Check for updates

PROGRAM OF THE

92ND ANNUAL MEETING OF THE AMERICAN ASSOCIATION OF BIOLOGICAL ANTHROPOLOGISTS

APRIL 3-5 & APRIL 19-22, 2023

To be held

Online and in Reno, Nevada

AABA Scientific Program Committee

Kristi L. Lewton, Chair

Donovan Adams
Francisca Alves-Cardoso
C. Eduardo Amorim
Benjamin Auerbach
Karen Baab
Shara Bailey
Heather Battles
Jonathan Bethard
Vanessa Campanacho
Tara Cepon-Robins
Colleen Cheverko
Maria Ana Correia
Susanne Cote
Miguel Delgado
Nathaniel Dominy
Amanda Ellwanger
Nicholas Ellwanger
Kori Filipek
Rebecca George
Rebecca Gilmour
Halszka Glowacka
Jesse Goliath
Mark Grabowski
Elaine Guevara
Lauren Halenar-Price
Angela Harden
Kevin Hatala
Amber Heard-Booth
Megan Holmes
Jennifer Hotzman
Kent Johnson
Saige Kelmelis
Brittany Kenyon-Flatt
Andrew Kim
Krystiana Krupa
Myra Laird
Nathan Lents
Christopher Lynn
Heli Maijanen
Lumila Paula Menéndez
Christina Nicholas
Heather Norton
Megan Perry
Marin Pilloud
Stephanie Poindexter
Sean Prall
Kathryn Reusch
Terry Ritzman
Gwen Robbins Schug
Krithivasan Sankaranarayanan
Amy Schreier
Maja Šešelj
Eric Shattuck
Michelle Singleton
Elizabeth St Clair
Katie Starkweather
Sean Tallman
Catherine Taylor
Nicole Torres Tamayo
Bethany Usher
Caroline VanSickle
Catalina Villamil
Amelia Villaseñor
Cara Wall-Scheffler
Kerryn Warren
Julie Wieczkowski
Scott Williams
An-Di Yim
Chi Zhang

AABA Meetings Director

Lori Strong, Burk & Associates, Inc.

Contributed Sessions Planning Committee

Francisca Alves-Cardoso
C. Eduardo Amorim
Karen Baab
Heather Battles
Jonathan Bethard
Tara Cepon-Robins
Amanda Ellwanger
Nicholas Ellwanger
Rebecca George
Mark Grabowski
Elaine Guevara
Kevin Hatala
Amber Heard-Booth
Saige Kelmelis
Krystiana Krupa
Myra Laird
Heli Maijanen
Marin Pilloud
Sean Prall
Gwen Robbins Schug
Krithivasan Sankaranarayanan
Eric Shattuck
Michelle Singleton
Nicole Torres Tamayo
Cara Wall-Scheffler
Kerryn Warren
Chi Zhang

Reno Advance Team

Jonathan Bethard
Leslea J. Hlusko
Steven R. Leigh
Kristi L. Lewton
Stephanie Meredith
Marin Pilloud
Richard Scott

Program Assistant

Amber Jaeger

Local Arrangements Committee

Marin Pilloud
Richard Scott

2022-2023 AABA Executive Committee

Steven R. Leigh
President

Leslea J. Hlusko
President-Elect

Kristi L. Lewton
Vice President and Program Chair

Graciela Cabana
Treasurer

Amy Rector
Secretary

Trudy Turner
Editor, *American Journal of Biological Anthropology*

Lyle W. Konigsberg
Editor, *Yearbook of Biological Anthropology*

Lauren Schroeder
Professional Development

Chelsey Juarez
Student Programs

Stephanie Meredith
Membership

Julienne Rutherford
History and Honors

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

MESSAGE FROM THE VP & PROGRAM CHAIR

Welcome!

It is my great pleasure to welcome you to the 2023 meeting of the American Association of Biological Anthropologists. This year's meeting is the 92nd gathering of our community. Like last year, we will convene in two venues: online only from April 3-5 and in-person and online in Reno, Nevada from April 19-22. However you participate, we hope you find the conference vibrant and intellectually stimulating!

The full AABA 2023 program includes 762 peer-reviewed scientific presentations by authors from all over the world.

The abstracts illustrate the remarkable breadth of our discipline, covering a range of research topics and approaches, and with global reach and incredible time depth. A total of 13 invited symposia (156 abstracts) are included in this year's program: five podium presentations will take place in Reno and be live-streamed onto the virtual platform, six poster symposia in Reno, and two symposia will be exclusive to the online program. There are 606 contributed abstracts. By subfield, these include Bioarchaeology (n=147, ~24%), Dental Anthropology (n=32; ~5%), Education in Biological Anthropology (n=9; ~1%), Forensic Anthropology (n=42; ~7%), Functional Anatomy & Tissue Biology (n=62, ~10%), Genetics & Genomics (n=55; ~9%), Human Behavior (n=9; ~1%), Human Biology (n=50; ~8%), Paleoanthropology (n=88; ~15%), and Primatology (n=114; ~19%).

This Program provides an overview of the activities planned for the online and Reno portions of our annual meeting. More details are available on AABA's annual meeting website and through the virtual platform. For the in-person program, the main conference hotel is the Peppermill Reno Resort. Many thanks to our Reno Local Arrangements Committee, Marin Pilloud and Richard Scott, for helping AABA articulate with the local community. They have put together a wonderful list of Reno attractions; check it out on our website!

Vaccination Requirement

Vaccination is required for attendance at AABA 2023, with very few allowable exceptions. We ask that all attendees be up-to-date on COVID boosters currently available to them. Exemption requests can be directed to AABA President, Steve Leigh, at bioanthpresident@gmail.com. Anyone granted an exception must submit a negative PCR test taken within 72 hours of the first day of the conference.

Masking Policy

Indoor masking is required for all attendees (vaccinated or unvaccinated) at the AABA 2023 conference with a few exceptions. KN95 masks will be available for all AABA attendees at the registration desk. A limited number of medical-grade N95 masks will also be available. Disinfectant wipes and hand sanitizer will be provided at each podium. Exceptions to the universal masking policy include:

- Vaccinated speakers have the option to lower their masks while presenting if there is at least 10 feet of distance between the speaker and the audience. The front row of seating in each room will be at least 10 feet from the podium.
- Attendees can momentarily shift their mask to sip a drink while inside meeting rooms, but prolonged unmasking to eat or drink is not allowed in meeting rooms.
- Prolonged unmasking to eat or drink is allowed in the exhibit portion of the exhibit hall and other common areas of the conference venue, but NOT in the meeting rooms or poster sessions. We encourage attendees to eat and drink outdoors when possible. Fortunately, our venue has several large outdoor areas available.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

MESSAGE FROM THE VP & PROGRAM CHAIR

Please be mindful of the variety of comfort levels with physical proximity. Ask colleagues before reaching out for a handshake or hug, and please pay attention to body language. Take a few steps back if someone looks uncomfortable.

If you have concerns about the Covid-19 safety policies or how they are being adhered to or implemented, Burk Associates Inc. (BAI), AABA's society management company, will have staff on the ground during the conference who will address safety issues and inform AABA attendees about our safety policies. We have established a call line for attendees to report COVID safety concerns during the meeting: 703-592-9946. BAI and members of AABA leadership will be available to respond to concerns raised in the conference center. They will also be regularly walking through conference spaces and available in-person.

The Online Program, April 3-5, 2023

Scientific programming for the online part of the conference begins on Monday, April 3 and runs through April 5. Because attendees of the online program are located all over the world including Africa, Asia, Australia, Europe, North America, and South America, we have scheduled the scientific sessions to accommodate presenters in their own time zone. There are 18 exciting sessions planned, with two of these being invited symposia: ***Archiving and sharing cranio-facial data: from 1D to 3D and beyond*** and ***Reconstruction of activity in the past: what's going on in Latin America***. In addition to these sessions, we have also planned a virtual Undergraduate Research Symposium on Wednesday, April 5.

The Reno Program, April 19-22, 2023

We are pleased to be joined in Reno by our partner organizations: the American Association for Anthropological Genetics (AAAG), the Dental Anthropology Association (DAA), the Human Biology Association (HBA), and the Paleopathology Association (PPA).

AABA 2023 programming in Reno begins on Wednesday, April 19 with the Committee on Diversity Undergraduate Research Symposium (open to everyone from 6:00-8:00pm) and the Opening Reception (8:00-11:00pm). On Thursday, April 20, scientific sessions scheduled for Reno begin. This portion of the program includes five invited podium symposia, six invited poster symposia, and 41 contributed sessions (20 poster and 21 podium sessions). All five of the invited podium symposia, the Business Meeting, and the President's Panel will be live-streamed on the virtual platform so that attendees can participate in these events either in-person or online.

Overview of Session Schedule and Presenter Information

Morning podium sessions begin at 8:00am and end by 12:00pm. Afternoon podium sessions begin at 2:30pm and end by 6:00pm (with a few exceptions). We have a few quarter-day podium sessions (half-morning or half-afternoon); be sure to check the Program for start times. The 2.5 hour lunch break allows for dedicated time to view posters as well as a variety of mid-day events including workshops and committee meetings between 12:15pm and 2:15pm. As in previous years, podium presentations need to be uploaded onto a central secure server in the Speaker Ready Room no later than a half day before the presentation. This server will then "push" presentations to the appropriate meeting room and will be available for the session. To ensure accessibility of presentations, we will be using voice-to-text subtitles in Powerpoint and ask all presenters to follow accessibility guidelines posted on the AABA website. Please note that all Invited Podium Symposia will be held in Tuscany A/B and live-streamed onto the virtual platform.

Contributed poster sessions and exhibitors booths will all be held in Tuscany D-F, a large open space where we can spread out for public health. Poster set-up will begin at 7:30am and should be completed by 8:00am. Posters should be taken down by 6:30pm. **Even-numbered poster presenters will stand by their posters from 4:00-5:00pm, with odd-numbered presenters attending from 5:00-6:00pm.** Invited Poster Symposia are held in smaller rooms and are assigned to a morning or afternoon time.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Joint sessions

The joint AAAG/AABA invited podium session *Born Which Way?: Biological and Genetic Engagement in Sex, Gender, and Sexuality Researc*h, organized by Christopher A. Schmitt & L. Zachary DuBois, will be held on Friday morning.

On Saturday at 12:30pm, we will hold the AABA Committee on Diversity, Committee on Community Partnership, & Presidential Panel: *Community Engagement in Biological Anthropology*. This panel will have broad-reaching interest and impact across disciplinary subfields as it considers how biological anthropologists can meaningfully engage and collaborate with communities.

Workshops

This year we have planned 12 exciting and innovative workshops throughout the week (four on Wednesday, four on Thursday, three on Friday, and one on Saturday) that occur in conjunction with our annual meeting. Because of space limitations, some of the workshops and events may require pre-registration (information is available on our meeting website; pre-registration closes March 31). Our workshops provide professional development, science communication, and methodological training that should be of broad interest to our membership.

Special Events

On Thursday morning (and online April 4th 6:00-8:00pm) we will host an AABA Forum and Listening Session on Disability, organized by Early Career Liaison, Dr. Katherine Kinkopf. This session will seek interaction around disability and help define steps our Association will take to promote full and open participation by all in our field. We hope to use information from this session to help future efforts and we welcome your ideas and feedback.

The AAAS Dialogue on Science, Ethics, and Religion (DoSER) and the Personal Genetics Education Project (pgEd) will host a screening and discussion of the film *Science As Mastery: A Film about Race and Power* on Thursday from 12:30-1:30pm.

On Thursday afternoon we are excited to hold our annual Auction! Each year the auction raises thousands of dollars to support Pollitzer Student Travel Awards and Cobb Professional Development Grants.

On Friday, following the conclusion of the scientific sessions, we will hold the Annual Business Meeting and Awards Presentation (6:30-8:30pm). This meeting is where the association comes together to review business of the past year (including annual reports from AABA Officers and committee chairs) and make a plan for the future. If you want to have a say in the organization, come to the business meeting! We strongly encourage and welcome attendance by all members and those interested in applying for membership. We will also take time to remember colleagues who passed away over the last year and celebrate this year's Cobb Professional Development Grant, Pollitzer Student Travel award, and COD Undergraduate Research travel award winners. We will also recognize this year's recipients of the Charles R. Darwin Lifetime Achievement Award (awarded to John Fleagle), the Gabriel W. Lasker Service Award (awarded to Andrea Taylor), and the AABA and Leakey Foundation Communication & Outreach Award in Honor of Camilla Smith (awarded to Cara Ocobock). Please join us in celebrating this year's outstanding winners!

Saturday brings our annual meeting to a close, with the Student Awards Ceremony and Closing Reception from 6:30-9:00pm. Please join us for a last-chance to network in person, say goodbye to new and long-time colleagues, and to learn who won the 2023 Student Presentation Awards!

As we approach the conference, we will be publicizing additional information regarding special events. These will be listed in the final meetings program and on our website.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

MESSAGE FROM THE VP & PROGRAM CHAIR

Acknowledgements and Appreciation

I sincerely thank everyone who helped organize the 2023 program. Tremendous thanks are due to our extraordinary business partners, Annual Meeting Executive Director Lori Strong and her team from Burk & Associates.

I am immensely grateful to the 69 talented, generous, and dedicated members of our Program Committee who conducted and completed symposium and abstract reviews thoughtfully, thoroughly, and expeditiously. Additional thanks go to the 37 members of the Program Committee who took on the task of organizing the contributed sessions for both the Reno and the Online programs.

I also want to express my deep gratitude to the Advance Team who met in Reno to set the schedule for the Reno program. Thank you to Jonathan Bethard, Leslea J. Hlusko, Steven R. Leigh, Stephanie Meredith, Marin Pilloud, and Richard Scott and to the extraordinary graduate student volunteers Ashley Baeza, Reecie Dern, Dori Kenessey, and Emily Smith. I also want to thank Maggie Hoffman for lending her incredible primate images to the AABA meetings swag!

Of course, none of the program organization would be possible without the immense effort of Ed Hagen, our website and abstract database developer. The Program Assistant Amber Jaeger has been a tremendous help and I am very grateful for her amazing organizational skills. I also want to thank the AABA Officers and members of the Executive Committee for their year-round hard work that makes our annual meeting possible. I am especially grateful to Steve Leigh and Leslea Hlusko for generously sharing their knowledge of meetings planning details.

The annual meeting would not be possible without the help of all these individuals, and I hope you will join me in thanking them when you see them in Reno or online!

Kristi L. Lewton
AABA Vice President and Program Chair

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

ABSTRACTS

Indigenous maternal inheritance and resilience in colonial lambayque, peru

LATEEFA ABEL[1], BETHANY L. TURNER[2], HAAGEN D. KLAUS[3] and LELAND L. ROGERS[4]

[1]Anthropology, The University of Tennessee, [2]Anthropology, Georgia State University, [3]Anthropology, George Mason University, [4]Anthropology, University of North Carolina

The Spanish conquest of Peru affected indigenous communities in myriad ways. On Peru's western coast, port towns became important nodes in the trans-Atlantic slave trade and trade between South America and the Far East, meaning that coastal colonial settlements brought together people from Africa, southern Europe, Asia, and the indigenous Central Andes with varying degrees of cultural and biological interaction. One such port town was Eten, located in the north coastal Lambayeque valley and containing two cemeteries associated with the Early (1536-1640 CE) and Middle/Late (1640-1750 CE) Colonial periods. Genomic investigations of the Central Andes are sparse and largely focus on pre-Hispanic contexts, which limits interpretations of population admixture and community dynamics during the Colonial period. This study begins to address this gap by sequencing the HVR1 mitochondrial segment of individuals (N=29) exhumed from Eten's colonial cemeteries. Authentic HVR1 sequences were obtained for 14 individuals using Sanger sequencing and quality controlled with Geneious Prime 2019, from which diagnostic SNPs were identified and used to estimate maternal inheritance. Results identified maternal haplogroups C and D, which vary in frequency between the two cemeteries. This suggests increasing genetic homogeneity, evidenced by an increase in Haplogroup D among individuals associated with the Middle/Late colonial period; this interpretation is supported by previous biodistance analyses, further suggesting changes in kinship and marriage networks related to ethnogenesis in response to Spanish domination. These results, while preliminary, provide a window into the resilience and adaptability of an indigenous community in the face of centuries of colonial oppression.

Effects of occupation-related physical activity on limb bone shaft strength among contemporary people in the United States

AMAYA ABEYTA-BROWN, TAYLOR BUSBY and IAN J. WALLACE

Department of Anthropology, University of New Mexico

Compelling evidence indicates that physical activity can enhance human limb bone shaft strength. Much of this evidence, however, comes from studies of people who engage in exceptionally high levels of activity, such as competitive and professional athletes. Less is known about how more subtle sources of variation in activity might affect bone shaft strength, including the effects of a person's occupation. Here, we investigate the influence of occupation-related physical activity on bone shaft strength among young men (aged 18-35 years) in the New Mexico Decedent Image Database, a collection of full-body CT scans of 21st-century individuals with documented occupations. Bone shaft strength was quantified in the humerus and tibia from CT scans. Physical activity intensity of each person's job was categorized based on an established classification scheme as either (1) sedentary or requiring light amounts of activity, or (2) involving moderate to large amounts of activity. Data collection for this study is ongoing, but preliminary results from a subsample of 50 individuals (n=25 per occupation group) suggest that humeral and tibial shaft strength properties (e.g., cortical bone area, second moments of area) do not differ significantly between people with and without jobs requiring moderate to large amounts of activity. If similar findings are obtained with a larger sample size, the results of this study may suggest that most jobs today are not physically demanding enough to provide substantial benefits for bone shaft strength. If so, activities outside the workplace may be critical for developing and maintaining strong limb bones.

Funding was provided by a Maxine Graves Undergraduate Award and John Campbell Award for Undergraduate Student Research (University of New Mexico) to A.A.-B.

Questioning Darwin: How woolly monkey sexuality challenges longstanding ideas based on the theory of sexual selection

LAURA A. ABONDANO[1,2], KELSEY M. ELLIS[2,3] and ANTHONY DI FIORE[2,4]

[1]Department of Biology - Project Dragonfly, Miami University, [2]Department of Anthropology - Primate Molecular Ecology and Evolution Lab, University of Texas at Austin, [3]Department of Anthropology, Miami University, [4]College of Biological and Environmental Sciences, Universidad San Francisco de Quito, Ecuador

Studies on sexuality and reproductive behaviors have traditionally focused on Darwin's (1871) theory of sexual selection. Darwin described males as individuals who actively seek and compete for reproductive opportunities, while females were characterized as more passive agents who choose male mating partners based on a set of physical or behavioral attributes. Over the last 150 years, as research has widened to include more taxa and perspectives from diverse scholars, there has been an increasing amount of evidence challenging Darwin's original ideas of animal sexuality. Here we present data on the sexual behaviors and reproductive strategies of four social groups of woolly monkeys (*Lagothrix lagotricha poeppigii*) in Amazonian Ecuador. While both males and females engaged in polygynandrous mating, intra-sexual competition was more prevalent among female woolly monkeys, with 20% of all observed copulations being interrupted by another female. Genetic parentage analyses revealed that male reproductive success was skewed towards one or two individuals in each social group. However, male woolly monkeys did not display overt aggressive behaviors towards other males for mating opportunities. Our results suggest that reproductive patterns in woolly monkeys may be influenced by females actively competing with each other for mating opportunities, in combination with potential male sperm competition. These observations add to the evidence challenging Darwin's notions about animal sexuality, which at the time were permeated by the social norms of the English Victorian era, inviting us to reflect on how scientific dogmas and narratives from the past can influence our current understanding of human sexuality.

Funded by NSF BCS-1540403, NSF BCS-1638822, the L.S.B. Leakey Foundation, the Wenner-Gren Foundation, and the University of Texas at Austin.

Ontogenetic biomechanical variation in diaphyseal morphology of the femur and humerus in anthropoid primates

BELKIS ABUFAUR

Anthropology Department, University of Florida

This project investigates ontogenetic patterns of association between locomotor ecology and diaphyseal morphology. Structural properties were extracted by using the newly developed R package *morphomap (ajpa.24140)*, in addition, material (bone density) properties were calculated for comparison to structural results. Prior analyses (*ajpa.24198, ajpa.22889, J.Anat,213:308–324*) suggest humeral midshafts reflect locomotor mode while femoral midshafts reflect body size, and distal sections exhibit higher genetic constraint. I examined area moments of inertia (I_x,I_y,*Imax*,*Imin*), polar moment of inertia (J), section moduli (*Z*), and cortical thickness of 61 cross-sections extracted from male and female long bones of Nano-Ct images of *Lagothrix* (n=4/4), *Alouatta* (n=4/4), *Aotus* (n=4/4), *Macaca* (n=3/4), *Hylobates* (n=6/6), *Chlorocebus* (n=3/3), *Colobus* (n=4/4), *Papio* (n=4/4) and *Pan* (n=12/10). My findings support previous results, suggesting that differences in diaphyseal shape (*Imax/Imin, Ix/Iy*) are not significantly different among species (ANOVA, p=0.32) and do not associate with the locomotor mode in the femur in contrast to the humerus. Cortical thickness is highly variable among species in juveniles regardless of the locomotor mode. The peak thickness in *Lagothrix* and *Hylobates* is detected mediolaterally at 42.5-67.5% of the diaphysis length, while anteriorly intensified thickness is seen at 42.5-80% in *Pan* and 55-80% in *Papio*. Mineral density (grey-scale value) distributions in distal diaphyses show high variation among juveniles. In addition, preliminary analyses show that standardized distal and

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

proximal femur bending strength (*Zp*) significantly associate with a greater range of locomotor diversity [*Alouatta* (arboreal quadruped) vs. *Lagothrix* (climber/leaper), and *Lagothrix*vs. *Hylobate*s].

This project is funded by UF Elizabeth Eddy Summer New Graduate Student Research Grant, 2022.

Prevalence of entheseal changes in modern male Colombian individuals

MARIA ALEJANDRA ACOSTA[1], CHARLOTTE HENDERSON[3] and EUGENIA CUNHA[1,2]

[1]Centre for Functional Ecology, Laboratory of Forensic Anthropology, Department of Life Sciences, University of Coimbra., [2]National Institute of Legal Medicine and Forensic Science, Portugal, [3]Independent Researcher, UK

Entheseal changes (EC) have been widely used in physical anthropology to infer physical activity levels in past societies. Factors such as age, sex hormones, and body mass index are involved in the presence of EC. However, other factors, such as population variability, have not been systematically considered in the analyses of EC and could affect the interpretation of results. In this study, the differences in the prevalence of EC between male individuals from two modern identified skeletal collections located in different cities, Bogota, and Medellin, were used to test the effect of population variability among contemporary male Colombians. EC in fourteen fibrocartilaginous entheses of 171 individuals were collected using the new Coimbra method. The results showed differences, with a small effect size, between the two collections. Differences were stronger when age was considered. Population variability affects the prevalence of EC and needs to be included in the analysis of EC. These results also invite us to reflect on the concept of population variability and its implication for the interpretations of previous research.

An analysis of phenotypic diversity and mortuary treatment of females at Early Bronze Age Karataş-Semayük, Anatolia (c. 2700-2300 BCE)

DONOVAN M. ADAMS[1], MARIN A. PILLOUD[2] and ALI METIN BÜYÜKKARAKAYA[3,4]

[1]Anthropology, University of Central Florida, [2]Anthropology, University of Nevada, Reno, [3]Anthropology, Hacettepe University, [4]Human Behavioral Ecology and Archaeometry Laboratory (IDEA Lab),

Previous work on Early Bronze Age Karataş-Semayük, a settlement in southwestern Anatolia, suggests that the site's population increase was partially driven by migration from multiple potential areas. This migration was likely influenced by a patrilocal residence pattern whereby females were more mobile and migrated to the site. This research seeks to identify if mortuary treatment of females at Karataş-Semayük shows comparable degrees and patterns of diversity. These results are used to examine the potential negotiation of individual and community identities as impacted by postmarital residence practices.

Odontometric and morphological data were collected on adults (males = 44, females = 40) and juveniles (n = 126). Shannon's and Simpson's Diversity Indices, Hill's Numbers (morphology), coefficients of variation (metrics), and possibilistic fuzzy c-means were calculated to assess phenotypic diversity for each sex. Mortuary architecture and inclusions for adults and juveniles were analyzed using these same techniques to evaluate patterns of archaeological diversity.

Female biological diversity was higher than males, supporting the possibility of a patrilocal residence system (*H'Female* = 2.669; *H'Male* = 2.441). Females exhibit significantly greater diversity in mortuary architecture (*H'Female* = 1.748; *H'Male* = 0.900). Further, burials that include juveniles show greatest overall diversity. Burial good diversity is only slightly higher in females (*H'Female* = 2.477; *H'Male* = 2.290). These results may indicate postmarital movement largely from similar cultural regions but with some degree of movement from other cultural regions that brought diverse styles into the mortuary record, some incorporation into local practices, and/or local variation in mortuary practices.

Research supported by NSF BCS#1848473, American Research Institute in Turkey (ARIT), UNR GSA Research Grant, UNR International Activities Grant, and Russell J. and Dorothy S. Bilinski Fellowship

Empty graves: Deciphering origins of human anatomical teaching specimens in U.S. institutions and calls for retirement and repatriation

ELISE J. ADAMS[1], LARRA M. DIBOYAN[1] and JESSE R. GOLIATH[1,2]

[1]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Cobb Institute of Archaeology, Mississippi State University

Human anatomical teaching specimens have been used in a variety of U.S. institutions for centuries; however, their provenience is rarely documented or acknowledged. While the illegal trade of human remains was banned in 1985, remnants of the trade still exist between impoverished Eastern Asian countries and U.S. institutions. In classrooms and labs nationwide, there are boxes of heavily handled and distressed human skeletal remains that have been used to train many aspiring anthropologists and medical professionals. Unfortunately, there is no standardized method of care for these skeletal remains when they are retired in institutions.

The objectives for this project include: 1.) a focus on the history of trafficking human anatomical specimens to the West, 2.) implementing a standardized method of care regarding handling of human skeletal teaching specimens, and 3.) developing ethical protocols for retiring and repatriating human skeletal specimens. Potential methodologies of repatriation and retirement were assessed through systematic review of relevant literature and human remains trafficking public forum discussions. From this review, we found an evident gap in the published academic literature relating to methodologies for care and strategies for addressing human remains trafficking. As a result, we propose several initiatives, such as the creation of a network of scholars and practitioners that work to create and implement protocols for these specimens, executing an institution-specific curation plan, and development of a 3D digital repository for retired remains. Through these efforts, we can impact the care and long-term curation of these remains currently stored in our institutions.

Experimental design matters: effects of clothing and carrion biomass load on forensically relevant scavenging in Cape Town, South Africa

KARA S. ADAMS[1], DEVIN A. FINAUGHTY[1,2] and VICTORIA E. GIBBON[1]

[1]Division of Clinical Anatomy and Biological Anthropology, Department of Human Biology, University of Cape Town, [2]School of Chemistry and Forensic Science, Division of Natural Sciences, University of Kent

Identifying unknown human decedents is a serious challenge in South Africa, complicated by a high murder rate. Locally, vertebrate scavenging has been shown to significantly impact the rate of decomposition, and failure to account for this may hinder accurate estimation of the post-mortem interval. While baseline data exist regarding scavenging, what is lacking is detailed understanding of the effects of experimental design on scavenging activity – a knowledge gap that extends internationally. Two 60kg clothed and uncaged pig carcasses were deployed in July 2021 and January 2022 respectively. The carcasses were observed by motion activated trail cameras, recording decomposition, scavenger species and activity. To assess the effect of clothing and carrion biomass load, a comparative sample of 16 unclothed carcasses deployed between 2014-2016 were analysed. The effect of scavenging activity on gross carcass depletion was assessed through time (24hr days) to specific weight loss milestones (25%; 50%; 75%). Three main findings were apparent: 1) it took significantly less time to reach the milestones in the summer, regardless of habitat or carrion biomass load; 2) the number of days needed to reach each milestone was more affected by mongoose scavenging in the winter; and 3) across both seasons, the single carcasses reached each milestone in less time than the multi-carcass deployments. However, the

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

difference between multi-carcass deployments was less pronounced in the summer than in the winter. This research suggests that experimental design can appreciably alter scavenger activity with potentially implications for PMI estimation based on methods developed through such research.

UCT Faculty of Health Sciences Discretionary Award, UCT Research Contracts & IP Explorer Funding; the South African National Research Foundation (Grant No. 115357).

Patterns of Craniofacial Trauma Among 19th Century Individuals From the Santa Clara Valley: Aspects of Structural Violence and Fighting

DEVIN ADCOX, SADIE FRIEND, TAYLOR LAMBRIGGER, CHEYENNE COLLINS, ERIC BARTELINK and COLLEEN MILLIGAN

Anthropology, California State University Chico

The application of structural violence to the past has become a productive framework with which to examine traumatic injuries in historic contexts. The embedded inequalities individuals experienced during life often become reflected in the injuries they sustain. Despite a body of literature examining trauma in skeletal samples, few studies have documented evidence of interpersonal violence in historic populations from the western US.

We analyzed patterns of craniofacial trauma among individuals from a late 19th to early 20th century pauper cemetery in the Santa Clara Valley, California and compared the data to other contemporaneous samples. We collected data on vault and facial injuries from 43 burials from the Santa Clara Valley Medical Center cemetery. Most interred in the cemetery worked as laborers in agricultural fields, orchards, and mines. Given that the cemetery was used for low socioeconomic status individuals, this research provides a unique opportunity to examine how structural violence shaped the lives of these individuals. Fourteen individuals (32.6%) showed evidence of craniofacial trauma, all of which was well-healed. This included four cranial vault fractures (9.3%) and ten facial fractures (23.3%). The overall prevalence of healed craniofacial trauma in the sample was significantly higher than that of San Francisco's Golden Gate Cemetery, Pittsburgh's Voegtly Cemetery, and Tucson's Alameda-Stone Cemetery ($p<0.05$) but was lower than that reported in the Terry/Hamann-Todd collections. We discuss how the high rates of craniofacial injuries relate to structural inequalities and violence these individuals likely experienced in life.

Predicting the position of hip bones within the pelvic girdle: A case study of the Kebara 2 Neanderthal

MAYOWA T. ADEGBOYEGA[1,2], MARK GROTE[2] and TIMOTHY D. WEAVER[2]

[1]Evolutionary Anthropology, Duke University, [2]Anthropology, University of California, Davis

The hominin fossil record is replete with fragmented pelvises. Many of them retain only one partially preserved hip bone, making it difficult to evaluate the biological processes they impacted. Pelvic bilateral symmetry allows us to reflect these preserved hip bones to create a more complete reconstruction however, the placement of the reflected side is still primarily determined by researcher expertise. This process can be especially subjective when the sacrum is either absent or poorly preserved such that it cannot be relied upon to orient the disarticulated hip bones.

In this study, we trained a reduced rank regression model to predict the translation and rotation matrices needed to transform a hip bone onto the location of its pair. To build this model, 44 landmarks and 72 curve semilandmarks were collected on a training sample of medical CT scans of 103 adults throughout the University of California Health system. We also fitted the model to 2 reconstructions of the Kebara 2 Neanderthal pelvis to assess the reconstruction of its poorly preserved left hip bone and to assess model performance with non *Homo sapiens* samples.

Our results suggest that regression modelling can reliably reconstruct incomplete pelvises by predicting the transformation matrix required to convert a hip bone to its pair. This model presents a new opportunity to recreate and articulate a missing side of the pelvis, even without the sacrum. Furthermore, this method can be employed in conjunction with other techniques to reduce subjectivity in the fossil pelvis reconstruction process.

A cost-effective way to conduct genotype-phenotype studies

KAMAR AFRA

Anthropology, University of Tennessee

The relationship between genotype and phenotype has been studied since the rise of Mendelian genetics in 1866. Molecular biology expanded to involve the study of gene expression, where Waddington (1957) developed a model for epigenetic landscapes, which was later refined by Hallgrimsson (2009). The analysis of complex gene interactions and epigenetic landscapes has resulted in new advances in the field focusing on the effect of pleiotropy, epistasis, and other phenomena acting on the phenotype. Genotype-phenotype research initially centered around disease manifestation, but in the last decade, the focus has shifted toward investigating human variation through population-based genome-wide association studies (GWAS). Unfortunately, students specializing in this area often lack a departmental DNA laboratory, making external laboratories their only option for conducting genomic research. Third-party laboratories are often accompanied by high DNA sequencing costs, which may lead to unattainable graduate research projects. This presentation reviews the history of genotype-phenotype studies in biological anthropology and presents a cost analysis associated with this process across several institutions in the country. The average costs for Miseq next-generation (NG) sequencing are $1500 per sample, demonstrating the considerable price tag molecular anthropologists must work with. This presentation also provides a cost-effective approach students can rely on to complete their analyses. The proposed methodology incorporates molecular and skeletal data procedures students can utilize to gain hands-on practical experience for their professional careers. The project aims to remove structural barriers and promote accessibility in research to advance diversity and equity in biological anthropology.

Evolvability and Morphological Integration Among the Human Basicranium, Limb Girdles, and Limb Segments

ELIZABETH R. AGOSTO[1], KRISTEN R.R. SAVELL[2] and BENJAMIN M. AUERBACH[3,4]

[1]Anatomy, Cell Biology & Physiology, Indiana University School of Medicine, [2]Biology, Sacred Heart University, [3]Anthropology, The University of Tennessee, [4]Ecology and Evolutionary Biology, The University of Tennessee

Evolutionary quantitative genetics allows researchers to explore evolutionary potential across anatomical regions. Agosto and Auerbach (*Journal of Human Evolution*, 2022) investigated relationships between the basicranium, limb girdles, and humerus in eight species of primates and found evidence of potential genetic constraint between the basicranium and limb girdles. While there is mutual evolutionary constraint among these regions, it is unknown how this may relate to the upper and lower limbs, which we have previously shown are not genetically independent. Here, we investigate the potential evolutionary relationships between human limb segments and limb girdles, as well as the basicranium.

Using a sample of 104 modern humans (55 female, 49 male), we estimated metrics of evolvability and morphological integration using simulated directional selection gradients. Our results mirror and elucidate previous findings. In evolutionary relationships among the basicranium, shoulder girdle, and pelvic girdle, there is greater evolutionary constraint between the basicranium and shoulder girdle than the basicranium and pelvic girdle, as previously reported. Novel to this study, we found that evolutionary

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

constraint between the basicranium and limb elements is the second strongest among the paired anatomical regions tested. Due to the lack of functional relationships and different genetic networks underlying their development, as well as low integration among these anatomical regions, this degree of constraint was not expected. Our results reinforce that potential evolutionary relationships exist among anatomical regions that have traditionally been thought as independent in anthropological studies. Further, we argue for a whole-organism approach to modeling morphological evolution in the primate skeleton.

Biohistory of a city. Exploring the population structure of ancient Thessaloniki, Greece

ASTERIOS AIDONIS[1], GEORGE LYRAS[2], SOULTANA PROTOPSALTI[3], STAVROULA TZEVRENI[3], STELA VASILEIADOU[3], KRINO KONSTANTINIDOU[3], ELENI KALLIGA[1] and CHRISTINA PAPAGEORGOPOULOU[1]

[1]Department of History and Ethnology, Laboratory of Physical Anthropology, Democritus University of Thrace, [2]Department of Historical Geology and Palaeontology, Faculty of Geology & Geoenvironment, National and Kapodistrian University of Athens, [3]Ephorate of Antiquities of Thessaloniki City, Ministry of Culture and Sports

Urban bioarchaeology provides context and theoretical background for studying human skeletal adaptation to urban environments. Thessaloniki was founded by Cassander in 315 BC. Its strategic position on the maritime and land routes made it an economic and political hub. Historical and archaeological records support that during the roman period (31 BC-324 AD) it became a multicultural urban center that attracted populations of different origins. Our study investigates the impacts of urbanization on the population structure of ancient Thessaloniki. We analyzed 208 individuals from Thessaloniki, spanning from the Hellenistic (323 BC) to the post-Byzantine period (15th c AD). In addition, 30 skulls from Mavropigi, a rural settlement of the late Roman period (4th c AD) were used for comparison. In order to reconstruct the secular patterns of the population, we investigate the morphological variation of the temporal bone with geometric morphometrics. The bones were digitized with a 3D scanner. Thirteen anatomical landmarks were collected. Procrustes ANOVA was used to test landmark measurement error. A Generalized Procrustes Analysis (GPA) was conducted to extract the geometric shape from the overall size. Principal components analysis (PCA) and Canonical variate analysis (CVA) were performed to examine temporal bone shape differences among individuals and chronocultural groups respectively. Results suggest variation among chronological groups, particularly between the Hellenistic and Roman periods of Thessaloniki. There is also variation between the urban sample from Thessaloniki and the rural from Mavropigi.

This research has been co-financed by the European Regional Development Fund of the European Union and Greek national funds under the call RESEARCH – CREATE – INNOVATE (project acronym: ECHOES T2Eδκ-00152)

Stable oxygen isotopic indicators of geographic residence in the early Colonial Basin of Mexico — the case of El Japón, Xochimilco, Mexico

EDGAR ALARCÓN TINAJERO[1,2] and DIANA K. MOREIRAS REYNAGA[3,4,5]

[1]Department of Anthropology, University of Georgia, [2]Center for Applied Isotope Studies, University of Georgia, [3]Department of Philosophy, The University of British Columbia, [4]Department of Anthropology, The University of British Columbia, Canadian Latin American Archaeology Society

The decades following sixteenth century Spanish colonization of Mesoamerica brought about large-scale demographic decline, epidemics, and successive events of political conflict. These series of events played a role in geographic relocation of individuals and communities. Stable isotopic approaches are beginning to cross-examine patterns of European colonization reconstructed primarily from texts. Skeletal samples from El Japón – an early Colonial period farming hamlet in the Basin of Mexico (1550-1650 CE) – present an opportunity to examine geographic residences within a population sample. Stable oxygen isotope ($\delta 18O$) analysis in archaeology serves as an identifier of geographic origin and residence during formation and renewal of biological tissues. The $\delta 18O$ in human bone renews throughout life permitting interpolation of geographic residence. $\delta 18O$ was analyzed from El Japón individuals (n = 74) via gas bench mass spectrometry from bone bioapatite samples representing an averaged value of several years before death. $\delta 18O_{apatite}$ facilitated calculation of $\delta 18O_{phosphate}$ and $\delta 18O_{drinking\ water}$ using published regression equations. Residence is identified from among Mesoamerican phosphate oxygen isotope regions using $\delta 18O_{phosphate}$. Marginally significant changes are observed between male and female adults (n = 64, Kruskal-Wallis test, p = 0.04). Residences do not change over time in pooled male and female subsamples (Kruskal-Wallis test, p = 0.5). Whole-sample variation is consistent through time (earlier burials SD = 1.17; later burials SD = 1.15). Consistent variation through time and absence of non-locals are likely rooted in continuity of cultural practices (e.g., kinship reckoning, marriage partner selection, and land tenure) within the Basin of Mexico.

Funded by the University of Georgia Graduate School Dean's Award (2021), the Department of Anthropology Melissa Hague Field Study Award (2021) and Janis Faith Steingruber Student Travel Award (2021).

Take a load off: Skeletal implications of sedentism in the feet of modern body donors

MALORIE E. ALBEE

Department of Sociology and Anthropology, Northern Michigan University

Studies considering the effects of sedentism on the foot have largely considered pathological changes to the gross foot without particular regard for the pedal skeleton. To address this gap in the literature, temporal trends in three aspects of tarsals and metatarsals, robusticity, osteoarthritis, and entheseal changes, were analyzed in the context of biodemographic and occupation data for recent modern humans. The sample utilized for this project is comprised of 71 individuals from the William M. Bass Donated Skeletal Collection, with birth years ranging from 1909 to 1993. Temporal trends in metatarsal robusticity, osteoarthritis, and entheseal changes were determined via a suite of statistical tests, including linear regressions and Spearman rank-order correlation tests, using year of birth as the explanatory variable. ANCOVAs were used to determine the direction and magnitude of changes in pedal morphology over time, using year of birth as the explanatory variable and age, sex, stature, BMI, tibial robusticity, and occupation as covariates. These tests were used to determine the extent to which temporal trends in pedal morphology can be attributed to temporal trends in biodemographic variables. The results indicate that entheseal changes and osteoarthritis have decreased over time, and these trends are statistically significant. The increase in sedentary behavior over time has usually been framed as a net negative for human health and well-being. However, considered in isolation, the decrease in entheseal changes and osteoarthritis presented here might be considered a positive development as they suggest overall less stress on the modern human foot.

The status of *Australopithecus*

ZERESENAY ALEMSEGED

Organismal Biology and Anatomy, University of Chicago

Australopithecus played a pivotal bridging role in the evolutionary history hominins owing to its morphological, behavioral, and temporal placement between the earliest archaic putative hominins such as *Ardipithecus, Orrorin* and *Sahelanthropus* and later hominins including *Paranthropus* and *Homo*. For long, our knowledge of *Australopithecus* came from both *A. africanus* and *A. afarensis*, and the genus was portrayed as a bipedal, non-stone tool using creature possessing largely chimpanzee-like cranium with a prognathic face and relatively small brain. This portrayal has, however, been substantially altered with more discoveries. Here, the paleobiology of *Australopithecus* is discussed based

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

on recent knowledge gained through fieldwork and the application of new data collection and analytical methods. The new emerging picture of *Australopithecus* suggests that it was a habitual biped, practiced arboreality, used stone tools, consumed animal resources using rudimentary stone tools, and possessed incipient childhood. The genus, whose ancestor remains elusive, was represented by *Australopithecus afarensis* from ~ 4.2 to 2.9 Ma, which gave rise to *A. platyops* and *A. africanus* before 3 Ma and to *Paranthropus*, *Homo* and *A. garhi* after 3 Ma.

The effect of cancer on pubic symphysis aging techniques using computed tomography scans

MAYA N. ALIBRIO[1] and SEAN D. TALLMAN[1,2]

[1]Department of Anatomy and Neurobiology, Boston University Aram V. Chobanian & Edward Avedisian School of Medicine, [2]Department of Anthropology, Boston University

Cancer and cancer treatments, particularly radiation therapies, are known to cause osteoporosis. While the primary sex organs regulate bone mineral density (BMD) through the production of estrogen, testosterone, and androgen, it is unknown whether cancer and cancer treatment affect age-related skeletal changes used in the biological profile of skeletonized remains. The present research examines the effects of cancer on skeletal age estimation using computed tomography (CT) scans of the pubic symphyses of 307 individuals from the New Mexico Descendent Image Database. The Suchey-Brooks method was applied to 125 individuals without documented cancer (control) and 182 individuals with documented cancer; however, the duration of cancer and/or cancer treatment was unknown. Individuals were correctly aged if their chronological age fell within the original study's 95% prediction range. Though not statistically significant in Kruskal-Wallis tests, the results indicated that females with cancer were aged correctly 74.7% of the time, while females without cancer were aged correctly 85.1% of the time, and males with cancer were aged correctly only 46.0% of the time, while males without cancer were aged correctly 55.7% of the time. Additionally, a total of 30 individuals were reanalyzed to examine intraobserver error, and a Cohen's kappa value (k=0.600) indicated a moderate level of agreement. While no differences were found between cancer and control groups, CT scans may lack the resolution needed to visualize the nuanced effects of BMD loss, if present, and overall quality of bone—necessary observations in updates on the Suchey-Brooks method—despite proven utility in skeletal analyses.

A Stable Isotopic Analysis of Diet across Three Millennia of Maya Settlement at Santa Rita Corozal, Belize

MEREDITH M. AMATO[1], ANGELINA J. LOCKER[1,2], ARLEN F. CHASE[3], DIANE Z. CHASE[4], ADRIAN SZ. CHASE[5], MELISSA BADILLO[6], LAUREN C. SPRINGS[7], TIFFINY TUNG[2], AUSTIN W. REYNOLDS[8] and RICK WA. SMITH[1,10,9]

[1]Department of Sociology and Anthropology, George Mason University, [2]Department of Anthropology, Vanderbilt University, [3]Department of Anthropology, Pomona College, [4]Claremont Graduate University, [5]Mansueto Institute for Urban Innovation and Department of Anthropology, University of Chicago, [6]Institute of Archaeology, Belize, [7]Department of Anthropology, The University of Texas at Austin, [8]Department of Anthropology, Baylor University, [9]Women and Gender Studies, George Mason University, [10]Indigenous Science, Technology, and Society Lab, Faculty of Native Studies, University of Alberta

The archaeological site of Santa Rita Corozal (SRC), located in north coastal Belize, has been home to Maya peoples for nearly three millennia. The city was occupied by some of the earliest Maya in northern Belize (ca. 742 BCE), rose to become an influential Postclassic Maya capital (900-1531 CE), and was the site where Spanish colonizers first invaded Belize (1531 CE). The peoples of SRC have therefore witnessed some of the most significant events across Maya chronology in Belize. However, few stable isotopic studies have been conducted at SRC, and an isotopic analysis of diet could help characterize foodways at this important place, how it compares to other Maya centers, and how it may have been shaped by social, political, and environmental events. Here we analyze dietary isotopes from 28 people at SRC whose interments span the Middle Preclassic (742 cal. BCE) through the Colonial Period (1630 cal. CE). We measured stable carbon and nitrogen from bone collagen (N=47) and stable carbon from bone apatite (N=49) and assessed preservation via Attenuated Total Reflectance Fourier Transform Infrared Spectroscopy (ATR-FTIR). This project was approved by the Institute of Archaeology in Belize and received support from Maya collaborators in Corozal, Belize. Preliminary $\delta^{13}C_{(VPDB)}$ values show an overall positive shift (p=0.003) from the Middle Preclassic (mean: -10.45‰) to the early Colonial Period (mean: -3.36‰). These data may indicate increased dependence on C4 plants and decreased dietary diversity over time, or a shift from terrestrial protein sources and an increased dependency on marine foods.

This work was funded by a Summer Research Fellowship to MMA from GMU; a Level 1 Grant to RWAS from The National Geographic Society; and NSF grants to AFC and DZC.

A Paleodemography Study of Violence: Age and Sex Distribution Patterns of Cranial Trauma in the 1st millennium BCE Turpan Basin, Xinjiang, China

LINGYU AN[1], ZIQIAN LI[2], WENXIN ZHANG[3], ANQI WANG[4] and QUANCHAO ZHANG[1]

[1]School of Archaeology, JilinUniversity, [2]School of Mathematics, JilinUniversity, [3]School of History, Classics and Archaeology, the University of Edinburgh, [4]Department of Archaeology, School of History, Xinjiang University

Introduction:

A paleodemography case study, using mathematical methodology doing relatively scientific observation on the human remains data, try to find a possible injury pattern for the three Bronze to early Iron Age populations (1,000–100 BCE) in the core hinterland of Central Asia.

Materials and methods:

345 individuals excavate from Subeixi culture in the Turpan Basin, Xinjiang, China. The total samples of these three populations were quantified by equal probability weighting and then marked based on skull injuries, observing differences in age and sex distribution of trauma.

Result:

Overall, the numerical mean age at death was 32.4 years old, with prime-aged males having the highest overall mortality rate, but females in youth and middle-aged at higher rates than males. Take the Jiayi cemetery (204 individuals) as an example: 48.2% of the males died in their young adulthood. Regarding the trauma rate, young and middle-aged females are only one-third of males. More than 1 in 10 children suffer from cranial trauma; all are relatively older individuals close to adulthood.

Conclusion:

The trauma fatality rate of middle-aged men shows that people in this area are at the core of Interpersonal conflict as the primary victim. Equally high rates of adult female and sub-adult trauma suggest that this population is exposed to violent conflict. Combined with other bioarchaeological evidence such as isotopes, starch granules in dental calculus, etc., the people in this area are also under extremely high survival pressure, and the resources of the attacked settlements are scarce.

Morphological differentiation of the hands and feet in primates: implications of hind limb dominance

ALISHA ANAYA[1], ROBERT RAVIER[2], SERGIO ALMÉCIJA[3,4,5] and DOUG M. BOYER[1]

[1]Evolutionary Anthropology, Duke University, [2]Mathematics, Duke University, [3]Division of Anthropology, American Museum of Natural History, [4]New York Consortium in Evolutionary

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Primatology, [5]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona

The evolutionary histories of the hands and feet are thought to be intertwined, whereby specialization of the feet for supporting locomotor demands allowed for functional and morphological diversification of the forelimb according to selective pressures unrelated to locomotion. This hypothesis predicts different magnitudes of variation in the hand versus the foot, and lower integration between hand and foot bones than between bones from the same autopod/extremity. The current study evaluates these predictions using taxonomically diverse samples and modern morphometric and statistical methods. Using a fully automated approach, we extracted 1,024, evenly distributed pseudolandmarks from samples of four bones (hamate, pisiform, talus, and calcaneus) with broad representation of haplorrhine and strepsirrhine primates (n=23 genera). R-square values were calculated on PC scores extracted from the pseudolandmarks to compare variance between bones. Results show that the talus and calcaneus are more strongly correlated to each other than either are to the hamate or pisiform. While the pisiform showed weak correlations with all bones, its R-square with the hamate was marginally higher than those with the foot bones. Thus, preliminary results suggest integration between hand and foot bones is lower than between bones of the same autopod and thus are consistent with the major hypothesis. These results will be further assessed by including additional tarsal and carpal bones, incorporating phylogenetic comparative methods, and by more nuanced assessments of geometric shape variation.

NSF BCS 1552848, NSF DBI 1759839, MCIEI (PID2020-116908GB-I00), Generalitat de Catalunya (CERCA Programme).

Population continuity or replacement in Monterenzio Vecchio, Italy revisited. Dental affinities during the 4th and 3rd centuries BCE

MALLORY J. ANCTIL[1] and JOEL D. IRISH[2]

[1]Anthropology, University of Alaska Anchorage, [2]School of Biological and Environmental Sciences, Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University

The relationship between the spread of Celtic material culture and/or population movement into northern Italy during the 4th-3rd century BCE has been a longstanding debate. Recently, a biocultural study advocated the latter, reporting, among other factors, significant gene flow between populations in northern Italy, Monterenzio Vecchio, and East Yorkshire, Britain. However, that study relied on pooled and composite samples (n=38 total individuals). In the present study phenetic affinity analyses were used to explore population demographic dynamics, to specifically discern whether gene flow between these populations is evident using distinct regional samples (n=209 individuals). In the process, it was assessed if the previous finding may have been an artifact of sample composition.

Here, the Arizona State University Dental Anthropological System was used to record 36 crown, root, and intraoral osseous discrete traits in four well defined regional samples of Celtic and Italian populations. These data were compared using the mean measure of divergence distance statistic and principal components analysis to yield inter-sample phenetic affinities and the identification of traits driving inter-sample variation. Comparative results indicate that: 1) phenetic heterogeneity is evident among samples; 2) evidence for significant gene flow between east Yorkshire and Monterenzio Vecchio populations is lacking; 3) these groups retained an overall degree of cultural autonomy and genetic divergence from the Celts; and 4) previous indications for significant gene flow between groups are likely a result of sample composition. As such, the presence of Celtic artifacts in northern Italy was likely due to cultural diffusion, not population movement.

Health and inequality during the Hellenistic Period in central Anatolia

CHERYL P. ANDERSON

Anthropology, Boise State University

The goal of this research was to reconstruct the health profile of the Hellenistic Period (ca. 300-100 BCE) human skeletal assemblage (n=28) at Kaman-Kalehöyük in central Anatolia. In particular, the aim was to further test the hypothesis that these skeletal remains may represent individuals of low social status as reflected in their burial context and through comparisons with other Celtic Galatian sites with similar pit burials, such as Gordion and Danebury. It has been proposed by some that the individuals found in these Galatian pit burials may be the victims of ritual violence, although thus far no evidence for perimortem trauma has been observed on the individuals from Kaman-Kalehöyük.

The results of this research show that for the individuals with observable teeth in this sample, 25.00% (n=5) had at least one linear enamel hypoplasia. In addition to dental pathology, the results show that the prevalence of cribra orbitalia in this sample is 21.42% (n=6) and the prevalence of porotic hyperostosis is also 21.42% (n=6), with a total of 11 individuals (39.29%) displaying either cribra orbitalia, porotic hyperostosis or both. Additionally, three subadults in this sample, all of whom had signs of cribra orbitalia, also display endocranial lesions. While the etiology of these lesions is unclear, they could be related to dietary deficiency or infection. The paleopathological data from this site complements previous studies concerning the burial context and antemortem trauma evidence to further support the idea that these individuals may have experienced inequalities potentially related to low social status.

Calcaneal Functional Morphology of Large-Bodied Fossil Colobines

MONYA ANDERSON[1], EMMALEIGH GRADY[1], JORDAN FRANKLIN-GARZA[1] and THOMAS C. PRANG[2]

[1]Anthropology, Texas A&M University, [2]Anthropology, Washington University in St. Louis

At least 3 large-bodied colobine taxa displaying postcranial morphology consistent with some degree of terrestriality are known from Plio-Pleistocene deposits within the Turkana Basin: *Cercopithecoides williamsi, Cercopithecoides kimeui,* and *Paracolobus mutiwa.* Although all share some functional morphology with terrestrial cercopithecines, *P. mutiwa* in particular displays a uniquely derived calcaneus making it an ideal taxon with which to explore broader cercopithecid locomotor evolution.

Here we present comparative analyses of calcaneal morphology from three large-bodied colobine specimens: *P. mutiwa* (KNM-WT 16827), *?P. mutiwa* (L895-1), and *P. chemeroni* (KNM-BC 3). The comparative Primate sample includes calcanei (N = 505) from 179 extant colobines, 173 extant cercopithecines, 181 hominoids, 66 platyrrhines, and 6 fossil cercopithecines. Quantitative analyses focus on 7 linear metrics, 5 functionally relevant indices, and body mass estimates.

Although the fossil sample size is small, when compared to extant colobines, KNM-WT 16827 and L895-1 are distinct from extant colobines and KNM-BC 3 in total length, posterior facet size, and tuberosity length. However, thy fall within the Colobinae pattern for body mass scaling distinct from cercopithecines, hominoids, and platyrrhines. Overall, the fossil ankle joints reflect a positional repertoire distinct from extant terrestrial and arboreal quadrupeds.

This research was supported by Texas A&M University, the University of Oregon, the National Science Foundation (Proposal No. 1650923), and the Wenner-Gren Foundation.

Profiling age-related patterns of gene expression in the hippocampus of rhesus macaques

TANNER J. ANDERSON[1], SAM PETERSON[2], MARINA WATOWICH[3,4], STEVEN KOHAMA[2] and KIRSTIN N. STERNER[1]

[1]Department of Anthropology, University of Oregon, [2]Division of Neuroscience, Oregon National Primate Research Center, [3]Department of Biology, University of Washington, [4]Center for Evolution and Medicine, Arizona State University

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

General patterns of brain aging are conserved among primates; however, pace of brain aging can vary between species and within individuals of the same species. To better understand how the hippocampus, a region particularly susceptible to aging, changes with age at the molecular level, we measured gene expression in 96 banked rhesus macaque hippocampus samples aged 3-35 years (~9 to 105 human years) using RNAseq. We used autoregressive integrated moving average models to examine age-related changes in gene expression while regressing out sex effects. We identified 2,037 genes with significant (pval < 0.05) nonzero trends that clustered into 4 distinct aging trajectories. Clusters 1 (n=1,042) and 2 (n=683) exhibited monotonic patterns of expression with age. Upregulated genes (Cluster 1) were enriched for immune responses while downregulated genes (Cluster 2) were enriched for neuronal formation and neurodegenerative disease pathways. Clusters 3 (n=159) and 4 (n=153) captured nonlinear trends in expression and were enriched for DNA replication, neuron differentiation and immune response. Next, we examined age-related gene expression patterns in males and females independently. We identified 1,253 (male dataset) and 1,376 (female dataset) genes with age-associated expression. As expected, most of these genes are conserved in both datasets and Clusters 1 and 2 of the original combined analysis. However, we identified 369 genes in males and 193 genes in females with sex-specific age-associated expression. Preliminary ontology analyses suggest enrichment for neurological-related pathways, warranting further analysis. Importantly, our study highlights molecular changes during midlife that may shape brain aging in longer lived primates.

This research was funded by the UO and OHSU Collaborative Seed Grant program, National Science Foundation Doctoral Dissertation Research Improvement Grant (2217961) and by ONPRC support (P51 OD 011092).

Skeletal evidence of health and disease in Cayo Santiago *Macaca mulatta*: Evidence of age differences in a single social group

SUSAN C. ANTÓN[1], SCOTT A. WILLIAMS[1], CBRU CAYO BIOBANK RESEARCH UNIT[2], JAMES P. HIGHAM[1] and CASSANDRA M. TURCOTTE[1,3]

[1]Center for the Study of Human Origins, Anthropology, New York University, [2]Department of Neuroscience, University of Pennsylvania, [3]Department of Anatomy, New York Institute of Technology College of Osteopathic Medicine

Degenerative and pathological changes to the skeleton are used in clinical, bioarchaeological, and forensic assessments of frailty and mobility in individual humans, and to infer stress and well-being in populations. Yet rarely can we assess contemporaneous skeletons known to have formed a single social group and of documented sex, age, resource base, and status. Here we consider skeletal signs of degeneration, trauma, and disease in the fore and hind limb of a single, low-ranked social group (HH) of *Macaca mulatta* from the free-ranging colony on Cayo Santiago, Puerto Rico. Individuals are housed in the CPRC-NYU Rhesus Macaque Skeletal Collection. Sixty-six monkeys (42 female, 24 male) ranging from 2.9-25.9 years of age at death were scored for evidence of periosteal reaction, osteoblastic/osteoclastic bone response, degenerative changes to joint surfaces (including marginal lipping, porosity of subchondral bone, and eburnation), and healed fracture.

Nearly the entire (97%) population exhibits evidence of at least one healed fracture in the bones examined, most commonly the foot and fibula. While nearly all adults exhibit some marginal lipping around joint surfaces, there is little evidence of subchondral bone porosity or eburnation that would suggest advanced joint disease. There is a fairly high frequency (80%) of light, non-specific periosteal reaction and of healed fractures, some related to interpersonal violence (bites), suggesting high levels of social stress. Although unrelated fractures do increase in number in older individuals, unlike in humans, these seem unrelated to decreased bone density or general frailty.

National Institutes of Aging R01-AG060931, AABA Cobb Grant (to CMT). National Science Foundation BCS-1754024, NSF RAPID 1648676, Leakey Foundation grant (to JPH, SCA, SAW). NIH #P40-OD012217.

The effects of uneven surfaces on walking biomechanics when barefoot compared to shod

ZACCHARIAH M. APOLITO and NICHOLAS B. HOLOWKA

Anthropology, University at Buffalo

Extensive biomechanical research on human bipedalism has been conducted in laboratory settings on mostly flat surfaces or treadmills, yet for most of human history, we have walked barefoot on natural, uneven terrains. We currently know little about how modern shoes alter the lower limb kinematics and muscle activation patterns required on such surfaces and therefore may be missing information necessary to understand how the lower limb is adapted to walk on natural terrains. To begin addressing this gap, we collected three-dimensional kinematic, kinetic, and electromyographic data from nine subjects (27.5±5 years, 66.9± 12.6 kg) who walked barefoot and in athletic shoes across an even surface (ES) and an artificial uneven surface (UES) consisting of tiered blocks of stiff EVA foam that caused a 1-2 cm height variation from step-to-step. When walking across the UES, subjects decreased their preferred speeds by 15% on average whether barefoot or shod but decreased their duty factors by roughly 35% for both surfaces when barefoot. Analyses of a subset of subjects (n = 6) indicated that when barefoot, peak foot eversion power during push-off was 90% lower on the UES compared to the ES. However, peroneus longus activation was similar on both surfaces when barefoot, in contrast to shod walking where the UES caused subjects to nearly double peroneus longus activation following foot strike. These results suggest that walking barefoot on uneven surfaces causes humans to alter their walking biomechanics in important ways, particularly at the subtalar joint.

The genomic landscape of Native American peoples

MARCOS ARAUJO CASTRO E SILVA[1], MAÍRA RIBEIRO RODRIGUES[2], PUTIRA SACUENA[3], MARIA CÁTIRA BORTOLINI[4], JOÃO GUERREIRO[3], FABRÍCIO SANTOS[5], JOSÉ GERALDO MILL[6], DAVID COMAS[1,7] and TÁBITA HÜNEMEIER[2,7]

[1]Departament de Medicina i Ciències de la Vida - MELIS-UPF, Universitat Pompeu Fabra, [2]Departamento de Genética e Biologia Evolutiva, Universidade de São Paulo, [3]Instituto de Ciências Biológicas, Universidade Federal do Pará, [4]Departamento de Genética, Universidade Federal do Rio Grande do Sul, [5]Departamento de Genética, Ecologia e Evolução, Universidade Federal de Minas Gerais, [6]Departamento de Fisiologia, Universidade Federal do Espírito Santo, [7]Population Genetics Department, Evolutionary Biology Institute (IBE/CSIC-UPF)

Latin America despite being one of the most culturally and environmentally diverse landscapes on earth is still largely understudied in relation to human genetic variation and how it was shaped by historical, environmental, and cultural factors. In order to bridge this gap, here we present the most diverse whole genome sequencing dataset ever assembled for indigenous American peoples, with data from 128 individuals belonging to 45 ethnic groups and 28 linguistic families, distributed across 8 countries. To examine the genomes of indigenous Americans in light of world genomic diversity, our new dataset was first combined with publicly available WGS databases, and quality control filters were applied. Here we present some preliminary analyses, which first demonstrated that newly sequenced individuals cluster with other Native Americans in the Principal Components Analysis and Admixture analysis, recapitulating the patterns of genetic diversity of global populations observed before. The results also evidence a general absence (71 individuals) or low proportion of admixture with Europeans and African ancestries, as well as the existence of more genetically differentiated groups such as the Karitiana and Surui, in addition to some Mesoamerican groups, indicative of more intense genetic drift effects. Finally, we performed a local ancestry inference to determine whether some genomic regions of these individuals had

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

a relative excess of Australasian ancestry; our findings suggest a putative adaptive role of this ancestry in specific regions of the genome, hence further analysis will be conducted to investigate this possibility.

This project is funded by the Maria Skłodowska-Curie COFUND (Id oficial 945380) EUTOPIA Science and Innovation Fellowship and the Fundação de Amparo à Pesquisa do Estado de São Paulo project 15/26875-9

A reassessment of *"Colobus" freedmani*

JULIA L. ARENSON

Program in Anthropology, The Graduate Center, CUNY, New York Consortium in Evolutionary Primatology (NYCEP)

"Colobus" freedmani is a fossil colobine from the Okote Member of the Koobi Fora Formation dated to ca. 1.5 Ma. However, this species exhibits a number of features that differentiate it from modern *Colobus*, and thus *"C." freedmani* was compared to a sample of 193 individuals representing 11 extant African colobine species to reassess its affinities. It is similar to *Piliocolobus* and *Colobus* in dental size and substantially larger than *Procolobus* (lower molar row length, *"C." freedmani N* = 3; ANOVA $F_{(3, 181)}$ = 119.2, p < 0.001). While the undulating inferior margin of the corpus and gonial expansion are more similar to *Colobus*, the robust *prominentia laterales* on the mandibular corpus and a moderately developed infraorbital ridge are more similar to *Piliocolobus* and *Procolobus*. The lower molars are more elongated like in *Piliocolobus* and *Procolobus* (M_2 shape, *"C." freedmani N* = 4; ANOVA $F_{(3, 167)}$ = 40.44, p < 0.001) and it lacks the buccolingual flare of the upper P^4 seen in *Colobus* (*"C." freedmani N* = 4; ANOVA $F_{(3, 109)}$ = 16.11, p < 0.001). A maxillary fragment suggests a shallow, relatively elongated face, more similar to *Colobus* and unlike the vertically taller face of *Piliocolobus*. In sum, *"C." freedmani* exhibits a mix of features, and it is not clearly aligned with *Colobus* to the exclusion of other African colobine genera. Cladistic analyses may clarify the polarity of these features among colobines and resolve its position within the Colobina.

Funding for this project provided by a NSF GRFP (Award No. 40F79-02 04), NSF DDIG (Award No. 2018093), and a Leakey Foundation Research Grant.

Enamel growth variation in pathological samples and its potential uses as a diagnostic tool in biological and forensic anthropology

CHRISTOPHER ARIS[1], KATIE HEMER[2], MARIE WEALE[3], EMMA STREET[4] and AMBER J. COLLINGS[1]

[1]School of Chemical and Physical Sciences, Keele University, [2]Institute of Archaeology, University College London, [3]School of Archaeological and Forensic Sciences, University of Bradford, [4]No affiliation, None

Analysis of amelogenesis and enamel growth through examining cross-striations has been vital in expanding insights into the variation of enamel physiology in humans. However, the study of the internal structures of enamel to date have been limited to predominantly individuals lacking observable pathology. This study produced histological thin sections of teeth, from individuals with a range of pathological conditions, to examine the daily rate of new matrix production. Included are an incisor talon cusp (accessory enamel growth) from a modern English individual, a premolar from a modern leprotic individual, and multiple teeth from pre-medieval Wales (n=5) and industrial-era England (n=26) with vitamin D deficiency. When compared to non-pathological teeth from their same populations (n≥17): the talon cusped incisor showed a significantly slower enamel growth pattern; the vitamin D deficient individuals presented significantly faster enamel growth for select enamel regions, and a significantly larger range and deviation in growth rates throughout the enamel cap. The leprotic individual also presented significant variation in enamel growth rates. These data collected present the first expansive evidence for variation in the daily rate of enamel growth in humans with identifiable pathology. Unique variations noted across three distinct conditions with varying rarities across historic and modern populations. Ongoing research will investigate teeth from individuals with different pathological conditions, as well as expand sample sizes for the rarer conditions presented here. The aim is to produce diagnostic models of pathologies lacking easily identifiable legions for use in biological and forensic anthropology.

This research was not supported by any funding body.

Cut marks at the BK II site, Olduvai, suggest broadening of extractive technologies during the early Pleistocene

MIRANDA J. ARMOUR-CHELU

School of Medicine, Georgetown University

The analysis of cut mark evidence from early archaeofaunas has focused on the process of meat acquisition and methods by which edible animal tissues were detached from bone. Cut marks are also known from non-meat bearing bones, such as distal, limb elements, and it has been suggested that they indicate skinning activity.

Six equid second phalanges were recovered from the excavations conducted by the Leakeys at the BK II locality, Olduvai. Three of these have a transverse or obliquely orientated cut marks along the palmar surface of the bone shaft. These are interpreted as evidence for tendon removal rather than skinning as the cut marks do not encircle the shaft of the bone. The location and orientation were found to closely match cut marks produced during the preparation of equid bones for museum vertebrate collections. Whilst several anatomical structures insert on the second phalanx it is concluded that the tendon involved is the deep digital flexor tendon which is connected to the shaft of the second phalanx by the T ligament.

Cut marks on equid second phalanges from the BK II site, Olduvai, suggest a novel use of tendon as a raw material. Manufacture of bone tools has been identified from sites of a similar age and the use of tendons as a binding material is likely of long duration. Tendon extraction at the BK II site would seem plausible and adds to the range of animal products utilized as raw materials during the early Pleistocene.

Sex differences in immune function and disease risk are not easily explained by an evolutionary mismatch

AUDREY M. ARNER[1,2], VARADA ABHYANKAR[3], LAUREN JN. BRENT[4], JAMES P. HIGHAM[5], JOSEPH KAMAU[6,7], FRANCIS LOTUKOI[8], DINO MARTINS[9], MICHAEL J. MONTAGUE[10], BENJAMIN MUHOYA[3,8,9], JULIE PENG[3], MITCHELL SANCHEZ ROZADO[11,12], MARINA WATOWICH[11,13], NOAH SNYDER-MACKLER[11], JULIEN F. AYROLES[3,9] and AMANDA J. LEA[1,2]

[1]Department of Biological Sciences, Vanderbilt University, [2]Evolutionary Studies Initiative, Vanderbilt University, [3]Lewis Sigler Institute for Integrative Genomics, Princeton University, [4]Centre for Research in Animal Behavior, University of Exeter, [5]Department of Anthropology, New York University, [6]Department of Biochemistry, University of Nairobi, [7]Institute of Primate Research, National Museums of Kenya, [8]Mpala Research Centre, Nanyuki, Kenya, [9]Department of Ecology and Evolution, Princeton University, [10]Department of Neuroscience, University of Pennsylvania, [11]Center for Evolution & Medicine, Arizona State University, [12]Department of Microbiology and Medical Zoology, University of Puerto Rico, [13]Department of Biology, University of Washington

The "Pregnancy Compensation Hypothesis" (PCH) posits that sex differences in the mammalian immune system reflect an adaptation to selection on female immunity during pregnancy, during which increased immunomodulation is required to reduce immune responses to the fetus, while maintaining the ability to respond to pathogens. In humans, fewer pathogens and lower parity in urban environments is expected to leave female immune systems under-stimulated, creating an "evolutionary mismatch" which exacerbates sex differences in immunity and autoimmune disease risk. Yet, robust tests of this mismatch hypothesis are rare. Here, we first confirmed a sex-bias in autoimmune disease prevalence in a biobank of urban U.S. individuals (BioVU). Second, we asked whether sex differences in immune function are affected by shifts toward urban, lower-parity lifestyles in a single population—the Turkana of northwest Kenya. We found that lifestyle alters sex differences in immune cell counts, but not in

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

gene expression. Contrary to expectations, parity did not explain the observed sex x lifestyle effects for cell counts within the Turkana. We then tested for generalizable trends across natural fertility mammalian populations versus urban humans (data from Turkana, NHANES, GTEx, Batwa and Bakiga, yellow baboons, and macaques). We did not find consistent relationships between lifestyle and sex-biases in immune biomarkers or between parity and the same immune outcomes. Taken together, our work suggests that while sex clearly influences disease risk in urban humans, these effects are not easily explained by evolutionary mismatch. Future work addressing how sex interacts with lifestyle change to generate disease is needed.

This research was funded by an NSF GRFP, the NIH (R35GM147267), the Chan Zuckerberg Initiative, the Searle Scholars Program, and the Canadian Institute for Advanced Research.

Parent-offspring affiliative behavior in white-faced saki monkeys

EMMA C. ASKREN and MAJA ŠEŠELJ

Anthropology, Bryn Mawr College

White-faced saki monkeys (Pithecia pithecia) are understudied platyrrhines who live in the rainforests of northern South America. Their social organization is highly variable, but centered around the breeding pair, and characterized by same-sex aggression. However, extra-pair adults are often stable members of the social group, and solitary individuals have also been observed. Researchers have proposed that competing selective pressures for territory defense and mate access have resulted in this high level of intraspecific variation. Further variation is found in zoos, with more unusual captive group compositions that may not reflect what is encountered in the wild.

We report here on an observational study of an all-male group of sakis living at the Philadelphia Zoo, one year after the death of the breeding female. One observer (E.A.) recorded general, affiliative, and agonistic behaviors of the father and his two sons. Due to sakis' reported tendency towards same-sex aggression, we expected to see more affiliative behavior between the father and each of his sons than between the sons. The father interacted with the more assertive son during the day, mostly by grooming, but slept on the same platform as the more reserved son during the night. The two sons rarely interacted, but the more reserved son scent-marked much more. The keepers reported the monkeys' sleeping behaviors changed following the death of their mate/mother. It appears that, adjusting to the new group composition, these males employed alternative strategies for maintaining parent-offspring relationships while exhibiting low levels of same-sex aggression.

Cognitive Demands of Bipedal Walking

DANIEL H. ASLAN[1] and DAVID A. RAICHLEN[1,2]

[1]Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California, [2]Department of Anthropology, University of Southern California

Humans and our hominin ancestors are the only mammals to habitually walk bipedally. Dual-task research (walking while performing cognitive tasks) has shown that bipedal walking requires attentional effort, which is linked to maintenance of dynamic postural stability. Yet, few studies have examined whether challenging dynamic postural stability affects the attentional demands of walking. Because human foraging combines complex cognition with walking, our goal is to understand how attentional demands of bipedal walking over ecologically relevant terrain impact cognitive performance on other tasks. Here, we tested the hypothesis that walking over uneven terrain would reduce performance on cognitive tasks compared with more predictable substrates. Thirteen young adults (23±4 years) walked back and forth on a 9.77m walkway for two minutes per trial. Participants walked on an even and uneven walkway while performing a cognitive dual-task (serial seven subtractions). Attentional demand outcomes were measured using audio recordings, and quantified as number of correct subtractions per trial. Across the experimental walking trials, the uneven walkway reduced cognitive performance by ~10% (p=.0058). Our preliminary results indicate that attentional effort dedicated to maintaining dynamic postural stability impacts cognitive performance. We discuss implications of our results for the evolution of bipedal foraging on complex landscapes and how the potentially unique stability demands of upright bipedalism affect dual-task performance in a foraging context.

No bones about it: human sexual polymorphism and ranges of morphological variation in human skeletal sex indicators

CLAUDIA M. ASTORINO

Department of Anthropology, The Graduate School and University Center, The City University of New York, NYCEP, New York Consortium in Evolutionary Primatology

While sex is often considered a binary, categorical variable in humans, there exists extensive variation in human sex traits that is often unacknowledged. Intersex individuals are those who are born with a combination of sex traits – some traditionally considered male, some traditionally considered female, and/or traits that are not traditionally considered either male or female – all in the same body. Little is known about intersex biology, with most previous studies focusing on medical (often surgical) means to alter intersex individuals' morphologies. This includes skeletal morphology – currently, no skeletal collections including known intersex individuals exist, and virtually nothing is known about how ranges of skeletal variation in individuals with different forms of intersex (or intersex variations) compare with typical (i.e., non-intersex) males and females, and also with one another. Predictions about skeletal sex indicator morphology intersex individuals, however, can be made based on sex traits known to be present in different forms of intersex; these include karyotype, alleles, internal sex organs, hormone types and levels, and gametes produced. Controlling for population differences, relative levels of skeletal robusticity were predicted to be generally high in hypospadias; intermediate in 5-α-reductase, CAH, PAIS, and Kleinfelter's; and low in CAIS, MRKH, Swyer's, and Turner's. These results have special relevance for human biology, forensic anthropology, and bioarchaeology.

Quantifying sexual dimorphism of the bony labyrinth and biological sex distribution in Lagoa Santa, Brazil

BRUNO ATHIE TERUEL[1], MARIA ANA CORREIA[2], ALEXANDRA UHL[1], ANDRÉ STRAUSS[2] and HUGO REYES-CENTENO[1,3]

[1]Department of Anthropology, University of Kentucky, [2]Museu de Arqueologia e Etnologia, Universidade de São Paulo, [3]William S. Webb Museum of Anthropology, University of Kentucky

Previous studies have shown quantitative variables of the human bony labyrinth to be sexually dimorphic and therefore useful in osteological sex estimation. The archaeological region of Lagoa Santa in the Brazilian state of Minas Gerais is notable for its wide occupation time frame, ranging from the early Holocene to post-colonial periods, and its expansive human osteological record. This study thus uses a sample of bony labyrinth endocasts from Lagoa Santa to sex individuals by applying discriminant functions developed from diverse comparative datasets. We verify the results against morphologically sexed individuals, as well as a subset of genomically sexed individuals. In addition, we apply geometric morphometrics methods to visualize shape variation across the Lagoa Santa series. Our results show that a discriminant function developed from a Native North American population was most successful in predicting the sex for the sample of individuals from Lagoa Santa, with 88.89 % overall accuracy (85.71% correct based on morphology and 100% correct based on genomics). In contrast, functions from other populations or global averages were less accurate at 33% correct classification. In addition, our shape analysis shows differences in the size of the cochlea and angle of the anterior canal between the sexes. These results have implications for the development and application of sex discriminant

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

functions based on the bony labyrinth, suggesting that further sampling is necessary in order to account for variation across wide geographical and temporal scales.

National Science Foundation Mid-scale RI-1 2131940 (EduceLab: Infrastructure for Next-Generation Heritage Science); University of Kentucky Vice President for Research and College of Arts & Sciences (Summer Undergraduate Research Fellowship)

How (not!) to perpetuate biological race in paleoanthropology

SHEELA ATHREYA[1] and REBECCA R. ACKERMANN[2,3]

[1]Anthropology, Texas A&M University, [2]Archaeology, University of Cape Town, [3]Co-Director, Human Evolution Research Institute

The 2022 Nobel Prize in Physiology/Medicine went to a geneticist for their work on ancient DNA; specifically for decoding the Neanderthal genome. Having one of Western science's highest honors go for the first time to paleoanthropological research was a significant moment for our field. Neanderthals play an important part in the history of our discipline, as the first-discovered hominins. Their position in models of human origins has been debated ever since, and their exclusion from our lineage was a key part of the argument that elevated a recent African origin (RAO) model for *Homo sapiens*. The decades-long dominance of the RAO model repeatedly involved the marginalization or downright erasure of voices that espoused a more nuanced understanding of our evolutionary history involving admixture and continuity. We explore several dimensions of this, including: 1) the elevated status given to Western lab science/scientists, and the erasure of other voices and kinds of scholarship in paleoanthropology, 2) how current paleoanthropological models are a repackaging not just of previous models of gene flow, but more concerningly of colonial ideas about human evolution that primitivize non-Whites; and 3) the myth that science and scientists are separate and therefore objective. These practices are in part why, despite our discipline's reckoning with its historical role in promoting the concept of race, paleoanthropology continues to reproduce typological and essentialized models that actually provide support for biological race. We use satirical comedy to explore these very serious issues and reveal how they serve to police the boundaries of humanness.

Demographic and Socioeconomic Trends in U.S. Home-to-Hospital Transfer Integration

MEREDITH AULDS[1], MELISSA CHEYNEY[2], MARIT BOVBJERG[3] and AMANDA VEILE[1]

[1]Anthropology Department, Purdue University, [2]Anthropology Department, Oregon State University, [3]College of Public Health and Human Sciences, Oregon State University

Births have occurred at home with family and trusted community members for the majority of human history. Although the evolutionary mechanisms underlying human birth complications remain debated, they occur peripartum in a small number of births and can negatively affect outcomes for birthing parents and newborns. When homebirthing parents in the United States experience complications, they may opt to transfer from the home to a hospital for biomedical care. There were ~30,000 homebirths per year, and an estimated 3,000-12,000 home-to-hospital transfers per year (pre-COVID). However, the decentralized US healthcare system, and state and hospital-level variation in midwifery integration (i.e., the degree to which midwifery care is incorporated into state-level legislation and hospital policy), produce nationally variable transfer rates and outcomes. Socioeconomic factors can further complicate the decision to transfer for many birthing people, necessitating investigation of barriers to home-to-hospital transfer. This research therefore examines demographic and socioeconomic trends in intrapartum, postpartum, and newborn transfers using the Midwives Alliance of North America (MANA) 4.0 database (a secondary anonymized dataset containing data from U.S. home births from 2012-2018). Preliminary results suggest an association between birther race and indicators of socioeconomic status (e.g., Medicaid eligibility, participation in the Special Supplemental Nutrition Program for Women, Infants, and Children (WIC) program) and intrapartum, postpartum, and newborn transfer rates. The landscape of home-to-hospital transfer integration is complex in the US. Social environments shape human birth variation, underscoring the need for better US transfer integration systems.

Are cribrous lesions a reflection of growth? An investigation of cranial and postcranial cribrous lesions in a British study sample

JENNIFER L.D. AUSTEN and MARY E. LEWIS

Department of Archaeology, University of Reading

With increasing use of postcranial cribrous lesions in bioarchaeological studies, there is a vital need to explore the aetiology of cribrous lesions. While these lesions are typically considered pathological, other aetiologies including growth should also be considered. Using a sample comprised of five British sites from Roman to Post-Medieval periods (n=531), this study explored the relationship between growth, cribra orbitalia, cribra humeralis, and cribra femoralis. Cribrous lesions were recorded using a scoring scheme devised by the authors and analysed through multinomial logistic regression to assess the relationship between cribrous lesions. Linear regressions were then used to determine whether age and crude prevalence rates of each cribrous lesion could predict humeral and femoral diaphyseal lengths in nonadults ranging from birth-18.0 years (n=191). Overall, age was a statistically significant predictor of cribra orbitalia in both adult and nonadult individuals. Age revealed further trends in lesion prevalence, with high prevalence rates found in age categories that have slow (2.6-6.5 years) and rapid (10.6-14.5 years) growth periods. In nonadults, age was found to consistently predict humeral (p<0.001) and femoral diaphyseal lengths (p<0.001) in every site. Conversely, all three cribrous lesions did not significantly predict humeral (p>0.05) or femoral diaphyseal lengths (p>0.05). St John's Church (Redhill, UK) was the only exception, whereby cribra orbitalia was found to significantly predict humeral diaphyseal length (p<0.05). These results demonstrate the complexity of cribrous lesion aetiology; while age is a key component, the relationship between growth and cribrous lesions is not as clearly defined and warrants further investigation.

Understanding Hidden Heterogeneity in Frailty through the Social Determinants of Health: A case study from Ancient Egypt

ANNE E. AUSTIN

History, University of Missouri - St. Louis

In 1992, Wood and colleagues published a landmark article discussing three key issues that challenge how we can interpret health in past populations: demographic nonstationarity, selective mortality, and heterogeneous frailty. The last of these remains a key issue as the underlying factors impacting individual levels of frailty are often hidden.

Around this same period, public health experts were similarly challenged to explain health disparities on a global scale resulting in the concept of the Social Determinants of Health: factors in one's social structure, environment, and behaviors that can explain health inequalities.

In this paper, I argue that applying the Social Determinants of Health to bioarchaeological contexts can help reveal hidden heterogeneity by identifying how social structures in the past could have directly impacted health outcomes. As an example, I present my research on enamel hypoplasias in three tombs – TT217, TT290, and TT298 – at the site of Deir el-Medina. The rates of these lesions in comparison to published data from other sites in ancient Egypt and Nubia suggest the people of Deir el-Medina had overall lower rates of this childhood stress indicator. To explain this, I model how social cohesion – one factor within the Social Determinants of Health – is evidenced in texts from the site. Aligning this

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

with results from public health research, I demonstrate processes through which social cohesion could lower rates of cribra orbitalia and enamel hypoplasias at Deir el-Medina.

This research was funded by the Antiquities Endowment Fund and the University of Missouri Strategic Investment Program.

A validation and assessment of interobserver error for the FSS method of frontal sinus identification

PATRICIA R. AVENT, JESSICA L. CAMPBELL and LAUREN N. BUTARIC

Anatomy, Des Moines University

Various methods of frontal sinus comparison are used for positive identification in forensics. One technique is the FSS method developed by Tatlisumak et al. (2007), which is named for the morphological analysis of the **F**rontal sinus's **S**epta, and **S**callops. Variables are scored and the resulting codes are compared to discriminate incorrect identifications. The goal of this preliminary study is to further validate Tatlisumak et al.'s claim of a 93% discrimination rate with a sample partially representative to the U.S. forensic population.

This study utilizes CT scans of 99 individuals of European and African descent from the New Mexico Decedent Image Database. Using 3DSlicer, frontal sinus morphology was scored; an additional subset (n=18) was coded by a second observer to assess interobserver agreement.

Weighted kappa results show that all variables had high interobserver agreement (k = 0.638-1, p = .005-<0.001), and 12 of the 17 interobserver pairs matched exactly. In the total sample, there were 62 duplicated codes; however, after correct interobserver duplicates were removed, 41 duplicates (35%) remained. The most frequently (five instances; 4.3%) duplicated code was "00--------" representing bilateral absence of the sinus.

Results of this study indicate that while agreement when scoring frontal sinus traits is significant (p<0.05), the usefulness of the FSS method in this sample is low given that it could only discriminate 65% of cases compared to the original study's claim of 93%. Caution should be taken when applying this method for frontal sinus comparison in US-based populations, particularly in instances of aplasia.

This project was supported by Award No. 2020-75-CX-0013, awarded by the National Institute of Justice, Office of Justice Programs, U.S. Department of Justice.

The relationship between dental wear and dental topographic measures in platyrrhine primates

JULIET O. AZE[1], CLAIRE E. TERHUNE[2], CLAIRE A. KIRCHHOFF[3] and SIOBHÁN B. COOKE[4,5]

[1]Ecology, Evolution and Environmental Biology, Columbia University, [2]Anthropology, University of Arkansas, [3]Biomedical Sciences, Marquette University, [4]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, [5]New York Consortium in Evolutionary Primatology Morphometrics Group

Paleontologists and functional morphologists have sought to establish correlations between primate tooth form and dietary habits, largely basing their analyses on pristine dentition. However, most dental remains are not pristine. Here, we examine whether dental topographic signals are maintained through the dental wear sequence. The sample includes three platyrrhines: *Alouatta seniculus* (n=23), a folivore; *Ateles geoffroyi* (n=23), a soft-fruit frugivore; and *Sapajus apella* (n=25) a frugivore-omnivore practicing durophagy.

Full dental rows were surface scanned and upper and lower second molars were cropped. To measure dental wear, the surface area of exposed dentin and the total occlusal surface of the upper and lower second molars was measured. The ratio of the surface area of exposed dentin to the occlusal surface area was calculated to provide an overall measure of wear. The measures of dental wear were then correlated with the dental topographic measures Orientation Patch Count Rotated (OPCR) and Dirichlet Normal Surface Energy (DNE). Results indicate that DNE and OPCR values remain largely species-specific with light to moderate dental wear (up to 30% dentin exposure); in *Alouatta* and *Ateles* both measures increased slightly with wear implying that greater complexity and curvature develop through use. These results suggest that patterns of dental wear are adaptive rather than random, and that worn teeth can be used for dietary reconstruction in a paleontological context. The findings indicate it would be beneficial to increase the sample size to determine the strength of correlations between the DNE and OPCR values and wear.

NSF BCS-1551669 (SBC), NSF BCS-1551766 (CET); NSF BCS-1551722 (CAK)

Exploring the effects of diabetes mellitus on isotopic ratios

JA'NET BAIDE[1] and NICHOLAS P. HERRMANN[2]

[1]Department of Anthropology, University of Utah, [2]Department of Anthropology, Texas State University

The use of stable isotope analysis (SIA) is a growing sector in anthropology and forensic sciences. While considering partnerships between academia and law enforcement industries, recent literature highlights objectives to refine methods in SIA. As of yet unaddressed is the potential for underlying disease to impact isotopic variations observed from bodily tissues. However, finding direct-pathological-induced variations in isotopic ratios is challenging without the ability to control diet, activity levels, or stress in an experimental population. Our research explores type 2 diabetes mellitus-related variations in tissue chemistry using a donated skeletal collection with known medical and residential histories. We procured samples from 24 individuals with the Texas State Donated Skeletal Collection for stable oxygen analysis (d18O). Individuals are self-identified as White, 52 years or older (median=73.50 years), of known sex (f=10, m=14), and have data regarding known diabetic status (nondiabetic=14, diabetic=10) and duration at last known residence (mean=30.5 years). Residents from San Antonio, TX (mean=-2.9107) have lower d18O values to Austin, TX residents (mean=-2.2571; p=0.07), and diabetics have lower d18O values (mean=-2.7821) compared to non-diabetics (mean=-2.4423; p=0.39). Among donors who were residents of San Antonio before death, d18O values vary more widely with underlying disease (diabetics mean=-3.2153; non-diabetics mean=-2.6932; p=0.35) in comparison to variation observed among donors who were Austin residents (diabetics mean=-2.3489; non-diabetics mean=-2.1915; p=0.76). Results indicate that, despite underlying regional variation, diabetics exhibit lower levels of oxygen enrichment than non-diabetics. Variation in enrichment among diabetics may suggest health inequities mediate the degree of impact diabetes has on individuals' health.

This material is based upon work supported by the Grady Early Research Endowment in Forensic Anthropology and the National Science Foundation Graduate Research Fellowship Program under Grant No. (1840989).

Age-at-death estimation: Accuracy and reliability of common age reporting strategies in forensic anthropology

CHRISTINE BAILEY[1] and GIOVANNA VIDOLI[2]

[1]Physical Anthropology, Cleveland Museum of Natural History, [2]Anthropology, University of Tennessee, Knoxville

Age-at-death estimation continues to be a challenge within forensic anthropology due to the uncertainty regarding method selection and the production of a final age estimation for law enforcement. The purpose of this research is to identify the age-reporting strategies, commonly implemented in forensic casework, that provide the most accurate and reliable (low inaccuracy and low bias) age-at-death estimations when evaluated by total sample, age-cohort (20-39; 40-59; 60-79), and sex. The age reporting strategies in this study were derived from six age-at-death estimation methods and tested on 58 adult individuals (31 males and 27 females) from the UTK

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Donated Skeletal Collection at the University of Tennessee, Knoxville. An experienced-based estimation was also assessed. Two-way repeated measures ANOVAs were conducted to determine if there were significant differences in reliability between the age-reporting strategies. The results show that the most accurate and reliable age-reporting strategy varied if the sample was evaluated as a whole, by age, or by sex. Accuracies ranged between 80%-100%, inaccuracies, 4.9-10.6 years, and bias, 0.1-5.3 years, for the best preforming methods. While none of the age-reporting strategies evaluated in this study were consistently the most accurate and reliable for all of the sample categories, the experience-based approach performed well for each group. This research sheds light on the performance of the different strategies for delivering a final age range for unknown remains to law enforcement and provides further support to the reliance on multiple aging indicators and professional judgment in developing a final age-at-death estimation.

The Prevalence of Childhood Metabolic Bone Disease and Growth Stunting in the Great Depression

LYDIA BAILEY

Department of Physical Anthropology, Cleveland Museum of Natural History

The Great Depression (1929-1939) caused a decline in overall childhood health due to homelessness, extreme poverty, and minimal access to nutritious food. Such environments affect the development and remodeling of the skeleton, and understanding the impact that dramatic socioeconomic events can have on metabolic bone disease is imperative. This study examines all juveniles (n=70) in the Hamann-Todd Osteological Collection (HTOC) to determine whether children who experienced the Great Depression have more skeletal evidence of stunted growth and metabolic bone disease than those who did not. To assess this, diaphyseal lengths of long bones were observed and recorded in addition to the severity of osteological stress indicators (cribra orbitalia, porotic hyperostosis, and long bone deformation). The individuals were separated into pre-Great Depression (n= 47) and Great Depression (n=23) groups for analysis. The data were analyzed using a chi square test and independent t-test. Results indicate that there is not a statistically significant difference in metabolic bone disease indicators between those who experienced the Great Depression and those who did not, though 75% of juveniles in the HTOC exhibit some evidence of metabolic bone disease regardless of what group they were in. However, the Great Depression group had shorter long bone measurements which are indicative of stunted growth resulting from extreme developmental stress. Although many juveniles in this sample experienced metabolic challenges, it is possible the Great Depression was not a direct cause of these challenges and other factors should be explored.

This research recieved funding through the Kirtlandia Research Internship Program.

Cranionasal sexual size dimorphism in proboscis monkeys (*Nasalis larvatus*) is associated with growth beyond dental maturity in males, but not in females

KATHARINE L. BALOLIA and PHILIPPA L. FITZGERALD

School of Archaeology and Anthropology, Australian National University

Enlarged noses in proboscis monkeys are associated with sexual selection, where among males, large noses serve as honest signals of sexual quality and competitive ability. In the research presented here, we investigate cranionasal sexual size dimorphism and adulthood growth in proboscis monkeys to assess the bony correlates of soft tissue nasal sexual dimorphism in this species. Using 3D landmark data taken from dry cranial specimens of 36 dentally mature proboscis monkeys (17 females, 19 males), we a) assess whether sex-specific cranionasal allometric scaling relationships diverge from isometry, b) test for the presence and degree of cranionasal sexual size dimorphism, and c) test for sex-specific cranionasal growth beyond dental maturity. Male proboscis monkeys show a positive association between cranionasal and craniofacial size, however this scaling relationship does not diverge from isometry. We found no significant relationship between cranionasal and craniofacial size among females. Proboscis monkeys show strong cranionasal size dimorphism, relative to the degree of overall cranial size dimorphism, which is associated with nasal growth beyond dental maturity in males, but not in females. Cranionasal growth in males is not associated with craniofacial growth beyond dental maturity. Our results are consistent with what is expected from a socially selected trait in primates living in social groups in which males attain social dominance later in adulthood. More broadly, our findings show evidence for hard tissue correlates of sexual dimorphism observed in a soft tissue feature, associated with visual signaling.

Investigating human migrations and genetic diversity in Northeast India over the last ~4,000 years using ancient genomics

ESHA BANDYOPADHYAY[1], CONSTANZA DE LA. FUENTE[1], DAVID WITONSKY[1], TIATOSHI JAMIR[2], DAVID TETSO[3], NIRAJ RAI[4] and MAANASA RAGHAVAN[1]

[1]Human Genetics, The University of Chicago, USA, [2]Department of History and Archaeology, Nagaland University, Kohima Campus, India, [3]Department of Anthropology, Kohima Science College (Autonomous), India, [4]Ancient DNA Group, Birbal Sahni Institute of Palaeosciences, India

Northeast India occupies a strategic position between South Asia, East Asia, and Southeast Asia. Archaeological evidence from cave and rockshelter sites along the border between the Northeast Indian state of Nagaland and Myanmar suggests that hunter-gatherer societies survived in the forested uplands of Northeast India spanning the mid-Holocene to as late as ~3,500 years before present (yBP). Archaeological records further reveal that the Neolithic transition in broader Northeast India postulated to date back as early as ~4,000 yBP, shared cultural features with the Neolithic period in East and Southeast Asia. Furthermore, genetic affinities have been reported between present-day Northeast Indian populations and Eastern Eurasians, though the temporal context and source of this genetic affinity remain unresolved. This raises an important question about the genetic relationships between hunter-gatherers, early farmers, and present-day inhabitants of the region and their genetic affinities over time with Eastern Eurasian populations.

In this study, we aim to characterize for the first time past genetic variation and genetic admixture in Northeast India by analyzing genome-wide data from two ancient samples from the rockshelter site of Photangkhun Longkhap in Nagaland. These individuals are radiocarbon dated to *ca.* 3,700 – 4,300 yBP calibrated BP. We find that the ancient individuals from Nagaland are genetically closest to present-day Naga and other populations in Northeast India and the eastern Himalayas, primarily speakers of Tibeto-Burman languages, and can be modeled using similar genetic components as present-day populations in Nagaland.

Blinded by the rift? Exploring the limitations of hominin habitat reconstructions based on spatially restricted species occurrences

W. ANDREW BARR

Department of Anthropology, Center for the Advanced Study of Human Paleobiology, The George Washington University

The Eastern African Rift System (the rift) preserves an outsized portion of the African fossil record, but represents less than 2% of the spatial area of the continent. Our understanding of hominin habitat use is likely impaired by the overabundance of fossils coming from this thin sliver of eastern Africa. To better understand potential biases, this study asks: how would our understanding of rift-dwelling extant mammal habitats be different if all we knew about was their occurrence within the rift?

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Using range data from IUCN, I compared each rift-dwelling terrestrial mammal range ($range_{full}$) to the subset of the range occurring within the rift ($range_{rift}$). I characterized $range_{full}$ and $range_{rift}$ in terms of percent grass cover and percent tree cover (from the Copernicus Global Land Cover service) and annual precipitation and annual temperature (from BIOCLIM).

The median spatial overlap between $range_{rift}$ and $range_{full}$ is only 2.8%. Using repeated measures ANOVA, tree cover was significantly lower in $range_{rift}$ ($F=96.4$, $df=1,146$, $p<0.001$, $range_{full}$ mean = 33.4%, $range_{rift}$ mean= 15.9%), as was annual precipitation ($F=29.2$, $df=1,146$, $p<0.001$, $range_{full\ mean}$ = 1010.46 mm, $range_{rift}$ mean = 887.94 mm). Grass cover and mean temperature showed no significant differences.

For modern rift-dwelling mammals, the rift comprises a tiny and environmentally unrepresentative fraction of most species ranges. To the extent the environmental differences between the rift and the rest of Africa were present in the Plio-Pleistocene, reconstructions of early hominin paleoenvironments are likely biased towards less wooded and drier portions of actual hominin ranges.

ANTERIOR TEETH AND THE MANDIBULAR SYMPHYSIS: A Morphometric Analysis of Correlation in Extant Hominids

ARIEL N. BARRERA and CHRIS A. ROBINSON

Anthropology, CUNY Graduate Center

Recent studies (microwear, isotopes, and FEA) challenged the consensus that differences in mandibular morphology between *Australopithecus* and later hominins are due to adaptations to processing mechanically resistant foods, suggesting that researchers explore alternative explanations for variation. One of the variables potentially affecting the shape of the mandible is the size and shape of the teeth since the mandible must have space to house those teeth. Consequently, this study assesses the hypothesis that the shape of the symphysis is influenced by the shapes of the incisors and canines, by examining covariation between their shapes. If spatial relationships are the cause of variation in symphyseal morphology, it would not be necessary to invoke mechanical explanations for variation in external mandibular form in hominids. Variation was assessed by collecting 3D semilandmarks on MicroCT scans of the root, crown, and midline symphysis outlines from seven specimens of each extant hominid genus. Two-blocks partial least squares analyses were performed on the Procrustes aligned data to assess the correlation between the shapes of the teeth and mandibular symphysis. Results suggest that covariation exists between the symphysis and overall canine and incisor crown shape when analyzing all taxa together, and the symphysis and the canine crown in *Homo*. However, given that no significant covariation was found between incisor crown and symphysis shape in individual genera and incisor root shape did not significantly covary with symphysis shape, it's plausible, that a third variable, such as diet, could be driving the relationship between the incisor crown and symphysis shape.

Social transmission of *Blastocystis* spp. in rural Madagascar: disentangling the effect of household, friendship, and close contact networks

TYLER M. BARRETT[1], GEORGIA C. TITCOMB[2], MICHELLE PENDER[3], JEAN YVES RABEZARA[4], VOAHANGY SOARIMALALA[5,6], RANDALL A. KRAMER[3,7], HILLARY S. YOUNG[8] and CHARLES L. NUNN[1,3]

[1]Department of Evolutionary Anthropology, Duke University, [2]Marine Science Institute, University of California, Santa Barbara, [3]Duke Global Health Institute, Duke University, [4]Science de la Nature et Valorisation des Resources Naturelles, Centre Universitaire Régional de la SAVA, [5]Association Vahatra, [6]Institut des Sciences et Techniques de l'Environnement, University of Fianarantsoa, [7]Nicholas School of the Environment, Duke University, [8]Department of Ecology, Evolution, and Marine Biology, University of California, Santa Barbara

Blastocystis spp. is a common intestinal protozoan that can cause diarrhea, which has significant health consequences in low-resource settings. Although *Blastocystis* is transmitted through the fecal-oral route, little is known about the social factors that influence its transmission. We investigated three types of social transmission and *Blastocystis* infection among 198 smallholder farmers in rural northeastern Madagascar. We hypothesized that more substantial social relationships that entail shared meals and living space would facilitate transmission better than brief interactions in the community and nearby agricultural lands. To test this hypothesis, we constructed household-proximity and close contact networks using GPS data and a friendship network using survey data. Infection was determined using DNA metabarcoding analysis of fecal samples. We applied a network permutation approach (network *k*-test) to assess the epidemiological significance of each network and examined the association between an individual's number of infected alters on each network and their odds of infection using generalized network autocorrelation models. These models also included age, sex, and handwashing behavior as covariates. Of the 198 participants, 127 (64%) showed evidence of infection. The network *k*-test revealed that connections on both the household-proximity (p=0.011) and friendship network (p<0.001) predicted infection. Number of infected alters was associated with infection in the household-proximity network (OR [95% CI]: 3.56 [2.43-5.69], p<0.001) and the friendship network (OR [95% CI]: 3.25 [2.03-5.52], p<0.001), but not the close contact network (OR [95% CI]: 0.98 [0.88-1.08], p=0.692). These findings suggest that sustained social interaction among family, friends, and neighbors is important for *Blastocystis* transmission.

NIH-NSF-NIFA Ecology and Evolution of Infectious Disease (R01-TW011493-01)

Best Practices for the Ethical use of Human Remains for Research and Teaching

ERIC J. BARTELINK[1], NICHOLAS PASSALACQUA[2], WENDY MCQUADE[3], DAWNIE STEADMAN[4], DONNA BOYD[5], KATE SPRADLEY[6], KELLY SAUERWEIN[7] and RANEE HO[8]

[1]Anthropology, California State University, Chico, [2]Anthropology and Sociology, Western Carolina University, [3]UNT Center for Human Identification, University of North Texas, [4]Anthropology, University of Tennessee, Knoxville, [5]Anthropological Sciences, Radford University, [6]Anthropology, Texas State University, [7]National Institute of Standards and Technology, National Institute of Standards and Technology, [8]Onondaga County Center for Forensic Sciences, Onondaga County Center for Forensic Sciences

As part of NIST's Organization of Scientific Area Committees (OSAC), OSAC Subcommittees are tasked with drafting standards, guidelines, and best practice recommendations specific to their forensic science discipline. These are then submitted to a standards development organization for further development and publication. Published documents are eligible for placement on the OSAC Registry, which encourages their implementation by making them freely available to the forensic science community.

Forensic anthropologists often use curated human skeletal remains for research purposes. Additionally, human skeletal remains are necessary to provide adequate education and training to students, anthropologists, and medicolegal professionals. Although most institutions curating large skeletal collections have policies and procedures addressing issues such as informed consent, there are no national guidelines for how human remains may be used in research and education contexts. Here we present the OSAC Forensic Anthropology Subcommittee's proposed guidelines concerning the ethical treatment of curated contemporary human remains and associated data. Core principles include seeking and obtaining appropriate permission(s) (i.e., informed consent) for the use of human remains in forensic anthropological research and/or education, as well as ensuring their proper handling and curation. The guidelines clarify which entities can provide consent based on the remains' origin (donated, unclaimed, or unidentified) and how obtained permissions—in addition to institutional policies and procedures—dictate the ethical use

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

of remains for education or research. Guidance is also provided for the use of information associated with remains (e.g., images, measurements), loaning of remains or associated data, and final disposition of remains.

No funding was provided for this research.

Vocal communication in black-and-white ruffed lemurs (*Varecia variegata*) at Mangevo, Ranomafana National Park, Madagascar

CARLY H. BATIST[1,2], MENDRIKA N. RAZAFINDRAIBE[4], FRANCOIS RANDRIAMANANTENA[3] and ANDREA L. BADEN[1,2]

[1]Anthropology, City University of New York (CUNY) Graduate Center, [2]Anthropology, CUNY Hunter College, [3]Research, Centre ValBio, [4]Animal Biology, University of Antananarivo

Studying vocal communication yields important insights into primate behavioral ecology. Black-and-white ruffed lemurs (*Varecia variegata*) are frugivorous lemurs that exhibit strong fission-fusion dynamics and communally rear litters that are parked. They are informally known for their raucous calls, but surprisingly only one previous vocal repertoire exists for *V. variegata* and even so, was generated from captive individuals. We qualitatively and quantitatively described the vocal repertoire and call usage of *V. variegata* from Ranomafana National Park, Madagascar. We characterized 11 call types using 33 bioacoustic parameters related to frequency, duration, tonality and composition (*warbleR* package). The repertoire consists of both monosyllabic and multisyllabic calls that are individually-given or emitted in contagious choruses. Eight of 11 call types were given in combination with other calls; for example, 76% of roar-shrieks were preceded by another call type and 49% were followed by another. We conducted a discriminant function analysis (DFA), which correctly assigned call types with 88% success, though this varied greatly by call type (range 1-64%) and is likely related to sample size. The repertoire thus appears graded and highly variable. We also identified statistically-significant demographic (sex, subgroup size) and contextual (behavioral state, fission-fusion events) influences on the usage of different call types. Vocal activity was fairly constant across time of day (no diel pattern) but decreased as rainfall increased (p=0.03). This study is the only complete vocal repertoire described from wild *V. variegata* and the only one that provides a quantitative bioacoustic analysis.

This study was generously funded by the CUNY Graduate Center Provost's Office.

Consequences of Lack of Qualifications and Unethical Behavior: The Need for Better Science Communication in Forensic Anthropology

MELANIE M. BEASLEY

Department of Anthropology, Purdue University

Since the 1970s, modern forensic anthropology has grown from an applied anthropology approach to investigate human skeletal remains into a sub-discipline of anthropology with continually evolving theory, methods, and ethical practices. Making the advances in the science and practice of forensic anthropology understandable to the broader field of biological anthropology and the public can remove existing stigma, misinformation, and bring confidence to the value of specialized training within the discipline. In recent years, media coverage has highlighted cases where pseudoscience, unethical practices of by unqualified individuals, and the unethical treatment of human remains had a negative impact to families, communities, and the discipline. With the exception of the state of Texas (where a doctoral degree is required to analyze skeletal remains related to medicolegal cases), there are no laws that guide qualifications to practice forensic anthropology in the United States. The misidentification of animal remains as human because of a lack of qualifications or promoting the pseudoscience of dowsing rods to locate clandestine graves has lasting consequences in the public perception of what assistance trained forensic anthropologists can offer investigators. In this presentation, I argue that science communication is key to moving new legislation forward for the ethical handling of human skeletal remains in forensic contexts because the current state of the science, the understanding by the public, and the laws regarding death investigation are not aligned.

Resolution: comparing isotopic weaning profiles in permanent and primary teeth from the Tooth Fairy Project

JULIA BEAUMONT

School of Archaeological and Forensic Sciences, University of Bradford

The aim was to investigate whether analytical methods using incremental dentine collagen carbon and nitrogen isotope ratio profiles of primary molar and M1 from the same individual show the same patterns: or does temporal blurring in M1 affect the quality of the potential interpretations? Dentine isotope profiles allow the investigation of dietary and physiological changes during modern and past childhood. The breastfeeding and weaning period is critical in infant life: breastmilk provides the best nutrition and maternal immunity for the first 6 months. The introduction of other foodstuffs, while essential to promote further development, can introduce infections and may vary in quality and composition until the child is weaned and consumes the family diet. Primary molar teeth develop from the last trimester of pregnancy with crown completed at about 9 months of age; permanent M1 crowns contain tissue from around birth to 3.5 years ± 6 months. Beaumont Method 2 (2013) in a primary molar gives isotopic profiles containing an in-utero value for the first ½ mm and an average of approximately 3 months per 1mm sample, while M1 yields approximately 7-9 months per sample. The temporal resolution from primary teeth is therefore better for the breastfeeding/weaning period. To address this, Curtis method (2022) of microdrilling 0.35mm samples of the same M1 crown dentine was applied.The 3 datasets from 18 individuals from the Tooth Fairy Project (with known breastfeeding histories) are presented as a guide to help researchers decide how best to interpret data from M1 in future.

Tooth Fairy project supported by the Rank Nutrition Prize, analyses for this study supported by the BA/Leverhulme small research grant no: SG2122\210221.

Osteological specimens and the human bone trade: An anthropological responsibility

JULIETTE BEDARD

Anthropology, Idaho State University

Anthropological education and research claim the use of anatomical specimens is invaluable; however, the commercial trade of human remains has deeply colonial and ethical consequences that have historically been ignored within institutions. The epistemic entitlement of biological anthropology to osteological specimens has thus contributed to the unethical standards of the human remains trade and teaching collections.

This study seeks to build a more accurate picture of the current state of collections within North American institutions, as well as understand the responsibility anthropologists have toward ethical collections. To do so, universities across North America were used as comparative case studies, specifically those with anthropology departments holding osteological collections. My analysis compared the condition of remains, knowledge of the remains' history, and information on provenience. In the case of legacy remains from a coroner's office in rural Idaho, there was little information on where the remains came from and were in poor condition.

A survey of collections and case studies across North America shows that contemporary ethical standards for building a teaching collection *de novo* tend to source remains from willed-body donation programs. Still, many anthropology departments across North America contain remains with no provenience, as there is no practical solution for meaningfully repatriating their remains. Other departments have not yet begun the effort to only have ethical and legal specimens.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Overall, there needs to be a cultural shift within anthropology to think beyond anthroposcopic analysis for education or research and consider how other forms of evidence could provide further avenues.

On the trunk muscles of Kebara 2 neanderthal

ELLA BEEN[1], MOSHE SACHAR[2], YOEL RAK[2] and ALON BARASH[3]

[1]Department of Sports Therapy, Faculty of Health Professions, Ono Academic College, [2]Department of Anatomy & Anthropology, Sackler Faculty of Medicine, Tel Aviv University, [3]Azrieli Faculty of Medicine, Bar Ilan University

Kebara 2 is the most complete Neandertal axial skeleton ever to be found. Previous reconstruction of the spine, pelvis, and thorax of the Kebara Neanderthal provides us with a unique opportunity to accurately reconstruct the dimensions of trunk and abdominal muscles and compare it to those of modern humans.

The aim of this research is to reconstruct the Neanderthal's trunk muscles, measure its length and torque (moment arm) and compare it to a sample of contemporary *H. sapiens*.

Using the Horos software, we measured muscle length and moment arms on the virtual reconstruction of Kebara 2, and CT scans of the fifty modern humans. Fascicular length of each spinal and abdominal muscle, their direction, and the torque arm available to them was measured in the sagittal, coronal, and horizontal planes. These measurements are based on well-established kinesiological methods.

The results of the study show that the moment arms of the lateral abdominal muscles of Kebara 2 are significantly longer compared to *H. sapiens*, as well as the length of the fascicles of the external oblique muscle and part of the fibers of Quadratus lumborum. There were no significant differences in the length and moment arm of the rest of the trunk muscles that were measured.

The skeletal morphology of the Neanderthal from Kebara, manifests differences in the length of the fascicles and the torque arm of spinal and abdominal muscles, compared to modern humans. This might imply differences in muscle function and movement pattern between the two species.

From "Brachiationist" to "Extended Limb Clambering." Extant and extinct positional behavior and the origin of hominin bipedalism

DAVID R. BEGUN[1] and MADELAINE BÖHME[2,3]

[1]Department of Anthropology, University of Toronto, [2]Senckenberg Centre for Human Evolution and Palaeoenvironment, Tübingen, [3]Department of Geosciences, Eberhard-Karls-University of Tübingen

Reconstruction of positional behavior in extinct taxa frequently relies on analogy with extant species. Yet, fossil morphology is often difficult to reconcile with extant positional behavior. Bipedalism in australopithecines is a well-known example. Miocene apes are even more unique in their combination of morphological attributes that are not immediately suggestive of any specific extant behavior. Extended limb clambering (ELC) in *Danuvius* is not analogous with known extant positional behavior but incorporates components observed in several extant taxa. Its vertebrae point to a stiff, relatively short lower back, as do the vertebrae of *Pierolapithecus* and the os coxae of *Rudapithecus*. Forelimb morphology in these apes is suggestive of high levels of mobility and below branch arboreality. The tibia in *Danuvius*, not known in other taxa, reflects habitually bipedal, load bearing postures while its hallux and that of many Miocene apes indicate powerful pedal grasping. New evidence of the second metatarsal of *Danuvius* reveals aspects of the biomechanics of its pedal grasping reflecting a unique foot form consistent with its unique positional behavior. Metatarsal shaft morphology is unlike most extant taxa and closer to *Rudapithecus.* A powerful hallux and unique foot morphology are also characteristic of *Ardipithecus ramidus.* The unique combination of attributes in *Danuvius* and other Miocene apes suggests that ELC may have been widespread among late Miocene apes and may be a better model for the ancestral positional behavior of hominin bipedalism than multi-stage models based on extant taxa.

Hammerschmiede excavations are supported by the Bavarian State Ministry of Research and the Arts, and by the Bavarian Natural History Collections (SNSB). Additional funding from NSERC (RGPIN-2016-06761).

Genetic ancestry testing within an Afro-Puerto Rican community: Expressions of cultural identity, race, and resistance

JADA BENN TORRES[1] and GABRIEL TORRES COLÓN[1,2]

[1]Department of Anthropology, Vanderbilt University, [2]American Studies Program, Vanderbilt University

Genetic ancestry testing may be appealing for some people because it is (mistakenly) assumed to explain the genetic underpinnings of race and cultural identity. Furthermore, for some test takers, genetic ancestry testing can be potentially life-altering because of the possibility of impacting fundamental ideas about self and one's affiliation to community. We sought to elucidate the relationship between genetic ancestry testing results, notions of race, and discourses of belonging among a group of 58 self-identified Afro-Puerto Ricans. In this ongoing community-engaged project, we genotyped mitochondrial and Y chromosome haplogroups and returned these results to participants. Analysis of these markers indicated ancestry derived from African (66% of the matrilines, 52% of the patrilines), Eurasian (5% of the matrilines, 44% of the patrilines), and Indigenous American (29% of the matrilines, 4% of the patrilines) populations. Additionally, three major themes became evident upon discussing results with participants. First, participants came to the study already immersed in a particular history of marginalization and socialization which impacted how the results were interpreted and ultimately valued. Second, socio-cultural cues that shape racial experience weighed more heavily on self-identification than genetic ancestry results. Third, for many involved, participation in this study was a form of resistance to anti-Black sentiment, an expression of being Black and being Puerto Rican, and an affirmation of relationships to larger African diasporic and Puerto Rican communities. Our study illustrates that both context and experience are central to understanding relationships between phenotypes and genotypes especially regarding issues of race and identity.

This work is supported by National Geographic Research Explorer Grant and Vanderbilt University grants from the Community Engaged Research Core and the Office of Equity, Diversity, and Inclusion.

Assessing Accuracy of Three Pelvic Age-at-Death Methods

KRISTA E. BENNETT

Geography and Anthropology, Louisiana State University

Age-at-death estimation of human skeletal remains often utilize pelvic joint surfaces. Each pelvic joint surface (i.e., the pubic symphysis and auricular surfaces of the ilium and sacrum) exhibits age-related degeneration at varying rates due to the location, type, and thickness of the cartilage present. This study examines three pelvic age-at-death methods: the pubic symphysis revised method (Hartnett, 2010a), auricular surface revised method (Buckberry and Chamberlain, 2002), and sacral method (Passalacqua, 2009). Paired sacra and os coxae (n=135) were randomly selected from the Texas State University Donated Collection for assessment. The sample included 50 females and 85 males (aged 18-102 years; xÃÖ=65 years). Joint surfaces were scored according to the associated age-at-death method and evaluated for accuracy (i.e., if chronological age fell within the estimated age range). The methods with the highest accuracy were the Passalacqua (2009) 95% confidence interval (CI) at 97.6% and the Buckberry and Chamberlain (2002) at 96.2%; however, these methods also have very wide age intervals. Conversely, Hartnett (2010a) and Passalacqua (2009) 68% CI showed 69.1% and 64.8% accuracy, respectively; these methods have lower accuracy but more narrow age intervals. Over 77% of the individuals inaccurately estimated by the Hartnett (2010a) and Passalacqua (2009) 68% CI methods were 65 years and older, which suggested these

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

methods are not ideal for senescent individuals. All three methods failed to estimate age-at-death accurately for four individuals, each of whom exhibited at least one pelvic anomaly; therefore, these methods should be used with caution if pelvic anomalies are present.

This research was funded in part by the Robert C. West Graduate Student Research Award from the Department of Geography and Anthropology at Louisiana State University.

Ontogenetic changes to trabecular bone microstructure compared to other measures of growth

AMY C. BERESHEIM[1], SUSAN PFEIFFER[2,3], MARC GRYNPAS[4,5] and CHRIS DUDAR[6]

[1]Anatomy and Cell Biology, Rush University Medical Center, [2]Anthropology, University of Toronto, [3]Anthropology, George Washington University, [4]Department of Laboratory Medicine and Pathobiology and Institute for Biomaterials and Biomedical Engineering, University of Toronto, [5]Lunenfeld-Tanenbaum Research Institute, Sinai Health, [6]Anthropology, National Museum of Natural History, Smithsonian Institution

The growth of immature individuals from archaeological samples often lags behind modern standards. However, it remains unclear how bone microstructural variation corresponds to growth-related changes in physical dimensions. This study quantifies changes to trabecular bone microstructure relative to changes in age and diaphyseal bone length.

A sample of 27 individuals (0–16 years of age) from a pioneer cemetery (Prospect Hill, Newmarket, ON (1824–1879 AD)) have age estimates based on dental development. Maximum femoral (n= 20) and humeral (n=23) diaphyseal lengths are available for most individuals. Mid-shaft rib sections were scanned using the SkyScan 1174 Micro-CT system at the Lunenfeld-Tanenbaum Research Institute, Toronto, ON. Quantitative trabecular bone parameters were derived using SkyScan CT-analyzer software. Both parametric and nonparametric tests were used for statistical analysis.

Bone volume fraction (BV/TV), trabecular number (Tb.N), and connectivity density (Conn. Dn) demonstrate significant negative relationships with age, while trabecular separation (Tb. Sp) demonstrates a positive relationship with age. Trabecular thickness (Tb.Th) and degree of anisotropy (DA) do not demonstrate significant relationships with age. Tb.Th markedly increases within the first two years of life but is highly heterogenous thereafter. Age-group comparisons reveal general similarities between children (2-10 years) and adolescents (10+ years), but infant (0-2 years) bone microstructure is more distinct. Tb.Sp demonstrates positive, while BV/TV and Tb.N demonstrate negative, covariance with increasing diaphyseal bone length.

The greatest changes to bone microstructural organization occur from 0-2 years. Mid-childhood and pubertal growth spurts are not obvious. BV/TV, Tb.Sp and Tb.N demonstrate predictable relationships with measures of linear growth.

Oxygen isotopes in herbivore enamel reveal Terminal Pleistocene mesic grasslands in northern Malawi: implications for forager territoriality

ALEX BERTACCHI[1], STANLEY H. AMBROSE[2], JORDAN A.G. WOSTBROCK[3], JESSICA C. THOMPSON[1] and POTIPHAR KALIBA[4]

[1]Department of Anthropology, Yale University, [2]Department of Anthropology, University of Illinois at Urbana-Champaign, [3]Department of Earth and Planetary Sciences, Yale University, [4]Malawi Ministry of Tourism, Culture and Wildlife, Republic of Malawi

Ancient DNA and material culture indicate Pleistocene long-distance social and demographic interactions between eastern and southern Africa declined around the Last Glacial Maximum (LGM; 26.5-15 ka), assuming a structure that was maintained into the Holocene. Local resources might have become richer and more predictable, favoring larger population sizes and the formation of stable territories. To test if this hypothesis is compatible with local paleoenvironmental proxies, we measured stable carbon and oxygen isotopes in 48 herbivore teeth (270 intra-tooth samples) spanning the last 30,000 years in northern Malawi. Our results indicate that overall precipitation in the LGM and the Terminal Pleistocene (TP) was comparable to the Holocene (mean $\delta^{18}O$ -2.7 to -3.3‰), despite a decline of large grazers in the fossil record. Seasonal variation in $\delta^{18}O$ of large grazer enamel was high (4.2±0.8‰ in the LGM), but individual TP zebras appear to have been buffered against seasonal variation through migratory behavior or drinking from non-evaporated sources (e.g., springs). The triple oxygen isotope composition ($\delta'^{17}O$) of a subset of samples indicates intra-tooth variation of ~20 per meg within individual zebra teeth, while intra-tooth differences in other specimens fall within measurement error, consistent with differences in drinking behavior. We propose that high atmospheric pCO_2 favored mesic C4 grasslands during the Terminal Pleistocene, whereas in the Holocene the region became dominated by drought resistant C3 woodlands. Our results are consistent with the hypothesis that during the Terminal Pleistocene northern Malawi included rich grassland ecosystems that supported larger and more territorial foraging communities.

This research was funded by NSF-DDIG #2211151, NSF-EARPF #1952615, and the Yale Institute of Biospheric Studies.

A theoretical framework for tracking evolutionary changes in optimal dental function

MICHAEL A. BERTHAUME

Mechanical Engineering and Design, London South Bank University

Comparative studies of mammalian teeth often begin with the assumption that teeth are optimal for their function, where function is often measured using a single metric. Function is highly dependent on the desired function (e.g., stabilization, crushing/shearing, resisting failure) and limited by trade-offs and developmental, phylogenetic, ecological, and physical constraints; this means there is no single test which can be used to quantify dental function, particularly across taxa with varying diets and other ecological demands. I present a model for testing dental function and visualize the results using a ternary plot, where the vertices represent tooth strength, food item breakdown efficiency, and trapability (the ability to trap/stabilize a food item). Where multiple metrics for strength, efficiency, and/or trapability exist, weights can be assigned to different performance metrics, creating a composite score. Using the ternary plot, it is possible to observe trade-offs between two metrics (e.g., strength and efficiency) without the third metric being affected (e.g., trapability). Traveling along these lines, it is possible for taxa to move towards global optima in two performance metrics while having suboptimal performance in the third metrics. When combined with phylogenies, as in principal component analyses, it is possible to see how taxa have evolved within this functional morphospace, and what areas of the morphospace are "unoccupiable" due to constraints. Here, I describe this functional model, and apply it to *Australopithecus africanus* and *Paranthropus robustus* lower second molars, showing how tooth strength played a more important role in *P. robustus* molars compared to *A. africanus*.

In partnership with the British Academy, Royal Academy of Engineering, and Royal Society ('the Academies') with generous support from the Leverhulme Trust, this research was funded by APEX award APX\R1\211183.

The sky's not the limit: Ultramarathoners and the metabolic ceiling

ANDREW W. BEST[1], AMANDA MCGROSKY[2], ZANE SWANSON[2], REBECCA RIMBACH[2,3], JOE MCCONAUGHY[4], CARA OCOBOCK[5] and HERMAN PONTZER[2,6]

[1]Biology, Massachusetts College of Liberal Arts, [2]Evolutionary Anthropology, Duke University, [3]Behavioural Biology, University of Münster, [4]Stringbean Coaching, LLC, [5]Department of Anthropology, University of Notre Dame, [6]Duke Global Health Institute, Duke University

Metabolic scope (MS)- total energy expenditure (TEE) divided by basal metabolic rate (BMR)- constrains many physiological processes. Recent research has identified an inverse curvilinear

26927691, 2023, S7S, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

relationship between MS and the time span over which an energetic effort is apportioned. Maximal sustained metabolic scope (susMS), which can be maintained for months or years without catabolizing body tissues, is apparently limited to ~2.5x BMR. Elite ultramarathon runners are an ideal population for testing this hypothesis as they maintain high training volumes supported by near-optimized nutrition and recovery. We used the doubly-labelled water method to measure TEE in 6 ultramarathon runners (age 35.8 ±5.3 years, 5 male and 1 female) during competition to further define the relationship between MS and event duration; and during a ~1-week baseline period of training. Using training records, we established a regression equation for each runner describing the relationship between running mileage and MS, and used this to calculate susMS (the average monthly MS over the 12-month period). Sustained MS ranged from 2.2-2.63xBMR (mean 2.39± 0.20). Combining our ultramarathon MS and susMS results with previously published MS data from endurance events ranging 0.53-365 days reproduced the robust curvilinear relationship previously described (r^2=0.88, p<0.0001). These data lend further support for the existence of a "metabolic ceiling" that is a function of effort duration and agree with previous results which place the sustainable limit of metabolic scope at or just above 2.5x BMR. Further research will gather additional MS data from ultrarunners and explore the causes of interindividual variation in susMS.

This research was funded in part by a Massachusetts College of Liberal Arts Faculty Incentive Award.

Investigating physiological stress and disease in St. Henry's Cemetery, East St. Louis, IL (11S1742), 1866-1908

KALEIGH C. BEST[1,2] and JESSICA R. SPENCER[1,2]

[1]Anthropology, Southern Illinois University-Carbondale, [2]Center for Archaeological Investigations, Southern Illinois University-Carbondale

During the latter part of the 19th century, East St. Louis attracted worldwide immigrants as one of the hearts of industry and westward expansion in the United States. St. Henry's Cemetery (1866-1908) served seven of the area's Catholic parishes, with the largest amount of people interred having German and Irish heritage. As part of a nationwide movement of cemeteries out of cities during the early 20th century, St. Henry's supposedly was relocated by 1926, and the land developed into a National Guard Armory, which it remains today. Excavations in the winter of 2021/2022 were conducted as part of planned utility work and confirmed the presence of burials, despite 'relocation.' Twenty-five burials excavated by February 2022 were analyzed for evidence of disease, trauma, and indicators of stress. It was expected that these rates would be relatively low, given the apparent affluent population buried in St. Henry's.

Results indicate that 64% of the analyzed individuals have dental disease, 32% have dental enamel hypoplasia, 16% have cribra orbitalia/porotic hyperostosis, 20% have periostitis, 52% have age-related pathologies, 20% have antemortem injuries, 4% have perimortem injuries, and 4% have postmortem injury. The hypothesis was supported, except for the higher rates of dental disease within the sample, which given the state of poor dental hygiene and the increase in simple sugars in American diets at the time, is not surprising. The findings of this analysis provide information about the lives of Victorian white inhabitants in East St. Louis at the turn of the 20th century.

The Fault of a Filling: A Case Study Analysis of Dental Fillings from 18th-19th Century Halifax, Nova Scotia

TRACY K. BETSINGER[1], AMY B. SCOTT[2], ADRIENNE LANGILLE[3] and KAARE LUND. RASMUSSEN[4]

[1]Anthropology, SUNY Oneonta, [2]Anthropology, University of New Brunswick, [3]Brookside Dental Clinic, Fredericton, New Brunswick, [4]CHART Lab, University of Southern Denmark

Dental fillings have a long history among modern humans and have been documented from various locations beginning in the Neolithic. Filling materials have included tin, gold, lead, and amalgam, among others. The earliest use of amalgam, typically containing mercury and silver, dates to the 7th century CE in China. In 1833, amalgam was introduced to the Americas. This case study focuses on the dental treatment of one individual in 18th-19th century Atlantic Canada. The Grafton Street Methodist Burial Ground in Halifax, Nova Scotia was in use between 1793 and 1844. Skeletal remains from this cemetery were analyzed and yielded one adult (21+ years) of undetermined sex with three dental fillings, including a small gold filling on the occlusal surface of the right mandibular M1 and two large amalgam fillings on the left maxillary P3 (distal surface) and P4 (mesial surface). Radiographs of the premolars show the entire dentinal area of both teeth was replaced with amalgam, effectively killing both teeth. Additionally, the amalgam was in contact with the pulp chamber of the roots. Laser ablation ICP-MS of the amalgam confirmed major signals for ^{202}Hg and ^{107}Ag. Trace metal analysis of trabecular femoral bone from this individual yielded an exceptional high concentration of 56 μg g^{-1}. Normal levels of Hg in non-exposed individuals are below 0.30 mg g^{-1} for trabecular bone, suggesting this individual may have been poisoned due to leaching from the amalgam. Alternative explanations are also considered including ground contamination, medical treatments, and occupational exposure.

This research was funded by the Social Sciences and Humanities Research Council (Canada) Insight Development Grant (grant #101003-4201).

Eat to Move, Move to Eat: A Graphic Non-Fiction Novel

MICHELLE BEZANSON[1] and ALLISON MCNAMARA[2]

[1]Anthropology, Santa Clara University, [2]Anthropology, University of Texas, Austin

Primate positional behavior (posture and locomotion) mediates all aspects of behavior with an individual's habitat. Understanding the skeletal and physiological traits that allow variation across the primate order, provides an in-depth view of primate evolution, primate ecology, and primate diversity. Here, we present a graphic non-fiction novel for children and adults. We integrate data from our studies of positional behavior, gait, and body mass. For example, using published data on primate positional repertoires, we found that body mass alone is not a reliable predictor of primate positional repertoires even though scholars have depended on a body mass framework to test and report their results for the past 40 years. Our analysis highlighted variability both within and across clades of primates. Species that used climb as their top locomotor mode ranged in body mass from 0.89 – 170.4 kg, and species that used leap as their top locomotor mode ranged from 0.125 – 8.75 kg. Therefore, many other factors influence positional patterns. Our graphic non-fiction novel will introduce the order of primates and then focus on the role of locomotion in influencing an individual primate's day. Our novel combines illustration, lacks jargon, and provides readers with more specific information than a typical children's book.

Turn of the Tidemark: Transitional Properties at Tendon Attachment Sites

HENNA D. BHRAMDAT and DAVID J. DAEGLING

Anthropology, University of Florida

Tendinous junctions are responsible for mediating the muscle-bone interface. Our understanding of tissue complexity at the insertion site, specifically at the tidemark, is lacking. We test the material properties of tendon surrounding the tidemark to better understand its structure and influence on the soft-hard tissue junction.

We tested the material properties of *Oryctolagus* anterior patellar and supraspinatus tendons (APt, SSt). Tendon tissue and their entheseal insertions were removed and kept in calcium buffered saline. A Knoop MicroHardness Tester was used to test the tendon (1) proper, (2) directly preceding the tidemark, (3) directly behind the tidemark,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

(4) beyond the tidemark. We calculated elastic modulus from the measured hardness values and used those data to create a finite element model to assess the stress and strain fields under tension. Both tendons display unique stiffness heterogeneity, including at and beyond the tidemark; the tidemarks share similar material characteristics with their respective tendons. APt's model reveals a concentration of high magnitude stress around the tidemark and bone; high strains are observed at the tidemark and are slightly lower in the tendon proper and bone. SSt's model distributes low stress magnitudes across tendon and bone; strain is consistent throughout the tendon and significantly lower in bone.

Tendons' performance is explained by their composition: APt's *large proteoglycan-rich area* enhances effects from physiochemical mechanisms, while SSt's *short* fibrocartilaginous region *abruptly* inserts to trabecular bone. Tendon structure-function variation is governed by the nature of these physiochemical mechanisms, which are consequential for building a secure soft-hard tissue junction.

Crowd-sourcing resources and solutions to aid forensic anthropologists in identification of transgender and gender-expansive decedents

SAMANTHA H. BLATT[1], MARIYAM I. ISA[2], AMY R. MICHAEL[3] and TAYLOR FLAHERTY[4]

[1]Anthropoogy, Idaho State University, [2]Anthropology, Texas Tech University, [3]Anthropology, University of New Hampshire, [4]Anthropology, University of Nevada, Las Vegas

In response to escalating rates of fatal violence against transgender and gender-expansive (TGE) individuals, forensic anthropologists must adapt a holistic biocultural approach and develop informed, practical strategies to improve identification of TGE decedents. Such practices will narrow identification, reject biological reductionism, and reduce postmortem harm.

Using TGE case studies entered into the LGBT+ Accountability for Missing and Murdered Persons (LAMMP) database, we demonstrate the necessity for gender-inclusive approaches. LAMMP generates forensic matches using data from aggregate sources and the National Missing and Unidentified Persons System (NamUs). The majority of the 247 decedents entered into LAMMP were default-listed in NamUs as "Male." Case descriptions include vague, conflicting, and even derogatory references to gender-affirming clothing and surgeries, while many submissions use pre-transition photographs and deadnames. Binary options, language-use, and lack of resources limit investigation into TGE identity for those entering cases into NamUs.

Here, we present a living draft of a document to assist practitioners in accurately reporting observations on sex and gender, as well as recognizing and documenting potentially gendered evidence that would help contextualize sex estimations. We invite the anthropology and LGBTQ2S+ communities to evaluate, beta-test, and contribute to the development of this document and associated resources. While we caution against a checklist approach to interpreting gender due to the highly individual, personal, and diverse nature of gender identity and performance, we provide guided suggestions to document evidence that may provide additional context to sex estimates and a first step in crowd-sourcing a practical resource to include in casework.

Ancient DNA insights into America's pre-conquest pathogen landscape

KELLY E. BLEVINS[1,2], STEVIE WININGEAR[3,5] and ANNE C. STONE[2,3,4,5]

[1]Department of Archaeology, Durham University, UK, [2]Center for Bioarchaeological Research, Arizona State University, [3]School of Human Evolution & Social Change, Arizona State University, [4]Center for Evolution and Medicine, Arizona State University, [5]Institute of Human Origins, Arizona State University

What pathogens did humans bring to the Americas, and what pathogens did First Peoples encounter in their new environments? Here we discuss what genetic data reveal about the origins of pathogens and the extent to which they inform and are informed by human migration routes into the Americas. For example, the diversity of pathogens that humans brought with them was likely limited by the hunter-gatherer and nomadic lifestyles of these groups and the apparent millennia of isolation of the Indigenous American source population in Beringea. Pathogens that could be maintained in these early populations include *H. pylori*, hepatitis B virus, treponemal bacteria, and opportunistically pathogenic gut microbes. Many pre-conquest pathogens, however, were new, likely resulting from zoonotic jumps as humans exploited new ecosystems and population densities increased. Human diseases that may have been acquired from animals include leishmaniasis, coccidioidomycosis, Chagas disease, and tuberculosis. As a case study for understanding how these zoonotic infections arose and disappeared, we explore the genetic epidemiology of contemporaneous tuberculosis cases (n = 8) from a pre-conquest Mesoamerican city. Lastly, we discuss the hurdles for recovering pre-conquest pathogens. The successful recovery of pre-conquest *M. tuberculosis* lineages reflects centuries of historical records and decades of modern and paleopathological/bioarchaeological characterization, i.e. we know how to recognize and target this disease. Many pre-conquest diseases remain invisible due to the eradication of medical knowledge and likely extinction of pathogens after the social disruption and population decline associated with violence and introduction of new pathogens during and after the conquest.

We would like to acknowledge NSF funding (BCS-1945812 and BCS-2217953) to ACS and KEB and a Fulbright-García Robles Fellowship to Mexico (to KEB).

Death in the forest: Quantifying predator density in a fragmented rainforest in Costa Rica

LAURA M. BOLT[1,4], LAROY S. E. BRANDT[2,4] and AMY L. SCHREIER[3,4]

[1]Department of Anthropology, University of Toronto Mississauga, [2]Department of Biology, Lincoln Memorial University, [3]Department of Biology, Regis University, [4]Maderas Rainforest Conservancy

Primates face predation throughout their ranges. As arboreal primates, platyrrhines are particularly at risk of predation in fragmented habitat areas. In order to better understand the risks to howler (*Alouatta palliata*), capuchin (*Cebus imitator*), and spider (*Ateles geoffroyi*) monkeys in degraded landscapes in Costa Rica, we used camera traps to determine predator density in a 3 km^2 fragmented tropical rainforest. From 2017-2020, 19 camera traps (Stealth Cam G42 No-Glo Trail STC-G42NG models) were placed at regular intervals throughout La Suerte Biological Research Station (LSBRS) to document sightings of primate predators. Over 3171 recording days (mean of 167 recording days/camera), there were 40 sightings of known primate predators, including *Leopardus pardalis* (21 sightings), *Canis familiaris* (9), *Eira barbara* (4), *Herpailurus yagouaroundi* (3), *Puma concolor* (2), and *Canis latrans* (1). Predator density at LSBRS was 16 animals/km^2. This predator density is higher than in comparable forest fragments, potentially due to extensive deforestation in the broader region limiting habitat area for prey animals. LSBRS also has a very high population density of monkeys, which may lead to this fragment supporting a larger number of monkey predators than forests in other regions. Understanding the range of factors that affect monkey populations in degraded landscapes is important for informing their conservation action plans.

Evidence from refits shows displacement of *Homo naledi* materials in the Dinaledi Chamber, Rising Star Cave, South Africa

DEBRA R. BOLTER[1,2], MARINA C. ELLIOTT[3], ASHLEY KRUGER[2,4], JOHN HAWKS[2,5] and LEE R. BERGER[2]

[1]Anthropology, Modesto Junior College, [2]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand, [3]Department of Archaeology, Simon Fraser University, [4]Department of Palaeobiology, Swedish Museum of Natural History, [5]Department of Anthropology, University of Wisconsin, Madison

26927691, 2023, S7S, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

The Dinaledi Chamber has yielded *Homo naledi* remains from at least 15 individuals, dated to 335-241,000 years ago. The majority of the 1647 bones excavated during the 2013-2015 field seasons were fragmented and highly commingled. 281 specimens were located on the surface of the chamber floor, and 1366 specimens were recovered from an excavation unit measuring 0.8m^2, to a depth of 160mm. Articulated elements including a hand, a foot and two partial lower limbs recovered from the unit suggest primary depositional context, yet the commingling of fragmented elements appears more consistent with secondary deposition and disturbance. Here we present an analysis of the distribution of the rare elements across the assemblage that have been reintegrated in the lab through refits (n=41). The refits fall into three broad categories: (1) elements recovered together, even though broken (41%); (2) surface scatter refits of fragments recovered from different areas of the 3 x 5m^2 chamber floor (27%); and (3) excavation unit fragments that were refit to other elements (32%). Of the excavation unit refits, some elements were reintegrated with surface scatter specimens. These included multiple cranial elements representing an "old adult" DH3 (22%). Less common were refits of bone fragments inside the excavation unit but at different depths and/or provenience (10%). The distribution of refits provides a basis to explore the patterning of elements within the Dinaledi Chamber and to investigate the use of space.

This research was funded in part by a Ben Barres Spotlight Award from eLife.

The Role of Genetic Essentialism and Behavioral Genetic Data in Sexual Identity Construction

ALEXANDER BORSA

Sociomedical Sciences, Columbia University, GenderSci Lab, Harvard University

Genetics research increasingly incorporates data on sexual behavior. In light of high-visibility genome wide association studies (GWAS) that purport a genetic basis of same-sex sexual behavior (SSB), and even the brief creation of a "How Gay Are You?" app, it is likely that genetic theories and tests about sexuality will become increasingly accessible. To investigate the roles of genetic essentialism and population genetics research in sexual identity construction, 50 in-depth qualitative interviews were conducted with participants of diverse genders and sexualities. The interviews focused on each person's sexual history, as well as their knowledge, attitudes, and beliefs regarding genetic research. Participants were informed of recent scientific developments in behavioral genetics, and then presented with one of multiple scenarios (revealed to be hypothetical afterwards), which detailed people receiving genetic test results that conflicted with their own sexual identities. Participants were then asked for their insights about these situations as a form of intuition testing. Many people, far from being rigid in their ideas about the relationship between genetics and sexuality, have shifting beliefs that can be drawn upon for different narrative and meaning-making purposes. Even some participants who were very skeptical of genetic research on sexuality demonstrated curiosity about taking a test, and using it as a basis to explore their erotic lives–perhaps with other genders–as a type of "genetic play." These findings contribute to the AAAG/AABA symposium by showing downstream effects of genetic research on sexuality, as well as by complicating the idea of a stable sexual phenotype.

Research supported by funding from the Precision Medicine and Society program at Columbia University. Author's training supported by the NICHD (grant no. 5T32HD049339-15) and the NSF (grant no. DGE 2036197).

Applying Queer Theory to Understanding Sex as a Spectrum

FATIMAH BOUDERDABEN[1] and DEREK BOYD[2]

[1]Anthropology, Boston University, [2]Anthropology, University of Tennessee at Chattanooga

Queer perspectives have been instrumental in breaking down cis-heteronormative paradigms in academia. Queer biological anthropologists have been at the forefront of these initiatives. One of the most harmful cis-heteronormative paradigms that is prevalent in biological anthropology is the binary model of sex in modern humans. While there has been development in moving away from the binary denotation of sex, the harmful binary still affects the field today. To combat the harms of a binary denotation of sex, understanding sex as a spectrum in humans is pivotal to the progress of the field. In an osteological study of the morphology and variation of modern human pelvises, significant overlap was found in the morphology. An instance of 19% of overlap of males (n=142) with females (n=56) was found. The existence of this overlap found between sexes of a cisgender population indicates the existence of the spectrum of sex. Using a binary model for sex with this sample would have led to the misidentification of those overlap individuals. Understanding this data through the lens of Queer theory can lead to the development of a new paradigm of a spectrum of sex model. Using this model not only allows for fewer misidentifications of cis individuals but leads to a model where transgender individuals may fit in as variations of sex on the spectrum can be identified. As more and more research is conducted on the variation of sex in modern humans, more and more evidence is found in support of sex as a spectrum.

First author is funded by the National Science Foundation Graduate Research Fellowship Program.

Osteological analysis and ethical considerations of teaching skeletons in West Virginia

JAY BOW, KRISTY HENSON and ALYSSA PETTRY

Natural Sciences, Fairmont State University

Human skeletal remains have a long history of use in natural science courses. Older teaching skeletons are considered antiques and these individuals tend to be forgotten and poorly stored as instructors switch to plastic teaching models. Plastic models are robust, cheap, and less likely to have questionable origins. At these institutions skeletons stay in storage and when institutions close many of these teaching skeletons end up forsale online or at antique shows. This project has three parts, we examined our state's laws on skeletal remains, we reached out to twelve undergraduate universities to inquire about their use and storage of antique teaching skeletons, and finally we conducted collected all of the real skeletal material in our department and applied museum quality curation to the remains while determining creating osteological profiles. Results were as followed: 1) West Virginia has one state law, §29-1-8a, which prevents grave robbing. It is legal to buy and sell antique human skeletons in this state. 2) Four of these institutions still have antique teaching skeletons, two use to plastic skeletons, two still uses human skeletons, the rest are unknown. 3) The MNI for this collection is 42. Age, sex, ancestry, height, visible pathology, and potential cause of death were all analyzed. All of the individuals are adults, 4 individuals were of indeterminate sex, 7 probably male, and 7 probably female. Twelve individuals were of Asian ancestry and 2 were of Caucasian ancestry. A protocol for antique teaching skeletons needs to be established in the United States.

NASA West Virginia Space Grant Consortium, Training Grant #80NSSC20M0055, the National Science Foundation through the First2 Network, National Science Foundation INCLUDES Alliance under NSF cooperative agreements HRD-1834569, HRD-1834575, HRD-1834586, HRD-1834595, HRD-1834601

On the other hand: testing for bilateral asymmetry as a result of hand use in non-human primates

LUCYNA A. BOWLAND and LESLEY H. EASON

Anthropology, University of Arkansas

Humans display a species-wide preference for right-hand dominance across tasks (right handedness), but this pattern has not been observed at comparable levels in non-human primates. The current literature regarding hand preference within non-human primates across tasks is ambiguous. Some authors claim that certain populations of non-human primates do exhibit handedness, while others claim it is unique to humans. However, before assuming primates are an appropriate comparative baseline for

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

handedness within humans, it is important to test whether there is asymmetry among non-human primates. The *m. opponens pollicis*, located on the first metacarpal, is responsible for abduction and adduction of the thumb and is heavily recruited during high dexterity activities, meaning it should elicit asymmetrical patterns of development if non-human primates habitually engage one hand over the other. Conversely, if handedness is limited to humans, other primates should not exhibit asymmetry. Using a sample of macaques (*Macaca spp.)*, gibbons *(Hylobates lar*), and gorillas (*Gorilla spp.*) we tested for bilateral asymmetry of the opponens pollicis enthesis muscle flange. Metacarpal base and head breadth, maximum length, and radial projection of the opponens pollicis flange were measured using calipers and an ANOVA was run on the measurements to test for variance between antimeres within individuals. Additionally, elevation maps were generated using the CloudCompare v12.2 software program to further test for asymmetry within individuals. Preliminary results indicate no significant differences (p=0.05) differences for taxa within this study. Future analyses will include modern humans to see if handedness does indeed induce skeletal differences.

This work is supported by funding from the department of anthropology at the University of Arkansas.

An intersectional Bayesian analysis of respiratory mortality in industrializing England

DEREK A. BOYD

Social, Cultural, and Justice Studies, University of Tennessee-Chattanooga

Intersectionality influences respiratory health in urban areas by differentially exposing urban dwellers to health-harming hazards, such as air pollution, poor sanitation, and crowded living. Yet, how systems of power intersected with oppressive identities in urban areas to shape respiratory health in the past have yet to be fully elucidated. This study evaluated the impact of classism, sexism, and regional inequalities on respiratory mortality among urban dwellers from industrial-era England. Associations between age-at-death, biological sex, social class, region of burial, and skeletal evidence of pleural disease (rib lesions) among 508 adults (18 years +) from four skeletal samples (ca. 1700-1857) were modeled using Bayes' Theorem and interrogated *post hoc* by estimating Kaplan-Meier survival functions for each intersectional group. I hypothesized that, among individuals with rib lesions, age-at-death would be lower for those with multiple social and economic marginalizations and higher for their multiply-privileged counterparts. Results indicated that lower/working-class London females with rib lesions were more likely to die younger than any other intersectional group; however, their chances of survival were similar to their counterparts without rib lesions (30.3 vs. 31.6 years). Conversely, middle/upper-class London males with rib lesions exhibited one of the highest average ages-at-death but experienced lower survivorship compared to their counterparts without rib lesions (34.8 vs. 62.8 years). While the devaluation of women's work combined with the squalid conditions in London created health disparities that resulted in premature death among working-class women, these findings suggest that respiratory disease was primarily a concern for those buffered against these conditions.

This project was funded by the McClure Scholarship for World Affairs and the Thomas Fellowship.

Looking Forward in Forensic Anthropology: Working to Address Systemic Public Health and Mortality Disparities Across Forensic Contexts and Improve the Human Condition

DONNA C. BOYD

Forensic Science Institute, Radford University

Forensic anthropologists engaged in casework in the U. S. have long since recognized patterning in the biosocial profile of the decedents they study and the contextual circumstances surrounding their death. While DEI initiatives are commonly applied to the living, they have rarely been applied to the deceased in a forensic public health context. The "marginalized" represent the majority of a forensic anthropologist's casework, including individuals living in endemic poverty with unequal access to basic health care, medicine, and nutrition and in environments (e.g., abusive, neglectful, discriminatory) with an elevated or targeted risk of fatal injury. These deaths are complexly interwoven and correlated with systemic socioeconomic and demographic (e.g., ethnicity or ancestry, gender, age) factors. Many are patterned and predictable deaths, thus potentially preventable. Some reflect not only health and mortality structural and systemic disparities but also a violation of universal human rights.

This paper addresses the effects of systemic health and mortality inequities on the contemporary human skeleton. It encourages the recording and reporting of osteological, contextual, and skeletal health data to ultimately be used for humanitarian reduction in mortality risk and outcomes. Forensic anthropologists are in a unique position to contribute to the broader national (and global) discussion regarding the causes and possible solutions to these mortality inequities and to take a more active role in extrapolating anthropological data toward not only understanding, but improving the human condition. The logistical and ethical challenges associated with this new role in Forensic Anthropology and its broadened application are considered.

Evaluating Dental Wear Methods in Estimating Age-at-Death

CASSANDRA A. K. BOYER

Anthropology, University of Nevada, Reno

Human dental remains are one of the most prevalent and intact elements found in the archaeological record, as well as in contemporary forensic analyses of charred and cremated remains due to tooth composition of collagen and hydroxyapatite. As such, dentition plays a primary role in age-at-death estimations in a variety of research contexts, typically following eruption sequences. After third molar eruption, however, teeth are susceptible to degradation and aging adult individuals at death from dental remains becomes more difficult. Despite the prevalence of dental wear, there are few age-at-death estimation methods that incorporate the degree of tooth wear into their estimations.

Utilizing meta-analysis, this study evaluates existing dental wear assessment methods with the intent to develop an accessible and in-field macroscopic age-at-death estimation methodology that will be useful for bioarchaeological and contemporary populations. Preliminary results suggests that existing methods are limited to specific populations (i.e., prehistoric vs. contemporary; shellfish reliant vs. agricultural), are subjective with high inter- and intra-observer error, require complete and healthy dentition, and/or require examining complex variables such as pathologies, temporality, geographical region, cultural modifications, and habitual behaviors. The wide range of applications, resources, and subjectivity demonstrate a need to establish a standardized protocol that prioritizes age, as opposed to diet, when examining dental wear. This research has several implications such as providing invaluable information regarding medico-legal investigations and aiding in bioarchaeological and mass casualty events where there is a need to reassociate commingled remains.

Individual and population-level variation in 3D genome folding among bonobos (*Pan paniscus*) and chimpanzees (*Pan troglodytes*)

COLIN M. BRAND[1,2], SHUZHEN KUANG[3], ERIN N. GILBERTSON[1,4], EVONNE MCARTHUR[5], KATHERINE S. POLLARD[1,2,3,4,6], TIMOTHY H. WEBSTER[7] and JOHN A. CAPRA[1,2,4]

[1]Bakar Computational Health Sciences Institute, University of California San Francisco, [2]Department of Epidemiology and Biostatistics, University of California San Francisco, [3]Data Science and Biotechnology Institute, Gladstone Institutes, [4]Biomedical Informatics Graduate Program, University of California San Francisco, [5]Vanderbilt Genetics Institute, Vanderbilt University, [6]Chan Zuckerberg Biohub, [7]Department of Anthropology, University of Utah

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Gene expression differences underlie much of the phenotypic divergence between related species, including both species of *Pan*. However, the molecular mechanisms and genomic changes underlying expression divergence are not well understood. Gene expression is regulated by distal non-coding sequences that physically interact with gene promoters, and these interactions are mediated by the 3D structure of the genome. While variation in individual regulatory elements has been characterized across some *Pan* lineages, the role of differences in 3D genome folding to expression divergence has not been studied. Here, we apply machine learning to predict genome-wide 3D genome contact maps from DNA sequence for 56 bonobos and chimpanzees, encompassing all five extant lineages. We use a pairwise approach to estimate 3D divergence between individuals from the resulting contact maps in 4,420 1-megabase genomic windows. As expected, most individuals have very similar contact maps for most of the genome; however, we identified 87 windows with at least one pair of individuals having high 3D divergence. Maximally dissimilar maps were largely driven by single individuals with rare variants producing unique 3D genome folding in a region. We also identified 63 genomic windows where bonobo-chimpanzee comparisons were significantly diverged and used *in silico* mutagenesis to identify 3D modifying variants. We found 44 unique variants among 28 different contact domains containing 151 genes. Our results unmask individual-level 3D genome variation and identify genomic regions where changes in 3D folding may contribute to phenotypic differences in our closest living relatives.

JAC and CMB were funded by National Institutes of Health grant R35GM127087.

Dry bone and virtual modality interchangeability for the estimation of sex on the human pelvis

SANDRA BRAUN[1], NICOLE SCHWENDENER[2], FABIAN KANZ[3], SANDRA LÖSCH[1] and MARCO MILELLA[1]

[1]Department of Physical Anthropology, University of Bern, [2]Department of Forensic Medicine and Imaging, University of Bern, [3]Forensic Anthropology Unit, Medical University of Vienna

Traditional osteological methods are typically based on both visual and tactile procedures. The latter are however excluded when investigating virtual models of skeletal remains. This raises the question of the reliability of virtual anthropological data when compared with the tactile modality, an urgent topic given the steady rise of virtual methods and accumulation of imaging data in biological and forensic anthropology. Here, we address this topic and quantify the deviation between the scoring on dry bone and virtual models of sexually dimorphic features on the human pelvis. To this aim, we applied the methods of İşcan & Derrick (1984), Bruzek (2002), Klales et al. (2012) and Bruzek et al. (2017) to 200 archaeological pelves, scoring and measuring each method-specific variable on dry bone and computed tomographic (CT) models of the same individual. We compared the scores and measurements from the two sets of observations using Cohen's κ tests and relative technical error of measurement (rTEM). Results show that: 1) metric traits are more repeatable than nonmetric traits; b) dichotomous variables are more repeatable than ordinal ones; c) most nonmetric traits show overall acceptable κ values; d) one metric variable (depth of the great sciatic notch) stands out due to an rTEM well above 5%. Overall, our data suggest that traditional scoring methods can be applied interchangeably to analogous and virtual specimens without obtaining substantially different information. Imprecise trait definition, more than other factors, is the main source of error between the two modalities.

Differential adult mortality risk from late medieval to early modern Berlin: Health consequences at the intersection of urban growth and climate change

EMILY J. BRENNAN

Anthropology, University of South Carolina

After its foundation in the late medieval period (*c.* 1200-1500 CE), the city of Berlin experienced marked urban growth into the early modern period (1500-1700 CE) in the context of climatic changes associated with the Little Ice Age (LIA). Since death is the ultimate signifier of poor health, this study uses paleodemographic analysis of adult skeletal individuals to determine how the intersection of urban growth and climatic variability effected the health of males and females. This project examined 274 adult individuals excavated from Petriplatz, the churchyard of St. Peter's Church dating to *c.* 1200, in the medieval city of Cölln/Berlin, now present-day Berlin. For adult individuals (those with complete epiphyseal fusion), MorphoPASSE was used to estimate sex while ages at death were estimated using Transition Analysis. The Gompertz and Gompertz-Makeham hazards models were used to assess variability in adult mortality. Based on the Gompertz-Makeham model, the most parsimonious, estimated females were found to have an increased risk of mortality compared to estimated males, for both time periods. For both estimated females and estimated males, the risk of mortality decreased in the early modern period, compared to the late medieval period. These results suggest that living in an urban area may have benefitted the population of Berlin even in the context of the climatic variability of the LIA, as wetter summers and colder winters destroyed crops and caused fluctuating grain prices. However, these results do suggest that males benefited more than females from these urban resources.

This study was funded by the National Science Foundation (Doctoral Dissertation Research Improvement Grant), the Rust Family Foundation, and the University of South Carolina Office of the Vice President for Research.

Transmigrations: Fiber art modeling of neutrophil evolution in primates

JESSICA F. BRINKWORTH

Anthropology, University of Illinois Urbana-Champaign

Larger mammals, including humans, maintain high circulating levels of a white blood cell called a neutrophil. Short lived and highly reactive, neutrophils are key limiters of bacterial pathogens via a range of self-sacrificing activities, commonly expelling their chromatin in an antimicrobial process known as neutrophil extracellular trapping (NETing). Neutrophils are an important aspect of understanding human immune system evolution because they are energetically costly, implicated in major human chronic diseases, and intensely coevolving with important human pathogens. As such they should feature in undergraduate curricula, such as biological anthropology, that prepare students for careers in clinical sciences or evolutionary biology. However, transmitting cell strategies and evolution to an undergraduate audience with no prior immunology education comes with challenges – including unfamiliarity with jargon, preconceived notions of cell function, limited background in pathogen-host evolution and poor understanding of the interconnectedness of cell-based defenses. One way to help students engage with complex materials on biological mechanisms is to use real world tactile materials as a proxies. Here we illustrate findings from our ongoing study of neutrophil evolution, via a fiber arts installation that allows students to engage with the processes of transmigration and NETing. This interactive installation illustrates both how NETing is executed, and how it is coevolving in humans with the bacteria *Staphylococcus aureus*. By being able to replicate NETing by hand, students learn the steps of its organization as well as its vulnerabilities as a tactic. The work is currently being tested in an undergraduate course in evolutionary medicine.

Orangutan gut microbiomes across temporal changes in their dietary landscape

REBECCA S. A. BRITTAIN[1,2], ETHAN C. HARRIS[3], MARIA A. VAN NOORDWIJK[4], SRI SUCI UTAMI ATMOKO[5], TATANG MITRA SETIA[5], ASTRI ZULFA[5], PRIMA LADY[5], HAIPENG SUN[6], MARIA GLORIA

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

DOMINGUEZ-BELLO[1,2,6,7], DANIEL J. NAUMENKO[8,9] and ERIN R. VOGEL[1,2]

[1]Department of Anthropology, Rutgers, The State University of New Jersey, [2]Center for Human Evolutionary Studies, Rutgers, The State University of New Jersey, [3]Department of Anthropology, University of Wisconsin-Milwaukee, [4]Comparative Socioecology Research Group, Max Planck Institute of Animal Behavior, [5]Faculty of Biology, Universitas Nasional, [6]Department of Biochemistry and Microbiology, Rutgers, The State University of New Jersey, [7]Institute for Food, Nutrition and Health, Rutgers, The State University of New Jersey, [8]Department of Anthropology, University of Colorado Boulder, [9]Institute of Behavioral Science, University of Colorado Boulder

The challenges of meeting energetic needs are exacerbated by unpredictable and variable environments, and such challenges should shape an organism's dietary strategies and energetics. Gut microbiota (GM) are increasingly recognized as powerful drivers of host energetics. We measured changes in orangutan GM communities and inferred functions across substantial fluctuations in fruit availability over a 5-year period. While orangutans prefer fruits, when fruiting is low they consume high proportions of cambium, leaves, and pith, experience considerable reductions in caloric intake, and subsequently catabolize fat. We hypothesized that GM energy production would increase with reduced energy intake, as found in previous studies.

We collected fecal samples from 48 orangutans (*Pongo pygmaeus wurmbii*) in Central Kalimantan, Indonesia. We sequenced the 16SrRNA-V4 region and used Picrust2 to infer functional pathway abundances. We fit mixed models using Maaslin2 to test relationships between fixed effects and microbial pathways or taxa.

Results indicate a significant positive association between fatty acid synthesis pathway abundances and caloric intake (coef=0.56, FDR=7.26e-05), and a two-fold increase with every percent increase in fruit abundance (coef=0.88, FDR=3.98e-13). Genera positively associated with caloric intake included potential short-chain fatty acid producers such as *Bifidobacterium*, *Blautia*, *Eubacterium*, and *Butyricicoccus*. We also found significant positive associations between caloric intake and pathways related to obesity and energy production by the GM. These pathways included starch/sucrose (coef=0.41, FDR=1.49e-12), galactose (coef=0.14, FDR=1.2e-11), and butanoate (coef=0.40, FDR=1.02e-09) metabolism.

We suggest increased GM energy production during periods of caloric abundance may facilitate orangutan energy storage to buffer periods of reduced caloric intake.

We thank the L.S.B. Leakey Foundation, National Science Foundation, Fulbright U.S. Student Program, Rutgers University Center for Human Evolutionary Studies, and American Institute for Indonesian Studies for supporting this research.

Odontometric sexual dimorphism in a U.S. subadult sample

KRISTEN A. BROEHL[1], LOUISE K. CORRON[1], ELAINE Y. CHU[1], MARIN A. PILLOUD[1] and KYRA E. STULL[1,2]

[1]Department of Anthropology, University of Nevada, Reno, [2]Department of Anatomy, University of Pretoria, South Africa

Currently, forensic anthropologists lack robust methods for estimating sex assigned at birth from subadult remains. Dental metric variables of deciduous and permanent dentition have shown promise, but many studies suffer from lack of access to subadult collections with adequate sample sizes. This study explores odontometric variation in a modern U.S. sample of 360 subadults (ages 6 months to 20 years) from the Subadult Virtual Anthropology Database (SVAD). For deciduous and permanent teeth, four measurements (maximum mesiodistal and buccolingual crown diameters, and mesiodistal and buccolingual cervical dimensions) were collected virtually per tooth (excluding permanent third molars and the buccolingual crown of the deciduous third premolars). Data were collected on teeth showing at least initial root formation. Measurements were evaluated for variation by sex assigned at birth.

Wilcoxon tests showed significant sex differences ($p < 0.05$) for 13.2% (5/38) of deciduous and 57.1% (32/56) of permanent measurements. After a Bonferroni adjustment, 2.6% (1/38) of deciduous and 21.4% (12/56) of permanent measurements showed statistical significance. The results largely align with trends described in prior human odontometric studies: deciduous teeth show little sexual dimorphism; permanent canines and molars are the most sexually dimorphic; and buccolingual diameters are generally more dimorphic than mesiodistal dimensions. Future studies will examine whether these patterns of dental variation have predictive value for estimating components of the subadult biological profile from dental CT scans. The ability to use permanent teeth would be valuable for sex estimations of subadults as these teeth emerge throughout childhood and adolescence.

This research was funded by the NIJ 2019-DU-BX-0039 Award

Identifying ambiguous bovids from the Gladysvale Cave External Deposits and their implications for paleoenvironmental reconstruction

JULIET K. BROPHY[1,2] and GREGORY J. MATTHEWS[3]

[1]Geography and Anthropology, Louisiana State University, [2]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand, [3]Department of Mathematics and Statistics, Loyola University Chicago

Gladysvale is a hominin bearing cave site located in the Bloubank Valley in the Cradle of Humankind World Heritage Site, South Africa, approximately 13 km northeast of Sterkfontein. Previous analyses of the fossil bovids from the external, deroofed deposits (GVED) identified a group as "medium sized alcelaphines". This study uses predictive models trained on a newly published database, B.O.V.I.D., to classify the sample to their genera/species. Accuracy levels for B.O.V.I.D. are between 80-90% in cross validation and 65-75% for species level depending on the tooth type and taxa. The GVED alcelaphine sample was photographed and converted into black and white images using the freeware GIMP. The coordinates of the edges of the binarized images were acquired with matlab and used to obtain size-and-shape information. Support vector machines were trained using the B.O.V.I.D. database and the taxa of the fossil teeth were predicted. Only one tooth predicted to be *Connochaetes taurinus*, the largest of the extant South African alcelaphines. The remaining teeth classified as Alcelaphini were predicted to be *C. gnou*, *Alcelaphus buselaphus*, and *Damaliscus dorcas*. Since even these closely related bovids have very particular habitat requirements, this process helps generate a more accurate paleoenvironmental reconstruction for GVED. The identification of *D. dorcas* and *A. buselaphus* individuals suggests the paleoenvironment was likely more wooded than previously suggested.

Funding was provided by the Louisiana State University Manship Research Grant and NSF #1812065.

Variation in volume fractions of multiple skeletal elements in a diverse sample of Holocene humans

DARA N. BRUCE[1], TEA JASHASHVILI[1,2], MARK R. DOWDESWELL[3], ELISA CHENG[1], EMILY ZHU[1], KIMBERLEIGH A. TOMMY[4], SHARON KUO[5,6], LILY J. DEMARS[5], JAAP P.P. SAERS[7], JOHN R. JOHNSON[8], ADAM D. GORDON[9], JAY T. STOCK[10,7], TIMOTHY M. RYAN[5] and KRISTIAN J. CARLSON[1,11]

[1]Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [2]Department of Geology and Paleontology, Georgian National Museum, [3]School of Statistics and Actuarial Science, University of the Witwatersrand, [4]School of Anatomical Sciences, University of the Witwatersrand, [5]Department of Anthropology, Pennsylvania State University, [6]Department of Biomedical Sciences, University of Minnesota, Duluth, [7]Department of Archaeology, University of Cambridge, [8]Department of Anthropology, Santa Barbara Museum of Natural History, [9]Department of Anthropology, University at Albany, SUNY, [10]Department of Anthropology, Western University, [11]Evolutionary Studies Institute, University of the Witwatersrand

Human skeletal health and structural integrity vary due to internal (e.g., nutrition and hormones) and applied external factors. Certain bones may manifest this variation differently based on their location. For example, cervical vertebrae are presumably less influenced by musculoskeletal

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

stresses and weight-bearing loads compared to long bones, but all of these elements presumably reflect the same systemic factors in an individual. Here, we investigate variability in vertebral bone volumes of several human groups compared to those in select long bones (femora and humeri). Since cervical vertebrae experience less activity-related loading than femora and humeri, we predict their volumetric measures will not exhibit the same between-group pattern as the long bones. Additionally, we predict femora and humeri will covary to a greater extent than either will covary with the vertebrae.

Skeletal elements (n=109 individuals) from sixteen human groups spanning a broad range of lifestyles, diets, terrains, and climates were scanned by µCT. Volumes of interest (VOIs) from cervical vertebral bodies were acquired to measure trabecular bone volume fraction (BV/TV). For comparison to vertebral BV/TV, we calculated long bone diaphyseal cortical volume fraction (CV/TV). The correlation between femoral and humeral CV/TVs is statistically significant ($p<0.05$). Correlations between either long bone CV/TV and vertebral BV/TV are non-significant ($p>0.05$). Group means in all three bones show significant differences. These findings indicate that, first, vertebral BV/TVs are responsive to a different set of factors than long bone CV/TVs, and second, groups differ in all three measures possibly according to their lifestyles, diets, terrains, and/or climates.

NSF BCS-1719140, NSF BCS-1719187, DSI-NRF (South Africa), ERC under European Union's Seventh Framework Programme (FP/2007–2013)/ERC Grant Agreement n.617627, RCUK/BBSRC grant BB/R01292X/1, USC Provost grant for Nikon Metrology XTS225ST micro-CT.

Sex differences in semi-free ranging chimpanzees: Insights into evolution of chimpanzee social behavior

MARGARET A. H. BRYER[1], PAIGE BARNES[1], KRIS H. SABBI[2], JOSHUA RUKUNDO[3], ZARIN P. MACHANDA[2,4] and ALEXANDRA G. ROSATI[1,5]

[1]Psychology, University of Michigan, [2]Anthropology, Tufts University, [3]Ngamba Island Chimpanzee Sanctuary, Uganda, [4]Kibale Chimpanzee Project, Makerere Biological Field Station, Uganda, [5]Anthropology, University of Michigan

Wild female chimpanzees are generally less gregarious than males, exhibiting less affiliative behaviors as well as lower social status. This may be due to intrinsic biological differences such as differences in body size, or it may reflect contextual responses to the higher costs of feeding competition and greater reproductive constraints female chimpanzees often face. Here we examine patterns of social behavior in semi-free ranging chimpanzees (*Pan troglodytes*) living in an African sanctuary to test these hypotheses; as these chimpanzees are provisioned and are on birth control, feeding constraints and female reproductive effort are ameliorated in this environment. Using a year of observational data comprising 3,356 ten-minute focal follows of 45 adult chimpanzees (17 males, 28 females), we investigated sex differences in grooming, aggression, and social status. Unlike in wild chimpanzees, males and females showed similar rates of grooming ($x^2(1)=0.85$, $p=0.36$). We found that males engaged in aggressive behavior more than females, whether we looked at displays ($x^2(1)=43.26$, $p<0.001$) or targeted aggression ($x^2(1)=27.08$, $p<0.001$). Despite the lower rates of aggression exhibited by females compared to males, we did not find a significant sex difference in proportion of aggression consisting of coalitions and protections ($x^2(1)=0.21$, $p=0.10$). Finally, patterns of dominance show that some adult females outrank some adult males. Overall, our findings suggest that some sex differences in wild chimpanzee social behavior may reflect a contextual response to feeding competition or infant care, rather than intrinsic differences, and contribute to our understanding of intraspecific variation in ape behavior.

This work was supported by National Science Foundation grants #1926653 to AGR and #1926737 to ZPM.

Factors influencing cranial variation among prehistoric Japanese forager populations

LAURA T. BUCK[1], LUMILA P. MENENDEZ[2,3], ISABELLE DE GROOTE[4], BRENNA R. HASSETT[5], HIROFUMI MATSUMURA[6] and JAY T. STOCK[7]

[1]School of Biological and Environmental Sciences, Liverpool John Moores University, [2]Department of Anthropology of the Americas, University of Bonn, Bonn, Germany, [3]Department of Evolutionary Biology, University of Vienna, Vienna, Austria, [4]Department of Archaeology, Ghent University, Ghent, Belgium, [5]Institute of Archaeology, University College London, London, UK, [6]School of Health Science, Sapporo Medical University, Sapporo, Japan, [7]Department of Anthropology, Western University, London, Ontario, Canada

Climate, diet, and population history are all well-established influences on cranial morphology, yet their effects are rarely compared within a single, variable population, limiting interpretations of their relative contribution. Jomon prehistoric foragers inhabited the Japanese Archipelago throughout its considerable climatic range and developed correspondingly varied subsistence practices. We previously demonstrated that a large group of Jomon crania exhibited no clear climatic pattern and here we subsequently evaluate the potential influences of population history and dietary variation in the same individuals. Following previous archaeologically-based schemes, we divide the Jomon crania into dietary groups and infer population history from geographic distance. We use 3D geometric morphometric methods to analyse correlates of cranial shape / size. There is evidence for diet-related influences on the shape of the neurocranium and, most markedly, of the temporalis region. These shape differences are congruent with regional dietary variation, but experimental biomechanical and nutritional evidence is needed to better support this link. Craniofacial size potentially shows the influence of population history, which is not evident in analyses of cranial shape. This intra-Jomon result contrasts with human cranial variation globally, where stochastic processes are the strongest influence on cranial shape and ecological factors influence cranial size. The determinants of Jomon cranial morphology are complex and dietary adaptation is likely mediated by factors including sex, social status, and chronology. These results contribute to our understanding of the complexity of selective pressures shaping human phenotypes on different geographic scales and of biological versus behavioural adaptive strategies during human evolutionary history.

The research underpinning this work was funded by a European Research Council grant (PI: J. Stock) under the European Union's Seventh Framework Programme (FP/2007-13)/ERC Grant Agreement n. 617627.

The ontogeny of sexual size monomorphism in Verreaux's sifaka (*Propithecus verreauxi*)

GABRIELLE L. BUENO and REBECCA J. LEWIS

Anthropology, The University of Texas at Austin

Sexual size dimorphism, exhibited by many primates, can develop through variation in growth rate, growth duration, or a combination of the two. Adult Verreaux's sifaka (*Propithecus verreauxi*) exhibit sexual size monomorphism, but whether the sexes experience the same developmental trajectory to reach this same adult body size is unknown. We used generalized additive mixed models to examine the growth rate and duration of 14 morphometric variables collected from a population of wild Verreaux's sifaka at Kirindy Mitea National Park in Madagascar between 2006 and 2019 (n=211 captures). Terminal adult weight was reached at age six for both sexes, later than other populations. Females exhibited longer growth duration in body, hindlimb, thigh, and forelimb lengths, and faster growth rates in hindlimb and forelimb lengths. Males exhibited longer growth duration in thigh and bicep circumferences, and faster growth rates in bicep circumference. Males reach terminal skeletal length earlier, but terminal musculature later, than females. Adult females had significantly longer hindlimb length than males, while adult males had significantly larger thigh circumference, bicep circumference, and a higher intermembral index. Because most of the intersexual differences appeared in adulthood, they may be associated with sex differences in infant carrying and intrasexual competition: as vertical clingers and leapers, adult female sifaka may need longer legs to compensate for dorsal infant carrying, while adult males may benefit

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

from larger thigh and bicep muscles in male-male contest competition over mates. These results demonstrate that the path to adulthood can vary greatly depending on sex and life history.

Elevated fecal glucocorticoid metabolite concentrations in juvenile rhesus macaques (*Macaca mulatta*) with strong peer social bonds

KATHARINE BURKE[1], MICHAEL HEISTERMANN[2], JAMES HIGHAM[3] and CAROL M. BERMAN[4]

[1]Anthropology, University at Buffalo, [2]Endocrinology Laboratory, German Primate Center, Leibniz Institute for Primate Research, [3]Anthropology, New York University, [4]Anthropology, University at Buffalo

Social bonds have been linked with lower GC concentrations and fitness related benefits in adult human and nonhuman primates. However, research on possible links between social bonds and physiological processes in juvenile primates is lacking. To address this gap, we examined relationships between the mean strength and number of social bonds with same-sex peers and mean concentrations of fecal glucocorticoid metabolites (fGCMs) in free-ranging juvenile rhesus monkeys (*Macaca mulatta*). We collected behavioral data and fecal samples on 44 juvenile monkeys on Cayo Santiago, Puerto Rico, and used composite sociality indices (CSIs) to measure the strength of dyadic affiliative social bonds between each juvenile and each of its same-sex peers. Furthermore, we tested whether physical activity and aggression rates were related to fGCM concentrations, social bond strength and numbers of strong and weak social bonds. Although we found no significant relationship between total numbers of affiliative peer bonds and fGCM concentrations, juveniles with relatively more strong relationships and high mean CSI scores displayed relatively high fGCM concentrations. However, fGCM concentrations were unassociated with physical activity or aggressive behavior. Thus hypothalamic-pituitary-adrenocortical (HPA) axis regulation in juveniles appears to differ from that of adults; unlike adults, many strong social bonds do not appear to moderate GC concentrations in juveniles. Instead, strong bonds appear to be associated with rises in metabolic demand that are unrelated to increases in physical activity or aggressive behavior. We speculate that the navigation of social bonds at this stage of life may involve increased metabolic demand.

This work was supported by the Leakey Foundation [#74929], the Nacey Maggioncalda Foundation [#415939], the Animal Behavior Society [Student Research grant], and the Mark Diamond Research Fund [SP-15-02].

Strepsirrhine gum-feeders have short skulls: searching for the evolutionary morphology of gummivory

ANNE M. BURROWS[1,2], CHRIS LAW[3], SERGI LOPEZ-TORRES[4,5,6], KEEGAN R. SELILG[7] and MARY T. SILCOX[8]

[1]Physical Therapy, Duquesne University, [2]Anthropology, University of Pittsburgh, [3]Integrative Biology, University of Texas at Austin, [4]Biology, University of Warsaw, [5]Paleontology, American Museum of Natural History, [6]NYCEP, New York Consortium in Evolutionary Primatology, [7]Evolutionary Anthropology, Duke University, [8]Anthropology, University of Toronto Scarborough

Most obligate gummivores are strepsirrhines that include gums as the majority of their year-round diet. Gummivory may have been an important adaptation of early primates, so understanding the craniodental signatures of extant gummivory is advantageous. Although previous work has shown that lorisoid, but not lemuroid, gummivores have robust toothcombs and small molars, whether gummivory also influences the evolution of the overall skull remains to be tested. Here we test the prediction that primate gum-feeding is associated with shorter heads in strepsirrhine gummivores. We also included the aye-aye (*Daubentonia madagascariensis*) because it gouges bark, even though they do not consume gums, because the demands on the anterior teeth are likely to be similar. We used sliding, digital calipers to take select craniodental traits from 494 specimens across 26 lemuroid and lorisoid species: obligate gummivores (158), facultative gummivores, (161) and non-gummivores (175). Because body sizes vary tremendously among strepsirrhines, we scaled all measurements by the geometric mean of each specimen, then tested differences in scaled means using one-way ANOVAs ($p<0.05$). Preliminary results show that obligate gummivorres/gougers have significantly shorter heads but there were no significant differences in palatal length or dentary length. Coupled with the lack of shared dental signatures for gummivory between lemuroids and lorisoids, preliminary results suggest that gummivory may have developed independently between lemuroids and lorisoids with differing selective pressures. As such, gummivory in lemuroids may be a relatively recent event.

New Tricks, Old Bones: Reassessing Assigned Sex at Birth Estimations of the Erie County Poorhouse Cemetery using MorphoPASSE

JENNIFER F. BYRNES, SILVIO E. MIRABAL TORRES, LIAM J. JOHNSON, SAMOURA L. HORSLEY, TAYLOR M. FLAHERTY and DAYANIRA LOPEZ

Anthropology, University of Nevada, Las Vegas

Bioarchaeologists and forensic anthropologists commonly use analysis of human skeletal traits to estimate Assigned Sex at Birth (ASAB). Traditional methods used to estimate ASAB relied on gross qualitative assessment, but advancements in statistical modeling offer a quantitative alternative with built-in accuracy rates. This study aimed to explore the viability of applying new methods to reassess ASAB of the reburied remains from the Erie County Poorhouse Cemetery using archival skeletal data. Using MorphoPASSE 1.0, we produced new estimations using: 1) all scorable traits (n=209) and 2) cranial traits only (excluding mental eminence) (n=245). Accuracy thresholds of 0.85, 0.65, and <0.65 were used to code for female/male, probable female/male, and unknown, respectively. Using Cohen's kappa, MorphoPASSE estimates substantially agreed with the previous ASAB estimations when all scorable traits were included (K=0.61) and tended to deviate towards more masculine scores. In contrast, when the pelvis and mental eminence were excluded, these new estimates fairly agreed with original ASAB estimations (K=0.34) and tended to deviate towards more feminine scores. Fewer individuals were reassessed as unknown ASAB compared to the original estimates, which could be a limitation of MorphoPASSE or our chosen accuracy thresholds. Other limitations include the imperfect translation of scores using old methods to align with new trait descriptions and scores. Some individuals' original ASAB also changed dramatically, which potentially highlights the original observers' inexperience and the benefit of gestalt evaluation.

Evaluating Entheseal Changes and Pathological Conditions in Bronze Age Arabia using the Patella

JANETH CABAÑAS[1], ANGELIQUE LINDBERG[2], LESLEY A. GREGORICKA[3] and JAIME ULLINGER[4]

[1]Anthropology, University of California Berkeley, [2]Anthropology, Boston University, [3]Sociology, Anthropology, and Social Work, University of South Alabama, [4]Sociology and Anthropology, Quinnipiac University

Umm an-Nar (ca. 2700-2000 BCE) tombs Unar 1 and Unar 2 (Emirate of Ras al-Khaimah, United Arab Emirates) contain cremated, commingled, and fragmentary skeletons. Intensification of oasis agriculture in this period led to several hypotheses: (1) a difference in the prevalence of entheseal changes (EC) and vastus notches over time, (2) association between these indicators, and (3) no bilateral asymmetry. Patellar entheses were evaluated for proliferative enthesophytes and osteolytic enthesopathy. Osteoarthritis (OA) was evaluated by degree of lipping, porosity, and eburnation. The presence of a vastus notch was also recorded.

Statistical analyses revealed no difference in EC ($x2=0.1$, $p=0.48$) or vastus notch presence ($x2=0.4$, $p=0.53$) between the tombs, and no bilateral asymmetry ($p>0.05$). A difference in OA prevalence on right patellae compared to the left

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

was observed in both tombs (x2=6.15, p=0.013). OA and EC were associated in Unar 1 (OR=3.3, p=0.0004), specifically for right patellae (OR=5.03, p=0.001). Unar 2 patellae with vastus notches were more likely to have EC on the left (OR= 2.4, p=0.007) and right sides (OR=2.8, p=0.001), while the same association was seen on only left patellae in Unar 1 (OR=2.7, p=0.03). Similarities in EC presence suggest participation in strenuous activity using both knees in both tombs. The greater frequency of OA in Unar 2 suggests more intensive agricultural activity, or that individuals interred within this tomb reached older ages-at-death. Vastus notch and EC association in both tombs may be due to stress, or similar kin group activity.

This research was funded by a National Science Foundation Research Experiences for Undergraduates Award (#1852426).

Sources of Variation in the Semi-Circular canals in Old World Primates

CAI CACCAVARI[1], BRIAN A. KEELING[1] and ROLF QUAM[1,2,3,4]

[1]Department of Anthropology, Binghamton University (SUNY), [2]Centro de Investigación UCM-ISCIII sobre la Evolución y Comportamiento Humanos, UCM-ISCIII, [3]Division of Anthropology, American Museum of Natural History, [4]Cátedra de Otoacústica Evolutiva y Paleoantropología (HM Hospitales-Universidad de Alcalá), Área de Antropología Física, Departamento de Ciencias de la Vida, Universidad de Alcalá

The primate bony labyrinth has been the focus of much research in biological anthropology. Variation in the inner ear anatomy of primates has been argued to be related to body mass as well as to differences in auditory function (cochlea) and locomotion (semi-circular canals) across taxa. We carried out a linear morphometric study on a taxonomically diverse (*n*=19) sample of Old World Monkeys and small-bodied apes to examine these sources of variation in the primate bony labyrinth. We found the geometric mean of canal dimensions to be positively correlated with body mass in both males (r=0.62) and females (r=0.51). To examine potential correlations of the bony labyrinth with locomotor behavior and habitat preference, we performed a series of ANOVA tests for the canal dimensions and locomotor (arboreal quadrupedal, terrestrial quadrupedal, and suspensory) and habitat (arboreal or terrestrial) categories. ANOVA results demonstrated a significantly larger relative anterior canal size (p<0.01) and a significantly smaller relative lateral canal size (p=0.03) in suspensory taxa compared with arboreal and terrestrial quadrupedal taxa, but no significant differences in any of the variables between habitat types. Principal component analysis of the bony labyrinth variables revealed no clear separation between specimens grouped by either locomotor or habitat type. These results confirm suggestions made in previous studies that variation in the primate bony labyrinth does not seem to be influenced by habitat type, but is influenced by both body mass and locomotor behavior.

Binghamton University (SUNY)

Living at the Intersections at Lisht

ALYSON C. CAINE

Anthropology and Heritage Studies, University of California, Merced

Egyptian archaeological research has emphasized elites over non-elites because of the plethora of material made for and by elites, which characterize the archaeological record from ancient Egypt. The site of Lisht was first excavated in 1906 and has yielded individuals of both elite and non-elite status. Although issues persist with this legacy collection because of excavation priorities and curation practices, the skeletal remains present an opportunity to explore variable experiences at Lisht. Recontextualization of archival documents and skeletal remains has resulted in 103 of 594 tombs connected to skeletal remains.

Osteological analysis of individuals associated with specific tombs from Lisht, comprise 167 individuals and 67 tombs. Females represent seventy-seven individuals, while males represent thirty-two individuals. Thirty-five individuals were of ambiguous sex and could represent a larger share of males as the population from Lisht was gracile. Non-adults represent eighteen individuals from these tombs and range from one to twenty years old at the time of death. Of the 67 tombs studied, the type of burial is evenly distributed with thirty-four shaft tombs, with single or multi-chamber burials, and thirty-three surface burials. Half of the non-adults represent surface burials, but these individuals were buried in coffins or cloth wrapping and represent 30% of individuals associated with coffins or wrapping in their burials. While there are differences between males and females and adults and non-adults, these differences are not significant. This suggests that age and sex were not determining factors for the type of burial or presence of a coffin at Lisht.

This project was funded by the Institute for Bioarchaeology Grant from the Department of Egypt and Sudan at the British Museum, London, UK.

The mechanical contribution of trabecular bone in the MC3 head during knuckle-walking

GRACE V. CALHOUN[1], HENNA D. BHRAMDAT[1] and ANNA J. RAGNI[2]

[1]Anthropology, University of Florida, [2]Institute of Human Origins, Arizona State University

Trabecular architecture is hypothesized to correspond to specific loading environments and is therefore potentially useful for reconstructing fossil locomotor behavior. Past studies have operated under the assumption that trabecular architecture preferentially aligns to the direction of loading. In this study, an idealized 2D finite element analysis (FEA) was used to test this assumption by investigating the effects of variation in trabecular anisotropy and orientation on shear strain within the third metacarpal (MC3) head of knuckle-walking apes. Trabecular anisotropy was modeled using heterogeneous material properties within a continuum model of the MC3 head. In addition, trabecular architecture was measured in four *Pan troglodytes* and four *Gorilla gorilla* MC3 heads. Under the assumption outlined above, we expected trabeculae in actual MC3 heads to be aligned with the assumed dorsodistal to proximopalmar direction of loading incurred during knuckle-walking, and that this trabecular arrangement would produce reduced shear strains compared to other anisotropies tested in FEA. In contrast, trabecular fabric aligned with the direction of loading produced the highest shear strains of all models tested. Shear strain decreased at this orientation with increasing anisotropy; however, other orientations produced similar or lower shear strains. Moreover, trabeculae in actual ape MC3 heads had low anisotropy and were oriented ~70º palmar to the assumed direction of loading. These results suggest that trabecular morphologies assumed to be mechanically beneficial are suboptimal, and that the interaction between trabecular anisotropy, orientation and loading governs shear strain in complex, nonlinear ways. Purely functionalist interpretations of trabecular architecture are likely incomplete.

Investigating bone length and intralimb proportion inheritance in healthy, growing twins from England

MICHELLE E. CAMERON[1], SARAH-LOUISE DECRAUSAZ[2], CARA WALL-SCHEFFLER[3], HELEN KURKI[2], JAY T. STOCK[4], JANE E. WILLIAMS[5], MARY S. FEWTRELL[5] and JONATHAN CK. WELLS[5]

[1]Department of Anthropology, University of Toronto, [2]Department of Anthropology, University of Victoria, [3]Biology Department, Seattle Pacific University, [4]Department of Anthropology, Western University, [5]Childhood Nutrition Research Centre, Population, Policy, and Practice Research and Teaching Department, University College London Great Ormond Street Institute of Child Health

Human growth trajectories can be predicted from observations of clinical child and adolescent growth studies and represent a balance between genetic and environmental influences. Body sizes and intralimb indices, or the ratio between proximal and distal limb segments, may have high heritability, but are also plastic in response to environmental stresses. Here, we examine the relationships of long bone lengths and intralimb indices within 65 twin pairs (n=130; m=78, f=52) from England between 6-19 years of age included in a contemporary cross-sectional growth study. Dual-energy x-ray absorptiometry (DXA) scans

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

were collected for each participant. Long bone lengths, including maximum humerus, ulna, femur, and tibia lengths, were collected from DXA scans. Brachial and crural indices were calculated to represent upper and lower intralimb indices respectively. All variables were converted to age- and sex-specific standard deviation scores relative to a UK reference sample. Skeletal traits were compared within 27 monozygotic (MZ) and 38 dizygotic (DZ) twin pairs using correlation analyses and paired samples t-tests. These preliminary analyses provide information on how genetic and environmental factors interact to affect skeletal growth.

Long bone lengths are highly correlated between MZ (r=0.90-0.94) and DZ (r=0.47-0.59) twin pairs, indicating genetic or shared environmental contributions to long bone lengths. Higher MZ twin correlations indicate potentially stronger genetic influences on long bone lengths. Lower MZ (r=0.69-0.70) and DZ (r=0.19-0.36) twin pair correlations for intralimb indices suggest stronger environmental influences on intralimb indices. Further analyses will clarify genetic and environmental contributions to skeletal development.

This research was supported by the Connaught Fund of the University of Toronto and the Natural Sciences and Engineering Research Council of Canada (RGPIN 2019-04048).

Visual comparisons for personal identification in forensic anthropology: a scoping review

JESSICA L. CAMPBELL, PATRICIA R. AVENT, ALEXIS L. VANBAARLE and LAUREN N. BUTARIC

Department of Anatomy, Des Moines University

Forensic anthropology often uses visual comparison to support personal identification; however, there exists no standard guidance for implementation. The purpose of this scoping review is to identify the range of methods and practices for visual comparison when establishing personal identification of skeletal remains. We investigate type of 1) imaging modalities, 2) skeletal elements, and 3) methodological strategies for completing visual comparisons. Relevant literature (n=68) was identified from five databases using PRISMA 2020 updated guidelines for systematic reviews. Two observers collected data to minimize observer error; data were then compared and consolidated. Disagreements were resolved by re-evaluation of the publication. Publications included case studies (n=31) and experimental research (n=36). Radiographs alone were more common (76.9%) than computed tomography (CT) or multiple modalities, though CT imaging has been increasing since 2012. The skull is most frequently used (41.5%) and several publications included elements from multiple regions. The highest frequency mapping specific features included anomalies, sinuses, and degenerative processes (combined, 80.2%), with trabeculae the next most frequent (8.6%). Experimental studies most frequently used 2-3 observers (40.0%); though survey-type studies used up to 106 participants. A secondary method to the visual comparison was used in 58.8% of experimental and 16.7% of case studies, and 41.9% of experimental studies provided a non-match option. There was no agreement for a recommendation of points/items of concordance. Overall, there was wide variety in how visual comparisons were completed. These results will help to inform research design into the use of visual comparisons for personal identification.

This project was supported by the National Institute of Justice (Award No. 2020-75-CX-0013).

Distribution and chronostratigraphy of *Australopithecus afarensis* specimens from Hadar, Ethiopia

CHRISTOPHER J. CAMPISANO[1,2] and ALAN L. DEINO[3]

[1]Institute of Human Origins, Arizona State University, [2]School of Human Evolution and Social Change, Arizona State University, [3]BGC, Berkeley Geochronology Center

The paleoanthropological site of Hadar, Ethiopia preserves a rich record of Pliocene hominins encompassing 556 specimens from 112 localities. These finds represent ~150 individuals, almost all of which are assigned to *Australopithecus afarensis*. This prolific site preserves ~90% of the entire *A. afarensis* record, yet all the Hadar occurrences are found within a relatively small ~85 km^2 area spanning just 0.5 Myr. New $^{40}Ar/^{39}Ar$ dating at Hadar confirms or slightly revises ages for the KHT, TT-4, and BKT-2 volcanic marker beds, and provides new ages for BKT-1 (~3.1 Ma) and some of the oldest Busidima Formation tuffs at Hadar (~2.5 Ma). Combined with previously derived ages, we provide a refined summary for the chronostratigraphic distribution of all Hadar *A. afarensis* specimens. The number of hominin-bearing localities, as well as the relative proportion of hominins, are highest in the oldest (SH-1) and youngest (KH-2) Hadar Formation submembers, indicating the absence of any temporal trend in *A. afarensis* distribution through time. The majority of hominin specimens are represented by postcranial elements (58%) followed by isolated dental remains (18%). Cranial (6%), mandibular (13%), maxillary (5%) specimens (with and without associated dentition) comprise the remaining 24%. In terms of discovery, the majority of hominin specimens were collected in the 1970s, followed by the 1990s, but are highly skewed by specimen rich localities such as A.L. 288, A.L. 333, and A.L. 444.

Postural behaviors in response to substrates and food size in non-housed bearded capuchin monkeys (*Sapajus libidinosus*) and ring-tailed lemurs (*Lemur catta*)

STEPHANIE L. CANINGTON[1], JANINE CHALK-WILAYTO[2], KRISTIN A. WRIGHT[3] and MYRA F. LAIRD[4,5]

[1]Center for Functional Anatomy & Evolution, Johns Hopkins University School of Medicine, [2]Department of Biomedical Sciences, Mercer University School of Medicine, [3]Department of Biomedical Sciences, University of Missouri Kansas City School of Medicine, [4]Department of Integrative Anatomical Sciences, University of Southern California, [5]Department of Basic and Translational Sciences, University of Pennsylvania

Postural behaviors displayed during feeding are thought to reflect anatomical constraints, substrate stability, and food properties. We compared the roles of substrate (arboreal/terrestrial), substrate size (if arboreal: small, medium, large), and food size (small, medium, large) on postural behaviors during feeding in tufted capuchins (*Sapajus libidinosus*; N=15; Fazenda Boa Vista, Piauí, Brazil) and ring-tailed lemurs (*Lemur catta*; N=16; St. Catherines Island, GA and Duke Lemur Center, NC). We predict that: **P1**, the more terrestrial *L. catta* employs more seated/crouched postures that promote stability during feeding on small substrates compared to the more arboreal *S. libidinosus* and **P2**, terrestrial-feeding sequences from size-matched foods yield similar postural behaviors for both species.

Focal animals were filmed continuously throughout feeding events, resulting in 3,125 observations that were scored for postural behaviors (N=15), substrate type, size, and food size. Lemurs had significantly greater postural variation on medium-sized arboreal substrates (n=10 postures), whereas capuchins had greater postural variation on small-sized arboreal substrates (n=7). On the ground, lemurs used a greater number of postures when feeding on small (n=7), medium (n=8), and large foods (n=7) compared to capuchins (n=5;6;3), and lemurs used sitting postures for all food sizes whereas capuchins favored them for small and medium foods. **P1** is unsupported, with capuchins demonstrating a greater range of seated/crouched postures on small substrates whereas lemurs used more non-seated postures. **P2** is partially supported for small and medium (but not large) foods. These results suggest the impact of food size on feeding postural behaviors is likely taxon- and food-specific.

St. Catherines Island Scientific Research and Advisory Committee, National Science Foundation (NSF-BCS-1440516, NSF-BCS-1440541, NSF-BCS 1440542, NSF-BCS-1440545, NSF-BCS-1627206), Zumberge Award-Office of Provost at USC, and São Paulo Research Foundation (FAPESP 14/13237-1).

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Social status and cognitive control in chimpanzees

AVERILL CANTWELL[1], PAIGE BARNES[1], KRIS SABBI[2], ZARIN MACHANDA[2] and ALEXANDRA G. ROSATI[1,3]

[1]Psychology, University of Michigan, [2]Anthropology, Tufts University, [3]Anthropology, University of Michigan

Dominance status can have a profound effect on animals' lives, impacting the social and ecological problems that individuals face. Dominance may therefore be related to cognitive performance, either because individuals with particular traits are more likely to ascend in rank, or because dominance shapes an individual's optimal responses. Yet the direction of this relationship is unclear. On one hand, high-ranking individuals may exhibit more flexible, 'intelligent' behavior because this is needed to strategically acquire and maintain rank. On the other, low-ranking individuals may need to employ flexible strategies to deal with the constraints imposed by their social status. We conduct behavioral observations and cognitive experiments with semi-free-ranging chimpanzees (Pan troglodytes) living in an African sanctuary to investigate relationships between rank and cognitive control, a suite of traits that enable flexible, goal-oriented behavior. We tested 42 adult chimpanzees on three cognitive control tasks, and extracted dominance information from one year of behavioral observations on interactions in their social group. We find that high-ranking individuals of both sexes show better performance in a reversal learning task assessing cognitive flexibility ($x^2(2)=35.93$, $p<0.01$), and high- and middle-ranking individuals outperform low-ranking individuals in a working memory task ($x^2(2)=9.76$, $p<0.01$), There was no impact of rank on inhibitory control performance ($x^2(2)=1.01$, $p=0.60$). These results indicate that high-ranking individuals may exhibit more robust abilities in some measures of cognitive control. In contrast, low rank was not associated with higher performance in any measure. We discuss these results in terms of the evolution of flexible behavior.

Leakey Foundation Research Grant to AC; NSF #1926653 to AR; NSF #1926737 to ZM

Strontium isotopes reveal mobility dynamics in the Middle Iron Age mixed-funerary ritual necropolis of Piovego, Padua, Northeastern Italy

GIUSY CAPASSO[1], FEDERICO LUGLI[2], MICHAEL ALLEN BECK DE LOTTO[3], LUCA BONDIOLI[1], MICHELE CUPITÒ[1] and MASSIMO VIDALE[1]

[1]Department of Cultural Heritage, University of Padua, Italy, [2]Department of Cultural Heritage, University of Bologna, Italy, [3]Department of Cardiac, Thoracic, Vascular Sciences, and Public Health, University of Padua, Italy

The Piovego necropolis, Padua (VI-IV century BCE) yielded 132 cremations, 25 inhumations including the grave of a man with a horse, and 6 horse burials. To explain this funerary inhomogeneity, it was hypothesized that the inhumed individuals may have been foreigners or belonged to a lower rank, as suggested by the poverty of grave goods and by cases of violent deaths. Moreover, a Celtic inscribed tombstone suggests the presence of foreign individuals. To highlight possible relationships between funerary inhomogeneity and mobility dynamics, we performed a strontium isotope analysis of dental enamel of the first permanent molars for the inhumed individuals (n=19) and of petrous bones for the cremated ones (n=40). $^{87}Sr/^{86}Sr$ ratios were determined through solution MC-ICPMS analyses. Due to the location of the necropolis in an urbanized area, we relied on the Italian Sr isoscape and the shape of the human sample distribution to identify outliers (i.e. possible non-local individuals). Based on Tukey's outlier detecting method, the local baseline likely ranges between 0.7087 and 0.7103. This range matches the isoscape values' distribution within a ~10 km radius from the site. Eight individuals fall outside this baseline, with the percentage of non-locals among the inhumed (n= 5, 26%) nearly quadrupling if compared to the cremated (n=3, 7.5%).The composition of grave goods of some of the outliers seems to indicate contact with the Alpine area. The isotopic signatures of the most radiogenic outliers, compatible with Alpine isotope values based on the Sr isoscape of Italy, seem to support this hypothesis.

Morphological variation in strepsirrhine nails

GABRIELLA K. CARD[1] and STEPHANIE A. MAIOLINO[2]

[1]Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, [2]Department of Anatomical Sciences, Renaissance School of Medicine at Stony Brook University

Wide, flat nails are thought to be related to the evolution of grasping in primates. However, nail shape appears to be highly variable, especially among strepsirrhines. It is possible that different shapes have different significance. For example, at least two strepsirrhine groups are known to possess keeled nails (nails that end in a sharp point and have a prominent ridge running down their midline) which have been described to play a role in vertical clinging. We conducted a study to describe the diversity of nail shapes among extant strepsirrhines and to investigate possible relationships among nail morphology, body size, positional behavior, and phylogeny. Manual nails from the skins of 83 strepsirrhines, representing 24 species and 20 genera of varying body sizes and positional behaviors were sampled. Based on observed diversity, we were able to define five qualitative nail shape categories. We also quantified nail shape using an outline-based morphometric approach. TpsDig2 was used to take 100 equidistant x-y coordinates of the dorsal outline shape from digital photographs. Elliptic Fourier analysis was conducted in R using Momocs and the resulting data were summarized using principal component analysis. The results of this study indicate that nail shape does not significantly vary among positional behavior groups and body size does not significantly vary among nail shape categories. Phylogenetic signal was found to be significantly low. While additional work is needed to understand the functional significance of nail shape variation, our results suggest that primate nails should not be treated as a homogenous character.

This material is based upon work supported by the National Science Foundation under Grant no. BCS-1341075 (SAM) and The Leakey Foundation (SAM).

Nasal trauma during the Jersey Bluff Phase of the Lower Illinois River Valley

MEGAN E. CAREY and ARION T. MAYES

Anthropology, San Diego State University

While the Middle Woodland (ca. 50 BCE – 400 CE) and Mississippian (ca. 1050 – 1300 CE) periods of the Lower Illinois River Valley have been much studied, the transitional Late Woodland (ca. 400 – 1050 CE) period, which featured major societal disruptions, such as the intensification of maize agriculture, has been relatively neglected. An analysis of an assemblage of crania from the Late-Late Woodland (ca. 800 – 1050 CE) Jersey Bluff site demonstrates an interesting phenomenon. An examination of archival materials, including photographic slides and x-rays, reveals a high prevalence of midfacial trauma. In a subsample (n=76) in which all nasal bones and maxillary frontal processes are present and observable, 34 (44.7%) exhibit marked antemortem nasal trauma, including fractures and dislocations. This sample includes 39 male/probable male and 32 female/probable female estimated individuals, as well as five individuals of indeterminant sex. Of these, 21 male individuals (53.8%) and 13 female individuals (40.6%) have observable trauma (OR=1.7; P=.269), as well as one individual of indeterminant sex. Most cases of trauma are mild, with 21 (61%) of the trauma cases ranking only a 1 on a 1-3 severity scale. Additionally, 14 (41.2%) injuries are estimated to be the result of an anterior-posterior direction of force. These patterns present an interesting issue. Two possible causes are considered. The first is widespread occupational injury with a lack of gender differentiation in labor roles. The second is a socially sanctioned system of violence, such as a system of conflict resolution.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Applied Expertise in Human Osteology: Legal Considerations in the United States

MELINDA L. CARTER, MD, PHD[1], RYAN M. SEIDEMANN, JD, PHD[2], JUSTINE L. NEWMAN, BS, JD[3] and EDWARD A. REEDY, PHD, MD[4]

[1]Biomedical Sciences, Edward Via College of Osteopathic Medicine, Auburn Campus, [2]Justice, Southern University Law Center, [3]Pre-Clinical, Southern Illinois University School of Medicine, [4]Montgomery Medical Examiners' Office, Alabama Department of Forensic Sciences

Anecdotal evidence suggests that many coroners, medical examiners, and justices of the peace rely on pathologists to examine skeletal cases as required by state law. However, residency and fellowship training in forensic pathology rarely include osteology, especially following the advanced standardized practices advocated by the American Board of Forensic Anthropology. Pathologists are legally responsible for conducting autopsies on human remains and, therefore, must be licensed by the states in which they practice and should be board-certified in forensic pathology. We address the disproportionate number of states in the U.S. that have passed laws to protect skeletal remains, by requiring and defining expertise, in archaeological but not in medicolegal contexts. Using a quantitative and qualitative analysis of the reception of purported forensic anthropology (FA) experts in U.S. courts over recent years, we assess the need for uniform standards nationwide and whether the judicial system is aware of this need. Based on these analyses, we propose that efforts to establish licensure for FAs, and thus to enhance employment opportunities and to standardize the field, must coincide with efforts to pass laws at the state level to improve death investigation and secure concomitant funding to establish positions. Ethical practice requires an expert be involved in the recovery and investigation of all skeletal cases, not only for high-profile cases. Ensuring the protection of people's civil rights and otherwise protecting the public through uniform FA training and education is critical to ensuring justice for all people.

Playing with Others' Expectations: Playful Teasing in Four Species of Great Apes

ERICA A. CARTMILL[1], ISABELLE B. LAUMER[2], SASHA L. WINKLER[1] and FEDERICO ROSSANO[3]

[1]Anthropology, University of California, Los Angeles, [2]Institute of Animal Behavior, Max Planck, Konstanz, [3]Cognitive Science, University of California, San Diego

Teasing, joking, and kidding walk a fine line between aggression and play. These intentionally ambiguous social behaviors draw on many complex cognitive abilities, including assessing relationship strength, predicting others' behaviors, and appreciating the violation of others' expectations. Playful teasing is a simple form of joking that appears in human infants by 12-months. Great apes also engage in infant-like playful teasing, but it has not been previously studied in a systematic way. Drawing upon methods from research on ape gesture, we developed an extensive behavioral coding system aimed at better identifying and quantifying primate teasing behavior. We applied this coding system to 75 hours of video of zoo-housed apes (chimpanzees, bonobos, gorillas, and orangutans) and found that all species engaged in intentionally provocative behavior frequently accompanied by play markers. We defined these interactions as playful teasing (as opposed to agonistic teasing). In addition to the presence of attention-getting (i.e., "provocative") behaviors, we found that ape playful teasing was characterized by one-sidedness, expectation of a response, repetition, and elaboration/escalation of behavior. We found many shared features of playful teasing across all four great ape species, including significantly more teasing initiated by juveniles. The specific actions used to tease differ across age classes, and for some species, we found preliminary evidence that adults may self-handicap. As playful teasing is present in all extant great ape genera (including Homo), it is likely that the cognitive prerequisites for joking evolved in the hominoid lineage at least 13 million years ago.

This work was supported by a grant to E.A. Cartmill from the Templeton World Charity Foundation (TWCF0318).

Investigating the ecological underpinnings of ethanol metabolism in wild primates

JULIA G. CASORSO[1], SUHEIDY ROMERO MORALES[2], ALLEGRA N. DEPASQUALE[1], SAÚL CHEVES HERNANDEZ[2], RONALD LOPEZ NAVARRO[2], KIMBERLEY J. HOCKINGS[3], MATTHEW A. CARRIGAN[4] and AMANDA D. MELIN[1]

[1]Department of Anthropology and Archaeology, University of Calgary, [2]Área de Conservación Guanacaste, Guanacaste, Costa Rica, [3]Centre for Ecology and Conservation, University of Exeter, [4]Department of Science, College of Central Florida

Although human-directed ethanol fermentation has occurred since 10,000 B.C.E., ethanol also occurs naturally in wild fruits and nectars, suggesting that frugivorous primates could have been ingesting ethanol throughout their evolutionary history. Intriguingly, humans and African great apes have a 40-fold higher efficiency for metabolizing ethanol relative to most mammals. The dietary exposure hypothesis posits that increased exposure to dietary ethanol selected for this adaptation in our last common ancestor with African great apes. However, our current understanding of naturally occurring ethanol concentrations, and variation within and across plant taxa consumed by different animal guilds, is limited, restricting our ability to investigate the role ethanol may play as a selective pressure on primate metabolism. To help fill this gap, we measured ethanol production in 70 wild fruit species in a tropical dry forest in Costa Rica, using a custom-adapted Mark V breathalyzer. We found that ethanol production was present in 76.3% of adequately-sampled species (n = 38), mainly when ripe, and ranged from trace amounts (0.01%) to 3.13%. We also observed strong phylogenetic signal in maximum ethanol production by ripe fruits (Pagel's λ=0.84). Notably, fruits with traits characteristic of a mammal/primate-dispersal syndrome (e.g. bigger, husked, low-contrast colours) produced significantly more ethanol per gram than fruits with bird-dispersal traits (e.g. smaller, dehiscent, high-contrast colours) (p < 0.05). Our findings offer support for a link between ethanol production and plant phylogeny, and for co-evolutionary relationships with different disperser guilds, shedding new light on the evolutionary origins of ethanol consumption in primates.

This research was funded by the Wenner-Gren Foundation.

Understanding the genetic relationships between height and skeletal endophenotypes in UK Biobank South Asian participants

CHELSEA C. CATALDO-RAMIREZ[1], MENG LIN[2], TIMOTHY D. WEAVER[1] and BRENNA M. HENN[1,3]

[1]Anthropology, University of California, Davis, [2]Biomedical Informatics, University of Colorado, Anschutz Medical Campus, [3]Genome Center, University of California, Davis

Biobank-level data has allowed for great advances in phenotype-genotype investigations, though not typically for phenotypes preserved in the fossil record. Height is one exception, but it's only well-characterized genetically in Europeans and its endophenotypes (e.g., femur length) have not been comparably assessed. Here, we investigate the genetic architecture of height and how it may be shared amongst related phenotypes in a UK Biobank (UKB) South Asian sample. An automated phenotyping pipeline was performed, extracting five 2D skeletal measurements from dual-energy X-ray absorptiometry (DXA) scans of participants with paired genotype, height, and environmental data. Two GWAS of height (utilizing different sets of covariates) were conducted (n = 5196), and their outputs used to train respective polygenic risk score (PRS) models (n = 1000). These PRS models, and published, well-powered height PRS's developed on European or East Asian samples, were applied to the participants with DXA images here (n = 280). Results suggest that incorporating appropriate environmental covariates in GWAS reduces the number of SNPs needed for the best-fit PRS model, and reduces the variance explained by genetic scores alone for height, average max femur length, and average tibia length. The out-of-population PRS's better predict height and vertebral column length than

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

the within-population PRS's, but do not always better predict related phenotypes (e.g., bi-iliac breadth). This reinforces the need for larger, more diverse genetic data to better characterize the specific genetic associations between related phenotypes, and also highlights the importance of including environmental covariates when conducting GWAS and training PRS models.

Potential effects of body size on skeletal maturation

MORTIMER CAVANAH and MAJA ŠEŠELJ

Anthropology, Bryn Mawr College

Skeletal age determined from the bones of the hand-wrist is often used in biological anthropology and biomedicine as a marker of skeletal maturation and a predictor of chronological age. Skeletal maturation is reportedly accelerated in individuals with overweight or obesity, though most studies focused only on overall bone age estimates. We examined the potential effects of body size on hand-wrist skeletal maturation using both a bone age estimate and individual hand-wrist maturity indicators of the Fels and Tanner-Whitehouse methods. One observer (M.C.) assessed 85 radiographs of children of known chronological age (5-18 years), sex (40 male, 45 female), and body mass index (BMI, range 14-33), who were previously enrolled in an ancillary study of the Bone Mineral Density in Childhood Study at the Children's Hospital of Philadelphia.

In this sample, BMI was not a significant predictor of Fels nor Tanner-Whitehouse bone age, though sex was a significant predictor after controlling for BMI. Neither BMI nor sex were significant after controlling for chronological age. BMI also did not appear to be associated with the maturation of the 13 individual hand-wrist indicators reported by Duren et al. (2015) as exhibiting secular trends, and thus potentially being more sensitive to environmental influences, in the Fels population. Given the preliminary nature of this study, future research should evaluate whether the impact of body size and adiposity on skeletal maturation differs based on the age at which adiposity emerges, ideally in a longitudinal context.

Signals of early hominin postural and locomotor diversity in the structural arrangement of the femoral neck

MARINE CAZENAVE[1,2,3], TRACY L. KIVELL[2,4], CHRISTOPHER J. DUNMORE[2] and MATTHEW M. SKINNER[2,4]

[1]Division of Anthropology, American Museum of Natural History, [2]School of Anthropology and Conservation, University of Kent, [3]Department of Anatomy, University of Pretoria, [4]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand

Variation in cortical bone distribution at the hip joint has been shown to reflect loading differences during habitual postural and locomotor behaviors in extant primates. Recent analyses of cortical thickness distribution across the whole femoral neck in *Paranthropus robustus* suggest its hip loading differed from both the typical human and chimpanzee patterns. However, it remains unknown if the *P. robustus* pattern differs from that of *Australopithecus africanus*.

Using microtomographic data and the Morphomap package in R, we assessed cortical bone distribution across the entire femoral neck in two *A. africanus* specimens from Sterkfontein Member 4 (StW 479 and StW 522) and two *P. robustus* from Swartkrans Member 1 (SK 82 and SK 97), South Africa, within an extant hominid comparative context. Both *A. africanus* specimens display a cortical bone thickness distribution similar to the human pattern and lack an anterior reinforcement in the lateral portion of the neck that uniquely characterizes both *P. robustus* specimens. The *P. robustus* pattern is most similar to the cortical distribution in chimpanzees.

These results indicate differences in postural and locomotor modes between the two fossil taxa suggesting they may have exploited different ecological niches. Given that at different eastern and southern African sites, *Australopithecus*, *Paranthropus* and *Homo* chronologically overlap, our results suggest that cortical bone distribution at the femoral neck represents a potentially valuable indicator for the taxonomic attribution of isolated specimens.

MC is funded by the RGGS program and the Division of Anthropology of the AMNH. This project has received funding from the European Research Council (grant agreement No. 819960).

Reconstructing demographic and admixture history of the Batwa and Bakiga in East-Central Africa

BRIDGET CHAK[1,2,3], GEORGE PERRY[4], MAANASA RAGHAVAN[3] and LUIS BARREIRO[1,2]

[1]Section of Genetic Medicine, University of Chicago, [2]Programme in Genetics, Genomics, and Systems Biology, University of Chicago, [3]Department of Human Genetics, University of Chicago, [4]Department of Anthropology, Pennsylvania State University

The Batwa are a rainforest hunter-gatherer population from southwest Uganda that maintained their traditional mode of subsistence until 1991, when their ancestral homeland was converted into the Bwindi Impenetrable National Park. The Bakiga are their Bantu-speaking neighbours who traditionally cultivated both plants and livestock. Ethnographic literature suggests there has been a co-association of the Batwa and Bakiga of at least 500 years, from trading to intermarriage. However, it remains unclear the degree and timescale of genetic exchange that has accompanied such cultural exchanges. We also lack a deep understanding of how admixture among the Batwa and Bakiga has shaped local adaptations and various complex traits.

Here, we have generated a new high-coverage (30x) whole-genome sequence (WGS) dataset comprised of 71 Batwa and 31 Bakiga individuals. We integrated this dataset with reference genomes originating from different regions in Africa to contextualize the genetic diversity and population structure of the Batwa and Bakiga, as well as to assess their genetic affinity with other populations. To interrogate the timescale and degree of genetic exchange between the two groups, we estimated admixture times among admixed Batwa individuals with >20% Bakiga-like ancestry (as inferred by ADMIXTURE). We further applied a suite of local ancestry inference methods to detect admixture-enabled selection. Our preliminary results suggest the genetic exchange between the Batwa and Bakiga occurred roughly around similar timescales as documented cultural exchanges.

Age-related variation in material and geometric properties of fruits in wild white-faced capuchins (*Cebus capucinus*)

JANINE CHALK-WILAYTO[1], JULIA G. CASORSO[2], RONALD LOPEZ NAVARRO[3], SAÚL CHEVES HERNANDEZ[3], AMANDA D. MELIN[2,3], BRIANNA S. LIU[4], SHAUN KIM[5], MARIANA DUTRA FOGAÇA[6], MEGAN A. HOLMES[7], CLAIRE E. TERHUNE[8] and MYRA F. LAIRD[5,9]

[1]Department of Biomedical Sciences, Mercer University School of Medicine, [2]Department of Anthropology and Archaeology, University of Calgary, [3]Área de Conservación Guanacaste, Guanacaste, Costa Rica, [4]Department of Human Evolutionary Biology, University of Southern California, [5]Department of Integrative Anatomical Sciences, University of Southern California, [6]Neotropical Primates Research Group – NeoPReGo, Sao Paulo, Brazil, [7]Department of Family Medicine and Community Health, Duke University, [8]Department of Anthropology, University of Arkansas, [9]Department of Basic and Translational Sciences, University of Pennsylvania

Capuchins (*Cebus* spp. and *Sapajus* spp.) routinely employ complex processing behaviors coupled with physical strength to access protected foods. Bearded capuchins (*Sapajus libidinosus*) have morphological adaptations for processing mechanically-challenging foods. Previous research has demonstrated that immature and adult bearded capuchins process foods of comparable food material properties (FMPs), suggesting these properties alone are not barriers to efficient food processing in juveniles. In contrast, *Cebus* spp., lacks these adaptations and the influence of FMPs on food selection in juveniles remains unclear. Here we compare the

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

material and geometric properties of fruits eaten by wild, habituated immature and adult *Cebus capucinus* and relate these properties to ontogenetic changes in facial width and jaw length.

Food material property data for 24 fruit species were collected using a FLS-II mechanical tester (Lucas Scientific, LLC). Facial width and jaw length measures were collected from 50 individuals using distance meter photogrammetry. Similar to bearded capuchins, weaned *C. capucinus* immatures and adults exploited fruits of comparable toughness and elastic modulus (p>0.05). Additionally, FMPs and food geometric properties were unrelated to facial width and jaw length, suggesting body size does not constrain access to fruits in juveniles. This preliminary analysis indicates that material and geometric properties do not limit immatures' access to fruits in *C. capucinus*. More broadly, these data suggest material and geometric properties of fruits selected during ontogeny are unlikely drivers of differentiation in feeding system morphology in these genera.

This research was supported by the National Science Foundation's Biological Anthropology directorate (BCS-1945771 [JCW], BCS-1944915 [MAH], BCS-1945283 [MFL], BCS-1945767 [CET]) and the Canada Research Chairs program 950-231257 to ADM.

Destruction or Transformation? Investigating Cremation burials from the Bronze Age of Scotland

ELISABETH CHAUMONT-STURTEVANT, REBECCA CROZIER and MARC F. OXENHAM

Department of Archaeology, University of Aberdeen

The challenging nature of cremation burials has meant a significant aspect of the osteoarchaeological record in Scottish prehistory has been underexploited and arguably often overlooked. This research seeks to not only demonstrate the potential of this important and rich resource, but to question if the practice of cremation during this time is focused on the destruction of the body, or transformation. Six reconstructions are presented, one each from the Bronze Age (2,100-750 BCE) sites; Seggiercrook, Toxside Quarry, Carmoustie, Beattie Lodge, Lowhill and Leucharbraes. These reconstructions not only document skeletal representation (allowing inferences on destruction, recovery, and preservation) but importantly, the generation of a theoretical heat map (color, fracture patterns). This 'mapping' represents a first step towards a more nuanced understanding of cremation burials. The nature of the evidence presented is argued to be more likely to speak to cosmological principles aligning with a framework of transformation, rather than simply being a more expedient form of discard or destruction of the body.

Home range size of Critically Endangered Coquerel's sifaka (*Propithecus coquereli*) across an anthropogenic landscape in northwest Madagascar

CORAL CHELL[1], HANITRINIAINA RAHARINIRINA[2], FERNANDO MERCADO MALABET[1] and SHAWN M. LEHMAN[1]

[1]Department of Anthropology, University of Toronto, [2]Mention Zoologie et Biodiversité Animale, Université d'Antananarivo

Primates subjected to environmental or anthropogenic habitat changes commonly adopt behavioural mitigation strategies, such as altering home range size. These strategies allow for groups to expand their ranging areas, potentially giving them access to higher quality food, but increasing chances for intraspecific competition. However, an opposite pattern has been observed in some species of *Propithecus*, where in fragmented and anthropogenic landscapes, they reduced their range and energy use, invoking an energy-minimizing strategy. Here we use home range size as a proxy for energy use in Critically Endangered Coquerel's sifaka (*Propithecus coquereli*), across an anthropogenic landscape in northwest Madagascar. We hypothesized that groups occupying edge and fragmented habitats would exhibit smaller home range sizes compared to conspecifics inhabiting relatively less disturbed interior forest, due to them taking less energy to utilise. We conducted day follows on four groups of *P. coquereli* occupying areas of differing levels of habitat disturbance in the Mariarano Forest Complex. Group movements were recorded using GPS data collected every 20 minutes throughout the day, and home ranges were modelled using kernel density estimates at 90%. Interior groups exhibited larger home range sizes (20.2 ha) compared to those in the edge/fragmented habitats (12.5-16.2 ha). Currently, our knowledge of how *P. coquereli* populations respond to anthropogenic habitat disturbance remains poorly understood. The species has recently moved onto the Primates in Peril world's 25 most endangered primates list, meaning research such as ours could be a key component to the species future persistence and survival in human-dominated landscapes.

Financial support was provided by the Department of Anthropology and the School of the Environment at the University of Toronto, and Natural Science and Engineering Research Council.

Evidence of emerging inequality in the Middle Period San Pedro de Atacama oases using entheseal patterns

COLLEEN M. CHEVERKO[1], SARAH A. SCHRADER[2], CHRISTINA M. TORRES[3,4], WILLIAM J. PESTLE[5] and MARK HUBBE[4,6]

[1]Division of Biomedical Affairs and Research, Edward Via College of Osteopathic Medicine-Louisiana, [2]Faculty of Archaeology, Leiden University, [3]Department of Anthropology & Heritage Studies, University of California Merced, [4]Instituto de Arqueología y Antropología, Universidad Católica del Norte, [5]Department of Anthropology, University of Miami, [6]Department of Anthropology, Ohio State University

The Middle Period (AD 400-1000) in the San Pedro de Atacama oases represents a time marked by demographic expansion, the development of interregional networks, and the formation of formalized social inequalities, all of which shaped the lives of local inhabitants within and between oases. In this study, we complement recent bioarchaeological investigations that have focused on these trends of emerging inequality in this region by investigating entheseal patterns among individuals (n = 210) interred in four Middle Period cemeteries that allow for investigations of potential differences between individuals living in a close geographic area. Solcor 3 and Casa Parroquial represent "elite" sites connected with the Tiwanaku state, while the later sites of Coyo 3 and Quitor 6 Tardío represent individuals who may have had lower status. Using ANCOVA to account for covariates in a single test, we identified differences in activity patterns among the cemeteries in several joints (left and right shoulders and wrists, and left elbow and hip, $p < 0.05$). Results highlight differences in entheseal patterns among individuals interred in cemeteries that were in close geographic proximity and in use over similar periods, highlighting possible differences in lived experiences for individuals interred in cemeteries categorized as "elite" and/or located within core oases compared to outside them.

Portions of this research were supported by NSF-BCS-1359644, NSF-BCS-1358753, and UCN-VRIDT 22/2011.

A transcriptomic and epigenomic atlas of cell types across the macaque brain

KENNETH L. CHIOU[1,2], XINGFAN HUANG[3,4], MARTIN O. BOHLEN[5], SÉBASTIEN TREMBLAY[6], DIANA R. O'DAY[7], CAILYN H. SPURRELL[7,8], AISHWARYA A. GOGATE[7,8], TRISHA M. ZINTEL[1,2], ALEX R. DECASIEN[9], CAYO BIOBANK RESEARCH UNIT[10], MADELINE G. ANDREWS[11], MELWEEN I. MARTÍNEZ[12], LEA M. STARITA[3,7], MICHAEL J. MONTAGUE[6], MICHAEL L. PLATT[13,14,6], JAY SHENDURE[15,16,3,7] and NOAH SNYDER-MACKLER[1,17,18,2]

[1]Center for Evolution and Medicine, Arizona State University, [2]School of Life Sciences, Arizona State University, [3]Department of Genome Sciences, University of Washington, [4]Paul G. Allen School of Computer Science & Engineering, University of Washington, [5]Department of Biomedical Engineering, Duke University, [6]Department of Neuroscience, University of Pennsylvania, [7]Brotman Baty Institute for Precision Medicine, [8]Seattle Children's Research Institute, [9]Section on Developmental Neurogenomics, National Institute of Mental Health, [10]Cayo Biobank Research Unit, [11]School of Biological and Health Systems Engineering, Arizona State University, [12]Caribbean

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Primate Research Center, University of Puerto Rico, [13]Department of Psychology, University of Pennsylvania, [14]Marketing Department, University of Pennsylvania, [15]Howard Hughes Medical Institute, [16]Allen Discovery Center for Cell Lineage Tracing, [17]School of Human Evolution and Social Change, Arizona State University, [18]ASU-Banner Neurodegenerative Disease Research Center, Arizona State University

Cataloging the diverse cellular architecture of the primate brain is crucial for understanding cognition, behavior and disease in humans. Here, we generated a brain-wide single-cell molecular atlas of the rhesus macaque brain encompassing single-nucleus RNA sequencing (snRNA-seq) and single-nucleus ATAC sequencing (snATAC-seq) data. Altogether, we profiled 2,583,967 transcriptomes and 1,587,880 epigenomes from single nuclei sampled from 30 cortical, subcortical, cerebellar, and brainstem regions spanning the brains of 5 adult macaques (3 female, 2 male) from Cayo Santiago. Our extensive sampling—in terms of both number of nuclei and number of brain regions—enabled us to identify 17 distinct cell types and 112 distinct cell subtypes across the dataset, including rare cell populations such as Purkinje cells. Cell-type and -subtype composition differed extensively across the brain, revealing cellular signatures of region-specific functions. Based on our snATAC-seq data, we identified 1,192,873 candidate *cis*-regulatory elements (peaks) which, after data integration and cell-type label transfer using our snRNA-seq dataset, allowed us to explore the landscape of *cis*-regulatory grammar and neurological disease risk in a cell-type-specific manner. Our multi-modal analysis of 4,171,847 nuclei combined enabled us to identify enrichment of transcription factor binding motifs among cell-type-specific open chromatin regions (e.g., *N*=433 in Purkinje cells). It also enabled us to jointly model gene expression and chromatin accessibility of similar cells, which revealed 142,324 peak-gene pairs showing evidence of regulatory function. Together, our multi-modal atlas provides an open resource for investigating the evolution of the human brain and identifying novel targets for disease interventions.

This research was supported by NIH grants U01-MH121260, R01-AG060931, R00-AG051764, R01-HG010632, R01-MH118203, R01-MH096875, R37-MH109728, R21-AG073958, R01-MH108627, R56-AG071023, R56-MH122819, T32-AG000057, K99-AG075241, P40-OD012217; NSF grants TIP-2110037, BCS-1800558; Kaufman Foundation grant KA2019-105548.

Defects of Non-survivors: Linear Enamel Hypoplasia in Juveniles at Umm al-Jimal

CECELIA CHISDOCK

Anthropology, University of Notre Dame

Linear enamel hypoplasia (LEH) is a particularly useful non-specific stress indicator as it is non-healing and its age-at-formation can be accurately estimated. When incorporated with juvenile mortality data, LEH may be used to examine patterns of stress, survival, and age-specific frailty. In this study, LEH and age-at-death were analyzed in the juveniles of Roman-Byzantine Umm al Jimal, Jordan, to investigate stress patterns at the site. A total of twenty individuals had permanent anterior dentition able to be examined. Each tooth (n=86) was analyzed macroscopically and with 10-20x handheld magnification. Age at formation was estimated using the exponential regression equations by Cares Henriquez and Oxenham (2018). Age at death for each individual was estimated from tooth development and dental eruption and ranged from 7.5 months to 17 years. In total, thirteen individuals presented LEH. Age at formation ranged from 1.18 to 5.34 years and averaged 3.28 years. Notably, nearly all teeth presented more than one defect, with only four demonstrating a single instance of LEH. Additionally, 78% of individuals over the age of 6.5 years (when anterior crowns are complete), presented LEH. No significant age-associated formation pattern could be determined though most were concentrated in the broad range of 2-4 years and no defects were formed before one year. In sum, juveniles at Umm al-Jimal experienced a high level of LEH-inducing stress in variable patterns consistent primarily in their high prevalence and general survivability, given their consistently high incidence in older age groups.

Supported by the National Science Foundation Graduate Research Fellowship under Grant No. 1841556 and the University of Notre Dame Institute for the Study of Liberal Arts Graduate Student Research Award

One of these is not like the others: Re-evaluating the association of nasal projection with climate

ELIZABETH O. CHO[1], LAUREN N. BUTARIC[2] and SCOTT D. MADDUX[1]

[1]Center for Anatomical Sciences, University of North Texas Health Science Center, [2]Department of Anatomy, Des Moines University

Ecogeographic variation in nasal projection is commonly cited as evidence for climatic adaptation among modern humans. However, previous studies examining nasal tip protrusion and nasal bridge elevation have primarily employed Europeans as the sole representatives of cold-dry environments, despite the existence of populations in Northern Asia and the Arctic Circle that inhabit similar or more extreme cold-dry environments. Accordingly, this study re-examines nasal projection within climatic contexts employing an ecogeographically diverse sample of modern human crania (n=769), including sub-samples from mid-to-high latitude areas of Asia and the New World. The results of a multivariate regression using 3D coordinates for fourteen nasofacial landmarks in conjunction with climatic variables (e.g., temperature, absolute humidity) from the CRU-TS3 database, indicate that nasal bone protrusion and bridge elevation are not among the aspects of external nasal morphology significantly correlated with climate across modern humans (r=0.518, P<0.0001). Rather, nasal tip projection and bridge elevation appear predominately restricted to populations from Europe, North Africa, and the Middle East. Conversely, populations from northern Asia and the Arctic Circle generally exhibit low levels of nasal projection, comparable to populations from tropical areas such as equatorial Africa and Melanesia. Thus, contrary to previous predicative models, our results clearly suggest that nasal projection is not a universal adaptation to cold-dry climates among modern humans. These results have important implications for understanding climatic adaptation in modern humans, and potentially, for interpreting the fossil record of Neandertals and other archaic humans inhabiting cold-dry environments during the Pleistocene.

National Science Foundation (#1847486, #2203808), Wenner-Gren Foundation (#7969, #9693), Leakey Foundation

The role of posteroanterior left knee radiographs and osteoarthritis in positive identification

TARA A. CHOAT[1] and SEAN D. TALLMAN[1,2]

[1]Department of Anatomy & Neurobiology, Boston University Aram V. Chobanian & Edward Avedisian School of Medicine, [2]Department of Anthropology, Boston University

While osteoarthritis (OA)—regularly diagnosed with posteroanterior (PA) knee radiographs—is the most common skeletal pathology today, it is unknown if the associated bony changes over time preclude antemortem-postmortem radiographic comparison. Therefore, this research examines the reliability of PA left knee radiographs for positive identification using comparative radiography over a seven-year timeframe. Radiographs from 12, 48, 72, and 96-month collection periods of the Osteoarthritis Initiative public database were compiled for 89 individuals; edited into single side-by-side images; divided into three-year (Series 1), five-year (Series 2), and seven-year (Series 3) comparisons; and included in a survey that was distributed to those with and without comparative radiography experience. Accuracies, sensitivities, specificities, positive predictive values (PPV), and negative predictive values (NPV) were calculated for the survey respondents (n=66), series, and respondent demographics. The overall results (accuracy=94.2%, sensitivity=54.7%, specificity=97.5%, PPV=65.6%, and NPV=96.2%) indicated that respondents performed only moderately well in matching correct radiographs. However, the performance of survey participants in the overall survey and in all three series was statistically significantly lower (α<0.05) for those

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

with no comparative radiography experience and those with little-to-no forensic casework experience. The performance of all participants became progressively lower with each series, with Series 1 demonstrating the best performance and Series 3 demonstrating the worst. Degradation in performance suggests that bony changes associated with OA and those used in making matches (e.g., morphology of the femur and tibia, joint space width) preclude radiographic matching of the knee over around three years between antemortem and postmortem image acquisitions.

Paleomagnetic-based age estimates of primates and associated vertebrate fauna from the middle Miocene locality of Ramnagar (Jammu and Kashmir, India)

DEEPAK CHOUDHARY[1], CHRISTOPHER J. CAMPISANO[2,3], CHRISTOPHER C. GILBERT[4,5,6,7], MOHAMMAD ARIF[8], SARVENDRA P. SINGH[8], BIREN A. PATEL[10,9], ROHIT KUMAR[1], WASIM A. WAZIR[1], PANKAJ KUMAR[1], BINITA PHARTIYAL[8] and RAJEEV PATNAIK[1]

[1]Department of Geology, Panjab University, [2]Institute of Human Origins, Arizona State University, [3]School of Human Evolution and Social Change, Arizona State University, [4]Department of Anthropology, Hunter College, CUNY, [5]PhD Program in Anthropology, The Graduate Center, CUNY, [6]Division of Paleontology, American Museum of Natural History, [7]New York Consortium in Evolutionary Primatology, NYCEP, [8]Palaeomagnetism Laboratory, Birbal Sahni Institute of Palaeosciences, [9]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [10]Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California

The middle Miocene locality of Ramnagar (Jammu and Kashmir), India is well-known for its fossil primates including *Sivapithecus indicus, Kapi ramnagarensis,* and *Ramadapis sahnii*. Since its discovery over 100 years ago, it has been considered equivalent in age to the Chinji Formation of the Potwar Plateau on the basis of faunal correlation. However, no precise geochronological age beyond a Chinji-level correlation (~14.0-11.4 Ma) has been available. Furthermore, the stratigraphic section at Ramnagar has yet to be satisfactorily documented. Here we present new paleomagnetic and revised stratigraphic data for a number of Ramnagar localities, and document a near-complete chronology of all the mammal-yielding sites belonging to the main 365 m thick Lower Siwalik section at Ramnagar. We anchor the paleomagnetic results using the existing micro-mammal biochronology, and further extrapolate ages using sedimentation rates to help constrain possible correlations to the Geomagnetic Polarity Timescale (GPTS). Based on the paleomagnetic results (three normal chrons with two reversals), a few correlations to the GPTS are possible. The most likely interpretation constrains the primate yielding sites to between ~12.9 and ~11.2 Ma, which supports a correlation to the Chinji Formation and bottom of the Nagri Formation in Pakistan. It also suggests that the top of the Ramnagar section, including the *Sivapithecus* site of Dalsar, probably correlates to the Middle Siwaliks. Moreover, the first appearance datums (FADs) of *K. ramnagarensis*, *S. indicus*, and *R. sahnii* can now be placed between 12.735-12.89 Ma (incorporating two possible correlations), potentially extending the FAD of *Sivapithecus* by >100,000 years.

Funding generously provided by: Leakey Foundation; NSF BCS Awards 1945736, 1945618, 1945743; MoES/P.O. (Geosci)/46/2015 and SERB-HRR/2018/000063; PSC-CUNY faculty award program; Hunter College; AAPA professional development grant program; USC; IHO/ASU.

Socially-mediated microbial transmission infuences the early life black-and-white colobus monkey gut microbiome

DIANA MC. CHRISTIE[1,2], EVA C. WIKBERG[3], PASCALE SICOTTE[4], BRENDAN BOHANNAN[2] and NELSON TING[1,2]

[1]Department of Anthropology, University of Oregon, [2]Institute of Ecology and Evolution, University of Oregon, [3]Department of Anthropology, University of Texas at San Antonio, [4]Department of Biology, Concordia University

Inter-individual variation in the adult primate gut microbiome is shaped by host demography, diet, environment, and social behavior, and evidence of socially-mediated transmission in wild mammals has been documented across a variety of taxa. However, less is known about the role of socially-mediated transmission in shaping gut microbial variation among young primates. Diverse early life social contact in the form of allomothering makes colobus an ideal system for examining the influence of social contact on early life gut microbiomes. We collected behavioral data and characterized gut microbiomes of wild black and white colobus monkeys (*Colobus vellerosus*) across 4 social groups and all age classes (2 -34 months and 4-26 years). We found that shared social environment (in the form of social group membership) shaped similarity between young individuals and non-maternal adult colobus monkeys (p>0.001). Further, mother's social position (centrality within the social network) has a strong impact on early life gut microbiomes; young colobus with more central mothers have more similar gut microbiomes to social group adults than those with less central mothers (p>0.01). Taken together, these results indicate that socially-mediated transmission of gut microbes may be an important factor in shaping early life gut microbiomes, either directly via contact between infants and non-maternal adults or mediated via social contact with the mother. Utilizing a smaller cohort of deeply behaviorally sampled infants, we intend to further explore this pattern by examining the influence of direct contact between infants and non-mothers (via allomaternal care behaviors) on infant gut microbiomes.

We would like to thank the National Science Foundation for funding this research under Doctoral Dissertation Research Improvement Grant BCS-1945914

Nonlinear modeling of long bone ontogeny to investigate final adult size

ELAINE Y. CHU and KYRA E. STULL

Department of Anthropology, University of Nevada, Reno

Skeletal long bone measurement definitions differ based on the stage of growth and development, such as the presence/absence or degree of fusion of the epiphyses. Subsequently, few explorations in the utility of both including and excluding epiphyses together in evaluations of long bone ontogeny have been attempted. A sample of 798 individuals aged between birth and 50 years-old from the Subadult Virtual Anthropology Database (SVAD, *n*=385) and Forensic Data Bank (FDB, *n*=413) were used to model the ontogeny of relative long bone lengths. Stature was used to calculate relative lengths from absolute measures. Mann-Whitney U tests found no statistically significant differences ($p < 0.05$) in the *relative* long bone lengths of overlapping ages from the SVAD and FDB. 500 simulations of a three-parameter asymptotic exponential equation were used to generate point estimates and 95% confidence intervals of each model parameter. The asymptote (α) is interpreted as final relative adult size, which ranged from 0.15-0.27 mm. The distal elements presented with greater sexual dimorphism than the proximal elements in final relative adult size, with the femur demonstrating almost no differences in α between males and females. Each point estimate of α was subsequently used to reverse-calculate the age at final adult size, ranging from 26-31 years-old. Females reached final adult size 2-5 years before males. Results of this study demonstrate the utility of nonlinear modeling to glean information on processes of long bone ontogeny and age at final adult size attainment.

Culture-bound attitudes surrounding Philippine politics, health, and stress in pregnant Filipina women

KRISTINE JOY CHUA[1], ZOE PAMONAG[2], LIA LOURDES L. FRANCISCO[3], JESSICA G. ASUNCION[4] and ABIGAIL W. BIGHAM[1]

[1]Anthropology, University of California, Los Angeles, [2]Public Health, Johns Hopkins, [3]College of Commerce and Business Administration, University of Santo Tomas, [4]Biological Sciences, Mariano Marcos State University

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Fear and concerns about the current socio-political environment are becoming a world-wide issue for maternal and fetal health. Particularly salient are policies from authoritarian governments that are resulting in the rise of preterm births. Yet, little is known concerning how mothers perceive and thereby, embody the socio-political environment around them. We identify the Philippines, a country experiencing intense State violence from former President Duterte's administration and policies, as a prime location to contextualize and inform our understanding on maternal perceptions and embodiment of the socio-political climate during pregnancy. We interviewed 21 pregnant and recently pregnant Filipina women from various regions of the Philippines. We asked them to describe their experiences regarding the current political situation (e.g., war on drugs, COVID-19 response) and how much they felt their socio-political environment contributed to the overall health of their pregnancy and overall security. Using content analyses to systematically identify themes, we identified four major themes contributing to perceived stress level among mothers and their concern over their children's safety: (1) degree of support for President Duterte's administration, (2) consumption and engagement with political news, (3) culture-bound attitudes that downplays stress, and (4) coping strategies. This is one of the first studies to examine how women conceptualize as well as embody politics and policies, and our findings contribute to understandings of how the socio-political climate impacts health of mothers during pregnancy.

Population-specific vs. pooled dental samples: an argument for more generalizable age estimation methods

LAURA E. CIRILLO

Anthropology, University of Nevada, Reno

Age estimation is the most important aspect of the biological profile in subadults and is popularly estimated through dental development. Neither sex nor ancestry are estimated in juveniles, yet many population-based methods require knowledge of these categorizations prior to use. As dental age estimation methods become more specific in their application, their generalizability in both forensic anthropology and bioarcheology decreases.

To test the need for population-specific methods, a pooled study sample of 2,656 individuals from 10 countries was used to compare ordinal development timing to that of the populations published in Nolla (1960), AlQahtani et al. (2010), and Kuremoto et al. (2022). The median stage of development was calculated for one-year age categories from 0 to 19 years and compared to the published median stages in the three studies, providing an average of eight points of comparison per study, per tooth. A difference of less than one age category (representing <1 year difference in timing) was not considered a meaningful difference. The pooled data was greater than one category different in only 13 out of 249 points of comparison between studies in mandibular teeth, and 20 of 255 points of comparison in maxillary teeth (<1% of the data). Differences between samples were most often seen in third molars and data divided by sex. Because most comparisons are within one category, there is no demonstrated necessity for population-specific dental methods. Previous interpretations of population-specific differences were most likely the result of inconsistent trends that were exaggerated by small sample sizes.

Hidden in Plain Text: Using history to uncover heterogeneity in frailty

MELISSA CLARK[1], DEBBIE GUATELLI-STEINBERG[2] and MARK HUBBE[2]

[1]World Languages, Literature, and Cultures, Cleveland State University, [2]Anthropology, The Ohio State University

Historical sources describe extreme wealth inequality in post-medieval (c. AD 1640-1800) Ireland following the Anglican colonization of the late medieval period (c. AD 1150-1640). During this time, colonial practices like transplantation and religious discrimination transformed who owned land in Ireland, what foods were available to them, and where they lived. These transformations produced a large lower class comprised of mostly Irish Catholics and a small upper class comprised of mostly of Anglican Protestants. Guided by a biocultural political economy framework, this study evaluates to what extent the vast socioeconomic inequality described in historical sources is reflected in biological variation on the skeleton. Specifically, we test the hypothesis that exposure to stressors and resource deprivation for a large portion of the population resulted in a lower age-at-death in the post-medieval than in the late medieval samples. Second, we hypothesized that there was more variation in the number of linear enamel hypoplasia (LEH) across sites in the post-medieval than in the late medieval samples. We tested these hypotheses on 526 adult skeletons from counties Dublin, Kildare, Louth, and Meath. Results showed that longevity increased between the late medieval and post-medieval periods, but that the gains in survivorship were smaller for women than men. The variation in LEH across sites was significant in the post-medieval (p=0.0149) but not the late medieval sample (p=0.7945). These results are consistent with historical descriptions of vast inequality in post-medieval Ireland and can be explained by the colonial transformation of resource distribution.

Central chimpanzees and bonobos exhibit more stress-related dental defects than eastern chimpanzees

JILLIAN N. CLARKE[1], JIMMY ERKENS[2], SABRINA MACCARON[1], MATTHEW WILLIAMS[1], EMMANUE GILISSEN[3,4] and KATE MCGRATH[1,5]

[1]Anthropology, State University of New York at Oneonta, [2]Anthropolgy, The Ohio State University, [3]African Zoology, Royal Museum for Central Africa, Tervuren, Belgium, [4]Laboratory of Histology and Neuropathology, Université Libre de Bruxelles, Brussels, Belgium, [5]Center for the Advanced Study of Human Paleobiology, The George Washington University

Linear enamel hypoplasia (LEH) describes the band-like grooves that are common in ape and human teeth. LEH defects occur when stressors like illness and malnutrition disturb the tooth's normal development. We created high-resolution dental replicas from 38 individuals of three species: central chimpanzees (Pan troglodytes troglodytes; N=11), eastern chimpanzees (Pan troglodytes schweinfurthii; N=15), and bonobos (Pan paniscus; N=12). We selected the best-preserved canine and assessed LEH presence and severity by viewing the dental replicas 'by eye' and using a hand lens. We tested for species and sex differences in LEH frequency and severity using Bayesian methods (Poisson-Gamma posterior-derived 95% credible intervals). Central chimpanzees and bonobos are expected to have more defects (P=0.935, 0.885, respectively) as well as more severe defects (P=0.988, 0.987) than eastern chimpanzees. However, when the chimpanzee subspecies are combined, the difference in expected defect number is diminished (P=0.75), though bonobos are still expected to have more severe defects (P=0.919). The probability that males have a greater expected number of defects than females is 0.933, while their probability of having a greater expected number of severe defects is 0.830. Previous research suggested that bonobos have more defects than chimpanzees, and our results suggest that eastern chimpanzees specifically have fewer defects than the other taxa. Defects might form in response to malnutrition from seasonal lows in fruit availability, diseases like parasites, Ebola, or SIV, and even cold stress. Future work will quantify defects in these groups and assess why eastern chimpanzees differ from the other members of Pan.

SUNY Oneonta's Summer Research Fellowship Program, the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No 798117, SYNTHESYS Project, and SUNY PRODiG program.

Paleogenomic Insights into the Composition of an Ancient Urban Neighborhoods Near the Puchituk Terminus, Caracol

CELIA D. CLEARY[1], ANGELINA J. LOCKER[1,2], DIANE Z. CHASE[3], ARLEN F. CHASE[4], ADRIAN SZ. CHASE[5],

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

MELISSA M. BADILLO[6], JADA BENN TORRES[2], AUSTIN W. REYNOLDS[7] and RICK WA. SMITH[1,8,9]

[1]Sociology and Anthropology, George Mason University, [2]Department of Anthropology, Vanderbilt University, [3]Claremont Graduate University, [4]Department of Anthropology, Pomona College, [5]Mansueto Institute for Urban Innovation and Department of Anthropology, University of Chicago, [6]Institute of Archaeology, Belize, [7]Department of Anthropology, Baylor University, [8]Department of Women and Gender Studies, George Mason University, [9]Indigenous Science, Technology, and Society Lab, Faculty of Native Studies, University of Alberta

Mesoamerican archaeology has been instrumental in understanding early urbanism globally. One of the most important cities shaping our knowledge of Mesoamerican urbanism was the large Maya metropolis of Caracol. Caracol was one of the greatest cities of the Classic Maya Period (250-900 CE) and, at its peak, was home to more than 100,000 people. Previous archaeological analyses have demonstrated that residential groups at Caracol shared city-wide commonalities in mortuary contexts. Compared to the city of Teotihuacan, where dense urban neighborhoods were divided by distinctions in mortuary treatments, the demographic composition of Caracol at the neighborhood level is less apparent from mortuary analyses alone. In this project, we assess DNA preservation and use paleogenomic data to characterize biological relationships among residents of eight residential groups across three neighborhoods near the Puchituk Terminus, located 3 km outside the city's epicenter. This study was conducted with approval and support from the Institute of Archaeology in Belize. We extracted ancient DNA from 53 dental and skeletal elements of people interred near Puchituk and screened them for the preservation of endogenous DNA. For 25 of these extracts determined to have sufficient preservation, we constructed double-stranded, partial UDG treated, dual-indexed Illumina libraries and enriched them using the myBaits Expert Human Affinities probes targeting more than 2 million SNPs and the complete mitogenome. Resulting sequence data were used to assess biological kinship relationships and evaluate the demographic makeup of residential groups near Puchituk, providing some of the first insights into the urban composition of Caracol.

This project was funded via GMU Summer Research Fellowship to CDC, a Neukom Institute CompX grant to RWAS, and funding from Alphawood Foundation and NSF to AFC and DZC.

16S rRNA Analysis of 17th and 18th Century New York African Burial Ground soil samples

CARTER CLINTON, COURTNEY ROBINSON and FATIMAH JACKSON

Anthropology and Biology, Pennsylvania State University

Next-generation sequencing (NGS) and the development of bioinformatics tools have allowed researchers to learn more about extinct hominins and animal species that lived thousands of years ago in cave sediments and soil. However, we know very little about the condition of burial soil and its ability to inform us about populations buried just hundreds of years ago. Our study investigates New York African Burial Ground (NYABG) grave soil samples to establish evidence of human existence and determine burial-specific details about each inhabitant. The NYABG is the oldest and largest burial site of free and enslaved Africans, used between ~1640 and 1797 in Lower Manhattan. Previous research includes historical, skeletal, and archaeological analyses of the population and site. We used 16S rRNA sequencing to observe the bacterial community composition of 69 burial samples and 7 non-burial samples. We observed significant differences between the relative abundance of bacteria of the two groups at each taxonomic level. Our findings suggest that the NYABG samples contain human microbiome signatures such as *Akkermansia muciniphila* found in the human intestine and *Acinetobacter lwoffii* found in the skin microbiome, while the control samples reflect wetland soils. We have identified bacteria associated with disease pathogens, such as *Aggregatibacter segnis* (periodontal infection) and potential disease-causing bacteria of the genera *Legionella* (Legionnaires Disease) and *Blautia* (cholera). The detection of human-associated bacteria gives insight into the lives and possible causes of death of the NYABG population and serves as proof of concept to explore human DNA in the NYABG grave soil.

Funding for this research was made possible by grants obtained from the National Geographic Society, the Cosmos Foundation, Sigma Xi, and the Just-Julian Fellowship by the Howard University Graduate School.

Preliminary study of endocranial variation among gibbons using an open access dataset

ZACHARY COFRAN[1], JULIA M. ZICHELLO[2], REYNALDO VALENZUELA[1], CHLOE MENGDEN[1] and DARLING GARCIA[1]

[1]Anthropology Department, Vassar College, [2]Anthropology Department, Hunter College, CUNY

The "lesser apes" of Southeast Asia, gibbons (family Hylobatidae) are the most taxonomically diverse yet poorly studied of the extant apes. Gibbons are especially underrepresented in analyses of the brain and surrounding bony endocast. We aim to fill this gap in our knowledge of ape brain evolution by surveying endocranial shape variation in a large sample of gibbons from the Morphosource online repository. Focusing on adults, *Hylobates* is well represented by N=67 individuals spanning eight species, while other genera are more poorly represented (*Nomascus* N=8 representatives of two species, *Symphalangus* N=7, and N=4 *Hoolock* of two species). We virtually extracted each endocast from its cranium and used 3D geometric morphometrics to analyze endocast shape with a template of 926 landmarks. Principal components analysis of endocranial landmarks distinguishes *Hylobates* and *Nomascus* from *Hoolock* and *Symphalangus*: the former pair are distinguished by a globular endocast and flexed cranial base, while endocast shape of the latter pair is mediolaterally narrower with a cerebellar fossa oriented more posteriorly. Additionally, to test if endocranial shape follows neutral patterns of variation within taxa, we compared endocranial diversity (pairwise Procrustes distances) with published estimates of Hylobatid genetic diversity. All four genera show comparable measures of shape diversity, in contrast to published evidence for disparate levels genetic diversity. On the other hand, within-species endocranial diversity more closely tracks intraspecific genetic diversity. These preliminary results point to new directions in the study of gibbon brain variation and evolution.

Modularity in the cranium of *Macaca fascicularis*

THEODORE M. COLE III

Biomedical Sciences, UMKC School of Medicine

Mammalian skulls are comprised of anatomical modules influenced by genetics, development, and function. These modules are thought to be autonomous to some degree, responding to selective forces somewhat independently, so that mosaic evolution is facilitated. Modularity is often assessed by analyzing patterns in the correlations among continuous measurements. This study takes such an approach in a preliminary exploration of modular organization in the cranium of *Macaca fascicularis*.

The sample consists of 68 wild-collected, adult *M. fascicularis* specimens (38M, 30F). Fifty-two linear distances were collected to describe cranial form. The data were used to compute a correlation matrix (with sex as a covariate), which is expected (in theory) to have a modular structure. To uncover this structure, the correlation matrix was transformed to a dissimilarity matrix that was then subjected to principal coordinates analysis, yielding a lower-dimensional space summarizing the original matrix structure. Scores on the first ten axes were subjected to nonhierarchical clustering.

The cluster analysis identified two major modules and one smaller one. The neurocranium comprises one large module, while the

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

facial skeleton and cranial base combine to form another. However, a smaller cluster is localized to the premaxilla, the nasal aperture, and the nasal bones, suggesting some degree of autonomy with respect to the surrounding facial skeleton. Future studies will address questions of whether the modular pattern observed for *M. fascicularis* is seen in other macaque species and if within-species modularity predicts patterns of macaque cranial disparity above the species level.

Data collection for this project was supported by a Funding for Excellence grant from the University of Missouri-Kansas City.

Individual differences in baseline cortisol and cortisol reactivity among wild chimpanzees (*Pan troglodytes*) at Kanyawara

MEGAN F. COLE[1], STEPHANIE A. FOX[1], MARTIN N. MULLER[1,2], EMILY OTALI[2], ZARIN MACHANDA[2,3], RICHARD W. WRANGHAM[2,4] and MELISSA EMERY THOMPSON[1,2]

[1]Department of Anthropology, University of New Mexico, [2]Kibale Chimpanzee Project, [3]Department of Anthropology, Tufts University, [4]Department of Human Evolutionary Biology, Harvard University

Longitudinal human studies have revealed consistent individual variation in baseline cortisol production and cortisol reactivity, detectable in controlled experiments, and that these traits predict behavior. Among wild primates, it is difficult to evaluate these trait-level features with opportunistic sampling, i.e., individuals with higher average cortisol may experience more frequent or severe stressors. We evaluated evidence for trait-level variation in cortisol in a large, longitudinal sample (13,525 urine samples from 47 adults across 13 years) from wild chimpanzees in the Kanyawara community of Kibale National Park, Uganda. After controlling for numerous temporal, demographic, and socioecological covariates, linear mixed effects models identified significant random effects of individual identity for both males (variance=0.038, $p<0.001$, $R^2=0.42$) and females (variance=0.022, $p<0.001$, $R^2=0.41$). We subsequently introduce a novel approach for quantifying individual-varying baselines as the local maxima of right-skewed frequency distributions. To examine reactivity, we compared individual variation during periods of low versus high socioecological stress and isolated cortisol responses to five natural stressors: aging, rank change, group hierarchy instability, heightened reproductive effort, and reduced diet quality. For each stressor, there was an individual difference in the slope of response ($p<0.001$), though individuals who were more reactive to one stressor were not necessarily more reactive to another. Consistent with the principle of initial values, individuals with elevated baseline levels appeared constrained in the magnitude of their responsivity. Our results suggest that cortisol production has a trait-level component in chimpanzees and points to prospects that individual variation in adrenal function may explain some dimensions of social behavior.

This study was funded by the National Institute on Aging of the National Institutes of Health (Award 1R01AG049395-01) and a National Science Foundation Graduate Research Fellowship.

Keep Calm and Carrion: A Re-evaluation of Scavenging Patterns in the Western United States and Implications for Search Structure in Medicolegal Investigations

CHEYENNE D. COLLINS

Department of Anthropology, California State University, Chico

Forensic taphonomic research has long indicated that non-human animal scavengers play an important role in the decomposition, dispersal, and destruction of human remains in outdoor environments. Regional differences in climate, species presence, topography, seasonality, niche specificity, and available food resources can all lead to fluctuations in scavenging patterns. Currently, there are few studies focusing on animal scavenging in the western United States and new research will provide forensic investigators regionally specific insight for estimation of postmortem interval and construction of searches that consider scavenging behaviors. The current study utilized game camera data from taphonomic projects at the MORTIS (Multidisciplinary Oregon Taphonomy Investigative Studies) facility in Eugene, Oregon. Over one million game camera images were analyzed spanning multiple years, all four seasons, and two different environments (woodland and open). Porcine proxies were utilized as human analogues and distributed across an 80-acre forested parcel of land as well as a separate four-acre disturbed meadow environment. Observed scavengers included: turkey vultures (*Cathartes aura*), black bear (*Ursus americanus*), Virginia opossum (*Didelphis virginiana*), coyote (*Canis latrans*), gray fox (*Urocyon cinereoargenteus*), striped skunk (*Mephitis mephitis*), spotted skunk (*Spilogale gracilis*), unspecified small rodent species, and various small bird species. Notable differences were found between animal behaviors previously reported in the Western United States and those exhibited within this project. The results of this study further indicate that many variables can influence the likelihood of scavenging behaviors by various animal species, which should be considered when constructing search protocols for human remains in outdoor environmental contexts.

Age-related remodeling and trabecular volume in the fibular midshaft using histology and micro-CT

BAILEY A.G. COLOHAN[1,2], VICTORIA M. DOMINGUEZ[1,2,3] and WILLIAM E.H. HARCOURT-SMITH[1,2,3,4]

[1]Anthropology, The Graduate Center, CUNY, [2]NYCEP, New York Consortium of Evolutionary Primatology, [3]Anthropology, Lehman College, CUNY, [4]Division of Paleontology, American Museum of Natural History

Understanding the effects of aging in humans is an integral part of understanding human biology from both a medical and evolutionary perspective. Regularly overlooked in research is the fibula, as it experiences less mechanical strain than other structures of the leg. Thus, metabolic influences related to age may be more apparent in both its gross anatomy and microstructure. This study aims to assess aging of the skeleton by analyzing the midshaft of the fibula for trabecular and cortical volume and remodeling events in the cortex. A modern American cadaveric sample of fibular midshafts from 9 females and 10 males (15 to 105 years old (sd 29.87)) were evaluated. Fibular midshafts were scanned at 35µ using micro-CT and analyzed for 3D trabecular and cortical volume using Dragonfly software. Histological slides were analyzed for intact, fragmentary, and drifting osteons. Data were analyzed using an ordinary least square regression to evaluate potential age-related relationships. Results indicate that both raw and relative trabecular volume significantly increase while average cortical area decreases with age. Additionally, results show an increase in fragmentary osteons with age and a decrease in drifting osteons. Increased trabecular volume with age is the result of both trabecularization of the cortex and the creation of struts within the medullary cavity. Remodeling events increase with age, particularly fragmentary osteons while drifting osteons are gradually replaced by smaller, symmetrical osteons. The increased amount of remodeling, including an increase in trabecular structures, indicates age-related signals in both these characteristics that warrant further investigation.

Growth hormone receptor (GHR) polymorphisms and their association with craneofacial variation in a sample of Mexican mestizo and Indigenous populations

MIGUEL A. CONTRERAS-SIECK[1], GASTÓN MACÍN PÉREZ[2], TÁBITA HÜNEMEIER[3], VICTOR ACUÑA-ALONZO[4] and JORGE A. GÓMEZ-VALDÉS[5]

[1]Anthropology, University of Minnesota, [2]PROTUL, National School of Anthropology and History, Mexico, [3]Departamento de Genética e Biologia Evolutiva, Instituto de Biociências, Universidade de São Paulo, [4]Bachelors Program in Physical Anthropology, National School of Anthropology and History, [5]Postgraduate Program in Physical

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Anthropology, National School of Anthropology and History

Several growth hormone receptor (GHR) polymorphisms have been associated with significant craniofacial differences in the mandibular region in East Asian cohorts. Independent replications with different geographic populations demonstrated heterogeneity in associations. This could result from differences in sample sizes as well as methodologies to capture mandible morphology or could reflect the complexity of craniofacial variation due to genotype-phenotype interactions coupled with environmental noise. To elucidate this complex scenario we genotyped five polymorphisms located in exon 10 of the GHR gene (5p13.1-p1) together with the collection of 3D data from 31 landmarks to characterize overall craniofacial morphology and genetic diversity in a cohort of Mexican mestizo and Indigenous individuals (N=64). Subsequently, we conducted a Generalized Procrustes Analysis on the 32 landmark configurations followed by a Principal Components Analysis and a series of Partial Least Squares Analyses (PLS) to test the possible influence of any of the GHR polymorphism genotypes on mandibular variation and the strength and magnitude of Morphological Integration and Modularity in the craniofacial región. Our results identified significant differences in allele frequencies between our sample and comparative populations from previous studies, including the 1K Genomes. The series of PLS suggest that the genotypes of polymorphism rs6182 and rs6184 of the GHR gene have a possible effect on the morphological variation of the mid and lower craniofacial regions, which is most evident in the protrusion and retrusion of the chin. These findings highlight the complexity of gen-phenotype interactions that need to be considered when studying craniofacial variation between human populations.

Lateral iliac flare does not correlate with gluteal abductor moment arms in humans

REBECCA W. COOK[1,2], JAY CHANDAR[1,3], INDYA THOMPSON[2,4], GABRIEL S. YAPUNCICH[1,2,5], CHRISTOPHER S. WALKER[2,6] and STEVEN E. CHURCHILL[1,6]

[1]Department of Evolutionary Anthropology, Duke University, [2]Department of Molecular Biomedical Sciences, College of Veterinary Medicine, North Carolina State University, [3]Herbert Wertheim College of Medicine, Florida International University, [4]Health Science Center, University of North Texas, [5]School of Medicine, Duke University, [6]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand

Evolution of the human bipedal pelvis entailed shifting the origins of *mm. gluteus medius* and *minimus* to a more lateral position, thus facilitating their role as abductors of the hip. Exaggerated lateral iliac flare, as seen in early hominins, has been hypothesized to increase the leverage of these muscles. However, while numerous methods of measuring iliac flare exist, they are poorly correlated with one another. Here we evaluate 24 such methods relative to their ability to capture variation in the moment arms of *mm. gluteus medius* and *minimus*, as determined from *in silico* models of 39 articulated *Homo sapiens* pelves and femora.

When standardized for body mass, none of the measures of iliac flare are significantly correlated (at $\alpha = 0.05$) with the moment arms of the small gluteal muscles in a pooled-sex sample. Femoral biomechanical neck length (BNL) is significantly moderately correlated with the moment arms of *m. gluteus medius* ($r = 0.5604$) and *m. gluteus minimus* ($r = 0.6476$) in this sample. Sex-specific samples reveal a few significant but weak to moderate correlations between some measures of iliac flare and muscle moment arms. Significant correlations between BNL and moment arms are stronger among males ($r = 0.7163$ - 0.7233) than females ($r = 0.6125$). Overall, these results suggest that the mechanical advantage of the small gluteal muscles was not the target of natural selection acting on lateral iliac flare in early hominin evolution.

Why is excess body weight associated with greater bone strength?

H. MITCH COOK-GRAVER, JANA VALESCA MEYER, MARIO ANTONIO PEÑA MUÑOZ, ALEXIS MARTINEZ, JORDAN MARTINEZ, ALEXANDRA R. HARRIS, ROBERTO RIOS, TAYLOR BUSBY and IAN J. WALLACE

Department of Anthropology, University of New Mexico

Excess body weight (overweight, obesity) is known to be associated with greater bone strength. The most common explanation for this phenomenon is that greater body weight engenders greater mechanical loading of bones, which stimulates greater bone formation, leading to greater bone strength. An understudied yet plausible alternative hypothesis is that excess body weight and greater bone strength are associated because both phenotypes result from a common cause: metabolic energy abundance. That is, people who have enough surplus energy to store a lot as adipose tissue may also be able to devote more energy to developing strong bones. Here, we evaluate these two hypotheses using data from 200 adults in the New Mexico Decedent Image Database, a collection of full-body CT scans with associated anthropometric data. Bone strength properties (e.g., cortical area, second moments of area) were quantified in the tibial midshaft from CT scans. Interestingly, our results provide support for both hypotheses. First, we found a significant positive association between body weight and tibial strength after controlling statistically for skeletal frame size (stature and pelvic breadth), suggesting that people who subject their bones to more weight (higher loads) have greater bone strength than explainable solely by their baseline skeletal size. Second, a significant positive association was found between waist circumference and tibial strength after controlling statistically for the effects of body weight, suggesting that people with more adipose tissue (a proxy for energy abundance) have greater bone strength than explainable solely by the contribution of adipose tissue to body weight.

Funding was provided by a Maxine Graves Undergraduate Award (to H.M.C.-G.) and the Alfonso Ortiz Center for Intercultural Studies (to I.J.W.).

The predictive power of immune system biomarkers in quantifying aging and mortality risk noninvasively in a free-ranging population of rhesus macaques

EVE B. COOPER[1,2], NINA BEEBY[2,3], CONNOR WHALEN[1], CAYO BIOBANK RESEARCH UNIT[4], LAUREN JN. BRENT[5], NOAH SNYDER-MACKLER[6,7,8] and JAMES P. HIGHAM[1,2]

[1]Department of Anthropology, New York University, [2]The New York Consortium in Evolutionary Primatology (NYCEP), [3]The Graduate Center, City University of New York, [4]Department of Neuroscience, University of Pennsylvania, [5]Centre for Research in Animal Behaviour, University of Exeter, [6]School of Life Sciences, Arizona State University, [7]Center for Evolution and Medicine, Arizona State University, [8]ASU-Banner Neurodegenerative Disease Research Center, Arizona State University

The role of the immune system in aging and mortality risk is an important but poorly understood proximate component of individual fitness. In the present study, we aimed to investigate the predictive value of two urinary compounds, neopterin and suPAR, as biomarkers of aging, as well as biomarkers of current and future mortality risk, in the free-ranging rhesus macaque (*Macaca mulatta*) population located on Cayo Santiago, Puerto Rico. Neopterin concentrations were significantly positively correlated with age (n=856 samples from 210 individuals), with a predicted increase of 38% in baseline concentrations over ten years of adult life on average at the population level. Among individuals that naturally died during the 18 months of this study (n=46 samples from 23 individuals), neopterin concentration was positively correlated with proximity to death, with a predicted increase of 14% per month approaching death within the final 14 months of life. Conversely, suPAR concentration was not correlated with adult age, and showed no association with proximity to death. Both neopterin and suPAR showed patterns of seasonality, being significantly higher at the end of the mating season. This effect was seen in both sexes, indicating that immune system-related impacts of the mating season are not sex specific. Our results indicate that both compounds have the potential to provide fine-scale and noninvasive

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

measurement of immune system responses in a free-ranging primate. Neopterin specifically holds promise as a biomarker of degenerative health due to aging and is predictive of death.

This work was supported by the National Institutes of Health (Grant: R01-AG060931).

A quantitative genetic analysis of selection in the non-human hominid cranium over four ontogenetic stages

MARIANNE J. COOPER[1], EVAN A. SIMONS[1,2] and NOREEN VON CRAMON-TAUBADEL[1]

[1]Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, [2]Department of Behavioral Neuroscience, Oregon Health and Science University

Prior studies have found high levels of integration within cranial modules, similar patterns of integration among species throughout ontogeny, and evidence of strong stabilizing selection in the hominid cranium. A direct investigation of selection strength on the cranium and within modules would provide insight into whether stabilizing selection within or between modules contributes to the observed differences in morphology among taxa. This study applies Lande's generalized genetic distance, a framework that can be used to test for selection, to examine selection in non-human hominid crania in an ontogenetic series (from fully erupted deciduous dentition to fully erupted adult dentition) of 252 specimens of *Pongo pygmaeus* (n = 54)*, Gorilla gorilla* (n = 59)*, Pan paniscus* (n = 63)*,* and *Pan troglodytes* (n = 76)*,* using 16 interlandmark distances (traits). First, all 16 traits were analyzed, then traits were analyzed by cranial module. Results from the analysis of all traits indicated that strong stabilizing selection characterizes all evolutionary transitions for all age groups except the transition from the last common ancestor of African apes to *G. gorilla,* for which drift cannot be rejected. Results from module-specific analyses, however, indicated that strong stabilizing selection characterized early age groups, but drift could not be rejected for many of the transitions in adult and late juvenile groups. These results indicate that stabilizing selection between rather than within modules may play a strong role in shaping the morphology of the non-human hominid cranium.

This research was funded by National Science Foundation Grants (BCS-1751885, BCS 1830745)

Associations between baseline central and peripheral oxytocin and vasopressin concentrations and individual social behaviors in baboon species (*Papio hamadryas* and *Papio anubis*)

DANIEL J. COPPETO[1], JORDAN S. MARTIN[2], PABLO MORALES[3], VITTORIO PALMIERI[3], GARY WHITE[4], ROMAN WOLF[4], LARRY J. YOUNG[5,6] and ADRIAN V. JAEGGI[2]

[1]Anthropology, Emory University, [2]Institute of Evolutionary Medicine, University of Zurich, [3]Veterinary Medicine, The Mannheimer Foundation, [4]Department of Pathology, Division of Comparative Medicine, University of Oklahoma Health Sciences Center, University of Oklahoma, [5]Silvio O. Conte Center for Oxytocin and Social Cognition, Center for Translational Social Neuroscience, Yerkes National Primate Research Center, Emory National Primate Research Center, [6]Department of Psychiatry and Behavioral Sciences, Emory University School of Medicine

Individual primates display a wide array of temperaments and behavioral biases. While some frequently engage in intimate affiliative interactions, others are more biased to aggressive responses to social stimuli. Proximate neurobiological mechanisms (such as differing concentrations of cerebrospinal fluid (CSF) serotonin metabolites) have previously been implicated in contributing to these individual differences in temperament and behavior (i.e. "personality"). Given this previous research and the known influence of the neurohormones oxytocin (OT) and arginine vasopressin (AVP) in mediating affiliative and aggressive behaviors, we investigated whether individual differences in personality were associated with baseline levels of AVP in the CSF, and OT in CSF, blood plasma, and urine. We predicted that OT would correlate most strongly with affiliative behaviors, and AVP with aggressive behaviors. Biosamples and behavioral observations were collected from 70 captive baboons and hormones were assayed using ELISA. We used a Bayesian multivariate multilevel model to detect stable individual differences in nine behaviors and test for associations with hormone levels. Interestingly, baseline plasma OT was positively associated with initiation of close proximity and grooming. In contrast, CSF AVP was negatively associated with time spent in close proximity. In addition, both urinary and plasma OT were associated with submissive behaviors, albeit in opposite directions. In sum, it is suggested that these differences in baseline OT and AVP may predispose individuals for certain temperaments.

Funded in part from the National Science Foundation's Doctoral Dissertation Improvement Grant (Award Number 1413395), and the Silvio O. Conte Center for Oxytocin and Social Cognition.

Structural and Physical Violence in Archaic Greece: The Bioarchaeology of the "Distinctly Different" in the Phaleron Cemetery

AVIVA A. CORMIER[1], JANE E. BUIKSTRA[2] and HANNAH LIEDL[3]

[1]Anthropology, Davidson College, [2]School of Human Evolution and Social Change, Arizona State University, [3]Anthropology, Durham University

The world's attention was captured by the 7th century BCE finds that emerged from the coastal sands of Faliro, the ancient Port of Athens. Seventy-nine young men had been violently executed and interred in three trenches. They lived and died during the political upheavals that culminated in the foundational democracy of Classical Athens. These, however, are but a fraction (<10%) of those buried at the site of Phaleron, excavated between 2012 and 2017 by Dr. Stella Chryssoulaki of the Ephorate of Antiquities of West Attica, Piraeus, and Islands.

Most of the 1000+ individuals buried nearby fall within an expected range of burial forms, including pits, cists, and jars. We focus here upon 82 additional "atypical" burials, interred collectively in mass graves or buried prone or tightly flexed in single graves, with some bound at the wrists and/or ankles. Those buried in mass graves were exclusively biological males, while females were included in atypical single graves (22%). Adolescents and young adults dominated mass graves, while individual graves included all adolescent and adult age categories. We found a significant difference between the two forms (mass graves and individual burials) in childhood stressors (7% and 31% with linear enamel hypoplasia, respectively) and those of adulthood (13% and 57% with carious lesions and abscesses, respectively). Approximately 1/3 of both groups showed healed, antemortem postcranial fractures. Here we explore these life history factors, emphasizing how their potentially violent life and death experiences may have impacted their identity construction, physical wellbeing, and resulting mortuary treatment.

NSF BCS-1828645, NEH RZ-255623, Wiener Laboratory of the American School of Classical Studies at Athens

Mandibular corpus shape as a taxonomic indicator through ontogeny

CESAR O. CORNEJO OCHOA[1], IRISA ARNEY[2] and JASON MASSEY[3]

[1]College of Osteopathic Medicine, Western University of Health Sciences, [2]Department of Medical Anatomical Sciences, Western University of Health Sciences - College of Osteopathic Medicine, [3]Department of Anatomy and Developmental Biology, Centre for Human Anatomy Education, Biomedicine Discovery Institute, Monash University

Mandibular corpus (MC) specimens are prevalent in the hominoid fossil record, making them useful to discern taxonomic relationships among extinct hominoids. 3-dimensional geometric morphometric (3DGM) methods applied to the MC have shown promise in distinguishing modern adult hominoid species, but less is known about the taxonomic reliability of MC morphology through development. In this study, we evaluate shape

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

differences in the MC between five extant African ape species and subspecies to determine at which developmental stage morphological differentiation occurs.

Four subregions of the MC were digitized using 346 landmarks and semilandmarks in a sample of 249 mandibular 3D surface scans. A series of MANOVAs and discriminant functions analyses (DFA) were run on pairwise groups (at the genus-, species-, and subspecies-levels) at four developmental stages.

MC morphology between *Gorilla* and *Pan* was significantly different by dP4 occlusion. Differences between species of *Gorilla* were distinguished by M1 occlusion, while differences between species of *Pan* were significantly different by dP4. MC morphology was indistinguishable between subspecies of *Pan troglodytes* at any dental developmental stage.

These findings suggest that MC morphology at the earliest post-natal developmental stages can be a useful taxonomic indicator to differentiate between great African ape species at higher taxonomic levels, but MC morphology at any taxonomic level has decreased predictive power at the subspecies and population level. These findings in comparison to previous studies also show that the MC – an element largely associated with dietary function – may be less taxonomically useful than cranial elements in closely related populations.

The bony labyrinth and the population history of pre-Colonial Brazil – A virtual anthropology approach

MARIA ANA CORREIA[1,2], MANUEL DIMITRI[2], TALITA LIMA[2], JOÃO VÍTOR MACRON[1], LUANA SPÓSITO[1,2], RODRIGO OLIVEIRA[2], VERONICA WESOLOWSKI[1] and ANDRÉ STRAUSS[1,2]

[1]Museu de Arqueologia e Etnologia, Universidade de São Paulo, [2]Instituto de Biociências, Universidade de São Paulo

Understanding relationships of kinship between populations is key to the archaeological interpretation of peopling of the world, including the settlement of the American continent. Traditionally, these studies focused on morphological comparisons of anatomical regions (e.g., crania) and, more recently, on molecular data (i.e., aDNA). However, archaeological crania often do not preserve anatomical integrity while aDNA is affected by diagenesis. The advance of computed tomography allowed anthropologists to study effectively other anatomical structures, such as the bony labyrinth. Located in the petrous part of the temporal bone, this structure (1) records genetic distances between populations, due to its conformation to a model of serial founder effects, (2) preserves well in the archaeological record and (3) its study is not destructive. To validate the use of this new method in a Brazilian context, we analysed the labyrinth morphology from four Brazilian archaeological groups (*Toca do Alexandre, Lapa do Santo, Piaçaguera,* and *Moraes*), collecting 20 landmarks that represent 10 measurements of this structure. Preliminary results indicate that at least three of these measurements differ between groups with nine presenting a high effect size, confirming that the morphology of the bony labyrinth differs between populations. Follow-up analyses suggest that *Piaçaguera* is the most distinct group (and not the oldest *Lapa do Santo* as previously hypothesised), which supports what was previously found through non-metric dental analyses. Thus, these preliminary findings pioneer Virtual Anthropology in Brazil and contribute with a new tool to reconstruct, explain, and model the narrative of past populations in Brazil and elsewhere.

Funding provided through grants 2017/16451-2 (AS), 2020/06729-6 (MAC), 2021/08346-0 (TM) and 2022/01850-7 (DM) by São Paulo Research Foundation (FAPESP)

Correlations of cortical and trabecular bone across ontogeny in *Pan troglodytes*

MIRANDA N. COSMAN, MAUREEN J. DEVLIN and LAURA M. MACLATCHY

Anthropology, University of Michigan

Both cortical bone geometry and trabecular bone microarchitecture reflect interspecific locomotor differences in adult mammals. It has also been shown that within species, including *Pan troglodytes*, changes in bone architecture during ontogeny are correlated with changes in locomotion. In this study, we use *Pan troglodytes* as a model organism to determine how trabecular and cortical bone correlate together in response to changing locomotor behavior across ontogeny.

We hypothesize that if trabecular and cortical bone both respond dynamically to locomotor transitions, then cortical and trabecular bone will exhibit traits associated with arboreality during infancy and juvenility, and traits associated with terrestriality during adolescence and adulthood. To test this, we scanned the proximal femur and humerus of *Pan troglodytes* infants (n=6), juveniles (n=5), adolescents (n=2), and adults (n=5, 1M, 2F, 2U) using microCT. Volumes were generated in Dragonfly, exported, and analyzed using BoneJ. Results showed a significant but modest linear relationship ($p = 0.04$, $r^2 = 0.24$) between relative cortical area (CA/TA) and trabecular bone volume fraction (BV/TV) that did not vary with age or bone. In the humerus, there was a significant overall relationship between the polar moment of area (J, mm^4) and BV/TV ($p<0.05$, $r^2 = 0.86$). Adult humeri had significantly higher J for a given BV/TV relative to infants ($p=0.0005$) and juveniles ($p=0.002$). Cortical and trabecular bone were not significantly correlated in the femur. These results indicate the relationships between cortical and trabecular bone differ in the femur and humerus across ontogeny, independent of locomotion.

Funding for this research was provided by the Leakey Foundation and NSF-DDRIG (1945692) to MNC.

Potential Health Correlates with Social Connectedness in Captive Olive (*Papio hamadryas anubis*) and Olive/Yellow Hybrid (*P. h. cynocephalus*) Baboons

SARA J. COTTON[1], CORRINE K. LUTZ[2] and FRANCES J. WHITE[1]

[1]Anthropology, University of Oregon, [2]Animal Behavior Program, Bioqual Inc.

Primate social behaviors mitigate the negative effects of stress. In wild baboons, social connectedness predicts longevity and health, but the relationship between social connectedness and biological health in captive baboons is less known. Studies often use glucocorticoids to measure stress, but neutrophil and lymphocyte levels are correlated with cortisol levels and are available from routine veterinary bloodwork. High stress is associated with high levels of neutrophils and low levels of lymphocytes. This study assessed the impact of connectedness through social grooming on neutrophil and lymphocyte levels. Subjects were 45 adult female baboons housed in social groups consisting of one male, 3 to 12 females, and associated offspring. Four 30-minute all-occurrence samples were used to collect social grooming data. Blood data was collected opportunistically through routine veterinary check-ups. When all of the data was considered together, there were no significant overall correlations between neutrophil levels and the other factors assessed. However, social grooming and lymphocyte levels were related, but were complicated by the relationship of lymphocytes generally going down with age. Females with few social grooming partners (2 or less) showed this expected significant negative regression of lymphocyte levels on age ($F=13.34$, $df=1,30$, $p<0.01$). Females with many social grooming partners (3 or more), however, showed no significant regression of lymphocytes on age ($F=0.40$, $df\ 1,11$, ns). It appears, therefore, that older female baboons with many social partners are buffered against age related decreases in lymphocytes and that connectedness is potentially acting to mediate the negative health effects of chronic stress.

Supported by P51OD011133.

Illustrating Allen and Bergmann's Rules: Challenges and Pitfalls

LIBBY W. COWGILL

Department of Anthropology, University of Missouri, Columbia

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Biological anthropologists have long been interested in how Allen and Bergmann's rules influence human body shape across the globe. Given this, accurate visual representation of the relationship between an organism's volume and surface area in both professional talks and teaching presentations is important. However, many of the images currently available are problematic both scientifically and artistically. Visual depictions of humans in traditional costumes representing specific populations can be both essentialist and alienating for students. This presentation explores unconventional representations of Allen and Bergmann's rules though both photography and original drawings. The ultimate goal is to create aesthetically pleasing and inclusive illustrations, that successfully enhance viewer understanding of core concepts in thermoregulation. High resolution digital copies are available to interested parties on site for incorporation into their own presentations.

Effects of culture, environment and ancestry on stature in Early Neolithic Europe

SAMANTHA L. COX[1,2], NICOLE NICKLISCH[3], KURT W. ALT[3], WOLFGANG HAAK[4], EVA ROSENSTOCK[5] and IAIN MATHIESON[1]

[1]Department of Genetics, Perelman School of Medicine, University of Pennsylvania, [2]Physical Anthropology Section, Penn Museum, University of Pennsylvania, [3]Center of Natural and Cultural Human History, Danube Private University, [4]Department of Archaeogenetics, Max Planck Institute for the Science of Human History, [5]Bonn Center for ArchaeoSciences, Universität Bonn

This abstract is part of the symposium: *Toward a holistic approach - Investigating the genetic underpinnings of phenotypic variation*.

Morphology, genetics, environment, and culture are all inexorably linked in human development and experience, but analysis of these factors is often limited by the exclusion of the others. Genetic effects in particular are known to be powerful, but are hard to interpret in isolation. In this study, we use genetic, skeletal metric, paleopathology, and dietary stable isotope data from 1311 individuals to co-analyze genetic and non-genetic effects on stature in Early Neolithic Europe. Polygenic scores (PRS) in Central Europe are consistent with male femur length, but females from this region are significantly shorter than genetic predictions. This increase in sexual dimorphism is not associated with either $\delta^{13}C$ or $\delta^{15}N$ values. Cribra orbitalia and linear enamel hypoplasias are significantly more prevalent in the North where dimorphism is most extreme and is associated with reduced stature. Extreme dimorphism and negative female-specific health effects are consistent with present-day cultures which exhibit male preference in resource partitioning. In Southern Europe, we see opposite trends: PRS for females in this region are the shortest of those studied, though femora are the longest on average; male femora are shorter, as predicted by PRS. This decreased sexual dimorphism is more consistent with stress response where the sexes are equally sharing the burden. By analyzing multi-disciplinary data, we are able to better understand interactions between genetic and non-genetic factors in producing phenotypes, leading to more nuanced and comprehensive interpretations.

Supported by the National Science Foundation, grant No. BCS-2123627 and German Research Foundation (DFG), grant Nos. RO 4148/1-1; Al 287/7-1 and 7-3; Me 3245/1-1 and 1-3.

B3GET: A generalized agent-based model of primate ecology, evolution, and social behavior

KRISTIN N. CROUSE, CLARENCE L. LEHMAN and MICHAEL L. WILSON

Ecology, Evolution and Behavior, University of Minnesota

Studies of our primate relatives provide opportunities to develop and test socioecological models, which can help explain the evolution of social structure and behaviors such as cooperation. However, current socioecological models are limited by the sheer number of variables involved and the difficulty of operationalizing ecological concepts like resource distribution. Agent-based models have great potential for advancing the field because they can handle many variables and incorporate individual variation, stochasticity, and emergent properties. However, they are often designed for a single species or area of research, limiting their application to broader questions. To promote greater understanding of primate socioecology, we developed B3GET, a generalized agent-based model of virtual primates with decision-making rules encoded in diploid chromosomes to dictate movement, body growth, inclination to mate, eat, and other behaviors. The virtual environment consists of plants that vary in their quality and distribution. B3GET users can edit the starting genotype and population files to create species-specific virtual primates, and then collect simulation data for hypothesis testing. We conducted 4608 simulations of four primate species — chimpanzees, geladas, hamadryas baboons, and olive baboons — and found that these virtual counterparts resembled the target species in many aspects of their group composition, dispersal patterns, and mating strategies. For example, 48% of the simulated chimpanzee females joined a neighboring community at sexual maturity, exhibiting a similar dispersal rate to that observed at Gombe National Park. Because B3GET can effectively emulate a broad range of primate species, it provides a promising approach for investigating human origins.

Impact of sample pretreatment on enamel strontium isotope data

BROOKE E. CROWLEY[1,2], EMILY M. B. SIMPSON[1], SARAH J. HAMMER[1], JOSHUA M. SMITH[3] and THOMAS M. JOHNSON[3]

[1]Department of Geosciences, University of Cincinnati, [2]Department of Anthropology, University of Cincinnati, [3]Department of Geology, University of Illinois Urbana-Champaign

Pretreatment methods used to prepare tooth and bone samples for strontium isotope ($^{87}Sr/^{86}Sr$) analysis vary tremendously. Researchers commonly assume that sample pretreatment has no isotopic impact, but this has not been validated. We compared 14 enamel pretreatment methods that are representative of published methods used by ecologists, archeologists and paleontologists. These included no prep other than powdering enamel; ashing; soaking in water, an oxidizing agent (bleach or hydrogen peroxide), or acetic acid (0.1M, 1.0M, and 1.0M buffered with calcium acetate); and a combination of these steps. We worked with molars from one modern Indian elephant, one Pleistocene mastodon, and one Miocene gomphothere, preparing and analyzing triplicate aliquots of homogenized powdered enamel from each tooth for each method.

Ranges in average $^{87}Sr/^{86}Sr$ across methods were 0.70999-0.71029, 0.71458-0.71502, and 0.70804-0.70817 for the modern, Pleistocene, and Miocene teeth, respectively. Variability in $^{87}Sr/^{86}Sr$ was small for the Miocene tooth, but there were significant isotopic differences among pretreatments. Variability in $^{87}Sr/^{86}Sr$ within and across pretreatments was larger for the modern and Pleistocene molars. These specimens contained relatively little strontium, and it is possible that small amounts of exogenous strontium from reagents, building materials, or dust affected some replicates.

We caution researchers to avoid combining data obtained using different methods, particularly for older specimens, as small differences in $^{87}Sr/^{86}Sr$ could impact data interpretations, especially in areas where variability in $^{87}Sr/^{86}Sr$ is small. Errors related to exogenous Sr will depend on the strontium content of a sample and the $^{87}Sr/^{86}Sr$ of both biogenic and contaminant strontium.

This project was supported by NSF Award No. EAR-2110297 to BEC.

Indigenous peoples in eastern Brazil: insights from 19th century genomes

DIANA IVETTE CRUZ DÁVALOS[1,2], YAMI OMMAR ARIZMENDI CÁRDENAS[1,2], MIRIAM JETZABEL BRAVO-LOPEZ[3], SAMUEL NEUENSCHWANDER[1,2], SILVIA REIS[4], MURILO Q.R. BASTOS[4], JESPER STENDERUP[5], FULYA EYLEM YEDIAY[5,6], VIRIDIANA VILLA-ISLAS[3], CARLOS S. REYNA-BLANCO[7], CLAUDIA RODRIGUES-CARVALHO[4], TÁBITA

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

HÜNEMEIER[8], MORTEN E. ALLENTOFT[5], CARLOS EDUARDO G. AMORIM[1,2,9], J. VÍCTOR MORENO-MAYAR[1,2,5], MARÍA C. ÁVILA-ARCOS[3] and ANNA-SAPFO MALASPINAS[1,2]

[1]Department of Computational Biology, University of Lausanne, [2]Swiss Institute of Bioinformatics, [3]International Laboratory for Human Genome Research, National Autonomous University of Mexico, [4]Departamento de Antropologia, Museu Nacional, Universidade Federal do Rio de Janeiro, [5]Lundbeck Foundation GeoGenetics Center, GLOBE Institute, University of Copenhagen, [6]The Institute of Forensic Sciences, University of Istanbul, [7]Department of Biology, University of Fribourg, [8]Departamento de Genética e Biologia Evolutiva, Instituto de Biociências, Universidade de São Paulo, [9]Department of Biology, California State Northridge

The 2010 census in Brazil indicates that one third of its Indigenous population speaks a Tupi language and one quarter speaks a language of the Jê family. While there is archaeological, linguistic and, more recently, genetic evidence for Tupi speakers to have migrated over vast regions of today's Brazil, less is known about the genetic affiliations and possible migration routes of Jê speakers. Linguistic studies have estimated that the two language stocks diverged prior to the Tupi expansions (thought to take place between 2,000 and 3,000 YBP) and up to 7,000 YBP.

To uncover part of the genetic history of Indigenous South Americans, we analysed the genomes of twenty-two ancient individuals from central-eastern Brazil, dated to the 16th-19th century. These individuals have been associated with "Botocudo" populations, a label usually given to Jê speakers with hunter-gathering lifestyles in the area. Our results indicate that these potential Jê speakers are indeed an outgroup to present-day Tupi speakers. However, under several demographic scenarios considered, the "Botocudos" and Tupi speakers diverge at most 1,000 - 3,000 YBP. Therefore, the genetic differentiation between these clades is rather small compared to their linguistic divergence. This implies that either a) "Botocudos" (and potentially other Jê speakers) might actually descend from the migrations associated with Tupi speakers, or that b) Tupi expansions took place earlier than expected, and migration and genetic diversification observed among present-day Tupi speakers occurred at faster rates than previously thought.

Dental morphological affinities among Precolumbian Costa Rica and their potential affinities with Mesoamerican Postclassic.

ANDREA CUCINA[1], ALLAN ORTEGA-MUÑOZ[2] and MONICA AGUILAR BONILLA[3]

[1]School of Anthropological Sciences, Universidad Autónoma de Yucatán, [2]Centro INAH Quintana Roo, [3]Escuela de Antropologia, Universidad de Costa Rica

From the bioarcheological perspective, little information is available on the populations that inhabited nowadays' Costa Rica (CR). Population affinities and demic relationships among CR's different regions (i.e., the Nicoya Peninsula, Central Valley, and others) still need to be explored from a biocultural perspective, in particular because material culture suggests cultural contacts between the Nicoya Peninsula and Mesoamerica in Prehispanic times.

The present study explores population relationships in CR through the analysis of dental morphological traits among two human skeletal collections from the Nicoya Peninsula (Jícaro and La Cascabel) and one from the Central Valley (Playskool, Agua Caliente and El Molino), all dated between the 9th and the 16th century AD. To get a wider view from a macro-regional perspective, they are contextualized with some Classic (AD 300-1000) and Postclassic (AD 1000-1520) Maya groups from Honduras and the Yucatan Peninsula. Statistical analyses indicate a closer relationship between La Cascabel and the Central Valley, suggesting a common regional morphological background in CR, while Jícaro diverges from the other two, despite its close geographical proximity with La Cascabel. From a macro-regional perspective, La Cascabel and Central Valley gather with Postclassic Maya groups from the Yucatan Peninsula; Jícaro and the Maya Classic period groups separate from all the others. Jícaro presents "foreign" cultural and biocultural traits that differ from those commonly found in CR, which explains its divergence from the other two groups from CR. Similarities with the Postclassic groups from Yucatan, instead, suggest more extensive contacts between Meso- and Centro-America in Postclassic times

This study was made possible by CONACyT grant CB-2017-2018-A1-S-10037 to A.C.

Sex-based differences in the nasal morphology of Lemur catta

JULIANA G. D'ORAZIO and STEPHANIE A. POINDEXTER

Anthropology, University at Buffalo

The most prominent forms of sexual dimorphism across primates are in body size and their canines. Primates also display dimorphism in their pelage and skeletal features. The bulk of this work focuses on haplorhines, who tend to display stronger trends in physical dimorphism compared to strepsirrhines, who tend show slight to no dimorphism in their body's, canine's, and pelage (with a few exceptions within the lemurs). Ring tailed lemurs are monomorphic in most physical measures,but display behavioral differences between males and females. For example they show differences in their feeding ecology, and olfactory behaviors. Additionally, ring-tailed lemurs utilize scent marking for purposes like territory marking and mating. Based on the variable role and use of olfaction in ring-tailed lemurs we investigated whether or not the internal nasal cavity displayed any signes of sexual dimorphism. To complete this project, we downloaded 26 sexed ring-tailed lemur craniums from Morphosource. To characterize the nasal cavity we placed 25 manual landmarks on two-dimensional coronal slices using ImageJ. In Morphologika, we performed a generalized procrutes analysis and a canonical variate analysis to determine if each skull could be identified based on sex alone. Based on this preliminary analysis, there was minimal clustering, but the level of clustering varied by slice moving inward towards the braincase. Our finding suggest that the behavioral sex-differences we see in ring-tailed lemur olfaction does not have a strong physical signature, but this may change with a large dataset or when we consider airflow.

Hair cortisol levels and gut microbiome alpha diversity in infant rhesus macaques (*Macaca Mulatta*): an exploratory analysis

KATHERINE DAIY[1], KYLE WILEY[2], JACOB ALLEN[3], MICHAEL T. BAILEY[4,5] and AMANDA DETTMER[6]

[1]Department of Anthropology, Yale University, [2]Department of Anthropology, University of California Los Angeles, [3]Department of Kinesiology and Community Health, University of Illinois, Urbana-Champaign, [4]Center for Microbial Pathogenesis, The Research Institute at Nationwide Children's Hospital, [5]Department of Pediatrics, The Ohio State University College of Medicine, [6]Yale Child Study Center, Yale School of Medicine

The gut microbiome may influence behavioral and psychological processes through interaction with the hypothalamic pituitary adrenal (HPA) axis, referred to as the gut-microbiome-brain axis. However, few studies have investigated whether early function of the HPA may influence the development of the gut microbiome. We evaluate the relationship between HPA function and the composition of the infant gut microbiome across the first 13 months of life in n=44 mother- and nursery-reared captive infant rhesus macaques. Infant hair samples were collected at various ages and hair cortisol levels (pg/mg) were assessed via enzyme immunoassays. Infant fecal samples were collected at day-of-birth (DOB), day 14 (D14), day 30 (D30) and 6 months postpartum; we performed 16S rRNA sequencing to determine the fecal microbiome composition. We ran Spearman's correlations between the relative abundance of specific taxa and infant hair cortisol, as well as regression models with microbiome diversity (Shannon index) predicting cortisol, with rearing style and infant sex as covariates. While there were no significant relationships between specific taxa and cortisol levels, as an exception, *Bacteroides* abundance at 6 months was associated with cortisol levels (rho = 0.333, p=0.047). Microbiome diversity – at either DOB,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

D14, D30 or 6 months – was not statistically significantly associated with hair cortisol levels at any time point. Previous studies have documented associations between cortisol and the gut microbiome; however, we did not find clear statistical associations in this study. Additional research is needed to investigate the role of the HPA in the gut-microbiome-brain axis.

This study was funded by the Division of Intramural Research at the NICHD and by the American Society of Primatologists Legacy Award (AMD).

Transitioning societies: Post-earthquake Kourion (KAGC) - Human behavior and health after a mass disaster.

ALYCIA C. DAVIS[1], HANNAH B. CARSON[2], HUNTYR HILL[3], MERADETH SNOW[2], MICHAEL GIVEN[4] and XENIA-PAULA KYRIAKOU[5]

[1]Cyprus Institute of Sciences and Humanities, Wrexham Glyndwr University, Wrexham, [2]Department of Anthropology, University of Montana, Missoula, [3]Forensic Studies, Department of Justice Studies, Florida Gulf Coast University, Fort Myers, [4]Archaeology, School of Humanities, University of Glasgow, Glasgow, [5]Legal Studies, Department of Justice Studies, Florida Gulf Coast University, Fort Myers

Cataclysmic events affect the environment and human behavior alike. The study of populations who outlived a natural catastrophe offer insights to sociocultural transitions and subsistence shifts that may directly impact their health. This study evaluates the commingled skeletal material from Kourion's Amathus Gate Cemetery (4^{th} – 7^{th} C.E.) in Cyprus to determine what may have been the post-disaster effects on the population. A total of 5000 commingled bones from 24 cist graves and 10 trenches were analyzed. Low frequencies were found for trauma (0.56%), degenerative (2.24%), metabolic (0.38%) and inflammatory/infectious (1.04%) diseases. Eleven cases of auditory exostoses were present. EC (entheseal changes) was found in low expressions. Low prevalence of pathology and EC may be considered as evidence of health and status in a population. Death however may have been acute in a way that does not present on the bones. The presence of infectious disease (TB) indicates survivability, adaptation to health stressors, and disease management through community or family-based support systems. Evidence of metabolic conditions associated with anemia are more likely to be genetically than environmentally induced. An isolated phenomenon of interpersonal violence is indicated by perimortem cranial trauma that afflicted individuals found buried in the same grave. These findings highlight a rather haphazard trend in health and status, though not confirmed. A degree of continuity that links the periods pre- and post-earthquake is evinced by the presence of auditory exostoses, a trait linked to subsistence activities commonly practiced by coastal populations, and found elsewhere in Cyprus.

Cranial morphological structure of North and South American populations: Implication for discussions about the early human occupation of the American continents

CASSANDRA DAVIS[1], MADELYN GREEN[1,2], DANIEL FIDALGO[3] and MARK HUBBE[1]

[1]Department of Anthropology, Ohio State University, [2]Department of Social Sciences, Columbus State Community College, [3]Museu de Arqueologia e Etnografia, Universidade de São Paulo, Brazil

The biological and morphological diversity of Native American populations has been a topic of intense scrutiny over the past decades, with recent studies demonstrating that the process of human dispersion across the American continents was complex and non-linear. Despite this, the two continents are often combined into one macro-continent in studies about past and present biological diversity, and the differences in human history and occupation between them are largely ignored or oversimplified. In this study, we contribute to the debate about past human dispersion in the Americas by analyzing the cranial morphological variation of 39 population samples from both North and South America. Cranial morphology was represented through 18 linear craniometric variables, and their morphological affinities were explored using multidimensional scaling (MDS) and k-means clusters based on Mahalanobis distances. The MDS results show that North and South American populations overlap considerably in their morphological affinities. However, the k-means results plotted over the geographic location of the series show strong similarities between high-latitude North and South American populations and high affinities among Andean South American populations and most North American series. Eastern South American groups differentiate themselves from other populations, highlighting the biological impacts of different population histories across the southern continent. These results contrast with previous perspectives of grouping the settlement of the two continents into a single large dispersion event. The high degree of cranial diversity seen in the American continents reinforces the need of discussing North and South American human occupation separately by considering their unique histories.

The Coastal Migration Theory: Testable Hypotheses and Research Progress

LOREN DAVIS[1] and DAVID MADSEN[2]

[1]Department of Anthropology, Oregon State University, [2]Department of Anthropology, University of Nevada-Reno

<blockquote> Paleogenetics studies indicate that the First Americans were derived from a founding human population that was isolated from other Asian populations after ~25,000 years ago and expanded into the Americas sometime after ~19,500 years ago. Archaeological discoveries at multiple sites south of the North American continental ice sheets show human occupation by ~16,000-14,000 years ago. This evidence predates any possible opening of an ice-free corridor (IFC) between the Laurentide and Cordilleran ice sheets. This array of data is now sufficiently large that it requires an organizational framework within which to consider the processes and chronology underlying the only reasonable alternative for the initial Pleistocene peopling of the Americas: A Pacific coastal entry way into the New World. This presentation discusses the core ideas of the Coastal Migration Theory, how it might be tested, and presents new information about the search for submerged landforms and late Pleistocene-aged sites along the Pacific coast of North America. </blockquote>

Comparative Methodological Approaches to Capturing 3D Data to Study Shape Variation of the Proximal Humerus and the Scapulae in Extant and Fossil Lemurs

LISA M. DAY[1,2], JESSIE TIGNOR[3], MARIE VERGAMINI[1,3] and AMY L. RECTOR[1]

[1]Anthropology, School of World Studies, Virginia Commonwealth University, [2]Biology Department, Virginia Commonwealth University, [3]Integrative Life Sciences, Virginia Commonwealth University

Previous work on shape variation of proximal ulnae and distal humeri in primates suggests there is a correlation between locomotor repertoires and synovial joint shape in extant Cercopithecidae (Rector & Vergamini, 2018). Often overlooked in studies of the forelimb, extant and subfossil Lemuridae have independently evolved many locomotor behaviors convergent with Cercopithecidae. Tests of the hypothesized relationship between locomotor adaptation and 3D variation in primate scapulae and proximal humeri are more robust when morphological variation of Lemuridae is included in analyses.

For this project, ~25 extant Lemuridae and ~3 subfossil lemur species assigned to substrate use and a range of phylogenetic and geographic relationships were included in the analysis. Thirty landmarks characterizing the shape of the proximal humerus and 25 landmarks characterizing the shape of the scapula were digitized with a 3D MicroScribe, and resulting shape variations in these joint surfaces were analyzed using Python and MorphoJ. Each specimen was also 3D scanned using photogrammetry via a DSLR camera and analyzed with MeshLab.

Results suggest that behaviors affecting shape variation in the Lemuridae scapula and proximal humerus are likely multifaceted and complex; the relationship between substrate use and this variation remains unclear. This research explores this relationship both functionally and phylogenetically,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

providing a better understanding of how shoulder mobility reflects locomotor behavior in primates. Additionally, results from the two data collection methods were comparable, providing support for the use of a time and cost efficient data collection technique.

Genomic profiling of the Priory Orchard site in Godalming (Surrey, UK, 800-1125 AD)

FLAVIO DE ANGELIS[1], ELIZABETH A. NELSON[2], NASREEN BROOMANDKHOSHBACHT[3], SAM LEGGETT[4], ROB POULTON[5], TODD C. RAE[6], LARS FEHREN-SCHMITZ[3], LIA BETTI[7] and CARLOS EDUARDO G. AMORIM[1]

[1]Department of Biology, California State University Northridge, [2]Microbial Paleogenomics Unit, Department of Genomes and Genetics, Institute Pasteur, [3]Department of Anthropology, University of California Santa Cruz, [4]School of History, Classics and Archaeology, University of Edinburgh, [5]Archaeological Unit, Surrey County, [6]School of Life Sciences, University of Sussex, [7]School of Life and Health Sciences, University of Roehampton

Priory Orchard in Godalming (POG), Surrey, is a rare early Christian churchyard cemetery from a rural area in Southern England. It was used between ca. 800-1125 AD, covering the Late Anglo-Saxon to Early Norman transition period. The archeological surveys returned about 300 articulated burials, mostly lacking grave goods. Here, we aim to provide a first glimpse into their genomic characterization to investigate the impact of the complex socio-political and cultural transitions on population structure and demography. Teeth and petrous bones from 76 individuals were sampled to generate Whole Genome Sequencing (WGS) data. Following the authentication of the data, we evaluated the kinship structure across the individuals, resulting in the identification of potential familial clusters up to second-degree relationships. Furthermore, the reads mapping on the sex chromosomes allowed for dissecting the POG demographics, supporting the osteological sex determinations. We filtered the genetic variants for the 1240K SNP panel and compared POG with roughly coeval and present-day populations to elucidate genetic similarities through PCA, Admixture, and F-statistics. Our results suggest a marked genetic variability for POG, consistent with the transitional period of cemeterial activity. Overall, POG genetic variation falls within the European one, with individual genomic characteristics following a South-North cline partially confirmed by the admixture analyses, which identify a not negligible continental European genetic signature for some individuals. Our data support that the multiple migration events throughout the early medieval period in Britain left differential genetic signatures seen in the ancestry of the POG individuals.

Research reported in this publication was supported by the National Institute of General Medical Sciences of the National Institutes of Health under award number R35GM142939.

A world between frontiers: evaluating genetic shifts and continuity in past populations from Southern Chile

CONSTANZA P. DE LA FUENTE[1], MICHAEL ORELLANA[2], ROBERTO CAMPBELL[3], PEDRO ANDRADE[4], MAURICIO MORAGA[2] and MAANASA RAGHAVAN[1]

[1]Human Genetics, University of Chicago, [2]Programa de Genética Humana, ICBM, Universidad de Chile, [3]Escuela de Antropología, Pontificia Universidad Católica de Chile, [4]Carrera de Antropología, Universidad de Concepción

Characterization of present-day genetic variation is key to our understanding of human population histories. How this variation was shaped over time and the evolutionary processes involved are essential questions where both social and natural sciences contribute alike. In the Americas, while studying present-day populations has greatly contributed to our understanding of past demographic events, this approach has limitations mainly due to the profound impact of European colonization on the local genetic structure and diversity. In this project, we implemented state-of-the-art paleogenomic tools for the analysis of ancient individuals from Southern Chile to (1) characterize the human genetic variation in the region during pre- and post-Columbian times and (2) evaluate the genetic consequences of the spread of ceramics, agriculture, and European colonization on the genetic diversity of population from the region. We evaluated the DNA content in bones/teeth from 35 individuals ranging from the Archaic Period to Historical times. The human endogenous DNA content ranges from 0.023% to 51%, with all samples showing characteristic damage patterns of ancient DNA. We were able to reconstruct whole mitogenomes for 15 individuals, finding South American-specific lineages haplogroups B2i2, C1b13, and D1g. Whole-genome analysis was possible for eight individuals, six showing strong genetic affinity with each other and with present-day populations from Southern Chile. Two historical individuals seem to have evidence of European genetic admixture. Overall, both mitogenomes and whole-genome data suggest genetic continuity within the region from at least the Early Ceramic Period (ca. 1550-950 cal BP).

National Geographic Society and American Association of University Women.

New Pliocene cercopithecoid primates from Laetoli, Tanzania (1998-2022)

ANDREW S. DEANE[1,2,9], HAYDEN HURST[1], ELICIA ABELLA[3], JEREMY DESILVA[5,6,9], ELLISON MCNUTT[4], SHIRLEY RUBIN[7], ELLIE GUSTAFSON[8], KELLER VINCENT[1], DEVRY BECKETT[8], MARIHA CORBIN[8] and CHARLES MUSIBA[8,9]

[1]Anatomy, Cell Biology & Physiology, Indiana University School of Medicine, [2]Department of Anthropology, Indiana University in Indianapolis, [3]Department of Anthropology, University of Arkansas, [4]Anatomy, Idaho College of Osteopathic Medicine, [5]Ecology, Evolution, Environment and Society, Dartmouth College, [6]Anthropology, Dartmouth College, [7]Anthropology, Napa Valley College, [8]Anthropology, University of Colorado Denver, [9]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand

Laetoli, Tanzania preserves the earliest fossils attributed to *Australopithecus afarensis* (3.7 Mya), however, recent re-analysis of the hominin trackway at footprints Site A supports the presence of at least two hominin taxa. Laetoli also preserves a diverse cercopithecine assemblage representing both more folivorous and arboreal colobines and more omnivorous and terrestrial cercopithecids, although the latter is more abundant. The relative proportion of each group's factors prominently in interpretations of the extent of closed woodland/forested environments and open scrub/bushland. This study uses standard dental morphometrics and relative cusp proportion analyses to establish the morphological affinity of 11 new cercopithecoid dentognathic specimens recovered from Laetoli between 1998 and 2022 to further clarify the paleoenvironmental context for early humans at Laetoli.

Discriminant function analysis (DFA) with an extant cercopithecoid sample (n=90; 18 genera), was used to predict taxonomic affiliation for 11 specimens, including two mandibles with associated dentition. Mandibular molars more reliably segregate colobines from cercopithcids (77.1% - 87.2%) than do maxillary molars (64.4% - 70.2%). Colobine hypoconids and metacones are expanded but they have reduced metaconids, entoconids and paracones relative to cercopithecoids. The most complete mandibular specimen is attributed to *Rhinocolobus* sp. and preserves the only known female canine for that taxon. These results confirm that colobine primates are a significant faunal component in the upper Laetolil beds and are consistent with the significant presence of closed woodland/forested habitats. This suggests that hominin taxa at Laetoli would have had access to a diversity of habitats including closed woodland/forested environments and arboreal substrates.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Field-optimized selective sequencing of MHC-containing chromosome 17 of the vervet (*Chlorocebus aethiops*) using Oxford Nanopore technology

REBECCA M. DECAMP[1,2], LINDSEY R. HAUFF[2,3], MORGAN E. CHANEY[4,5], ANTHONY J. TOSI[4,5] and CHRISTINA M. BERGEY[2,6]

[1]Anthropology, Rutgers University, [2]Center for Human Evolutionary Studies, Rutgers University, [3]Ecology, Evolution, and Natural Resources, Rutgers University, [4]Anthropology, Kent State University, [5]School of Biomedical Sciences, Kent State University, [6]Genetics, Rutgers University

The Oxford Nanopore MinION is a portable third-generation sequencing technology that allows researchers to sequence DNA or RNA from samples in the field. While the MinION is most useful for sequencing smaller genomes, sequencing larger genomes, like those of primates, with the platform can be cost-ineffective. Adaptive sampling is a method of targeted sequencing using Oxford Nanopore Technology in which DNA strands can be computationally accepted or rejected in real time based on similarity to a predefined target. Adaptive sampling therefore offers an avenue for targeted sequencing of genes or chromosome regions when whole-genome sequencing is impractical. Here, we report a successful adaptive sampling experiment using the Oxford Nanopore MinION (Mk1B) in which we enriched chromosome 17 of a vervet monkey (*Chlorocebus aethiops*). We isolated high molecular weight DNA from a captive monkey sample from a population originating in St. Kitts and Nevis, and prepared the library using the Field Sequencing Kit (SQK-LRK001). We programmed the MinKNOW software to enrich sequences within our targeted chromosome, and used the Guppy and MinKNOW software to perform live GPU-powered basecalling of our sample. Our adaptive sampling experiment generated over 5,500 reads covering over 5 million basepairs. After enrichment, chromosome 17 had the highest density of reads longer than 1 kilobase in length (19.45 vs. genome average of 7.53 reads per 100 megabases). Overall, the success of this experiment paves the way for future adaptive sampling in the field using the MinION.

Funding for the work provided by Rutgers University and an NSF grant to CMB and AJT (BCS1717188).

Rethinking cranial base angle in light of primate ontogeny

VALERIE B. DELEON[1], KATHERYN P. FRANKLIN[1], EMILY R. BRYSON[1], ANDREANA S. CUNNINGHAM[1], SIOBHAN A. SUMMERS[1] and TIMOTHY D. SMITH[2]

[1]Anthropology Department, University of Florida, [2]School of Physical Therapy, Slippery Rock University

Cranial base angle (CBA) is a critical variable in paleoanthropology, primate comparative anatomy, and clinical studies. Generally, CBA describes the midsagittal angle between anterior and posterior cranial fossae, capturing changes in midsagittal basicranium produced by brain expansion through developmental and evolutionary time. Multiple definitions of CBA are well-reviewed in the literature; all are defined as a single angle. However, multiple midsagittal growth centers in the basicranium generate multiple points of midsagittal rotation. CBA should be conceptualized as a composite variable rather than a single angle, emphasizing the relationship between clival plane and planum sphenoidale ("CBA4").

To demonstrate this preferred approach for comparative studies of primate ontogeny, we studied cranial CT reconstructions for newborn and adult non-hominoid primates (N=110) from 30 representative species. Landmark data were collected at foramen cecum, sphenoidale, posterior clinoid process, and endobasion, producing two angles and three segments. We also measured endocranial volume and used multiple regression and morphometrics to study the effects of ontogeny and phylogeny on CBA.

As expected, total length of the cranial base had negative ontogenetic allometry relative to endocast volume. Basicranial elongation was most pronounced in the posterior segment. Flexion at the anterior angle associated with encephalization occurred in some but not all taxa, with a significant phylogenetic effect. However, in most taxa, retroflexion at the posterior angle resulted in overall ontogenetic retroflexion between planum sphenoidale and clival plane. For a subset of our sample, we used diceCT images to visualize the relationship of these metrics to associated soft tissue structures.

Funded by National Science Foundation grants BCS-1830919 and BCS-1830894.

Revisiting variation in the mandibular teeth of *Australopithecus afarensis*

LUCAS K. DELEZENE[1], AMELIA VILLASENOR[1] and JEREMIAH E. SCOTT[2]

[1]Department of Anthropology, University of Arkansas, [2]Department of Medical Anatomical Sciences, Western University of Health Sciences

From the time of its recognition, *Australopithecus afarensis* has drawn attention for its polymorphic nature, with some studies pointing to variation that seems high with reference to extant primate populations. However, other researchers have concluded that variation in *A. afarensis* can be accommodated within a single, highly dimorphic species. Discoveries in the last two decades have expanded the geographical and temporal representation of the taxon and have increased the range of morphological variation present in the taxon's dental hypodigm. This, along with recent evidence for Middle Pliocene taxonomic diversity in eastern Africa, raises concerns that *A. afarensis*, as conventionally defined, is an excessively variable wastebasket taxon. Using resampling procedures, we compared coefficients of variation for linear measures of mandibular tooth size in *A. afarensis* to five extant hominoid species, including humans. In line with previous studies, we find that few aspects of *A. afarensis* tooth size evince unusually high levels of variation, especially when accounting for differences between the Laetoli/Kantis and Afar region samples. The canine and P_3 show high levels of variation in comparison to humans, probably reflecting greater sexual dimorphism in these teeth in *A. afarensis* than in humans. Recently published fossils of *A. afarensis* from Laetoli, Hadar, Dikika, and Woranso-Mille expand the sample to include smaller-canined individuals, pointing to a possible male sex bias in the early collection of *A. afarensis* fossils. Thus, despite greater temporal and geographic sampling, dental size variation in the *A. afarensis* hypodigm points to the presence of a single species.

Kinship, postmarital residence patterns and dental diversity among Muisca chiefdoms in the Northern Andes

MIGUEL DELGADO[1,2,3], DANIEL BENITEZ[4] and HUGO REYES-CENTENO[4,5]

[1]División Antropología, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata. Paseo del Bosque s/n. (B1900FWA), La Plata, República Argentina., [2]Consejo Nacional de Investigaciones Científicas y Técnicas, (CONICET), Buenos Aires, República Argentina., [3]Ministry of Education Key Laboratory of Contemporary Anthropology Collaborative Innovation Center of Genetics and Development, School of Life Sciences and Human Phenome Institute Fudan University, Shanghai, China, [4]Department of Anthropology,, University of Kentucky, 211 Lafferty Hall, Lexington, KY 40506 USA, [5]William S. Webb Museum of Anthropology, University of Kentucky, 1020 Export St., Lexington, KY 40504 USA.

The Muisca societies emerged nearly 1800 years ago on the eastern highlands of Colombia, developed an economy focused on agricultural production, and reached high sociopolitical complexity. Previous ethnohistoric, archaeological and paleogenomic studies investigating Muisca social organization and kinship have suggested mixed patterns of sociopolitical inheritance and distinct postmarital residence practices. The aim of this study was therefore to examine postmarital residence patterns among Muisca settlements from the eastern highlands of Colombia through quantitative genetic analyses of dental morphology. We investigated 145 individuals from distinct sites: Portalegre (977–500 cal BP), Candelaria La Nueva (979–499 cal BP), Las Delicias (1180–739 cal BP), and Marín (726–330 cal BP) and scored 24 dental nonmetric traits following the ASUDAS standard. The individuals were sexed using bioarchaeological and paleogenomic methods. We used the R-matrix

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

approach to estimate inter-sex diversity, F_{ST} values, and biodistances (pseudo-Mahalanobis D^2). The kinship coefficients indicate greater within- than between- population diversity as well as higher biological diversity among females than in males in the sites investigated. The overall F*ST* value 0.0962 suggests high biological diversity at the regional level and the biodistances show that at Marin and Candelaria La Nueva/Las Delicias males and females are less similar to each other than in Portalegre. These results are in agreement with previous ethnohistoric and archaeological research which hypothesized a virilocal residential pattern and various levels of local exogamy among Muisca chiefdoms. The degree of inter-site male/female biological differentiation reveals distinct patterns of social organization and mobility across time and space.

Wenner-Gren Foundation for Anthropological Research (Grant No. 939); Consejo Nacional de Investigaciones Científicas y Técnicas (Argentina). University of Kentucky's Office of the Vice President for Research.

The Cost of Being Qualified: Current Barriers Faced by Students in Forensic Anthropology

THOMAS A. DELGADO[1], RAPHAELA M. MELORO[2], RANDI M. DEPP[3], KATHERINE M. LANE[4] and JAXSON D. HAUG[5]

[1]Anthropology, California State University, Chico, [2]Anthropology, University of Florida, [3]Anthropology, University of Akron, [4]Anthropology, University of Central Florida, [5]Anthropology, Southern Methodist University

When considering the best ethical practices in forensic anthropology, one must consider how accessible the field is to new students that are responsible for driving the future of research, pedagogy, and the field as a whole. While there is no denying that there are multiple barriers to accessing academia (e.g. racism, sexism, xenophobia, etc.) the cost of a graduate education is a key factor that affects the diversity of people that are able to enter the field. Here, the cost of several universities prominent in the education of forensic anthropologists are considered in tandem with the opportunities for funding offered by these institutions and average costs of living for the respective surrounding areas. Demographic data for the universities at the graduate and undergraduate level was additionally compared to the demographics of the cities surrounding the universities. Funding, excluding loans, was shown to be greatly below cost of living in university cities, and often did not match the costs of attendance estimated by institutions. Including the cost of living, the average graduate degree costs over $59,000 per year while the median stipend for graduate students is $34,658 which necessitates the need for loans or out-of-institute support. White individuals were overrepresented in graduate enrollment when compared with surrounding area demographics, even when undergraduate demographics did match those of the surrounding area. Overall, findings highlight the inaccessibility of pursuing higher education for minority groups and demonstrate the need for institutions to develop funding programs to promote diversity in higher education.

This project is not affaliated with any funding or sponsorship.

Picking pithy plants: Criteria for pith selection by a wild frugivorous primate (*Cebus imitator*)

ALLEGRA N. DEPASQUALE[1], ALICE POIRIER[1], CINTHIA VILLALOBOS-SUAREZ[2], MEGAN A. MAH[1], ADRIAN GUADAMUZ[3], SAUL CHEVES-HERNANDEZ[3], RONALD LOPEZ-NAVARRO[3], JESSICA M. ROTHMAN[4], OMER NEVO[5] and AMANDA D. MELIN[1,6]

[1]Department of Anthropology and Archaeology, University of Calgary, [2]Escuela de Ciencias Biológicas, Universidad Nacional de Costa Rica, [3]Área de Conservación Guanacaste, Costa Rica, [4]Department of Anthropology, CUNY Hunter College, [5]iDiv & Institute of Biodiversity, Friedrich-Schiller University Jena, [6]Department of Medical Genetics, University of Calgary

Understanding primate food selection is a central goal in biological anthropology. In particular, elucidating when and why primates consume non-preferred resources can offer insight into their nutritional ecology as well as their behavioral and morphological adaptations to food scarcity. In this study, we examine the mechanical, chemical, nutritional, and ecological basis of plant pith selection by a wild frugivorous primate, the white-faced capuchin monkey. We test the hypothesis that pith is a fallback food, consumed when fruit is less abundant, and we look for differences between eaten and putatively avoided pith species. We test dietary and non-dietary pith species for mechanical hardness, macronutrient concentrations, relative pith volume, and volatile organic chemical composition. We unite these data with 2+ years of "pith patch" visits analyzed in relation to monthly fruit availability. We find that the capuchins eat pith from 10 plant species (5.9% of ca.170 species in the dry forest). Further, pith consumption occurs primarily during seasonal transitions and is not correlated with fruit abundance. Relative to common non-dietary species, dietary species are softer, have relatively higher pith volume, and contain significantly more terpenes, a class of bioactive compounds known for their anti-parasitic properties. Our results suggest that pith volume, hardness, and chemistry are important selection criteria. Further, we find that seasonality is linked to the timing of pith consumption, possibly driven by seasonal shifts in parasite load. This study advances our understanding of how seasonality shapes primate foraging behavior and enlightens the multifactorial criteria underpinning primate food selection.

National Geographic Early Career Grant (EC-59267R-19); NSERC Discovery Grant (RGPIN-2017-03782); Canada Research Chair Program (950-231257)

Female-female social relationships are enduring in mountain gorilla group

RILEY N. DERBY[1], ROBIN E. MORRISON[2], WINNIE ECKARDT[2], TARA S. STOINSKI[2] and AARON A. SANDEL[1]

[1]Anthropology, University of Texas-Austin, [2]The Dian Fossey Gorilla Fund, Musanze, Rwanda

Social relationships between female primates have been a central focus in primatology, but less is known about whether these relationships are enduring. Mountain gorillas live in stable social groups and females remain in their natal group, disperse, or even emigrate between groups multiple times throughout their life. Although gorilla social relationships have been the focus of numerous studies, the extent to which female gorillas form relationships with each other remains understudied. Female gorillas are proposed to have weak social connections, but maternal relatives may have stronger ties and some preferences have been documented among non-relatives. However, no prior study has clearly determined whether female gorillas form enduring social relationships. We use 13 years of two-meter proximity data collected by the Dian Fossey Gorilla Fund to assess a mountain gorilla group (n = 7-20) in the Volcanoes National Park, Rwanda. We calculated strength of proximity ties, identifying females' top partner each year. Mountain gorillas formed enduring female-female relationships. On average, females had the same top partner for approximately 2 years, but some pairs lasted up to 13 consecutive years. The most enduring relationships were between mother-daughter pairs, lasting on average 5.5 years longer than other pairs. This is the first evidence of enduring female-female social relationships in gorillas, and demonstrates that mothers remain important throughout adulthood. In ongoing work, we are assessing social relationships in ten additional groups. Future work should assess how female-female gorilla relationships compare to other primates, and clarify what is meant by a "social bond".

This research was made possible by the many donors who have supported the Dian Fossey Gorilla Fund.

Biodistance Analysis of Nonmetric Dental Variation in Medieval and Early Modern Hungary

LARESA L. DERN[1], SÁNDOR ÉVINGER[2], TAMÁS HAJDU[2,3], TAMÁS SZENICZEY[2,3], MARIN A. PILLOUD[1], ARIELLE J. PASTORE[1], JENEVIEVE L.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

WALBRECKER[1], LUCA KIS[4,5], ROSE L. PERASH[1] and G. RICHARD SCOTT[1]

[1]Anthropology, University of Nevada, Reno, [2]Anthropology, Hungarian Natural History Museum, [3]Biological Anthropology, Eötvös Loránd University, [4]Anthropology, University of Szeged, [5]Research Centre for Archaeogenetics, Institute of Hungarian Research

The Carpathian Basin is an ideal route for migrations between Europe and Asia. Three major migrations shaped the basin's demography in the medieval and early modern periods: 1) the Avar migration, 2) the Magyar conquest, and 3) the invasion of the Ottomans. Using biodistance analysis of dental nonmetric data this study examines the impact of these migrations on the relationship between Hungarians and other Eurasian populations. ASUDAS scores for 36 nonmetric dental traits collected from the medieval and early modern bioarchaeological collections at the Hungarian Museum of Natural History and Szeged University (Avar = 139, Carolingian = 226, Post-Magyar Conquest Medieval = 481, Ottoman = 381) were compared to a medieval Byzantine sample from Turkey (çatalhöyük = 115) and the medieval, early modern, and modern European and Central Asian samples from the C.G. Turner II database (k = 9, n= 1013).

Biodistance analyses based on Mean Measures of Divergence support three conclusions: 1) Hungarians have distinct dental morphology relative to other primarily Northern European groups; 2) Avar period Hungarian diversity reflects their connection to the Pontic Caspian steppe; 3) major influxes of migrants from the Balkans may have shaped the demography of the basin in both the Carolingian and Ottoman periods and likely played a major role in characterizing medieval and early modern Hungarian biological diversity. Expanding nonmetric dental data in Central and Southeastern Europe and beyond promises to further refine these interpretations and expand our understanding of diversity and variability shaping modern human variation across Europe and Asia.

This study was funded by the University of Nevada, Reno Graduate Student Association Research Grant and the Ozmen Institute for Global Studies Graduate Student Research Grant.

Developmental Plasticity of the Spinal Column: A NMDID case study

JEN DEWEY

Anthropology, University of Oklahoma

This research addresses fetal programming, developmental plasticity, and the Developmental Origins of Health and Disease Hypothesis (DOHaD). The study focused on the vertebral column, evaluating each vertebra from a life course perspective. The evaluation of each vertebra was situated in their developmental context, which constitutes multiple developing stages and tissues of origin, while also understanding that the mechanisms that control the development and fusion of each element are subject to potential developmental stressors. These stressors can cause disruptions potentially predictive of future disease risk, as the abnormalities could indicate a shared developmental timing window or developmental ontology. The number, duration, type, and timing of these stressors during development windows may manifest in irregular segmentation, asymmetries, or delay in the fusion timing that can be evaluated with contextualized measurements of the resulting vertebrae (vertebrae neural canal (VNC); vertebral body-height (BH); pedicle length (PL) and height (PH)) and presence of known abnormalities. To establish the utility of this approach, an individual from the NMDID database has been evaluated in consideration with their medical history (evidence of idiopathic dextroscoliosis, degenerative changes of superior endplate of T7, ununited components of the cleft neural arch S2-S5). Data analysis of BH (ratio of SIP/SIA L & R) and PH and PW (ratio of PH/W L & R) highlighted T3, T8, T12, and L5 as potential areas of developmental delay, while VNC (APD/MLD) highlighted transitions between T2-T3; T10-T11; and T12-L1. These preliminary findings suggest that developmental factors potentially were influential in this individual's health and disease development.

Examining the complex interaction of the human gluteus maximus and hamstrings during hip extension using biomechanical parameters: an investigation into climbing as a possible selective pressure for hominins

RAE DIAS[1], ALISON MURRAY[1], JOSHUA W. GILES[2] and HELEN KURKI[1]

[1]Department of Anthropology, University of Victoria, [2]Department of Mechanical Engineering, University of Victoria

There are key differences in the pelvis and upper leg musculature between humans and apes that are thought to result in a trade-off between locomotor abilities. Human ischia morphology enables hyperextension of the hip that is necessary for efficient bipedal locomotion while simultaneously reducing the effectiveness of the hamstrings in powering hip extension when the hip is in a fully flexed position, as is typical of vertical climbing. An interdisciplinary approach was utilized to test whether the enlarged gluteus maximus (glmax) in humans compensates for the reduced ability of the hamstrings during hip extension. Musculoskeletal 3-D modeling, motion capture, and electromyography were used to assess the relative function of these muscles across two movement trials: 1) walking, and 2) standing up from a deep squat. It was predicted that the glmax would be utilized more than the hamstrings to power hip extension from the flexed position of the squat, and that the hamstrings would play a greater role in powering the legs and hips during the walking motion. Results supported the first prediction in general, and for the second prediction results showed that during walking there are specific points when the hamstrings are in a less optimal position to power this motion. At these points, the glmax plays an important complimentary role, particularly during the stance phase. Results contribute to the growing body of research that indicates that it is important to consider a broader range of human locomotive repertoires as of evolutionary significance, beyond solely one form of locomotion.

Macroscopic assessment of dental pathology from the Meroitic Nubian cemetery 8-B-5.A on Saï Island, Sudan

ANELIS DIAZ[1], STEPHANIE M. FUEHR[1], AMANDA O. LIMA[1], TOSHA L. DUPRAS[2] and VINCENT FRANCIGNY[3]

[1]Department of Anthropology, University of Central Florida, Orlando, Florida, [2]College of Arts and Sciences, Texas Tech University, Lubbock, Texas, [3]CNRS, UMR 8167, Orient & Méditerranée, Sorbonne Université, Paris, France

Saï Island, Sudan is the largest island situated within the Nile River. During the Meroitic period (300 BCE–350 CE), this island was of religious and administrative importance, evident from archaeological and mortuary evaluation. As the extent of osteological analysis from cemetery 8-B-5.A is comprised of only unpublished biological profile assessments, a dental pathological analysis was performed to assess health. The dental remains of 13 individuals were macroscopically analyzed to examine dental pathology of individuals living in ancient Nubia. Dental wear, carious lesions, abscesses, calculus build up, and antemortem tooth loss (AMTL) were examined in both maxillary and mandibular dentition. Pathological conditions were distinguished and categorized utilizing acceptable discipline standards. AMTL (n=61) was the most frequently observed pathological condition, followed by the presence of calculus (n=25), abscesses (n=22), and carious lesions (n=7). The lower presence of the latter pathological conditions was likely attributed to the extensive poor dental health that resulted in significant AMTL. The results indicate that the population at this site, although of elite religious status, had poor dental health that would have affected the consumption of particular resources. Additionally, environmental conditions and food preparation may have contributed to poor dental health. This preliminary assessment of pathological conditions can serve as a proxy for future research regarding dental health and dietary practices of Meroitic Saï Island populations. The research on this sample validates the use of smaller skeletal collections as valuable for understanding the lived experiences of individuals from the past.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Mitonuclear Discordance and Metabolic Function in Admixed Polynesian Populations

RACHEL R. DICKERSON[1], RIKU TAKEI[2], MURRAY CADZOW[3], STEPHANE CASTEL[4], ANNE-KATRIN EMDE[4], KAJA WASIK[4], THEODORE G. SCHURR[1], ANNA L. GOSLING[5] and TONY R. MERRIMAN[2,3]

[1]Anthropology, University of Pennsylvania, [2]Clinical Immunology and Rheumatology, University of Alabama at Birmingham, [3]Biochemistry, University of Otago, Dunedin, [4]Variant Bio, Variant Bio, [5]Anatomy, University of Otago, Dunedin

Mitochondrial function relies on a combination of products from both mitochondrial and nuclear genes. As mitochondrial genomes are inherited maternally, many individuals have different ancestral sources for their nuclear and mitochondrial genomes. The potential incompatibility between genetic ancestries may cause suboptimal mitochondrial function and result in energy-related pathologies such as metabolic disfunction. In this study, we examined the effect of mitonuclear discordance in an admixed population of 2417 individuals with Polynesian ancestry recruited in Aotearoa New Zealand. Mitochondrial haplogroups were assigned using HaploGREP software and proportions of broad regional nuclear ancestry were determined using ADMIXTURE. We defined mitonuclear discordance as the proportion of the nuclear genome not derived from the same ancestral source as the mitochondrial haplogroup. We then tested for associations between mitonuclear discordance and phenotype data for gout, type 2 diabetes, and chronic kidney disease. The results indicated that increasing mitonuclear discordance correlated with a decreased chance of experiencing gout (p=0.035) among individuals with Polynesian genetic ancestry. We also found that increasing mitonuclear discordance correlated with a decreased chance of experiencing type 2 diabetes specifically in individuals , a mtDNA haplogroup that is present in approximately 20% of individuals in West Polynesia and <10% in East Polynesia. These results deviated from our expected outcomes and indicated that increased admixture of nuclear and mitochondrial genomes may be protective against type 2 diabetes and chronic kidney disease in individuals with Polynesian ancestry. These results also indicated that mitonuclear interactions may play a role in metabolic disfunction in admixed Polynesian populations.

This project was made possible through funding from Variant Bio and the University of Pennsylvania Department of Anthropology.

The daily grind: Ecological variations in activity patterns among southern African hunter-gatherer/herders from the Holocene

ELIZABETH S. DINKELE and VICTORIA E. GIBBON

Division of Clinical Anatomy and Biological Anthropology, Department of Human Biology, University of Cape Town

Physical activity patterns, subsistence strategies and lifeways in hunter-gatherer/herders during the Later Stone Age in southern Africa were dynamic through space and time. By assessing activity-induced entheseal changes (ECs) we can obtain insight into the evolution of subsistence strategies, social organisation and the material culture in modern humans. The Coimbra method was used to score ECs in long bones of 118 southern African hunter-gatherer/herders (sAHGH) from the Holocene. Associations between ECs and sex, age, ecological biomes, and temporality were assessed. Our sample comprised 67/118 males and 42/118 females, most representative of the fynbos (59/118), forest (30/118) and succulent karoo (16/118) biomes. Results suggest a complex pattern of physical activity in sAHGH with differences attributable to regional ecology (*p=0.001)* rather than age or sex. More prominent ECs were identified in individuals from the forest biome, relative to the fynbos and succulent karoo biomes. These were consistent with resource search and processing costs, and terrain differences in these ecozones. No statistically significant differences in ECs were detected temporally relative to the infiltration of pastoralism (at 2000BP). This study provides intriguing evidence of the central role that regional ecology played in driving activity patterns regardless of social or cultural organisation in southern Africa during the Later Stone Age.

Financial assistance of the National Research Foundation (NRF) towards this research is acknowledged (Grant no. 467192). Opinions and conclusions in this work are not necessarily attributable to this funder.

Habitat acoustics and the evolution of human auditory sensitivity

NATHANIEL J. DOMINY[1,2], STANISLAUS M. KIVAI[3] and HANNAH TER HOFSTEDE[2]

[1]Department of Anthropology, Dartmouth College, [2]Department of Biological Sciences, Dartmouth College, [3]Department of Conservation Biology, Institute of Primate Research, Kenya

Human auditory sensitivity is greatest between 2 and 4 kHz, a derivation from chimpanzees that corresponds closely to the dominant frequencies of spoken language. This congruence has led some authors to argue that the acoustic properties of speech shaped the evolution of human audition, but recent evidence favors the reverse direction of causality. Termed sensory drive, this process has motivated discussions of habitat acoustics to better understand why humans evolved exceptional hearing in the 2-4 kHz frequency range. The acoustic properties of African savannas have drawn the greatest attention, but this "acoustic niche hypothesis" is difficult to assess. Published data exist for a single site in Kenya described as typical thornbush. To understand the sound-attenuating properties of wide-ranging habitats in Kenya and Uganda––from grasslands to savanna-woodlands to woodlands and closed-canopy forests––we broadcast and recorded (at distances of 5, 10, 20 and 30 m) a series of pure tunes at constant amplitude. We found that frequencies of 2-4 kHz travelled farther in the understory of closed-canopy forests compared to other habitats, in part because these frequencies are reflected by the forest floor but absorbed by savanna grasses. In grasslands, there was almost continuous loud cricket song in the range of 5-8 kHz. The masking effects of cricket noise above 5 kHz begin to explain the selective pressure on hearing in the 2-4 kHz frequency range––it is the optimal frequency range for audition and vocal communication in the forest understory and adjacent grasslands.

Funding was received from the Fulbright Africa Regional Research Program (award no. PS00289758), the Neukom Institute for Computational Science, and the Paul S. Veneklasen Research Foundation.

A 3D geometric morphometric study of the central longitudinal axis of the radius across primates

MADELYNNE M. DUDAS

Center for the Study of Human Origins, Department of Anthropology, New York University, New York Consortium in Evolutionary Primatology

The curvature of the radius can be both functionally and phylogenetically informative. Because the curvature of long bones does not approximate the arc of a circle, common measures such as radius of curvature and included angle are not as applicable as they are to other elements. Additionally, the s-shape of the radius and the multiple planes in which curvature can occur along the shaft make assessing curvature challenging. However, the centerline or central longitudinal axis of the bone can be used to compare curvature. In this study, the Vascular Modeling Toolkit in 3D Slicer (Fedorov et al., 2012) was utilized to extract the central longitudinal axis for surface models of 110 specimens from 33 primate genera. This centerline was then resampled into 23 semilandmarks and two proximal and distal end landmarks. Because this approach consisted of one curve of semilandmarks per bone, an additional landmark was placed on the medial edge of the radial head to counteract the loss of orientation of the curve during the Procrustes fit. A principal component analysis was performed with and without this additional landmark. When included, this orientation landmark allowed for better separation of taxonomic groups along PC2 and PC3. PC2

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

consisted of shape changes in the projection of the two vertices of the s-shape and PC3 consisted of changes in the plane of curvature. Although there was significant overlap between taxa, hylobatids did separate out from other hominoids along PC2. This approach has future applications for comparing long bone curvature.

Canine crown sexual dimorphism in a sample of the modern Croatian population

JELENA DUMANCIC[1], G. RICHARD SCOTT[2], SANDRA ANIC MILOSEVIC[3], NATASA MEDANCIC[4] and HRVOJE BRKIC[1]

[1]Department of Dental Anthropology, School of Dental Medicine University of Zagreb, [2]Department of Anthropology, University of Nevada Reno, [3]Department of Orthodontics, School of Dental Medicine University of Zagreb, [4]Private Dental Practice, Zagreb

Sex assessment is a key part of forensic analysis to establish the identity of unknown deceased individuals. While skeletal sexual characteristics develop during puberty, development of permanent teeth takes place early in childhood and the influence of sex chromosomes is expressed in the sexual dimorphism of tooth crowns and roots. Previous studies have shown that canines are the most dimorphic teeth, but population-specific data are necessary for forensic methods. This study explores sex dimorphism in canine crown dimensions and morphology in a contemporary Croatian population. Hypothesis: both canine crown dimensions and morphology can be used for sex estimation.

The material consisted of 302 dental casts (147 females, 155 males) of orthodontic patients and dental students (11-25 years). Distal accessory ridge (DAR) of the upper and lower canines was evaluated using the Arizona State University Dental Anthropology System. Mesiodistal (MD) and buccolingual (BL) crown dimensions were measured on 120 casts.

Sex differences in MD and BL dimensions were significant ($p<0.05$, Student t-test) for all the canines (upper and lower, left and right) while in DAR only for lower canines ($p<0.000001$, Kruskal-Wallis tests). When all variables were put in model, backward stepwise discriminant function analysis isolated lower canine DAR and lower left canine MD as the two independent variables differentiating sex with an accuracy of 73.5%.

This study shows that both canine crown morphology and dimensions are useful for sex determination, especially for lower canines. These methods can be applied in children as lower canines erupt at about 9 years of age.

This research was funded by the Croatian Science Foundation within the project: IP-2020–02-9423 — Analysis of teeth in forensic and archaeological research.

A Hidden Thread: Detections of Systemic Inflammation via the European History of Health Project Database

MEGAN DUNCANSON[1], FABIAN CRESPO[2], MARK HUBBE[1] and CLARK SPENCER LARSEN[1]

[1]Anthropology, The Ohio State University, [2]Anthropology, Center for Archaeology and Cultural Heritage, University of Louisville

The European continent has been the site of dynamic changes over the past two millennia in climate as well as economic and sociocultural environments. With this ongoing change, the health of local populations varied dramatically over space and time. The expression of health is a complex phenomenon, and it can be influenced by systemic vulnerabilities (e.g., systemic infections; chronic inflammation) in ways that are compounded over the individual via exposure to stressors and pathogens. Here, we test the hypothesis that there is evidence of systemic threats to health over the history of European social development through the analyses of the European History of Health Project (EHHP). This dataset includes data for more than 15,000 individuals from over 100 localities, ranging from the 3rd to the 19th century CE. The prevalence of skeletal markers associated with infection (osteoperiostitis (OP), antemortem tooth loss (AMTL), dental abscesses, and dental caries), and inflammation (osteoarthritis (OA)) were selected for analysis. The association between markers was tested through Pearson correlation tests between pairs of markers for the entire dataset. Positive significant correlations are observed between OA and OP ($r=0.13$; $p<0.001$); between dental caries and OP ($r=0.045$; $p<0.001$); and between caries and OA ($r=0.19$; $p<0.001$). Although the correlations are weak ($r^2 < 0.036$ in all cases), they suggest underlying systemic vulnerabilities to individuals, and to potential underlying connections between disparate observations on the skeleton. The common causes driving these associations likely include demographic as well as biocultural factors among past European societies.

Global History of Health Project funded by NSF SES-0138129 and NSF BCS-0527658.

A burial shrouded by the remnants of life: how mortuary treatment and reconstruction of life course can reveal personhood of an infant from Victorian San Francisco

SANDY DURDEN

Cultural Resource Management, Sonoma State University

This research asks if personhood of an infant can be discovered through the mortuary treatment and reconstruction of the life course, from in utero to after death. A late nineteenth century infant, from San Francisco, helps to answer that question. Positing this social status of the youngest members can lead to the discovery of important social systems, food systems, health and disease, family finances, and home-life cultures. Differential access to these variables still effects people today.

Osteological analysis revealed the lesser wings and body of the sphenoid bone, the squama of the temporal bone, and the squama of the occipital bone displayed porous bone and abnormal new bone formation consistent with nutritional mineral deficiency. Differential diagnosis includes scurvy, rickets, anemia, and infection. Historical research shows the site's household occupants were known to consume mostly good quality beef steaks, little seafood, and an absence of side dishes that required complex cooking. The survival of an infant living outside the womb is highly dependent on its mother eating a nutritionally balanced diet. Proper nutrition can be hindered by poverty, accessibility, ignorance, or illness. Midwives and medical care were available in the 1870s, but prenatal care was unheard. Victorian San Franciscans regarded infants as little more than animals and delayed their attachment, a practice fueled by death rates and burial costs. As discovered during excavation, the infant was buried without dignity. Life course analysis and mortuary setting supports disallowed personhood for this infant.

Beyond the Border: Standards and Methods Towards the Forensic Identification of Undocumented Persons

ISIS SL. DWYER[1], E. ROSE BRYSON[1], SIOBHAN AE. SUMMERS[1] and AMANDA N. FRIEND[2]

[1]Anthropology, University of Florida, [2]SNA International

Undocumented Border Crosser (UBC) profiles aid forensic anthropologists and the medicolegal community in recognizing decedents as potentially undocumented persons. Along the United States (U.S.)-Mexico Border, forensic practitioners have created UBC profiles based on patterns of recovery contexts, cultural items, as well as the likely population affinities typical of the undocumented persons entering the U.S. However, the UBC profiles of the Southwestern U.S. cannot be universally applied. The demographics of undocumented populations vary widely across the country, due to distinct trends of migration in different regions. Additionally, UBC profiles currently cannot account for the recovery and identification of undocumented persons beyond border contexts. Through critical literature review of forensic standards and practices regarding the identification of undocumented persons at the U.S.-Mexico border, this presentation puts forward a prospective model for the creation of regional Undocumented Person (UP) profiles - towards the goal of recognizing decedents as undocumented persons outside of border recovery contexts. Typical methods for positively identifying citizens or permanent residents, including medical

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

records, dental records, and forensic identification databases, are not always applicable or safe options for undocumented persons or their families. As a result, undocumented persons are more likely to be underserved by the medicolegal system. We assert that the identification of undocumented persons throughout the country must reflect an awareness of local demographics of undocumented populations, employ more in-depth methods to estimate population affinity and geographic origin in the initial biological profile, and incorporate post-hoc case analyses to evaluate efficacy.

This material is based upon work supported by the National Academies of Science, Engineering and Medicine Ford Foundation Predoctoral Fellowship.

Patterns of Morphological Variation Among Cercopithecid Fossil Femora

LESLEY H. EASON[1], LUCAS K. DELEZENE[1], THIERRA K. NALLEY[2], AMY L. RECTOR[3], DAGMAWIT GETAHUN[4] and J. M. PLAVCAN[1]

[1]Department of Anthropology, University of Arkansas, [2]Department of Medical Anatomical Sciences, College of Osteopathic Medicine of the Pacific, Western University of Health Sciences, [3]Department of Anthropology, School of World Studies, Virginia Commonwealth University, [4]Department of Anthropology, The Graduate Center, City University of New York (CUNY)

Postcranial fossils are typically assigned to taxa based on morphological similarities with extant species. For instance, descriptions of fossil femora assigned to *Theropithecus* cite morphological similarities with *T. gelada* as basis for taxonomic assignment and behavioral reconstruction. However, the pattern and magnitude of *Theropithecus* femoral variation has never been evaluated using 3D geometric morphometric techniques (3DGM). This study uses 3DGM to evaluate the pattern and magnitude of femoral shape variation among extant and fossil cercopithecidae (N=150). Landmarks are set on the femur to capture patterns of shape variation at the generic, specific, and subspecific levels. Principal component analysis is used to collapse and compare variation. Fossils assigned to *Theropithecus* (n=4), *Parapapio* (n=2), *Macaca* (n=1), *Paracolobus* (n=2), *Cercopithecus* (n=1), and *Lophocebus* (n=1) are compared against patterns of variation in the extant sample to evaluate taxonomic and functional hypotheses. Results demonstrate that femoral shape discriminates among extant taxa at the genus level. The clearest distinction occurs between *Papio* and *Theropithecus.* Most fossils group within or near their extant congeners. However, three of four fossils assigned to *Theropithecus* group within or near extant *Papio.* Additionally, variation among fossils assigned to *Theropithecus* is greater in magnitude than intraspecific variation in the extant geladas. These results suggest that variation among fossils assigned to *Theropithecus* more closely resembles patterns of interspecific variation seen in *Papio*. The results also suggest that closer examination of taxonomic and behavioral reconstructions is necessary when postcranial fossils are not associated with craniodental remains.

Development and Challenges for longevity in big data resources

HEATHER J.H. EDGAR[1] and SHAMSI DANESHVARI BERRY[2]

[1]Anthropology; Office of the Medical Investigator, University of New Mexico, [2]Homer Stryker M.D. School of Medicine, Western Michigan University

The New Mexico Decedent Image Database (NMDID) is a free access, documented dataset of 15,242 whole body decedent postmortem computed tomography scans. Made available to qualified researchers in February 2020, as of September 2022 NMDID had 760 users from 54 countries. Fifty-five papers, theses, and dissertations have already been published drawing on NMDID as a research resource. Considering that the primary goals for creating NMDID were to allow research on topics not previously possible and to provide a resource to researchers without access to such comprehensive data, we consider these statistics an early sign of success.

Challenges in the development of NMDID were myriad, including privacy protections and data deidentification, anonymization, standardization, storage, and accessibility. Additional challenges related to acquiring funding for a project that would serve many fields of inquiry, working a multidisciplinary team including computer scientists, information technology professionals, a biomedical informatician, medical examiners, and anthropologists. While NMDID is now accessible, improvements to the project are in process, including adding cases, metadata, and segmented images. Perhaps more importantly, the team is working to respond to feedback from the research and wider community about sensitive issues surrounding family participation, privacy, and ethics. Here, we discuss lessons learned and provide suggestions for the development process for future large data-sharing projects.

National Institute of Justice 2016-DN-BX-0144

Short- and Long-Term Effects of Common Consolidants on DNA Degradation/ Analysis

STACY EDINGTON[1], SAVANNAH KNUTSON[1], RICK WA. SMITH[2,3,4] and AUSTIN W. REYNOLDS[1]

[1]Department of Anthropology, Baylor University, [2]Department of Sociology and Anthropology, George Mason University, [3]Women and Gender Studies, George Mason University, [4]Indigenous STS Lab, Faculty of Native Studies, University of Alberta

Ancient DNA (aDNA) is widely used to understand the population histories and evolution of humans and other species. aDNA is most often recovered from skeletal remains that are excavated from archaeological and paleontological sites. Some ancient skeletal remains are too fragile for a complete excavation and require the use of consolidants to stabilize remains for safe removal. Two of the most common consolidants used are PVAc and B-72. These materials are excellent for excavation and preservation of the skeletal remains themselves as they act as a reinforcement or glue, but their potential to inhibit and/or damage the aDNA that is extracted from treated samples is not well understood. We conducted an experiment to test the immediate effects of both PVAc and B-72 on DNA. Using qPCR, we quantified the amount of DNA recovered after exposure to the consolidants. We found that PVAc and B-72 significantly reduce (Tukey's HSD p-value = 5.7x10-4 and 1.7x10-5 , respectively) PCR efficiency but do not completely inhibit amplification. We next tested the long-term effect that these consolidants had on the preservation of DNA. The same concentration of DNA was incubated separately with PVAc or B-72 for 72 hours, 6 months, and 9 months at a constant temperature (4C). Fragment length distributions were then measured with a Tapestation to determine if extended exposure to consolidants results in greater DNA fragmentation. This study can be used as an important resource to inform sampling decisions as paleogenomics becomes a more prevalent research tool.

Differential Stature for Men and Women in the Southwest (A.D. 900-1425): A Biocultural Examination of Gendered Patterns

EMILY R. EDMONDS, J. CRISTINA FREIBERGER and DEBRA L. MARTIN

Department of Anthropology, University of Nevada, Las Vegas

Research on the Ancestral Puebloan Southwest is extensive, and bioarchaeological data has added a complimentary dataset for thinking about the effects of drought, migration, and violence on overall population well-being. Regional comparisons between sites and across time are possible due to the availability of published bioarchaeological data. This project provides a first look at femur length, which serves as a proxy for achieved adult stature. There is abundant clinical and experimental research showing the strong correlation between adult stature and morbidity burden during childhood growth and development. Maximum femur length (n=88) from five Ancestral Puebloan sites throughout the Southwest were analyzed. Average female femur length decreased from the Pueblo I (413.8 mm) to the Pueblo III (391.7 mm) but increased from the Pueblo III to the Pueblo IV (404.2 mm).

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

This decrease in average female femur length after the depopulation of the Northern San Juan approaches statistical significance, with a medium-high effect (two-sample t-test: t_{20}=-1.7965, p=0.08754, Cohen's D=0.7789979). Despite the changes in average female femur length, average male femur length from the Pueblo I (425.4 mm) to the Pueblo IV (430 mm) remained generally unaffected (ANOVA: $F_{3,41}$=1.33, p=0.278). Changes in femur length are related to both nutritional adequacy and pathogen load that might have been more pronounced for females than for males. During times of crop failure, climate change, migration, and warfare in the Southwest, males may have been buffered from physiological stressors. The post-migration increase in average female femur length during Pueblo IV supports this hypothesis.

Investigating the costs and benefits of gregarious foraging

MARCY EKANAYAKE-WEBER[1], NAMITA MATHEW[2], DEANNA CUNHA[3], NATHANAEL PAYEN[2], VOLKER GRIMM[4,5] and ANDREAS KOENIG[1,3,6]

[1]Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, [2]Department of Computer Science and Department of Applied Mathematics and Statistics, Stony Brook University, [3]Department of Anthropology, Stony Brook University, [4]Department of Ecological Modeling, Helmholtz Center for Environmental Research - UFZ, [5]Institute of Biochemistry and Biology, University of Potsdam, [6]Graduate Program in Ecology and Evolution, Stony Brook University

For primates, group-living appears to incur a high cost by intensifying feeding competition. These costs raise the question of how gregariousness (i.e., the tendency to aggregate) could have evolved to such an extent in our order. When attempting to test the potential benefits and costs, previous foraging models demonstrated that group-living might be beneficial by lowering variance in intake, but that it otherwise reduces overall foraging efficiency. However, these models did not account for how ecological characteristics might interact with behavior to affect feeding competition. Here, we present an agent-based model for testing how ecological variables impact the costs and benefits of gregariousness. In our simulations, primate agents foraged on a variable resource landscape while either ignoring or maintaining spatial cohesion with conspecifics, and the agents' foraging efficiency was recorded. Using Morris Elementary Effects, we tested the sensitivity of 13 model parameters, of which 2 controlled gregarious behavior and 8 controlled food resources, including resource abundance, resource distribution, patch size, speed of calorie extraction, and resource regrowth. We found that, while gregariousness generally increased feeding competition and decreased foraging efficiency, the costs of gregariousness were much lower when resource abundance was high and resource extraction was slow. We also found that gregariousness resulted in lower variance in energy intake, but only when combined with fast resource extraction. Thus, it appears that the costs and benefits of gregariousness are strongly influenced by the interactions between specific resource characteristics, namely resource abundance and extraction speed.

This work was funded by the SBU Presidential Dissertation Completion Fellowship, the GWIS National Fellowship, the Louis Stokes Alliance for Minority Participation, and the Dean of CAS of Stony Brook University.

Sniffing out the difference: intraspecific variation in nasal cavity morphology

ANGELINA M. EMMONS, MILENA ROMANO and STEPHANIE A. POINDEXTER

Anthropology, University At Buffalo

A variable degree of intraspecific variation may occur in primate species. Examining interspecific differences in nasal cavity morphology in primates is a popular approach to answering evolutionary questions. When using limited representatives for interspecies analysis, opportunities to lose potentially meaningful intraspecies variation can occur. Here, we hypothesize that primates in different forest types have faced variable selection on their olfactory regions that may have resulted in different levels of intraspecific variation. To test our hypothesis, we assessed the intraspecific variation of the internal nasal cavity in two primate species: the Senegal Bushbaby (*Galago senegalensis*) and the West African potto (*Peridicticus potto*). We used publicly available computerized tomography scans from Morphosource (G. senegalensis =14; P. potto = 20). To characterize the internal geometry of the nasal cavity, we placed 20 manual landmarks across 4 2-D coronal slices from the nasal inlet to the base of the nasal cavity in ImageJ. In Morphologika, we started with a Procrustes alignment, then conducted a Procrustes regression for allometry and other covariates (including forest type). Within each of the two species the internal slices show the most variability compared to distal slices. The morphological variation seen in this small dataset suggests that comparative studies should take steps to ensure that they use multiple samples of species when looking for meaningful interspecific differences. We will present this research as a visual narrative with the hopes of reaching a broader audience and providing an unconventional form of displaying the importance of acknowledging intraspecific variation.

Ecological Advantages of Color Vision and Color Vision Deficiency in Capuchin Monkeys Under Controlled Conditions

SEDONA L. EPSTEIN[1], MATTHEW H. BABB[2,3], FRANCES J. WHITE[1], BENJAMIN WILSON[4,5] and SARAH F. BROSNAN[2,3,6,7]

[1]Department of Anthropology, University of Oregon, [2]Department of Psychology, Georgia State University, [3]Language Research Center, Georgia State University, [4]Department of Psychology, Emory University, [5]Emory National Primate Research Center, Emory University, [6]Department of Philosophy, Georgia State University, [7]Neuroscience Institute, Georgia State University

Tufted capuchin monkeys (*Sapajus [Cebus] apella)* show a sexually dimorphic pattern of color vision where all males are dichromats (red-green color-vision-deficient), and females can be dichromats or trichromats. The niche differentiation hypothesis for color vision differences posits that trichromats and dichromats occupy distinct foraging niches, resulting in reduced intragroup feeding competition whereby trichromats have an advantage in finding red objects on green backgrounds (such as fruit) and dichromats have an advantage in finding objects through red-green camouflage (such as cryptic prey). We used two computerized discrimination tasks to determine if these advantages are apparent in a controlled environment without other sensory/social cues. In task 1, most males failed to complete training of detecting the image with an apple when it was red, suggesting a dichromat disadvantage. Capuchins then had to choose the green scene hiding a red apple over a green scene hiding a green apple. Females showed a strong preference for red, consistent with hypothesized trichromat behavior, but two females had no preference, suggesting that they may be dichromats. The one male who reached testing showed no preference, again supporting a dichromat disadvantage. Genotyping is currently being conducted to verify these predictions. For task 2, capuchins chose the outline of an apple between two scenes with red-green or blue-yellow camouflage: in probe trials, apples were present in both. However, capuchins chose at chance, suggesting a floor effect, which we hypothesize was due to stimuli complexity. We are exploring other ways to test a possible dichromat advantage for camouflage.

New Y-SNP in QM3 indigenous populations of Colombia

MARISOL NAYDU ESPITIA FAJARDO[1], NELSON RIVERA FRANCO[1], YAMID BRAGA GOMEZ[2] and GUILLERMO BARRETO RODRIGUEZ[1]

[1]Biology, University of Valle, [2]Group Biology, Languages and History., Corpodihva

In studies of the evolution of human populations based on the Y chromosome, most of the Native Americans belong to the QM3 lineage. Therefore, it is necessary to have a higher resolution of the

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

tree to delve into the history of the groups that inhabit the north of South America. The objective of this work was to identify new SNPs of the QM3 lineage that would allow evaluating the phylogenetic relationships between Andean and Amazonian populations of Colombia. For this, previously obtained sequences of two Y chromosomes from Amazonian populations were used, from which 14 potential SNPs were selected and typified in 175 Amazonian samples from the Vaupés region and in 60 samples from the Pasto, Nasa, Embera, Arhuaco and Kogui from the Andean region. It was found that all the SNPs are present in the Amazonian samples and only 3 of them are shared with the Embera, Nasa and Pastos, but none of them are shared with the Kogui and Arhuaco from the north of the Andes, in the Colombian Caribbean. Combining the 14 variants of the present study with 13 previously found by our group and using TMRCA, a new QM3 tree with 17 sublineages is generated that allows establishing differences between the different Amazonian populations of Vaupés, as in the case of Kubeos and Pisamiras, the latter in serious risk of disappearing. The methodology used here allows to increase the QM3 sublineages with better resolution, useful for microevolutionary studies of South American populations.

Universidad del Valle and Minciencias

Para-masticatory dental wear: Patterns of variation between Paleolithic, Mesolithic and Neolithic populations from Northern Spain

ALMUDENA ESTALRRICH

EvoAdapta Group/ Anthropology, University of Cantabria/ University of Arkansas

One of the proxies used for the study of past human behavior is the analysis of the non-masticatory dental wear, the use of "teeth as tools". This study analyzes non-masticatory dental wear patterns in the permanent dentition from Upper Paleolithic to the Chalcolithic period in individuals from Northern Spain in order to trace the expression of behavioral patterns and cultural habits among these populations.

Activity-related dental wear features recorded include cultural striations, chipped enamel, toothpicking grooves, subvertical grooves within the interproximal contact facets, incisal grooves, and polished enamel. The sample was analyzed using an optical digitial microscopy. The cultural striations that were frequent in the Mousterian, Aurignacian and Magdalenian periods, become scarce during the Azilian and Mesolithic periods and absent during the Neolithic and Chalcolithic periods. Polished enamel appeared during the Magdalenian until the Chalcolithic. Incisal grooves appeared only during the Azilian and Mesolithic. The only two features that were recorded in all periods are the chipped enamel and toothpicking grooves.

The results indicate a change in the frequency and type of the non-masticatory dental wear features pattern. The diversification of stone tools (i.e. Microliths) that allowed for new tools that could have replaced the need for the "stuff-and-cut" behavior associated with the cultural striations. The life-style change from the Neolithic, favored a change in dietary habits and could have eliminated the need of pre-processing food using the mouth as a third hand. The widespread of toothpicking could be associated with an increase of oral hygiene or therapeutic habits.

This research is funded by a H2020-MSCA-IF project No. 891529 (3DFOSSILDIET).

Ecological influences on terrestrial behavior across the primate order

GENE R. ESTRADA

Anthropology, University of Michigan

Primates are masterfully adapted to life in the trees. However, many primates engage in terrestrial behavior either habitually or facultatively. Determining the current ecological factors associated with primate terrestriality could help uncover the environmental conditions that drove shifts to terrestriality in some primate lineages. We compiled published terrestriality data for 518 primate taxa, spanning 33 countries across the Americas, Africa, and Asia. We also collected ecological data and species characteristics data from online databases and published literature. We then used Bayesian phylogenetic models to determine the influence of ecological variables on primate terrestriality. We predicted that primate terrestriality would be: 1) positively influenced by forest structure characteristics such as forest height; 2) positively influenced by temperature; and 3) negatively influenced by rainfall. We found that annual rainfall and average forest height were the only significant predictors in our models. Body mass was included in all models as a control and was not a significant predictor. As we predicted, forest height was positively associated with terrestriality, while rainfall, which was the strongest predictor, was negatively associated with terrestriality. Maximum temperature, temperature seasonality, and rainfall seasonality were not significant predictors. Our results show that across the primate order, ecological variables are more reliable predictors of primate terrestrial behavior than physical characteristics such as body mass. This challenges popular hypotheses of the evolution of primate terrestriality and highlights the need for a better understanding of the role of ecology in primate behavior, locomotion, and evolution.

English Monkeys? Multi-isotope analysis of three possible *Chlorocebus* individuals from Nottingham Castle

KATIE E. FAILLACE[1], KRIS POOLE[2] and RICHARD MADGWICK[1]

[1]Department of Archaeology and Conservation, Cardiff University, [2]York Archaeology

The presence of "exotic" animals in post-medieval England is well-attested in the historical record, notably increasing through the Georgian period (late 18th century). However, despite their status as luxury commodities, accounts of the transport and maintenance of these animals are conspicuously absent, and archaeological evidence for them is rare. Recent excavations at Nottingham Castle recovered three animals, thought to be of the *Chlorocebus* genus, from a Georgian fill, presenting an unusual opportunity to investigate the origins and diet of these individuals through multi-isotope ($\delta^{13}C$, $\delta^{15}N$, $\delta^{34}S$, $^{87}Sr/^{86}Sr$, $^{206/207/208}Pb/^{204}Pb$) analysis.

Two immature individuals (1344 and 1346) have evidence suggestive of an origin in coastal or island West Africa, but had different diets. 1344 has $\delta^{13}C$ and $\delta^{15}N$ values consistent with an omnivorous C4 diet, while 1346 has values consistent with a C3-based diet, potentially due to being reared in captivity, as their Pb values reveal anthropogenic interference. 1346 had an $^{87}Sr/^{86}Sr$ value of 0.7039, incompatible with the British Isles and continental Europe, and in greater accordance with volcanic islands like Cape Verde, where *Chlorocebus* monkeys are documented at this time. Both immature individuals had $\delta^{34}S$ values consistent with a marine environment (11.1‰ and 14.8‰, respectively), inconsistent with inland Nottingham. The final individual, 1345, is an adult whose $\delta^{13}C$, $\delta^{15}N$, and $\delta^{34}S$ values were consistent with long term habitation in England.

Using isotopic analysis, this study has illustrated a diversity of experiences and origins among these three individuals, with implications for understanding the wider trade of "foreign" animals in Georgian England.

Chewing efficiency and abrasive diets explain tooth size variation in a community of African primates

LUKE D. FANNIN[1,2], DEBBIE GUATELLI-STEINBERG[3], JAKE ARFT-GUATELLI[4], MARCUS CLAUSS[5], NATHANIEL J. DOMINY[1,6] and W SCOTT. MCGRAW[3]

[1]Anthropology, Dartmouth College, [2]Ecology, Evolution, Environment, and Society, Dartmouth College, [3]Anthropology, The Ohio State University, [4]Philosophy, University of California, Berkeley, [5]Clinic for Zoo Animals, Exotic Pets and Wildlife, Vetsuisse Faculty, University of Zurich, [6]Biological Sciences, Dartmouth College

The evolution of postcanine tooth size variation is a topic of enduring debate within paleoanthropology. One explanation posits that larger teeth

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

enhance food fragmentation during mastication, improving both chewing efficiency and energy acquisition. Competing hypotheses have stressed the advantages of larger teeth for mediating the costs of masticatory effort and/or dietary abrasivity. Here, we test these mutually compatible hypotheses by focusing on premolar teeth in a community of cercopithecoid primates inhabiting Taï Forest, Ivory Coast. We found that larger premolar tooth sizes were strongly associated with (1) greater chewing efficiency, as evidenced by smaller relative mean fecal particulate sizes (FPS), and (2) greater dietary abrasivity, as shown by higher levels of fecal siliceous particulate matter (SPM). Dung samples from larger-toothed colobines and sooty mangabeys (*Cercocebus atys*) were distinguished from those of frugivorous guenons by higher levels of ingested opaline phytoliths, but only the mangabeys showed excessive intake of exogenous grit (crystalline quartz), suggesting a primary role in the evolution of their megadontia. In contrast, the average number of postcanine mastications per ingestive event––our proxy for cyclical loading stresses––was a weak predictor of premolar size. Our findings indicate that larger premolars facilitate increased food fragmentation, either by increasing the number of food particle contacts per chew or by promoting larger bite forces that permit stress-limited foods to be shattered. At the same time, greater tooth size may enhance the functional longevity of teeth among species with abrasive diets, especially those with a proclivity for terrestrial foraging.

This project was supported by the National Science Foundation (BCS 0840110, 0921770, 0922429; GRFP 1840344), the Explorers Club, the Primate Society of Great Britain, and a JEB Traveling Fellowship.

Breastfeeding and complementary feeding practices among mothers in Belém, Brazil: Dietary diversity and infant nutritional implications

STEPHANIE R. FANNIN[1], BARBARA A. PIPERATA[1], ANA CAROLINA BRITO DE AZEVEDO[2], CLAYCIANE SANTOS DO NASCIMENTO[2], ROSEANE BITTENCOURT TAVARES OLIVEIRA[2], CLARISSA ARAUJO DA PAZ[2], JACQUELINE MENDONÇA FREIRE PEREIRA[2] and VALLÉRIA DE CÁSSIA TAVARES DA SILVA[2]

[1]Anthropology, The Ohio State University, [2]Anthropology, Universidade Federal do Pará

International health organizations recommend six months of exclusive breastfeeding followed by a period of up to two years of complementary feeding to support infants' rapid growth and development during this stage of the life course. However, studies demonstrate that mothers' adoption of these guidelines is influenced by their sociocultural context. This study has two aims: (1) to characterize breastfeeding and complementary feeding patterns of Brazilian infants living in the Amazonian city of Belém, and (2) explore maternal logic guiding feeding decisions. To address these aims, we collected 24-hour dietary recall data from a sample of 65 infants over three measurement rounds (1 month, 3 months, and 9 months of age). Using the dietary data, we then developed a pile sorting exercise, which we administered to a sub-set of 30 mothers, that explored both when these foods should ideally be introduced and the factors that influenced these decisions. At one and three-months, 81% and 58% of infants were exclusively breastfed. By 9-months, 71% of infants were still receiving breastmilk, however, all but one was consuming a range of complementary foods. Following the FAO, we calculated an average dietary diversity score of 3.9 (out of 9) in round three. Foods given fell primarily into the FAO categories "starchy staples," "other fruits and vegetables," "meat and fish," and "milk and milk products." Results from the pile sort exercise indicate that adhering to public health guidelines on infant nutrition more than maintaining larger infant size influenced mothers feeding decisions.

This work was supported by the National Science Foundation [BSC 1921592].

The energetics of seasonality in captive Coquerel's sifaka (*Propithecus coquereli*) from non-invasive thyroid hormone measurement

CASEY M. FARMER[1], SARA HAAS[2,3], ANNE CROWLEY[4], SAVANNAH LO[3], LAURENCE R. GESQUIERE[3], MITCHELL T. IRWIN[1] and ELAINE E. GUEVARA[4]

[1]Anthropology, Northern Illinois University, [2]Environmental Science and Policy, Duke University, [3]Biology, Duke University, [4]Evolutionary Anthropology, Duke University

The energetic state of an animal has vital consequences for its fitness – persisting in negative energy balance can lead to reproductive failure and death. However, behavioral responses to stress are variable, leaving researchers unable to reliably identify populations under stress through observation alone. There is an urgent need for non-invasive markers of energetic state, particularly those that reflect energy balance but not social stress. Thyroid hormones, specifically triiodothyronine (T3), represent a non-invasive biomarker that can be used for this purpose - they regulate and reflect metabolic state in mammals, and can be detected in feces as metabolites (mT3); this has been assayed haplorrhines, but not strepsirrhines. We measured mT3 in captive, seasonally semi-free ranging Coquerel's sifaka at Duke Lemur Center across two seasons (77 samples across 14 individuals). mT3 was reliably recovered and validated via radioimmunoassay. Sifaka have higher mT3 concentrations in winter; this was unexpected, as animals are provisioned year-round and don't experience food scarcity; it is possible their metabolism slows during winter as an evolved response to seasonality in the wild. Intriguingly, there was no effect of sex or age, diverging from wild studies on nonhuman primates. This may be due to dietary provisioning and limited sample size. The response to seasonality should be taken into account when applying this tool to wild populations, but the lack of response to age and sex would simplify its application. This captive study establishes a baseline for comparison in technical and biological validation of this assay in wild lemurs.

This research was made possible by Duke University's Faculty Teaching/Research Enhancement Grants Code: 4511022.

Ontogenetic shape changes in the hominoid clavicle and the morphology of the *Australopithecus afarensis* juvenile DIK-1-1

HANNAH N. FARRELL and ZERESENAY ALEMSEGED

Organismal Biology and Anatomy, University of Chicago

The clavicle plays a central structural role in the hominoid shoulder acting as the only bony articulation between the upper limb and thorax. The bone is also known in modern humans to be one of the first to ossify *in utero* and has one of the last epiphyses to fuse in early adulthood. This allows the clavicle (and osteocytes comprising it) ample time to (re)model in response to how an individual uses its upper limb throughout life. Previous work has shown clavicular shape to separate adult non-human apes in morphospace, but the addition of juveniles into analyses has resulted in conflicting conclusions between 2D and 3D methods. Here, we use surface shape data from 120 extant hominoid clavicles, with ages ranging from early infancy to adulthood, and a 3D landmark scheme to quantify clavicular shape through ontogeny. Preliminary results indicate the varying presence of shape plasticity across taxa. In the few where ontogenetic trends could be identified, the morphological differences present between juveniles and adults are subtle. Additionally, despite the relatively clear separation of most taxa in the morphospace, *Homo* and *Pan* occupy overlapping regions and DIK-1-1, an infant *Australopithecus afarensis*, falls within that shared shape space. Further, given the vast overlap between *Homo* and *Pan* in morphospace, we suggest that curvature alone cannot be used to discriminate between 'ape-like' and 'modern human-like' clavicular morphology. Other traits should be considered when exploring the connection between form and function within the context of hominin evolution.

Face stimuli anonymization from known databases

ARODI FARRERA[1], KATYA RODRÍGUEZ VÁZQUEZ[2], LUIS FERNANDO CUEVAS REMIGIO[3], GUSTAVO

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

ORTIZ LAGUNES[3], SERGIO PADILLA REYNAUD[2] and GERMÁN PALAFOX PALAFOX[3]

[1]Instituto de Investigaciones Antropológicas, Universidad Nacional Autónoma de México, [2]Instituo de Investigaciones en Matemáticas Aplicadas y en Sistemas, Universidad Nacional Autónoma de México, [3]Facultad de Psicología, Universidad Nacional Autónoma de México

The study of facial features has been fundamental for forensic investigation. For instance, research on face identification and recognition, and eyewitness memory commonly uses face databases as experimental stimuli or to compare and evaluate software used for identification. Although there has recently been an increase in available databases, there is still a lack of diversity in the groups represented, which affects the generalizability of the findings or could lead to the amplification of these biases. One reason for this diversity bias is that some existing databases may not be available due to ethical reasons related to image sharing. In this contribution, we address this problem by proposing a reproducible approach to generate synthetic faces and assess their similarity in shape relative to the faces used to create them. Synthetic faces were produced by averaging randomly selected "parent" faces from the original sample. We used geometric morphometrics methods and principal component analysis to calculate a measure of similarity between the synthetic and parent faces. We chose the Euclidean distance among principal component scores as a measure of the degree of similarity: the smaller it is, the more correspondence there is between configurations. We found a tradeoff between the degree of similarity and shape variation present in the synthetic databases: using fewer parent faces results in synthetic faces with greater facial diversity but more similar to the faces used to create them, and vice versa. We conclude with some guidelines to generate synthetic faces and their ethical use.

This project was supported by UNAM-PAPIIT IT102422.

Lives on the move: the dietary and biomechanical impact of mobility in transhumance populations. The case of the Pindus Vlachs, Greece

CHRISTIANNE L. FERNÉE, ALICE R. HOLLAND, ELENA SANDOVAL and KONSTANTINOS P. TRIMMIS

Anthropology and Archaeology, University of Bristol

Transhumance is a form of pastoralism that involves the seasonal droving of livestock. It is a global practice that, in some localities, has been using the same routes for hundreds of years. The transient nature of this practice has meant that it has largely been studied using ethnography as it is difficult to study archaeologically. Consequently, very little is known of the impact that this movement had on the individuals that took part in it. This paper explores the impact of transhumance, looking at differences in diet, mobility and limb biomechanics, within the group and between their sedentary counterparts.

A sample of transhumant 19th/20th century Vlach pastoralists from the village of Samarina, Greece, was studied alongside a 'sedentary' comparative sample from the Thessalian Plain, Greece. Osteological analysis was combined with stable isotope and biomechanical analyses. A multi-isotope and multi-element approach was used to reconstruct a timeline, from childhood to adulthood, of diet (d13C and d15N) and mobility (87Sr/86Sr). Upper and lower long bones from each individual (both humeri and left femur and tibia) were scanned using medical computed tomography (CT). Biomechanical analyses were then carried out using geometric morphometrics and cross-sectional properties to explore differences in cultural practices (upper limb) and locomotion (lower limb).

The results show biomechanical and dietary differences between the Transhumant Vlachs of Samarina and sedentary group from the Thessalian plain. Within-group differences were also observed in the upper limb biomechanics between sexes, giving a unique insight into the lives and cultural practices of these transhumant pastoralists.

This research project was funded by the Erasmus + Key Action 2 and the University of Bristol Cabot Institute Innovation Fund.

Community knowledge and personal experiences with long-tailed macaques in Leyte and Bohol, Philippines

LORI L. FIELDS

Anthropology & Geography, Coastal Carolina University

The Philippine archipelago is home to two species of nonhuman primates: the long-tailed macaque, *Macaca fascicularis* and the Philippine tarsier, *Carlito syrichta*. While long-tailed macaques inhabit many of the island provinces, tarsiers are found only in the Visayas and Mindanao. Both primates can typically be found living in proximity to humans in forests, protected areas, tourist sites, and as pets. In 2014-2015, I conducted 210 interviews in 14 barangays in Leyte and Bohol, Philippines. These provinces each have existing tourist areas with captive and free-ranging macaques, where I asked questions about their habitats, if macaque populations were noticeably increasing or decreasing, and how their habitats changed over time. Here, I share results from these communities, including personal perspectives and experiences related to hunting and eating macaques. Results showed that participants had little knowledge about whether macaque populations were increasing, decreasing, or staying the same. However, specific habitats (e.g., mangroves, caves, forests) were accurately identified across the two provinces. Community members also noticed that macaques were moving into different areas of the barangays due to damage caused by a typhoon and earthquake in 2013. Attitudes toward conservation were also influenced by personal experiences and negative interactions with macaques (i.e., fear of disease or bites). Approximately 22% of participants discussed their beliefs and experiences with hunting and/or eating macaques. Given the updated IUCN Endangered status of *M. fascicularis*, this study points to the need for further inquiry about macaque populations in other areas of the Philippines.

This project was supported by the Fulbright U.S. Student Program and the Department of Anthropology and College of Liberal Arts at Texas A&M University

Effect of exercise, selection, and genetic background on metatarsal cross-sectional geometry in mice

MARA G. FIELDS[1], AMANDA N. SMOLINSKY[2], CAROL V. WARD[1] and KEVIN M. MIDDLETON[3]

[1]Pathology and Anatomical Sciences, University of Missouri, [2]Department of Biology, St. Norbert College, [3]Division of Biological Sciences, University of Missouri

Long bone cross-sectional geometry is commonly used to infer loading environments and locomotor specializations in fossil primates and other animals. Monkey, ape, and hominin metatarsals vary in length and cross-sectional proportions among taxa, suggesting that metatarsal mid-shaft geometry may reflect locomotor behavior and so could be used to infer locomotor specialization in fossils. However, comparing taxa with independent evolutionary histories might introduce potentially confounding sources of variation, given that studies of femoral cross-sectional morphology in experimental systems have found that theoretical loading response is influenced more by genetic background, age, and body mass rather than habitual locomotor activity.

We explored the effects of activity, selection, and genetic background on cross-sectional properties of metatarsals in an experimental animal model, *Mus musculus*. We compared metatarsal cross-sectional properties in six mice from three lines that were developed as part of an experimental evolution study: (1) Mice from a wild-type line selected for high levels of voluntary wheel-running, (2) Mice from this same line but with myosin deficiency, and (3) A randomly bred control line. Two mice from each cohort were assessed, one with access to wheel activity and the other sedentary. After micro-CT imaging, we assessed midshaft bone cross-sectional properties that reflect bending and torsional rigidity. Although explicit statistical comparisons were not possible given the small sample size, we found larger differences among lines than between exercise

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

treatments within lines. Our results suggest that caution is warranted when inferring locomotor behavioral differences among individuals representing groups that are genetically distinct.

New Oldowan Locality Sare River (ca. 1.7 Ma) Provides Evidence of Diverse Hominin Behaviors on the Homa Peninsula, Kenya

EMMA M. FINESTONE[1,2], THOMAS W. PLUMMER[3,4,5], THOMAS H. VINCENT[6], SCOTT A. BLUMENTHAL[7,8], PETER W. DITCHFIELD[9], LAURA C. BISHOP[6], ANDY IR. HERRIES[10,11], CHRISTOPHER V. PALFERY[10], TIMOTHY P. LANE[6], ELIZABETH MCGUIRE[7], JONATHAN S. REEVES[12], DAVID R. BRAUN[12,13], SIMION K. BARTILOL[14], NELSON KIPRONO ROTICH[14,15], JENNIFER A. PARKINSON[16], CRISTINA LEMORINI[17], ISABELLA CARICOLA[17,18], RAHAB N. KINYANJUI[19,2,5] and RICHARD POTTS[19,5]

[1]Department of Physical Anthropology, Cleveland Museum of Natural History, [2]Department of Archaeology, Max Planck Institute for the Science of Human History, [3]Department of Anthropology, Queens College, [4]Department of Anthropology, The CUNY Graduate Center, [5]Human Origins Program, National Museum of Natural History, Smithsonian Institution, [6]Research Centre in Evolutionary Anthropology and Palaeoecology, School of Biological and Environmental Sciences, Liverpool John Moores University, [7]Department of Anthropology, University of Oregon, [8]Department of Earth, Ocean, and Atmospheric Sciences, University of British Columbia, [9]School of Archaeology, University of Oxford, [10]The Australian Archaeomagnetism Laboratory, Dept. Archaeology and History, La Trobe University, [11]Paleo-Research Institute, University of Johannesburg, [12]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, [13]Center for the Advanced Study of Human Paleobiology, George Washington University, [14]Institute of Nuclear Science and Technology, University of Nairobi, [15]Institute of Nuclear Chemistry and Technology, Warsaw, [16]Department of Anthropology, University of San Diego, [17]LTFAPA Laboratory, Department of Classics, Sapienza University of Rome, [18]School of History, Classics and Archaeology, Newcastle University, [19]Department of Earth Sciences, National Museums of Kenya

Some of our most in-depth insights into Oldowan hominin landscape behaviors are known from the Homa Peninsula, southwestern Kenya. Hominins at Kanjera South (~2 Ma) invested in procuring a diversity of raw materials from over 10 km away and strategically reduced them to economize exotic cobbles in a grassland-dominated ecosystem. Here, we report new findings from Sare River, a ~1.7 Ma Oldowan locality situated 12 km southeast of the Kanjera locality. Sare River has yielded 1,754 artifacts in low-energy silts and sands. Stable isotopic analysis of pedogenic carbonates suggest that hominin activities were carried out in a grassland-dominated setting with similar vegetation structure as Kanjera South. In contrast to Kanjera South, the paleo-conglomerate near Sare River was composed of high-quality stone raw materials (e.g., quartz, rhyolite, quartzite) that were locally abundant within 200 meters. Toolmakers at Sare River opted for an expedient strategy focused on producing angular waste (92.5% of assemblage) from quartz pebbles (84.0% of assemblage), in contrast to raw material procurement and reduction at Kanjera South. Although stone tool behavior at Sare River was technologically simple, toolmakers efficiently produced cutting edges, made few mistakes, and exhibited a mastery of platform management. Expedient technical strategies do not necessarily indicate a lack of skill or lack of suitable raw materials. Lithic procurement and reduction patterns on the Homa Peninsula through time may reflect varied responses to local resource contexts rather than large-scale evolutionary changes that might imply expanded mobility, energy budgets, or toolmaker cognition.

Funding provided by the National Science Foundation (grants DDIA#1836669 and #1327047), the L.S.B. Leakey Foundation, the Peter Buck Fund for Human Origins Research, Smithsonian Institution, and NERC CIAF Grant (9170-0416)

Within and between community correlates of urinary testosterone in adult male chimpanzees (*Pan troglodytes)*

BENJAMIN J. FINKEL[1], SHARIFAH NAMAGANDA[1], MELISSA EMERY THOMPSON[2] and JOHN C. MITANI[1]

[1]Department of Anthropology, University of Michigan, [2]Department of Anthropology, University of New Mexico

The challenge hypothesis proposes that the steroid hormone testosterone (T) mediates aggression by increasing only in fitness-enhancing situations. Consistent with this hypothesis, male chimpanzees (*Pan troglodytes*) exhibit elevated T when competing for estrous females and when participating in territory defense. However, few studies have simultaneously evaluated the effects of within and between group aggression on T. A fission of the Ngogo chimpanzee community in 2018 provided an opportunity to investigate this. We present data from adult males (n = 20, 21-53 years) in two adjacent communities with urinary testosterone (n = 320 samples) collected over 12 months in 2018 and 2019. We built generalized linear mixed models to examine the influence of within and between competition on T. Males in the Ngogo West community had higher T levels (mean=111.3 ng/ml, sd=53.4) than those in the Ngogo Central community (mean=79.3 ng/ml, sd=45.9), consistent with their higher rates of territorial boundary patrols and inter-group encounters during the study period. While the ratio of parous estrous females to adult males explained some of this variation in T (Beta=0.17±0.09, >95% ω), the effect of community remained (0.21±0.13, >90% ω), suggesting that both intra- and intergroup aggression may simultaneously affect T levels. Neither dominance rank nor age were reliable predictors of T. We discuss the implications of these findings in relation to those derived from prior research on chimpanzees and other animals.

National Science Foundation (BCS-1927384), The Leakey Foundation (N025458), American Philosophical Society, International Primatological Society, University of Michigan.

Applying Queer Theory to Biological Anthropology: History, Discourse, and the Introduction of a New Reference Library

TAYLOR FLAHERTY[1], KATHLEEN D. STANSBURY[1], SAMANTHA BLATT[2], AMY MICHAEL[3] and MARI ISA[4]

[1]Department of Anthropology, University of Nevada, Las Vegas, [2]Department of Anthropology, Idaho State University, [3]Department of Anthropology, University of New Hampshire, [4]Department of Anthropology, Texas Tech University

Historically, biological anthropology has implemented dominant identity lenses limiting intersectionality and the equitable flow of knowledge. To challenge this, we advocate *Queering* the discipline. To *Queer* anthropology means challenging static identities and rethinking binaries not only in terms of sex/gender, but also in socio-cultural, -political, and -economic milieus. This also entails centering marginalized viewpoints and challenging biases. Some anthropologists do not believe that queering the discipline is necessary. However, rejection of the sex/gender binary will create more nuanced research that better speaks to individual experiences.

Our presentation adds to this discussion by exhibiting how queer theory challenges and transforms scientific knowledge. We begin with a history of queer theory and queer anthropology, highlighting the contributions of scholars such as Judith Butler and Pamela Geller. Critical theories that should be used in concordance with queer theory (i.e., intersectionality, critical race theory) will also be addressed. Next, discourse will be discussed and a case study will be presented to illustrate the utility of queer theory and downfalls of failing to Queer analyses. Finally, our open access reference library containing examples of queer theories, methods, and interdisciplinary pedagogical techniques will be introduced. This will help biological anthropologists access resources for classroom instruction, research, and personal edification. We argue that failure to develop tools aiding in the implementation of queer theory will continue to harm marginalized individuals. The proposed resource will promote the use of queer theory throughout anthropological subdisciplines and emphasize the need to deconstruct and decolonize dominant identity lenses.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Forensic Anthropology Standards: Development, Relevance, and Implementation

JULIE FLEISCHMAN[1], WENDY E.P. MCQUADE[2], ERIC BARTELINK[3] and JASON WIERSEMA[1]

[1]Harris County Institute of Forensic Sciences, [2]Center for Human Identification, University of North Texas Health Science Center at Fort Worth, [3]Anthropology Department, California State University, Chico

Forensic Anthropology standards development in the U.S. has been a decade-long process beginning with the Scientific Working Group for Forensic Anthropology (SWGANTH), which drafted a series of consensus guidelines. In 2014, dozens of forensic science SWGs were reorganized under the Organization of Scientific Area Committees (OSAC), which provided funding, a hierarchical structure, and technical support. Overseen by the Forensic Science Standards Board, the OSAC Forensic Anthropology Subcommittee began drafting formal, consensus-based standards. Because OSAC is not a Standards Development Organization, the AAFS Standards Board (ASB) was developed in 2015 to publish the OSAC-developed standards.

Lacking discipline-wide standards, differences exist among Forensic Anthropologists with regard to education and training, quality assurance, evidence handling, case documentation, method application, and reporting. Unfortunately, despite the urgent need for formalization, the standards development and publication process is complicated and time-consuming. This is challenging not only for those working to develop and publish standards, but also those waiting to implement them. Factors resulting in delays include: fluctuating group membership, the involvement of two nearly distinct groups (OSAC Subcommittee and ASB Working Group) writing and editing each standard, the volume of public comments requiring adjudication at both the OSAC and ASB levels, and the difficulty of writing standards that are applicable to forensic anthropology yet meet the technical merit requirements designed for more quantitative disciplines (e.g., DNA). This presentation discusses the history of Forensic Anthropology standards development, why standards are needed to formalize Forensic Anthropology practice, and the challenges associated with their development and implementation.

You are What You Eat: The Dietary Composition and Activity Budget of the Mantled Howler Monkey (*Alouatta palliata)* at La Suerte Biological Research Station in Costa Rica

MICHELLE L. FLEISHMAN

Primatology, University of Alabama

It is widely known that mantled howler monkeys are folivorous, but some studies suggest that howler monkeys (*Alouatta paliata*) consume fruits when available. I studied the food preferences of howler monkeys at the La Suerte Biological Research Station (LSBRS) from 4 – 13 July 2022 by conducting 1484 focal samples at one-minute intervals among 50 individuals. I observed feeding behaviors to assess sex differences in preferred food choices. Additionally, I collected fecal samples (n = 3) from focal individuals and analyzed the content of plant material. While I observed one incident of males and juveniles consuming unripe fruit, I did not observe either sex eating fruit during the focal sampling. However, all fecal samples contained seeds from fruit that had been ingested. Male howlers in my sample ate more mature leaves than females, and females spent more time foraging for higher-quality food than males. The observed sex differences may be related to females' greater physiological needs of gestation and lactation, motivating them to seek out higher-quality food such as young leaves and fruit. However, the effect of the high population density and the seasonal variation during the observation period at LSBRS may also influence food availability and howler monkey activity budgets. Overall, mantled howler monkeys at LSBRS adhered to a more folivorous diet, despite the availability of fruits within their home ranges.

Oral Health and Microbiome Diversity in 18th Century African Descended Individuals from Charleston, South Carolina

RAQUEL E. FLESKES[1,4], SARAH J. JOHNSON[2,3], TANVI P. HONAP[2,3], JOANNA K. GILMORE[4,5], LA'SHEIA OUBRÉ[4], ADE A. OFUNNIYIN[4,5], CECIL M. LEWIS[2,3] and THEODORE G. SCHURR[4,6]

[1]Department of Anthropology, University of Connecticut, [2]Department of Anthropology, University of Oklahoma, [3]Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, [4]Anson Street African Burial Ground Project, Charleston, SC, [5]Department of Sociology and Anthropology, College of Charleston, [6]Department of Anthropology, University of Pennsylvania

The Anson Street African Burial Ground project is a community engaged study focused on understanding the histories of 37 persons recovered during construction in Charleston, South Carolina. Previous archaeological, osteological, and genomic analyses indicated they were primarily of African descent and lived during the 18th century. Successive engagement with community partners indicated a strong interest in understanding the health and life experiences of these individuals. Thus, to understand the oral health of the Anson Street Ancestors, we collected dental calculus samples from 14 individuals prior to the reinternment of their remains in 2019. Twelve of these Ancestors displayed signs of poor oral health, including antemortem tooth loss, carious lesions and/or abscesses. DNA was extracted, and partial uracil deglycosylase treated double-stranded libraries were built and shotgun-sequenced on an Illumina HiSeq. SourceTracker analyses indicated that 12 calculus samples contained predominantly oral-associated microbial communities, verifying their authenticity. Taxonomic profiles generated using MetaPhlAn3 showed presence of oral commensal bacteria and known opportunistic pathogens such as *Tannerella forsythia* and *Pseudoramibacter alactolyticus.* Using a reference-based mapping approach, we reconstructed one *T. forsythia* strain and three *P. alactolyticus* strains from the Ancestors as well as multiple strains from comparative datasets. Phylogenetic analyses showed that the *T. forsythia* and *P. alactolyticus* strains from the Ancestors clustered with those from historic European and African individuals but differed in the extent of their replacement of New World strains. Overall, our results revealed unique features of oral microbiome diversity in 18th century African descended individuals in the colonial U.S. South.

Penn University Research Foundation (T.G.S.), National Science Foundation SPRF-FR-2105384 (R.E.F.), National Science Foundation BCS-2045308 'Hominid Dental Metagenomes for Pathogen Evolution Research' (C.M.L., T.P.H.).

The scaling of motor unit density in skeletal muscle as a framework for understanding functional adaptation and evolution

ADAM D. FOSTER[1], JUSTIN BAIRD[2], SARAH BOGAN[2], AMAAD CHOUDRY[2], PARTH DOSHI[2], VENKATESA MURUGANANDAM[2] and MAXX TOLER[1]

[1]Anatomy, Campbell University School of Osteopathic Medicine, [2]Medical Student, Campbell University School of Osteopathic Medicine

Previous work on functional anatomy relies on long established scaling relationships from experimental and morphological evidence. However, there is a significant gap in the literature describing a relationship between muscle size, location, functional role, and motor unit density (MUD, number of neurons controlling a muscle). Clarifying this relationship would inform both functional and evolutionary questions including adaptational differences between upper and lower extremities that are relevant to human and non-human primate evolution. We predict that muscles used for fine motor tasks will be controlled by a proportionally greater number of neurons compared to those that generate gross limb movements. In this study, we excised the first lumbrical in the hand and foot from n=8 human cadaveric donors and recorded the weight and volume of the muscle. All nerve branches supplying each muscle were sampled, placed in 10% formalin, stained with potassium ferricyanide, and scanned for virtual microscopy. MUD was calculated by quantifying

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

the number of motor axons supplied to each muscle in the sampled nerve using ImageJ. Our results suggest that there is a significant relationship between muscle weight and MUD (p=0.01). There were no significant differences between the hand and foot lumbricals, but there was a trend toward hand lumbricals having a greater MUD (p=0.07). These results are the first to explore MUD differences using this framework and have important implications for testing questions relevant to human evolution. Future work should expand the number of muscles tested and how these variables scale across taxa.

Funding was provided by Campbell University School of Osteopathic Medicine.

Signals of Dietary Adaptation in the Hardness and Stiffness of Primate Tooth Enamel

FREDERICK R. FOSTER[1], ROBERT S. SCOTT[1] and ADRIAN B. MANN[2]

[1]Anthropology, Rutgers, the State University of New Jersey, [2]Material Science and Engineering, Rutgers, the State University of New Jersey

Tooth enamel plays an important role in digestion by breaking down foods in their most mechanically challenging state. High mechanical properties (stiffness and hardness) in enamel allow teeth to transmit bite forces into food particles over many chew cycles. However, in critical regions of the cusp where stress is concentrated during chewing, high mechanical properties can reduce the bite forces required to cause fracture and wear, reducing dental competence. This problem may be solved by gradients in mechanical properties, where stiffness and hardness change from the tooth surface to the enamel-dentine junction (EDJ). One hypothesis is that gradients represent a trade-off adaptation promoting chewing efficiency in regions where high stiffness and hardness are needed while guarding against tooth failure in critical regions. These gradients have been observed in primate enamel, but their relationship to tooth failure in critical regions has not been explored. To address the role of gradients in tooth failure, nanoindentation was used to measure stiffness and hardness throughout the enamel in 22 molar teeth from 10 primate species. Signals of adaptation were identified near the EDJ in the top and base of the cusp, where a sharp reduction in stiffness increases fracture resistance. The steepest gradients were observed in large bodied species that can generate high bite forces, and in species with mechanically challenging diets. Scanning electron microscopy was used to characterize the microstructure of each specimen, and implicated tooth disease and microstructural orientation as major drivers of variation in the mechanical properties of primate tooth enamel.

This research was funded by the National Science Foundation Doctoral Dissertation Research Improvment Grant (NSF BSC-1847941) and the Rutgers University, Center for Human Evolutionary Studies ALbert Fellows Award.

Tracking the life histories of enslaved individuals from 18th and 19th century mid-Atlantic North America using stable isotopes: comparison to the African site of Elmina, Ghana

CHRISTINE A M. FRANCE[1], DOUGLAS W. OWSLEY[2], KARIN S. BRUWELHEIDE[2], EMILY S. RENSCHLER[3], KATHRYN G. BARCA[2] and CHRISTOPHER R. DECORSE[4]

[1]Smithsonian Museum Conservation Institute, Smithsonian Museum Conservation Institute, [2]Anthropology Department, Smithsonian National Museum of Natural History, [3]Museum of Archaeology and Anthropology, University of Pennsylvania, [4]Anthropology Department, Syracuse University

This study uses stable isotope analyses in skeletal remains of 18th and 19th century African Americans from the Mid-Atlantic region of North America to explore the origins of this historically marginalized population. In 1808, the United States slave trade was officially banned, yet legal slavery continued until 1865. During the apex of North American slavery, thousands of Africans and African Americans were trafficked and born into this system. A critical component of understanding this population involves tracing individual origins, yet written and historic records are rare. Oxygen, carbon, and nitrogen isotopes from African Americans and Caucasian Americans were compared to individuals from the cosmopolitan site of Elmina, Ghana, the population therein representing stable isotope values typical of West African slave export sites. Results show oxygen isotope values from Elmina are higher than those from North American Mid-Atlantic sites. These oxygen isotope values track geographic differences in drinking water, differentiating Elmina from Mid-Atlantic sites and identifying outliers as potential recent arrivals from West Africa. Given that very few outliers were identified in the Mid-Atlantic sites, this data lends insight into the establishment of slavery as a self-perpetuating system in the early United States. Additional results from carbon and nitrogen isotopes facilitate inferences on food choices in West Africa and suggest African Americans retained certain cultural food preferences. Overall these results show great promise for our ability to use biochemical techniques as a means to investigate and understand the identity of enslaved individuals whose life stories historically have been underrepresented.

Funding provided by Rice Endowment for Forensic Anthropology, Smithsonian Museum Conservation Institute Federal and Trust funds, and NSF REU Site Grant SMA-1156360.

Periodontal and systemic disease in the Cayo Santiago Rhesus macaques

GEORGE FRANCIS and QIAN WANG

Department of Biomedical Sciences, Texas A&M University School of Dentistry

Periodontitis has been associated with a myriad of comorbid diseases. Among skeletal remains, advanced stages of periodontitis are frequently employed as markers of poor oral health, though their role as part of the systemic health of individuals is often overlooked or elusive. In this study, 1482 individuals (868 females and 614 males) of Rhesus macaques (*Macaca mulatta*) from the Cayo Santiago skeleton collection were examined for periodontal disease and subsequently for bony manifestations of disease in craniofacial and postcranial skeletons. One hundred and one individuals (6.85 %) were identified with periodontitis via observation of alveolar bone recessions and/or periodontal abscessing. Of this subsample, 52 (51.5%) exhibited some form adjacent disease, including spondyloarthropathies (25.7%), porous infectious lesions (17.8%), periosteal lesions (8.9%) and osteomyelitis (7.9%). Periodontal disease was significantly associated with spondyloarthropathies ($x2 = 90.178$, $p = <0.001$), porous infectious lesions ($x2 = 20.597$, $p = <0.001$), and osteomyelitis ($x2 = 4.185$, $p = 0.04$). The phenomenon of positive associations between oral and systemic disease may reflect the direct spread of infection from one locale to another, the increasing susceptibility to a second infection after contracting a first, or overall diminished immune capabilities that predispose the individual to frailty and diseases. Future investigations may benefit from the elucidation of such associations in attempting to understand periodontal disease within the context of a systemic health condition.

Funding Sources: The Cayo Santiago colony is supported by NIH 5P40OD012217 to Caribbean Primate Research Center. This project is supported by NSF grant #1926601 to Q. Wang.

The Ontogeny of Nocturnal Primate Auditory Anatomy

KATHERYN P. FRANKLIN[1], TIMOTHY D. SMITH[2] and VALERIE B. DELEON[1]

[1]Department of Anthropology, University of Florida, [2]School of Physical Therapy, Slippery Rock University

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

The auditory morphology of nocturnal primates is understudied in comparative anatomy. Analysis of these auditory adaptations allows greater understanding of the evolutionary success of this population. The multichambered trabeculated middle ear cavities are of particular interest due to their proposed functional significance, including stabilization of middle ear pressure variation. We hypothesize that middle ear structure is associated with hearing sensitivity and nocturnality, and this variation can be distinguished throughout ontogeny.

We created 3D models of auditory apparatuses using 3DSlicer, combining conventional CT and diffusible iodine-based contrast-enhanced CT (diceCT) data. Metric data include volumes of all middle ear accessory cavities, tympanic membrane surface area, stapedial footplate area, and interaural distance. Our sample of newborn and adult primates representing strepsirrhines (e.g., *Daubentonia madagascariensis*, *Cheirogaleus medius*) and haplorhines (e.g., *Aotus nancymaae*, *Tarsius syrichta*) allows us to examine structural changes through an ontogenetic lens. We included diurnal foils (*Lemur catta* and *Saguinus midas*) to compare based on activity patterns.

Pneumatization of accessory cavities of newborn primates initiates early and foreshadows adult morphology and species distinctions. Consistent variation in the accessory cavity and spatial relationships of the ossicles distinguishes species clearly. For example, newborn *Tarsius syrichta* exhibit prominent anterior accessory cavities, and newborn *Nycticebus pygmaeus* exhibit pronounced posterior cavities. Additionally, large total cavity volume indicates a sensitivity to low-frequency sounds, among other factors.

This investigation highlights the complexities of the auditory system, allowing for a better understanding of the audible frequency estimation of each species by activity pattern and the morphology that supports this function.

Funded by National Science Foundation grants BCS-1830919 and BCS-1830894.

Cellular immune activity is both costly and energetically constrained during development in an East African monkey

LUCIA FREEDBERG[1], ERIN VOGEL[2], JAMES HIGHAM[3], MICHAEL HEISTERMANN[4], MARINA CORDS[5] and NICOLE THOMPSON GONZALEZ[1]

[1]Department of Anthropology, UC Santa Barbara, [2]Department of Anthropology, Rutgers University, [3]Department of Anthropology, New York University, [4]German Primate Center, Leibniz Association, [5]Department of Ecology Evolution and Environmental Biology, Columbia University

The activities of the immune system constitute a major energetic investment. During development, immune activation may detract from energy balance and compromise growth. On the other hand, energy balance and developmental priorities of growth may limit investment into immune function. In this study, we examine the potential energetic costs and constraints (c-peptide) to cellular immune activation (neopterin) during development, its potential trade-offs with lean body mass (LBM) and growth at different timescales, and the role played by HPA axis activity (fecal glucocorticoids) in their relationships. To do so we use non-invasive biomarkers from 620 urine and 627 fecal samples of 41 wild, juvenile blue monkeys (M = 21, F = 20) collected over 8 months. We find that neopterin was unrelated to age, sex, or maternal rank. Instead of detracting from energy balance and LBM at a broad timescale, neopterin increased with energy balance (ß = 0.30, $p < 0.001$) and LBM (ß = 0.11, $p < 0.001$), overall suggesting energetic constraints on juvenile cellular immunity. Such constraints were only weakly regulated by HPA activity during low energy states. At a short timescale, higher neopterin did diminish subsequent growth (ß = -0.10 , $p < 0.001$). Our results suggest that cellular immune activity is both costly and limited by energy availability in wild developing primates. These findings bear health implications for the social and seasonal factors that influence energy balance.

To NATG: Leakey Foundation (PG 007662), Animal Behavior Society, American Society of Primatologists. To MC: Leakey, Wenner-Gren, National Science Foundations (SBR 95-23623, BCS 98-08273, 05–54747, 10-2847, DGE 09-66166) and AAAS-WISC.

Integrating shape, cortical thickness, and bone modeling data: ontogeny and robusticity in the chimpanzee mandible

SARAH E. FREIDLINE[1], ALEXANDRA SCHUH[2], ZEWDI TSEGAI[3,4] and SÉLIM NATAHI[5,6]

[1]Department of Anthropology, University of Central Florida, [2]CNRS, MC, PACEA, UMR 5199, Université de Bordeaux, [3]Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, [4]Department of Organismal Biology and Anatomy, University of Chicago, [5]Center for Interdisciplinary Research in Biology, Collège de France, [6]Department of Comparative Cultural Psychology, Max Planck Institute for Evolutionary Anthropology

Cranio-mandibular robusticity, defined as thick bone and superstructures, plays an important role in hominin species definitions and diagnoses. Its underlying cause is unclear and likely involves a complex interplay between genetics, behavior, and ontogeny. Robusticity is often measured by cortical thickness. However, how cortical thickness relates to bone shape during ontogeny has been minimally explored. In this study, we use a novel method to evaluate the relationship between cortical thickness, bone modeling and shape in juvenile and adult *Pan troglodytes* mandibles. Data were collected on an ontogenetic sample of 10 mandibles classified into four age groups based on dental development. Morphometric maps of cortical thickness of the entire mandible were generated from microCT scans using a full width at half maximum technique. To evaluate changes in bone modeling patterns, molds were made on the periosteal surfaces of the mandibles. Patterns of bone formation and resorption were quantified and transformed to digital bone modeling maps. Finally, mandibular shape data was collected by digitizing landmarks and semi-landmarks on three-dimensional surface models.

We find that there are consistent patterns in cortical thickness, bone modeling, and shape throughout ontogeny. With age, cortical thickness increases, and is always thickest along the inferior corpus and thinnest at the symphysis and ramus. Thick cortical bone does not always correspond to bone formation or the greatest amount of shape change between ontogenetic stages. Together these results suggest that the relationship between these features is not straightforward and likely involves compensating mechanisms related to mechanical stress during mastication.

We acknowledge the Fyssen foundation (AS and SN), the Marie Skłodowska-Curie Grant #101025719 (ZJT), the University of Central Florida, and the Max Planck Society for funding.

Phylogenetic signal in the *Pan* talus and medial cuneiform

SARAH E. FRIESEN[1,2], RYAN P. KNIGGE[3], LAUREN SCHROEDER[1,4] and MATTHEW W. TOCHERI[2,5,6]

[1]Department of Anthropology, University of Toronto Mississauga, Mississauga, Ontario, Canada, [2]Department of Anthropology, Lakehead University, Thunder Bay, Ontario, Canada, [3]Department of Integrative Biology and Physiology, University of Minnesota Medical School, Minneapolis, Minnesota, USA, [4]Human Evolution Research Institute, Department of Anthropology, University of Cape Town, Rondebosch, South Africa, [5]Human Origins Program, National Museum of Natural History, Smithsonian Institution, Washington, District of Columbia, USA, [6]Australian Research Council Centre of Excellence for Australian Biodiversity and Heritage, University of Wollongong, Wollongong, New South Wales, Australia

A recent study found that the talus and medial cuneiform covary as a functional unit in *Pan*, and that differences in shape between taxa are related to documented differences in their styles of climbing. The phylogenetic relationships among *Pan* likely play a role in talus and medial cuneiform shape variation, but this has yet to be tested. Here, we present the results of phylogenetic analyses on 3D landmark data from a sample of 126 tali and 127 medial cuneiforms derived from bonobos and four chimpanzee subspecies. A phylogenetic tree was generated for these analyses using estimated divergence dates: bonobos-chimpanzees, 1.5 million years (Ma); eastern-western chimpanzees, 0.6 Ma; Nigeria/Cameroon-western chimpanzees, 0.25 Ma; central-eastern

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

chimpanzees, 0.15 Ma. Phylomorphospace analysis, phylogenetically aligned component analysis, and phylogenetic principal components analysis showed that the talus and medial cuneiform data had weak phylogenetic signals with significant ($p<0.05$) multivariate K statistics of 0.52 and 0.55, respectively. Additionally, using the univariate K statistic we found that more variation exists among chimpanzee subspecies in the talus and medial cuneiform than predicted by a Brownian Motion model of evolution. However, bonobos have changed less since their divergence with chimpanzees than predicted. This suggests that there may be functional or adaptive constraints on these bones in bonobos, but not in chimpanzees. These results provide new details about how foot bone morphology differs among *Pan* taxa.

Ontario Ministry of Colleges and Universities; QEII GSST; Social Sciences and Humanities Research Council of Canada, Award Number: 435-2017-1234; Canada Research Chairs Program; Wenner-Gren Foundation, Grant Number: 7822

Updated biochronology of South African Plio-Pleistocene fossil assemblages using cercopithecid monkeys

STEPHEN R. FROST[1], FRANCES J. WHITE[1], HAILAY G. REDA[1] and CHRISTOPHER C. GILBERT[2,3,4,5]

[1]Department of Anthropology, University of Oregon, [2]Department of Anthropology, Hunter College of the City University of New York, [3]Ph.D. Program in Anthropology, Graduate Center of the City University of New York, [4]New York Consortium in Evolutionary Primatology, [5]Division of Paleontology, American Museum of Natural History

Recent analyses, several employing methods only recently applied in paleoanthropology, have made new geological age estimates for South African hominin sites, some significantly different from previous consensus estimates. Biochronology provides an independent and well-understood control for these estimates based directly on the fossil assemblages themselves. Cercopithecid primates have previously proved reliable for this purpose: they are common and diverse elements of Plio-Pleistocene faunas from hominin localities, evincing both significant turnover and anagenetic evolution. The most recent cercopithecid biochronological assessments were published over 30 years ago, and since that time significant new fossil material has been discovered and chronological and taxonomic refinements have been made. Therefore, we directly examined all available African fossil cercopithecid collections (housed in African, European, and North American institutions) to produce an updated assessment of species time ranges and occurrences across sites. Additionally, we built a statistical model using the trend for increasing molar size over time in the highly abundant *Theropithecus oswaldi* lineage based on ANCOVA with log-transformed molar size as the dependent variable, geological age as the independent, and 6 molar tooth positions as categories. The sample included 1263 molars of *T. oswaldi* and spanned from 3.9-0.5 Ma. Geological age and molar size are highly correlated (r^2=~0.83) and where sample sizes are sufficient our model provides reliable age estimates. We find no support for any hominin-bearing sites in South Africa greater than approximately 2.8 Ma. Our results suggest some localities, such as Swartkrans Member 3 and Cooper's D are somewhat older than previously estimated.

This study was supported by the Wenner-Gren Foundation (#8523, Hunt Fellowship #8928), NSF 0966166 (NYCEP IGERT), PSC-CUNY Faculty Research Award, University of Oregon Faculty Research Award.

A Neolithic special: The headless dead from Vráble, Slovakia (5250-4950 BCE)

KATHARINA FUCHS[1], ZUZANNA HUKEĽOVÁ[3], ALENA BISTÁKOVÁ[3], IVAN CHEBEN[3], MARTIN FURHOLT[2], TILL KÜHL[2], KATA SZILÁGYI[2] and MARIA WUNDERLICH[2]

[1]Institute of Clinical Molecular Biology, Kiel University, [2]Institute of Prehistoric and Protohistoric Archaeology, Kiel University, [3]Institute of Archaeology, Slovak Academy of Sciences

7300 years ago, a new variant of the Neolithic way of life was established in Central Europe, archaeologically known as Linear Potter Culture (LBK). In village communities founded on the fertile loess soils, the first farmers established a fully agricultural economy. Burials and depositions of human remains generally witness certain norms in ritual and social practice. Nevertheless, skeletal remains from mass graves with signs of lethal violence or special treatment of the bodies give food for thoughts that sociopolitical crises, warfare, or ritual killings could have resulted from increasing socioeconomic pressure among these societies.

Stemming from a long-term project, we present a new and unique case in this respect: the dead of the settlement site Vráble, Slovakia. Here, three closely neighboring settlements with 313 houses agglomerated in a short time, which is already exceptional for the LBK context. Particularly special are the remains of 73 individuals, most of which have been found in a ditch surrounding the southwestern settlement. 45 of them were headless, with a concentration of 37 individuals in the same ditch area.

According to the recent state of research, the paper focuses on (1) presenting archaeological as well as first osteological results including taphonomic aspects and evidence of manipulation and/or violence, (2) discussing scenarios for this find by comparing it to other exceptional LBK cases, and (3) reflecting on the significance of head removals in the context of death.

This research has been conducted in the scope of the CRC 1266 'Scales of transformation' at Kiel University, funded by the German Research Foundation (DFG – Projektnummer 2901391021 – SFB 1266).

The cultural landscape of Homo naledi

AGUSTIN FUENTES[1], JOHN HAWKS[2] and LEE BERGER[3]

[1]Anthropology, Princeton University, [2]Anthropology, University of Wisconsin, Madison, [3]Centre for Exploration of the Deep Human Journey, University of the WITWATERSRAND

Since 2013 explorations at the Rising Star cave system have produced an unparalleled skeletal record of a nonhuman hominin species in the time and place (Late Pleistocene Southern Africa) many archaeologists argue that modern humans evolved. More than 150 collaborators have participated in the discoveries and analyses of copious fossil, archeological and geological contents and contexts producing a wealth of articles about the site and its denizens. Specific analyses of fossil remains and recent excavation and exploration in the Rising Star system has expanded the record and interpretive frame enabling a shift from envisioning Rising Star as just a fossil site to seeing it as a cultural landscape for *Homo naledi*. Here we present state the art modeling, augmented virtual reality, and unpublished hi-resolution images. Using these data we revisit previously published assertions regarding complex social and material behavior in the small-brained Homo naledi, that was until recently assumed to be primarily, or exclusively, found in Homo sapiens and other large brained hominins. Evidence that creates a paradox and questions the nature of *H. naledi* and our own species.

The genetic architecture of modern human dental and face morphology: new insights from admixed Latin American

MACARENA FUENTES-GUAJARDO[1], BETTY BONFANTE[2], QING LI[3], GUANGRUI YANG[3], YINGJIE CHEN[3], DANIEL BENÍTEZ[4], HAO LUO[3], CLÉMENT ZANOLLI[5], PIERRE FAUX[2], KAUSTUBH ADHIKARI[6], MIGUEL DELGADO[3,7] and ANDRÉS RUIZ-LINARES[2,3]

[1]Biomedical Science, Health Science Faculty, University of Tarapaca, Arica-Chile., [2]Laboratory of Biocultural Anthropology, Law, Ethics, and Health,, Aix-Marseille University, France., [3]Ministry of Education Key Laboratory of Contemporary Anthropology and Collaborative Innovation Center of Genetics and Development, School of Life Sciences and Human Phenome Institute, Fudan University, Yangpu District, Shanghai, China., [4]Department of Anthropology, University of Kentucky, 211 Lafferty Hall, Lexington, KY 40506 USA., [5]CNRS Researcher, Laboratory PACEA, UMR 5199, Univ. Bordeaux, Pessac, France., [6]School of

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Mathematics and Statistics, The Open University, United Kingdom., [7]CONICET- División Antropología, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata, Argentina.

The CANDELA consortium has been focused on the genetic underpinnings of physical appearance in Latin American people for nearly 10 years. We have performed GWAS, admixture mapping, etc., using ~700,000 SNPs from ~7000 individuals using both quantitative and qualitative methods to assess the facial and dental phenotypes. First, we reported four genomic regions showing associations (P-value $<5\times10^{-8}$) with three traits related to nose morphology. Furthermore, we detected an association of SNPs in the *EDAR* gene with chin protrusion, and we also documented alterations of mandible length in mice with modified *Edar* function. Recently, we reported a GWAS using 2D facial landmarks in profile images, and we found nine newly genomic regions associated with different facial traits, and the association between lip thickness and 1p12 genomic region involves SNPs in a region with evidence of adaptive introgression from archaic hominins (Denisovan). Subsequently, we investigate shovel-shaped incisors (UI1, UI2) and performed the first dental size GWAS in humans using 3D images from dental casts from >1,000 Latin Americans. We implemented automatic procedures for image segmentation, teeth orientation and measurement of buccolingual and mesiodistal diameters, height, and 3D mesh attributes. We detected significant association for 456 SNPs at 11 genome regions. The most robust association was observed between mesiodistal diameters of several teeth and *EDAR* gene. Several association signals detected are novel and many involve genes previously implicated in dental development. Our results provide novel biological insights into the genetic architecture of human facial and dental morphology with remarkable evolutionary implications.

First Steps to Fossil Site Prediction in South Africa: Exploring Multispectral and Digital Elevation Data

MARGARET J. FURTNER

Geography & Anthropology, Louisiana State University

The purpose of this study is to explore physical properties of the South African landscape in association with fossil-bearing cave localities to isolate suitable variables for a predictive model of fossil sites in the region. Many existing sites have been discovered due to limestone mining or by chance encounters. Machine learning models using remotely sensed imagery could reduce reliance on serendipity by using information about existing fossil localities to find areas with similar characteristics. Factors derived from multispectral and elevation imagery in relation to existing fossil sites in the region were applied within the Cradle of Humankind to determine if trends could be discerned for future application.

Unsupervised classification via k-means was employed on multispectral imagery of an 8 x 8 km area of interest located within the Cradle. The classes associated with the two hominin fossil sites in the area were extracted and compared to high-resolution imagery to determine possible trends. Spectral profiles of these fossil sites show similar spectral signatures, indicating that they may share physical properties that influence their reflectance values. Overall, the extraction reduced the surveyable land area by 81.3%, and the extracted classes appear to fall along western/southwestern hill faces in the area. Drainage channels were calculated by converting digital elevation models into flow direction and flow accumulation rasters and indicate that fossil sites cluster along drainage pathways. The results of this preliminary study demonstrate that multispectral data and factors derived from elevation data would make informative predictors in a future machine learning model.

Evidence Of Selection In The *Fabp4* Gene Region Suggests Thermoregulatory Adaptation To Cold Temperatures In Savanna Monkeys

CHRISTIAN M. GAGNON[1], HANNES SVARDAL[2], ANNA J. JANINSKA[3,4], NELSON B. FREIMER[3], PAUL J. GROBLER[5], TRUDY R. TURNER[5,6] and CHRISTOPHER A. SCHMITT[1]

[1]Department of Anthropology, Boston University, [2]Department of Biology, University of Antwerp, [3]Center for Neurobehavioral Genetics, University of California, Los Angeles, [4]Institute of Bioorganic Chemistry, Polish Academy of Sciences, [5]Department of Genetics, University of the Free State, [6]Department of Anthropology, University of Wisconsin

Fatty acid binding protein 4 (FABP4) has been identified as a key molecule involved in the process of nonshivering thermogenesis (NST) in brown adipose tissues (BAT). Heat production via NST is an adaptation most common among mammals believed to have played an indispensable role in overcoming the dangers of living in cold environments. Heat produced by NST comes from the metabolism of free fatty acids (FFA). Due to FABP4's role in providing FFA uptake into BAT, we hypothesize that variants in the *FABP4* gene region that increase the efficiency of FFA uptake would have undergone selection in cold-adapted populations. To test this hypothesis, we conducted an analysis of the variation present in the *FABP4* gene region in a sample of 72 savannah monkeys (*Chlorocebus* spp.) representing a range of climatic conditions across southern and eastern Africa. Our analyses included 10 kb flanking regions of *FABP4* to capture variation in potential cis-acting regulatory regions. Principal component analyses of the *FABP4* gene region show differentiation between taxa and local populations consistent with phylogenetic distance. Linkage-based analyses (iHS and EHH) suggest recent positive selective sweeps at 5 loci. Although these loci do not appear in coding regions of the gene, 2 appear near a known promoter region (8:76902505, piHS=2.94; and 8:76903607, piHS= 2.05) suggesting they could contribute to *FABP4* regulation and FFA uptake into BAT. These findings have important implications for the expansion of hominins beyond equatorial Africa, as well as how contemporary non-human primates cope with changing global climate.

Dental microwear reflects maturity-related feeding behavior in Virunga mountain gorillas

JORDI GALBANY[1,2,3], WINNIE ECKARDT[4], TARA S. STOINSKI[4], ALEJANDRO PÉREZ-PÉREZ[5], ANTOINE MUDAKIKWA[6], MICHAEL R. CRANFIELD[7], KIRSTEN GILARDI[7], RICHARD MUVUNYI[6], SHANNON C. MCFARLIN[3,4] and ALEJANDRO ROMERO[8]

[1]Section of Psychobiology, University of Barcelona, Barcelona, Spain, [2]Institute of Neurosciences, University of Barcelona, Barcelona, Spain, [3]Center for the Advanced Study of Human Paleobiology. Department of Anthropology, The George Washington University, Washington DC, [4]Gorilla Program, Dian Fossey Gorilla Fund International, Atlanta, GA, [5]Department of Evolutionary Biology, Ecology and Environmental Sciences, University of Barcelona, Barcelona, Spain, [6]Department of Tourism and Conservation, Rwanda Development Board, Kigali, Rwanda, [7]Mountain Gorilla Veterinary Project, University of California at Davis, [8]Departamento de Biotecnología, Universidad de Alicante, Alicante, Spain

Dental microwear reflects the abrasiveness of foodstuffs consumed by extant primates and it is commonly used to trace dietary adaptations in fossil hominins. However, the impact of feeding events and ecological constraints on micro-scale tooth wear formation processes remain unclear. Here, we use dental buccal-microwear analysis to test age-related effects of physical food processing on tooth-use in a naturally accumulated skeletal assemblage from the well-documented population of mountain gorillas from Volcanoes National Park, Rwanda. We analyzed dental microwear pattern of single teeth belonging to individual skeletons: 14 deciduous m2 (aged 1.2-6.08 years) and 39 permanent molars (~90% M2) of adult gorillas (10.69-44.55 years, 25 males and 14 females). Our results indicate that adult gorillas present more abraded molar buccal surfaces, with significantly higher densities and longer micro-striations, than immature individuals, which reflects the abrasive potential of ingested foods and the micro-striation cumulative process. However, we also found that dental buccal-microwear variability was not

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

associated with age when only adult gorillas were considered. Thus, gorillas from this population present a stable microwear pattern through adulthood, despite intraindividual variability in feeding ecology. Our findings show the cumulative process of dental buccal-microwear as immature mountain gorillas increase their intake of solid foods and develop an adult diet; but also, the stability of this pattern when diet over time is stable. We confirm that dental buccal-microwear variability is a reasonable proxy for feeding ecology in primates, although seasonality, habitat variability and diet proportions at individual level should be considered in future studies.

Funding: NSF (BCS 0852866, 0964944, 1520221, 1753651), The Leakey Foundation, National Geographic Society's Committee for Research and Exploration (8486-08), and the Spanish Ministerio de Ciencia e Innovación grant PID2020-114517GB-I00.

Comparing computational methodologies for adult skeletal age-estimation: DRNN and the MCP

JACQUELINE GALIMANY[1], KYRA E. STULL[1] and DAVID NAVEGA[2,3]

[1]Department of Anthropology, University of Nevada, Reno, [2]Department of Life Sciences, University of Coimbra, Portugal, [3]National Institute of Legal Medicine and Forensic Sciences, Coimbra, Portugal

Multi-trait computational methods are becoming the future of macroscopically-based skeletal age-estimation. In particular, increased precision is documented for middle and older adults with the use of traits from throughout the skeleton. Navega et al (2022) proposed a new method using Deep Random Neural Networks (DRNN) and 64 macroscopic skeletal traits on a sample of 500 identified skeletons. Tested with cross-validation, they report a ~6 year mean absolute error (MAE) across the entire adult age span. Stull et al (2022) proposed the Mixed Cumulative Probit (MCP), a new algorithm that is a generalization of the cumulative probit used in transition analysis that offers flexible modeling for nonlinear, heteroskedastic, and conditionally dependent mixtures of ordinal and continuous variables. We generated age-estimation models in the MCP with the data used to develop the DRNN to compare and contrast the performance of the two types of methods. Preliminary models generated on random selections of traits (m=12) and Navega et al's (2022) pre-specified trait sets resulted in similar (Wilcoxon test p>0.05) MAEs for the median of predicted ages calculated using conditionally dependent MCP models. While pubic symphysis and sacroiliac MCP models resulted in higher MAEs, acetabulum and first rib MCP models resulted in lower MAEs than presented by Navega et al. Random-trait-sets perform better than those limited by anatomical structures or regions. The comparison of these multi-trait age estimation methods contributes to the improvement of adult age estimates in forensic and bioarchaeological settings and the discussion regarding appropriate statistical analyses for complex biological data.

Applicability of Malocclusion Scoring Within the John A. Williams Human Skeletal Collection

SEAN J. GALLAGHER and REBECCA L. GEORGE

Anthropology & Sociology, Western Carolina University

Malocclusion is a common dental condition that is often associated with low socioeconomic status. Many studies available on malocclusion in modern populations are from orthodontic publications outside of the United States, so it is not well known how beneficial it might be in forensic anthropological or orthodontic contexts to understand the prevalence of this condition in a modern, U.S. sample. The John A. Williams (JAW) Human Skeletal Collection is a modern sample with access to biographical information, such as socioeconomic status or even orthodontic treatment, for many donors, making it ideal to explore the utility of scoring malocclusion. The purpose of this study was two-fold: to explore the utility of the Pilloud (2018) malocclusion and diastema scoring in a modern sample and to test its ease of use by examining intra- and interobserver error rates between a novice and more experienced scorer. Twenty individuals with at least 50% of the dentition per dental quadrant were scored using the Pilloud (2018) methodology with at least one week between observations. Diastemas and malocclusion were present within most donors scored, though these do not align with socioeconomic status as 87.5% of scored donors with available information were at least middle class at some point throughout their lives. Intra- and interobserver error rates indicate that this method requires some training as Cohen's kappa values for interobserver error were no higher than 0.606. Cohen's kappa values for the novice scorer ranged from 0.25 to 1 and from 0.571 to 1 for the more experienced scorer.

Mosaicism in the hominoid cranium and its impact on phylogenetic inference using 3D landmark data

JULIA GALWAY-WITHAM

Center for the Study of Human Origins, Department of Anthropology, New York University, New York Consortium in Evolutionary Primatology, (NYCEP)

Phylogenetic signal is the expectation that closely-related species are more similar phenotypically than distantly-related species. Given its statistical effects, we must account for phylogenetic signal, which requires a phylogeny. Traditionally, discrete anatomical features are used to construct phylogenies, but these may under-sample complex 3D morphology. I expand the exploration of using 3D landmark data for phylogenetic inference using crania from seven genera of extant catarrhines (N = 55), analyzed as single elements and partitioned into six modules based on a Maximum Likelihood analysis of modularity (EMMLi). I estimated phylogenetic signal in the crania and their modules using a multivariate extension of Blomberg's K (*Kmult*), which quantifies congruence between data and the expectation under neutral evolution. Distributions of shape variation were visualized using phylomorphospace analysis and phylogenetically aligned component analysis. In total evidence analyses implemented in TNT, I iteratively pruned molecular data from each taxon, designating each one as a 'pseudofossil'. The results support previous research that found both selection and neutral evolution to have shaped cranial variation in hominoids. Only two taxa were correctly placed as 'pseudofossils.' Different parts of the cranium demonstrate different phylogenetic signals and are variably accurate for phylogenetic inference. A combination of data from the cranial vault and the nasal region produces the most accurate hominoid phylogeny, with phylogenies that use data from the entire cranium performing less well overall. This mosaic evolution helps to explain the challenge of inferring hominoid phylogeny from cranial morphology alone and is important in the phylogenetic placement of fossils.

This research was jointly supported by the National Science Foundation Graduate Research Fellowship Program and the New York University MacCracken Fellowship.

Oral Microbiome Indicators of Systemic Disease Associated Frailty In Ancient Britain: A Paleoepidemiological Approach

ABIGAIL S. GANCZ[1] and LAURA S. WEYRICH[1,2,3]

[1]Anthropology, The Pennsylvania State University, [2]Huck Institutes of Life Sciences, The Pennsylvania State University, [3]Australian Centre for Ancient DNA, University of Adelaide

Noncommunicable diseases (NCDs) exact devastating emotional, physical, and economic tolls on modern populations, but little is known about their evolutionary histories. While NCDs do not generally leave diagnostic markers on human remains, in modern populations it has been shown that NCDs have strong associations with the oral microbiome (OM), and so their signals might be preserved in dental calculus. Using an ancient British population of 127 individuals dating from the Medieval to the Post-Medieval period (1066 to 1853 CE), we investigated whether OM signatures recovered via ancient DNA could be used as indicators of NCDs-associated frailty or mechanistic pathways via which dietary, social, and environmental factors became pathologically embodied. To do this, we used ADONIS tests to compare individuals exhibiting and not exhibiting pathologies, and found that overall pathology, periostitis,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

osteophytic lipping, joint porosity, and periodontitis were associated with significantly different OM communities. In order to assess which specific taxa were driving these trends, we used ALDEx2, a differential abundance analysis tool, to analyze whether specific species and genera were more common in pathological versus non-pathological individuals. We found that specific species, including *Streptococci* and *Methanobrevibacter*-associated taxa, were differentially more abundant in individuals with nonspecific periostitis and overall pathologies, respectively. Finally, we also used CCLasso to conduct correlation analyses that revealed overall OM community structures in pathology-exhibiting and non-exhibiting individuals. Our findings from this research indicate that, as in modern populations, ancient OM characteristics are related to systemic health and are promising markers of health-associated traits in past populations.

NSF-GRFP Grant No. DGE1255832. Any opinions, findings, and conclusions or recommendations expressed in this material are those of the authors and do not necessarily reflect the views of the NSF.

Crime concealment and body disposal using hydrochloric acid: A taphonomic and genetic appraisal

ATCHANA GANESALINGAM[1], LAURA J. ROYLE[2], VICTORIA E. GIBBON[3], GIUSEPPE SILVESTRI[4] and DEVIN A. FINAUGHTY[3,5]

[1]School of Anthropology and Conservation, Division of Human and Social Sciences, University of Kent, Canterbury, United Kingdom, [2]Division of Forensic Medicine and Toxicology, Department of Pathology, Faculty of Health Sciences, University of Cape Town, Cape Town, South Africa, [3]Division of Clinical Anatomy and Biological Anthropology, Department of Human Biology, Faculty of Health Sciences, University of Cape Town, Cape Town, South Africa, [4]School of Biosciences, Division of Natural Sciences, University of Kent, Canterbury, United Kingdom, [5]School of Chemistry and Forensic Science, Division of Natural Sciences, University of Kent, Canterbury, United Kingdom

Use of acids in crime concealment has necessitated research into its effects upon biological materials. Published research to date has lacked forensic realism and/or replicability in experimental design. Therefore, this study investigated whole-forelimb (porcine) dissolution in 36% hydrochloric acid, with immersion volume standardised using the following sample weight:acid ratios: 1:0.75 (experiment 1) and 1:1.1 (experiment 2 and 3). In experiment 1, a fleshed limb was immersed and macroscopic soft- and osseous tissue taphonomic artefacts were regularly recorded. Epidermal rupture occurred within 30mins, muscle fibre dissociation and bone exposure within 3hrs, 50% soft-tissue dissolution within 7hrs, and whole bone destruction by 19.5hrs. By 45hrs, only a small portion of humeral mid-shaft remained. Experiment 2 saw fleshed and de-fleshed limbs from one porcine specimen dissolved in equivalent volumetric concentrations. At 24hrs, the fleshed sample's mid-shaft retained soft-tissue, whilst the de-fleshed limb was largely dissolved. These taphonomic observations provide a benchmark timeline for whole limb dissolution in high-strength acid and illustrate the protective effects of soft-tissue, the latter suggesting future research should be conducted with fully fleshed limbs. In experiment 3, DNA was extracted from the soft-tissue of six fleshed limbs immersed for 24hrs, alongside positive and negative controls. While DNA from controls yielded a mean of 399.5ng of DNA, as measured by fluorometry, no detectable DNA was recovered from immersed samples. These results, combined with the taphonomic observations, suggest that mid-shaft cortical bone may be a better target for DNA recovery. Follow-up research will evaluate DNA recoverability from these tissues using qPCR.

We gratefully acknowledge the financial contributions of the School of Anthropology and Conservation for making this research possible.

Investigating the urban side of diet: reconstructing infant and adult diets through sequential and bulk isotopic collagen in the multicultural site of ancient Thessaloniki

ELISSAVET GANIATSOU[1], ANGELIKI GEORGIADOU[1], NEFELI CHOUPA[1], ASTERIOS AIDONIS[1], ANGELOS SOULELES[1], TANIA PROTOPSALTI[2], STAVROULA TZEVRENI[2], KRINO KONSTANTINIDOU[2], STELLA VASILEIADOU[2] and CHRISTINA PAPAGEORGOPOULOU[1]

[1]History and Ethnology, Democritus University of Thrace, [2]Ephorate of Antiquities of Thessaloniki City, Ministry of Culture and Sports

Carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotopic ratios in bone and dentine collagen from human remains provide the potential to reconstruct ancient diets in time-bound periods of life. In this study, we employed a multi-tissue isotopic approach to reconstruct infant and adult diets of the population of ancient Thessaloniki, which was founded in 315 BC and became one of the largest urban centers of the Greco-Roman world. We measured the $\delta^{13}C$ and $\delta^{15}N$ ratios of 240 individuals (315 BC-4th c. AD) and examine intra-site differences between historical periods, sex and cultural context. Infant diet (birth-7 years old) was based on the measurement of 1000 dentinal collagen samples obtained from sequential sampling of 100 first permanent molars and adult diets were reconstructed from 140 collagen samples from femurs. The results suggest that the dietary breadth in the site reflects the urban character of a large metropolis. Infant feeding practices varied greatly: breastfeeding initiates after birth and completes between the ages of 2.0 and 3.5 for the half of the dataset. Twenty infants were breastfed for less than two years and eight were breastfed for an even shorter period or were never breastfed. The long-term averaged adult diets consisted of animal protein and C3 plants. The consumption of C4 plants/small fish was detected during infancy and was less frequent during adulthood. Isotopic compositions have uncovered the dietary breadth in the site adding into our understanding of diachronic trends in the diet through illustrious turning points in Greek history.

This research has been co-financed by the European Regional Development Fund of the European Union and Greek national funds under the call RESEARCH – CREATE – INNOVATE (project acronym: ECHOES, T2EDK-00152).

The Largest Headhunting in Prehistoric Asia: Human Skull Hunting at the Honghe Site in Heilongjiang, China

GUOSHUAI GAO[1,2], QUN ZHANG[3], XIAOFAN SUN[1,2], WEI ZHANG[4], QUANCHAO ZHANG[1,2] and QIAN WANG[5]

[1]Bioarchaeology Laboratory, Jilin University, [2]School of Archaeology, Jilin University, [3]School of Society and Humanity, Xiamen University, [4]Department of Archaeology, Heilongjiang Institute of Archaeology, [5]Department of Biomedical Sciences, Texas A&M University College of Dentistry

Prehistoric human headhunting has a long history in various regions of the world, but osteological research on its evidence is relatively scarce, especially in Asia. Archaeological and osteological analysis of 39 headless individuals unearthed from Neolithic sites in northeastern China's Heilongjiang province revealed that the dead were beheaded using stone tools. We observed the bones of the deceased with a electron microscope, and in 5 cases, multiple artificial cutting marks were found in the front of the second cervical vertebra. Demographic and burialological information on the deceased reflect violent slaughter and headhunting of the tribe. The study provides evidence of the largest prehistoric headhunting in Asia to date.

Periodontal pathogens and osteoclastogenesis: How osteoimmunology can complement paleopathology

ELIJAH P. GARDNER[1], MICHAYLA G. GATSOS[1], ARUNA VASHISHTA[2], SILVIA M. URIARTE[2] and FABIAN CRESPO[3]

[1]Anthropology, University of Louisville, [2]Oral Immunology and Infectious Diseases, University of Louisville, [3]Anthropology and Center for Archaeology and Cultural Heritage, University of Louisville

During chronic oral infections, oral pathogens colonize surfaces in the oral cavity and activate the host immune system, triggering the release of inflammatory cytokines. These immune factors enhance the cellular response against oral pathogens and may induce excessive bone destruction

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

through the differentiation and activation of osteoclast cells. Alveolar bone loss associated with periodontal disease (PD) is identified in skeletal remains and can provide context for overall health status in past human populations. We propose that it is crucial for paleopathological reconstructions to address the interplay between periodontal pathogens, inflammatory factors, and osteoclastogenesis, which ultimately can inform about the severity and magnitude of PD. We exposed peripheral blood mononuclear cells (PBMCs) and neutrophils from healthy human donors to four periodontal pathogens: *Porphyromonas gingivalis, Filifactor alocis, Peptoanaerobacter stomatis,* and *Aggregatibacter actinomycetemcomitans*. In addition, monocytes from the same healthy human donors were differentiated into osteoclasts to explore how inflammatory cytokines (IFNg, TNFa, and IL6) expressed from the primed PBMCs and neutrophils impact osteoclastogenesis. Our preliminary results show that *A. actinomycetemcomitans* induced the highest expression of inflammatory proteins. However, osteoclastogenesis was reduced in the conditions that demonstrated the highest cytokine expression, mainly TNFa produced either by PBMCs or neutrophils. These results show us that the species of oral pathogen has a differential impact on inflammatory cytokine expression and, ultimately, osteoclastogenesis. Thus, we must consider the oral microbial composition when exploring the severity and bone loss observed in PD in skeletal samples.

Investigating diachronic dietary patterns in the ancient Greek colony of Ambracia: Stable isotope analysis ($\delta^{15}N$, $\delta^{13}C$) from bone collagen of human and animal remains

ANGELIKI GEORGIADOU[1], ELISSAVET GANIATSOU[1], KIRIAKOS XANTHOPOULOS[1], VARVARA PAPADOPOULOU[2] and CHRISTINA PAPAGEORGOPOULOU[1]

[1]Laboratory of Physical Anthropology, Department of History and Ethnology, Democritus University of Thrace, [2]Ephorate of Antiquities of Arta, Ministry of Culture and Sports

The Greek colonial expansion of the early 1st millennium BC spread people, goods, ideas and lifestyles across the Mediterranean and the Black Sea. The relationships between the mother-cities and colonies were profitable for both entities, and occasionally the colonies preceded the motherland in terms of cultural and political developments. Within this context, the reconstruction of dietary habits can shed significant light on these interactions, as food in ancient Greece was regarded as a marker of ethnic and cultural differentiation. To address pending questions about subsistence in ancient colonies, we analyzed carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) isotopic ratios in bone collagen to present the diet in the colony of Ambracia, from its foundation by Corinth (625 BC) up to its decline (323-33 β.C). We analyzed a total of 217 human individuals (25 subadults and 192 adults) to reconstruct the diet during childhood and adulthood together with 17 faunal remains. The results suggest that terrestrial animal protein played a pivotal role in the diet of the population with a lesser contribution of C3 plants and marine resources. These preferences were similar between chronological periods and contemporary sites in the broader region of Greece indicating a uniform diachronic pattern in diet. Sex-specific dietary differences were not detected but isotopic variability is greater in the subadult population showing that dietary breadth during childhood was possibly larger. Our study provides a comparative lens to our understanding of the subsistence techniques that developed during the second Greek colonization.

This research has been co-financed by the European Regional Development Fund of the European Union and Greek national funds under the call RESEARCH – CREATE – INNOVATE (project acronym: APOIKIA, T6ΥΠ;β-00191).

Chemical niche divergence in sympatric lemurs: understanding species' food selection

CHLOÉ NM. GHERARDI[1], JEAN-LUC RAHARISON[2], BRUNO RAMORASATA[3], VOLOLONIRINA RAHALINARIVO[3], JEAN-FREDDY RANAIVOARISOA[3], JEANNOT RANDRIANASY[3], JESSICA M. ROTHMAN[4,5], KAREN E. SAMONDS[1,2] and MITCHELL T. IRWIN[2,6]

[1]Biological Sciences, Northern Illinois University, [2]ONG, SADABE, [3]Anthropobiology and Sustainable Development, University of Antananarivo, [4]Anthropology, Hunter College, [5]Graduate Center, CUNY, [6]Anthropology, Northern Illinois University

Nutritional ecology being integrated into primatology has provided considerable insight into primate feeding strategies, and the ecological factors limiting populations - critical knowledge for addressing habitat change. The eastern rainforest of Madagascar possesses one of the world's most diverse primate communities, however, the ecological mechanisms by which these species coexist are not well understood. We quantified the nutritional chemistry of foods eaten by six sympatric lemurs (*Avahi laniger*, *Lepilemur mustelinus*, *Eulemur fulvus*, *Eulemur rubriventer*, *Hapalemur griseus*, and *Propithecus diadema*) to assess their niche separation. We also compared the nutritional chemistry of foods and non-foods (foods not eaten by any of these lemurs) to examine what drives food selection in these species. High dietary diversity in foods consumed was found with very little overlap – only 55 out of 213 foods tested being shared by at least two lemur species. Overall, both plant secondary metabolites (PSMs) and macronutrients appeared to drive food selection. Leaf selection depended on diet type and adaptations of different species: the frugivorous *Eulemur* species selected high-protein leaves, while two of the folivores (*A. laniger* and *P. diadema*) tolerated low-protein leaves. *A. laniger* and *P. diadema* tolerated high levels of tannins in their diet, while as *L. mustelinus* and *H. griseus* avoided them, confirming previous studies on the influence of PSMs on food selection. 33 of 53 non-foods collected were also found to contain tannins. Understanding the nutritional requirements and divergent dietary strategies of primates are essential for developing more effective conservation efforts, like reforestation and restoration projects.

Funding was provided by Global Wildlife Conservation, Primate Conservation Inc., NIU Department of Biological Sciences, NIU Department of Anthropology, and NIU Graduate School.

Helicobacter pylori's historical journey through Siberia and the Americas

SILVIA GHIROTTO

Life Sciences and Biotechnology, University of Ferrara

The gastric pathogen *Helicobacter pylori* has been associated with anatomically modern humans for at least 100,000 years and it is currently infecting more than half of the world population. Due to a high mutation and recombination rate, *H. pylori* strains show a clear phylogeographic signal and a pattern of genetic diversity that mirrors the one of their hosts. While *H. pylori* strains from Africa, Europe and Southeast Asia have been thoroughly investigated, sequences from northern Asia have yet to be reported. In this work we generated data and modeled the evolution of 556 new *H. pylori* sequences from 16 ethnically diverse human populations across Siberia to help resolve whether ancient northern Eurasian populations persisted at high latitudes through the last glacial maximum and the relationships between present-day Siberians and Native Americans. The genetic diversity across Eurasia and the Americas was structured into three main populations: *hpAsia2*, *hpEastAsia*, and *hpNorthAsia*. *hpNorthAsia* is closely related to the subpopulation *hspIndigenousAmericas* from Native Americans. Siberian bacteria were structured into five other subpopulations, two of which evolved through a divergence from *hpAsia2* and *hpNorthAsia*, while three originated as a consequence of Holocene admixture, supporting both Pleistocene persistence and Holocene recolonization of Central Asia and Siberia. We also reconstructed the evolutionary history of *hspIndigenousAmericas* through approximate Bayesian computation, supporting a colonization of the New World in a single migration event associated with a severe demographic bottleneck followed by low levels of recent admixture across the Bering Strait.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Comparative analysis of dietary intake and body composition among two ethnically distinct tribal populations from India

SUDIPTA GHOSH

Anthropology, North-Eastern Hill University

The present paper is an attempt to understand ethnic variations in the association of dietary intake with body composition in two geographically and genetically diverse adult populations, i.e., Santhal, an indigenous group from the plain regions of eastern India and Monpa, an indigenous population from the high-altitude regions of north-eastern India. A total number of 200 adult Monpa and 204 adult Santhal were recruited for the present investigation. Multiple and multivariate regression analyses were used to evaluate the influence of dietary intake on body composition. In somatotype, the Santhal were found to be predominantly mesomorphic, whereas the Monpa were predominantly endomorphic. Similarly, significantly ($p<0.001$) greater body fat was found among the Monpa males (23.41%$_{Monpa}$ vs. 11.27%$_{Santhal}$) and females (35.79%$_{Monpa}$ vs. 20.41%$_{Santhal}$), as compared to the Santhal. Despite the fact that both these tribes are engaged in primitive technology-based agriculture that requires a lot of physical labour, such difference in their body composition could be due to fundamental differences in the physical environment and great dietary/nutritional intake. In fact, it was found that Monpa follow a daily diet that is highly rich in dairy fat and animal protein, as compared to their counterpart Santhal. However, despite these dietary differences the present study found no significant influence of dietary intake on the body composition of these populations. Hence, an adaptive vis-a-vis evolutionary approach is proposed to understand the substantial proportion of body composition variations in these two ethnically distinct populations.

Ministry of Tribal Affairs, Government of India and by the University Grant Commission (UGC) Raman Post Doctoral fellowship to Indian for studying in USA.

How are Childhood Experiences Associated Variation in Inflammation among Sexual and Gender Minority Young Adults

JAMES K K. GIBB[1], BRIAN MUSTANSKI[2,3], JOSHUA M. SCHROCK[2] and THOMAS W. MCDADE[1,4]

[1]Department of Anthropology, Northwestern University, [2]Institute for Sexual and Gender Minority Health and Wellbeing, Northwestern University, [3]Department of Medical Social Sciences, Northwestern University, [4]Institute for Policy Research, Northwestern University

Childhood experiences can have a profound influence on adult physiological function and risk of adverse health outcomes later in life. However, little is known about the role adverse and positive childhood experiences plays in shaping variation in adult physiological function among sexual and gender minority (SGM) people. We examine how childhood experiences (both adverse and positive) shape variation in inflammatory biomarkers among SGM young adults. We used data from a racially and ethnically diverse Chicago-based cohort study of youth assigned male at birth who identify as SGM (ages 18–32, n =547), to test how childhood experiences are associated with C-reactive protein (CRP), and interleukin 6 (IL-6). Linear regression analysis adjusting for sexual orientation, gender, race/ethnicity, age, education, HIV status, body mass index, smoking status, showed that elevated levels of CRP were associated with rarely being able to talk to one's family (β: 0.517; SE: 0.253); as well as never feeling supported by friends (β: 0.788; SE: 0.410). Further, elevated levels of interleukin 6 was associated with rarely feeling like they had at least 2 non-parent adults who took a genuine interest in them was associated with elevated levels of interleukin 6 (β: 0.278; SE:0.134). Our analysis reveals that reporting fewer positive experiences during childhood, rather than reporting greater adverse experiences, is associated with elevated levels of CRP and IL-6. We discuss the implications of our findings for understanding variation in inflammation and chronic disease risk among SGM people.

JKG is supported by a Canadian Institutes of Health Research Doctoral Foreign Study Award (Funding Reference Number: 181602).

Restitution with community-centered science in South Africa: Sutherland Nine

VICTORIA E. GIBBON[1], LORETTA FERIS[2], JOSCHA GRETZINGER[3,4], KATHRYN SMITH[5,6], SIMON HALL[7], NIGEL PENN[8], TINASHE EM. MUTSVANGWA[1], CAROLINE M. WILKINSON[5], STEPHAN SCHIFFELS[4], SIANNE ALVES[9] and JUDITH C. SEALY[7]

[1]Human Biology, University of Cape Town, [2]Department of Public Law, University of Cape Town, [3]Max Planck Institute for the Science of Human History, Max Planck Institute, [4]Max Planck Institute for Evolutionary Anthropology, Max Planck Institute, [5]Face Lab, Liverpool John Moores University, [6]Department of Visual Arts, Stellenbosch University, [7]Department of Archaeology, University of Cape Town, [8]Department of History, University of Cape Town, [9]Office of the Deputy Vice Chancellor for Transformation, University of Cape Town

The historical unethical procurement of human skeletal remains and their use in race "science" haunts the discipline of biological anthropology. Between 1925-1927, human remains of nine San or Khoekhoe people, eight of them known-in-life, were removed from their graves on the farm Kruisrivier, near the town of Sutherland in South Africa without their families' knowledge or consent. Nearly 100 years later, as part of a restitution process, the descendant community requested a full range of analyses of the situation and the remains themselves. Historical and archaeological investigations have identified where the nine individuals came from and how they came to be at the University. Interdisciplinary historical, archaeological and analytical studies (osteobiographic, craniofacial, ancient DNA, stable isotope) of the nine individuals allow us to reconstruct the stories of their lives and in some cases their deaths. Craniofacial reconstruction and depiction, visualising the faces as they might have appeared in life, enable viewers to relate to these people as individuals, restoring personhood. The entire process of study, restitution and redress prioritised the descendant families' memories, wishes and desire to understand the situation, and learn more about their ancestors. They have described the process having helped them to reconnect with their ancestors and their heritage and culture. The approaches taken in this study contribute to restorative justice, reconciliation and healing while confronting historical trauma. These nine individuals were exhumed as specimens, but they will be reburied as people.

UCT; Max Planck Society; Liverpool John Moores; ZAMANI, National Geographic Society (EC-60001R-19); National Research Foundation SA (115357/120816); SA Research Chairs (84407); Biogeochemistry Research Infrastructure Platform, Depart. Science & Innovation SA.

Reanalysis of *Kapi ramnagarensis* supports its classification as a stem hylobatid

CHRISTOPHER C. GILBERT[1,2,3,4], ALEJANDRA ORTIZ[5], KELSEY D. PUGH[4,6], CHRISTOPHER J. CAMPISANO[7,8], BIREN A. PATEL[10,9], NINGTHOUJAM P. SINGH[11], JOHN G. FLEAGLE[12] and RAJEEV PATNAIK[13]

[1]Department of Anthropology, Hunter College, CUNY, [2]PhD Program in Anthropology, The Graduate Center, CUNY, [3]Division of Paleontology, American Museum of Natural History, [4]New York Consortium in Evolutionary Primatology, NYCEP, [5]Department of Anthropology, New York University, [6]Division of Anthropology, American Museum of Natural History, [7]Institute of Human Origins, Arizona State University, [8]School of Human Evolution and Social Change, Arizona State University, [9]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [10]Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California, [11]Biostratigraphy Group, Wadia Institute of Himalayan Geology, [12]Department of Anatomical Sciences, School of Medicine, HSC, Stony Brook University, [13]Department of Geology, Panjab University

Kapi ramnagarensis, described from the Indian Lower Siwaliks as a ~12.5-13 Ma stem hylobatid, was recently suggested to be a pliopithecoid stem catarrhine instead. We re-analyzed the character matrix used to hypothesize *K. ramnagarensis* as a krishnapithecid pliopithecoid, correcting a number of errors (e.g., codings for non-existent teeth), coding decisions inconsistent with previous anatomical descriptions, and character

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

modelling inconsistent with presumed character state transitions (i.e., ordered vs. unordered). We also added a character known to be important in catarrhine evolution, namely body size. The revised 161 character matrix was analyzed using parsimony, with and without *Krishnapithecus* included. The resulting three most parsimonious trees (MPTs) in both iterations place *Kapi* as a derived stem hominoid or stem hylobatid; *Kapi* is never reconstructed as a pliopithecoid. We then conducted 2D geometric morphometric analyses on the occlusal morphology of *Kapi* and a sample of 29 stem and 136 crown catarrhine M_3s to further assess whether *Kapi* is more likely to be a stem or crown catarrhine taxon. A discriminant functions analysis (DFA) on 24 principal components classifies 97.6% of specimens correctly (93.3% cross-validated), with *Kapi* classified as a crown catarrhine (98.0% probability). If we restrict the DFA to hylobatids versus stem catarrhine taxa, 87.2% of specimens are correctly classified (78.0% cross-validated), with no stem specimens incorrectly classified as hylobatids. *Kapi* is classified as a hylobatid (69.0% probability). Thus, despite only being known from a single M_3, all currently available data suggest that *Kapi* is most likely a stem hylobatid, as originally described.

Funding generously provided by: Leakey Foundation; NSF BCS Awards 1945736, 1945618, 1945743; MoES/P.O. (Geosci)/46/2015 and SERB-HRR/2018/000063; PSC-CUNY faculty award program; Hunter College; AAPA professional development grant program; USC; IHO/ASU.

Rural Embodiment and Community Health (REACH) study: Testing associations between environmental exposures and intestinal health in low-resource U.S. communities

THERESA E. GILDNER[1], ELIZABETH K. MALLOTT[2], ANGELA ZHANG[1], SOPHIE WAIMON[1], JADE B. THOMAS[1], KATHERINE L. NEMETH[1], ALEXANDER SHING[1] and TARA J. CEPON-ROBINS[3]

[1]Anthropology, Washington University in St. Louis, [2]Biology, Washington University in St. Louis, [3]Anthropology, University of Colorado Colorado Springs

Harmful environmental exposures (e.g., contaminated water and soil) are a key source of pathogen transmission; however, links between exposure and health outcomes remain poorly tested in low-resource U.S. regions. We assess whether drinking water source or reports of household flooding are associated with poor intestinal health outcomes using data collected from 85 adults (aged 18-84 years) living in low-resource communities within the Mississippi Delta and Southwestern Illinois that experience regular flooding and contaminated drinking water. Participant stool samples were used to assess fecal calprotectin levels (FC; a marker of intestinal inflammation) and *Helicobacter pylori* infection status (a gut bacteria linked with stomach ulcers and cancer in severe cases). 67% of participants exhibited clinically elevated FC levels, while 45% tested positive for *H. pylori*. Concerns about water quality were expressed in both communities, yet 26% of participants relied on unfiltered tap water. Further, 29% reported experiencing standing water in their basement. Unexpectedly, logistic regression analyses controlling for age, sex, and BMI suggest that drinking water and household flooding were not related to FC or *H. pylori* status (all $p > 0.08$), although higher BMI was associated with lower odds of *H. pylori* infection (OR = 0.934, $p = 0.047$). It is possible that the documented high rates of FC elevation and *H. pylori* infection are associated with broader community-level exposures, rather than individual household factors. 6S and 18S rRNA gene sequencing of community soil samples are underway to test whether local pathogen exposure patterns are associated with poor intestinal health.

Boettcher Foundation's Webb-Waring Biomedical Research Grant; WUSTL Seeding Projects for Enabling Excellence & Distinction (SPEED) Award; WUSTL Anthropology Department & Biology Department; University of Colorado Colorado Springs Anthropology Department

Stages? don't forget ages: Modeling cortisol-testosterone coupling across early to mid-pubertal ages among Indigenous Qom girls

DELANEY J. GLASS[1,2], MARGARET K. CORLEY[3], JESSICA GODWIN[2], ELEANNA BEZ[1], ELEANOR BRINDLE[2], CLAUDIA R. VALEGGIA[3] and MELANIE A. MARTIN[1,2]

[1]Department of Anthropology, University of Washington, [2]Center for Studies in Demography and Ecology, University of Washington, [3]Department of Anthropology, Yale University

The hypothalamic-pituitary-adrenal (HPA) and gonadal (HPG) axes partially regulate the timing of child-to-adult phenotypic transitions. 'Hormonal Coupling' describes relationships between 2+ hormones (e.g., cortisol, testosterone), leveraged to understand why HPA-HPG crosstalk is expected in adolescence. Evolutionary theorists suggest the HPA and HPG inhibit or co-activate depending on developmental demands such that cortisol and testosterone positively couple (associate) during puberty and de-couple as an adult phenotype is attained. While some find positive cortisol-testosterone coupling across pubertal status, evidence is sparse for detection of age-related trends of cortisol-testosterone coupling. We predicted cortisol and testosterone would not couple at pre-pubertal ages, positively couple at pubertal ages, and de-couple post-puberty. We used morning urinary cortisol, testosterone, and age data from Indigenous Qom girls (n=46, ages 8-14) who had samples 8-16 months apart (sample n = 92). We modeled the relationship between testosterone, age, and an age-testosterone interaction on cortisol using random-intercept models adjusting for participant identifiers. We observed evidence of coupling. Relative to cortisol and testosterone levels estimated at age 8, estimated interaction terms between age and testosterone on cortisol were indicative of positive and increasing coupling from ages 9-10 (b= -0.08 [-0.58,0.42]), 10-11 (b = 0.14 [0.36,0.63]) and 11-12 (b= 0.28 [-0.12,0.67]), de-coupling at ages 12-13 (b= - 0.18 [-0.78,0.42]), and positive coupling again at 13-14 (b=0.20 [-0.61,1.00]). We discuss our results from evolutionary and human biological perspectives on adolescent phenotypic transitions. We further investigate Bayesian approaches and analytic considerations for non-linear hormone data and age, relevant to future studies.

Funding for this analysis came from NSF BCS-0952264, UW Department of Anthropology Pilot Fund, and UW Center for Studies in Demography and Ecology (NICHD P2C HD042828, T32 HD101442-01).

An evaluation of the use of developmental simulations for taxonomic assessment

HALSZKA GLOWACKA[1], JASON S. MASSEY[2] and TERRENCE B. RITZMAN[3]

[1]Department of Basic Medical Sciences, University of Arizona College of Medicine-Phoenix, [2]Department of Anatomy and Developmental Biology, Centre for Human Anatomy Education, Biomedicine Discovery Institute, Monash University, [3]Department of Anatomy, Midwestern University

Bill Kimbel's contributions to the discovery and analysis of fossils are legendary; however, his research on hominin skull ontogeny, which includes co-authoring descriptions of important subadult fossils and significant studies at the intersection of taxonomy and ontogeny, is, perhaps, equally influential. In recent work on the remains from Malapa, South Africa, Bill questioned the taxonomic assessment of subadult hominins using direct comparisons to adults due to significant changes of the skull during ontogeny. One approach to address this issue is to use geometric morphometrics to simulate the development of subadult specimens using extant ontogenetic trajectories. Developmental simulation of adults can be performed using: (1) a linear method, whereby regression coefficients (shape variables on developmental stage) are multiplied by the number of age groups, or (2) a non-linear method, whereby regression coefficients are derived from each developmental stage. In the present study, we compare the performance of these two methods using an ontogenetic sample of five great ape species (n = 274 skulls) and fifty-seven 3D landmarks. Simulated adults were compared to the mean of true adults using Procrustes distances. Both methods performed well at classifying simulated adults to correct species, and the differences between methods were not statistically significant. Interestingly, when simulated adults were misclassified, they

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

were most often assigned to *Pan troglodytes* and both methods performed relatively poorly at classifying *Gorilla gorilla*. Overall, these results suggest that both methods of developmental simulation adequately assign the taxonomic identity of immature remains, but that there are potentially important differences among species.

Funding provided by NSF-DDIG 1540338, Wenner-Gren Foundation Doctoral Fieldwork Grant, Leakey Foundation Research Grant, James F. Nacey Fellowship, Elizabeth H. Harmon Research Endowment, and Donald C. Johanson Paleoanthropological Research Endowment.

Accuracy and Observer Agreement in the Determination of Trauma Timing in Human Ribs

CHRISTOPHER M. GODEN, EMMA T. BRZEZINSKI, AMANDA M. AGNEW and ANGELA L. HARDEN

Injury Biomechanics Research Center, The Ohio State University

Assessment of skeletal trauma timing is an important component of forensic anthropological analyses. The Standard for Analyzing Skeletal Trauma in Forensic Anthropology (ASB 147) states that trauma timing should be classified as antemortem, perimortem, or postmortem based on defect characteristics. However, standardized criteria for assessing trauma timing are lacking and when provided are typically limited to long bones or cranial examples. The objective of this research was to evaluate trauma timing in human ribs following current forensic anthropological definitions. Fractures (n=83) were classified as perimortem, postmortem, or undetermined by two analysts, novice and proficient, determined by previous trauma analysis experience. A word bank, compiled from recently published definitions of perimortem trauma and postmortem damage, was provided for the analyses. Accuracy rates of assessing trauma timing were 75.9% and 67.4% for the proficient and novice analysts, respectively. For both analysts, observations of plastic deformation were heavily weighted in differentiating peri- from postmortem timing. Interestingly, 39.5% and 31.3% of fractures correctly designated as perimortem by the proficient and novice observers, respectively, were described with language consistently used for postmortem damage (e.g., jagged or irregular fracture margins). Interobserver observations exhibited only fair agreement in timing classifications (Cohen's Kappa = 0.278), supporting the general opinion in forensic anthropology that experience is a critical component of trauma analysis. These results suggest that current descriptive characteristics for assessing trauma timing may not be appropriate for human ribs. Standardized criteria and language in assessing trauma timing should be further evaluated across various skeletal elements.

Assessing Classification Performance and Interobserver Error of the (hu)MANid Program on a Sample of Prehistoric Southwest Native American Individuals

ALIYA M. GODOY[1], NADIA C. NEFF[2,3] and DAWN MULHERN[1]

[1]Anthropology, Fort Lewis College, [2]Anthropology, University of New Mexico, [3]Center for Stable Isotopes, University of New Mexico

The need for reliable methods of determining population affinity from unknown or uncertain contexts is commonly encountered by anthropologists, including in repatriation efforts. While there has been substantial research and standardization efforts like the Macromorphoscopic Databank and (hu)MANid program, morphoscopic analysis can be problematic under such circumstances. With new data surfacing and validation studies exposing variability within ancestry classification groups, expanded representation is needed, particularly in Southwest Native American populations. We assessed classification performance of the (hu)MANid program on an archaeological sample of 29 Southwest Native American individuals dating to the Puebloan and Coalition periods. (hu)MANid data collected separately by two researchers on a subsample of 15 individuals were then used to evaluate potential interobserver error (IOE). After testing for normality, paired t-tests or Wilcoxon signed-rank tests were used to assess IOE of metric traits, and Cohen's Kappa was calculated for morphological traits and population classification for individuals based on the two sets of data.

The (hu)MANid program correctly classified 15/29 individuals using the prehistoric and historic reference groups. Within the pooled Hohokam and Arikara reference groups, 12 were correctly classified. The IOE analysis showed significant differences ($p<0.05$) in 3/11 metric traits, and slight or poor agreement (Kappa <0.4) in 2/6 morphological traits. Agreement between classifications based on all traits of the two samples resulted in a low percent agreement (26%, Kappa=0.2, p=0.23). These results indicate that (hu)MANid does not reliably identify the Southwest Native American groups tested here, stressing the need for additional reference groups.

I would like to thank the Fort Lewis College Student Research, Scholarly and Creative Activity Grant for funding this research.

Whole-bone shape variation of the manual third proximal phalanx in anthropoid primates

DEANNA M. GOLDSTEIN[1], CHRISTINE M. HARPER[2] and BIREN A. PATEL[3,4]

[1]Department of Anatomical Sciences, Stony Brook University, [2]Department of Biomedical Sciences, Cooper Medical School of Rowan University, [3]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [4]Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California

Paleoanthropologists have long noted that musculoskeletal adaptations in primate hands reflect their locomotor behaviors. For example, isolated features of proximal phalanges, including curvature, articular surface orientation, and diaphyseal proportions can distinguish extant terrestrial primates from extant suspensory primates. These traits are useful in reconstructing locomotion in extinct primates such as Miocene hominoids and the earliest hominins. Here, we use a combination of weighted spherical harmonic and sliding semilandmark analyses (SPHARM-sliding) to quantify whole-bone proximal third phalanx shape, and then analyze shape variation to identify aspects of phalangeal morphology linked to locomotion and phylogeny.

A SPHARM-sliding analysis with 2562 landmarks was performed on a large sample of anthropoids (N=75) including *Homo*, *Gorilla*, *Pan, Pongo, Hylobates, Symphalangus, Erythrocebus, Macaca, Nasalis, Papio,* and *Ateles*. Shape variation was summarized using principal component analysis. Procrustes distances were calculated and resampling statistics run to test for pairwise differences among taxa.

A majority of taxa exhibit significant differences in phalangeal shape ($p<0.05$). Taxa separate on PC1 (69.6% of variance) along a locomotor gradient driven by phalangeal curvature. Suspensory taxa exhibit curved/mediolaterally narrow phalanges, while terrestrial taxa exhibit straight/mediolaterally wide phalanges; taxa with more generalized locomotor profiles plot in between. Separation along PC2 (10.1% of variance) is driven by differences in proximal epiphysis shape. Additional results demonstrate that whole-bone, high-density landmark analyses can highlight nuanced features that disconnect manual phalanx shape from locomotion, as significant differences were also detected between closely related taxa that share similar locomotor repertoires (e.g., *Pan troglodytes* vs. *Pan paniscus*, p=0.04).

National Science Foundation (BCS #1539741, BCS #1317047); The Leakey Foundation; University of Southern California (URAP Program).

Structural and systemic barriers to entry in forensic anthropology: our history and our future

JESSE R. GOLIATH[1,2], ERIN B. WAXENBAUM[3], ISIS DWYER[4] and TAYLOR S. BORGELT[5]

[1]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Cobb Institute of Archaeology, Mississippi State University, [3]Department of Anthropology, Northwestern University, [4]Department of Anthropology, University of Florida, [5]Department of Anthropology, Purdue University

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

This presentation will address the persistent implicit and explicit barriers to building a culture of belonging in the field of forensic anthropology. These barriers create vulnerabilities, especially among marginalized groups, that need to be addressed as the field expands and diversifies. The lack of diversity in biological, and specifically forensic, anthropology is well documented. At the same time, recent years have seen a significant upswing in academic programs focusing on forensic anthropology at both the undergraduate and graduate levels. From 2000-2018, college enrollment of students from underrepresented populations has increased, however, these forensic programs are not addressing the pervasive structural barriers that exist and continue to impede the growth of diversity in our discipline. Barriers like the hierarchical power structure, illusion of objectivity and impartiality, racial and cis-gender biased methodologies, and belonging uncertainty are discussed. Numerous researchers have highlighted the value of indigenous and POC inclusion in both research and practice. However, these voices are not given equitable access and previous attempts of inclusion are shallow and seen as tokenism. Pedagogical and professional best practices that promote inclusive learning environments are also proposed. For example, peer engagement, beginning at the undergraduate level through emeritus status may both semantically and structurally allow for a bridge between the past and the future. Ultimately, pedagogical approaches that combat current systemic barriers need to be implemented to foster the expansion of diversity, inclusion, and equity in the field.

Behavioral Locomotor Patterns in Relation to Acetabular Shape Variation of African Great Apes

ASHE L. GOODEN and HANNAH E. MARSH

Anthropology, University of Central Missouri

The African great apes implement diverse locomotor patterns, including arboreal suspension, terrestrial quadrupedalism and occasional bipedalism. This locomotor diversity could be reflected in the shape of the acetabulum, a spherical region that is known to vary allometrically. Structural differences driven by locomotor patterns would help us interpret acetabular functionality of fossil groups, such as *Australopithecus* and other fossil apes. This study investigates the impact of locomotor patterns of four African apes, *Gorilla beringei; Gorilla gorilla; Pan paniscus; Pan troglodytes*, and *Homo sapiens* on the acetabulum shape through an acetabular notch index (ANI), consisting of the quotient of the distance between acetabular horns over the maximum diameter of the acetabulum. The use of an index removes the effects of size, thus negating the known effects of allometry for acetabular comparisons. The results showed there were statistically significant ANI differences between apes with varying primary locomotor patterns, with humans exhibiting a large ANI similar to *Gorilla*, and larger than either *Pan* species. Specifically, humans exhibit larger horn distances than the gorillas despite weighing less, which places total body weight on the joint, as opposed to quadrupeds who load partial body weight on each limb joint at a time. This trend suggests that other obligate bipedalists, such as the australopiths, would have ANIs larger than chimpanzees, most likely driven by large horn distances, even when they are predicted to weigh less than chimpanzees.

Funding provided by Ronald E. McNair Postbaccalaureate Program.

Examining the Dual Hormone Hypothesis in Wild Male Mountain Gorillas (*Gorilla beringei beringei*)

NICHOLAS M. GREBE[1], WINNIE ECKARDT[2], JOSEPHINE SCHMIDT[1], DOMINIC MAYO[1], ROSE UMUHOZA[2], RACHEL M. SANTYMIRE[3], TARA S. STOINSKI[4] and STACY ROSENBAUM[1]

[1]Department of Anthropology, University of Michigan, [2]Karisoke Research Center, [3]Department of Biology, Georgia State University, [4]Dian Fossey Gorilla Fund International

The Dual Hormone Hypothesis (DHH), originally developed via psychological research in humans, proposes that glucocorticoids block androgenic influences on status-seeking behaviors such as aggression and intrasexual competition. Numerous studies have provided supportive evidence for this hypothesis, showing negative interactions between androgens and glucocorticoids in predicting an array of target traits or behaviors. However, complications including null results, contradictory findings suggesting synergistic androgen-glucocorticoid interactions, and inconsistent contextual moderators demonstrate that the boundary conditions and robustness of the DHH remain underexplored. Remarkably, despite the wealth of studies examining endocrine predictors of social behavior in non-human primates, it is essentially unknown whether the DHH might apply to species other than humans. Gorillas serve as a particularly relevant comparative model, given their strong male intrasexual competition and heavy investment in androgen-mediated behaviors and morphological traits. In this study, we analyzed 960 fecal samples and matched behavioral observations from wild male mountain gorillas (*Gorilla beringei beringei*) at the Dian Fossey Gorilla Fund's Karisoke Research Center in Volcanoes National Park, Rwanda. We assayed glucocorticoid and androgen metabolites from fecal samples and examined whether androgens, glucocorticoids, or their interaction predict rates of displays, aggression, and sexual behavior. While we find limited evidence of androgens being weakly predictive of target behaviors, these associations do not generally depend on concurrent glucocorticoids, contrary to the DHH. We discuss potential reasons for null results and implications of the current study for primatology and future development of the DHH.

We would like to acknowledge support from donors to the Karisoke Research Center, the NSF Graduate Research Fellowship Program, and the University of Michigan.

The costs of women's work: maternal foraging energetics in an acorn subsistence economy

ALEXANDRA M. GREENWALD[1,2], ALEXANDRA NICLOU[3,4], GREGORY R. BURNS[1,5], HAYLEY KIEVMAN[1], ABBY BAKA[1], A. JA'NET BAIDE[1] and CARA OCOBOCK[4,6]

[1]Department of Anthropology, University of Utah, [2]Natural History Museum of Utah, University of Utah, [3]Pennington Biomedical Research Center, [4]Department of Anthropology, University of Notre Dame, [5]Yosemite National Park, Department of the Interior, [6]Eck Institute for Global Health, University of Notre Dame

The energy expenditures and return rates of mothers foraging with infants is an understudied and important consideration in our understanding of the evolutionary role of foraging and sexual division of labor. We replicate acorn foraging conditions representative of Holocene California hunter-gatherers and compare the energetic costs of acorn foraging in females (n=6, ages: 21-37 years) under three different infant-carrying conditions. We measured physical activity levels through accelerometry and metabolic rate (MR, Kcal/h) through indirect calorimetry of foraging "unloaded" and carrying a 10lbs load (mimicking a newborn) in a traditional California basketry cradle and in a sling. Average energy expenditure while foraging unloaded was 194 kcal in a 1 hour bout, 197 kcal while utilizing cradle technology, and 186 with sling technology. Average caloric value of foraged acorns was highest for unloaded bouts (11,066 kcal), followed by cradle-carrying bouts (10,616 kcal) and sling-carrying bouts (9,446 kcal). While cradle-carrying resulted in greater caloric expenditures compared to foraging unloaded or with a sling, foragers using cradles experienced higher return rates and greater foraging efficiency than foragers carrying infants in a sling. Basketry cradles and cradleboards, a traditional western North American technology, provides greater freedom of movement than the more constrictive sling-carrying method and was an important technology in subsistence economies relying primarily on women's labor to gather and process plant resources.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Structured Violence in Northern Egypt during the Hyksos Period

JULIA GRESKY[1], MANFRED BIETAK[2] and EMMANUELE PETITI[1]

[1]Divison of Natural Sciences, German Archaeological Institute, [2]Austrian Archaeological Institute, Austrian Academy of Sciences

This paper presents the results of the first systematic bioarchaeological analyses on severed hands from the excavations of M. Bietak at Avaris/Tell el-Dab'a 2011. The 12 articulated right hand bones were found in three pits in front of the throne room of the Hyksos palace (15thdynasty, c.1640–1530BC).

The presence of mainly complete hands and the absence of bones belonging to other anatomic districts indicate that the hands were detached shortly before or after death and that the tendons and ligaments of the wrist were carefully removed. The hands were then arranged into the pits with wide-splayed fingers, mostly placed on their palmar sides.

The bioarchaeological data presented here are the first direct evidence of one of the recurring propagandist motives in Egyptian written and figurative sources, known as the "gold of honor". Being introduced to Egypt already before the New Kingdom by the Hyksos, these sources refer to victorious soldiers presenting the chopped right hands of foes to the Pharaoh in order to receive a commensurate reward.

Our contribution, grounded on a trans-disciplinary methodological framework, focuses on the rhetoric of dominance conveyed by body parts as trophies in war contexts, such as for the case reported here. The accurate preparation of the body parts suggests a strictly codified language of violence, which translates into a rationalized de-personification and eternal removal of power of the enemy. Yet, the factual dimension is claimed by political propaganda, generating the disproportion between the narratives delivered by figurative sources and the hard bioarchaeological evidence.

Locomotor energetics in *Propithecus coquereli*: costs of terrestrial locomotion using arboreal anatomy

NEYSA GRIDER-POTTER[1,2], AMANDA MCGROSKY[3], ROSHNA WUNDERLICH[4], NICK HESLEP[4], ANGEL ZEININGER[3] and DANIEL SCHMITT[3]

[1]Cell Systems and Anatomy, University of Texas Health San Antonio, [2]Southwest National Primate Research Center, Texas Biomedical Research Institute, [3]Evolutionary Anthropology, Duke University, [4]Department of Biology, James Madison University

Arboreal to terrestrial transitions are rare among mammals. Obligate bipedalism is rarer still, making it challenging to study the functional morphology and selective pressures associated with the evolution of terrestrial bipedality in hominins. Nevertheless, facultative bipedalism has evolved convergently as a mode of terrestrial (and arboreal) locomotion in several arboreal primates, including gibbons, sifakas, and presumably early hominins. These species provide an ideal opportunity to study the energetic costs of transitioning to terrestrial bipedalism because they rely on bipedal gaits when moving terrestrially despite lacking musculoskeletal adaptations typically associated with obligate bipedalism. This study tests the prediction that mechanical energy expenditure is higher during terrestrial locomotor modes than during arboreal locomotion in sifaka. Triaxial acceleration was collected in three male captive sifaka (*Propithecus coquereli*) across three arboreal and three terrestrial locomotor experimental sessions. Overall dynamic body acceleration (ODBA), a proxy for mechanical energy expenditure, and average peak acceleration across each session were calculated. Linear mixed models demonstrate no significant difference in ODBA or average peak force between arboreal and terrestrial sessions, indicating that sifaka expend similar amounts of mechanical energy and experience similar peak forces during terrestrial bipedalism and arboreal locomotion despite lacking bipedally adapted morphology. Not only do these results suggest that early hominin locomotor anatomy did not hinder terrestrial bipedal locomotion but it may also suggest that sifaka locomotion is robust to the deforestation that their habitats are currently experiencing.

This study was supported by the Duke Lemur Center Director's Fund.

Religion/Spirituality has differential effects on CVD risk for Black people over the life course

ERIC E. GRIFFITH and KEISHA L. BENTLEY-EDWARDS

Samuel DuBois Cook Center on Social Equity, Duke University

One in four deaths in the United States is caused by cardiovascular disease (CVD). Although the occurrence of CVD is similar between White people and Black people, the latter are 30 percent more likely to die from CVD. It is imperative that researchers seek explanations that go beyond the doctor's office and into cultural and community settings to better understand cardiovascular health among Black people. As such, religion and spirituality (R/S) have been acknowledged for their positive influence on social behaviors and emotional health, but have not been sufficiently explored for their role in attenuating or exacerbating physical health outcomes – in particular, the risks associated with CVD for Black people.

Research Question: Do dimensions of R/S compound or mediate CVD risk over the life course for Black people?

Methods: This study examines the nature of the relationships of R/S and CVD risk factors by age, gender, education, income, using cross-sectional and longitudinal data for Black people from the Jackson Heart Study (n=5,301) and ADD health study (n=3,000). We employ mediation analyses to identify both direct and indirect effects.

Results: We find that the relationship between R/S constructs, as measured by the Daily Spiritual Experiences Scale (e.g., feeling God's love/presence) and rate of attendance in R/S events, do vary over time. These findings suggest that changes/shifts in religious participation over time merit additional study as they are associated with behaviors that affect CVD risk factors.

This research was supported by a grant from NIH/NIMHD (Religion, Spirituality, and CVD Risk: A Focus on African Americans, R01 MD011606-01A1).

The human pubic symphysis is an evolutionary trade-off

NICOLE D.S. GRUNSTRA

Evolutionary Biology, University of Vienna, Mammal Collection, Natural History Museum Vienna

Fast and high-impact locomotion requires stable pelvic joints while birthing relatively large fetuses may favor pelvic joint mobility. Humans posses a cartilaginous pubic symphysis, capable of a limited amount of expansion which appears obstetrically advantageous. But other mammals have even more flexible pubic joints, possessing a syndesmosis (a pubic "gap"), which is an adaptation to birthing single large fetuses (e.g. Chiroptera). Here, I test the hypothesis that increased mobility in the human pubic joint, while selectively advantageous given our large-headed babies, is evolutionarily constrained by our bipedal running locomotion. I studied variation in adult pubic joint morphology among 153 mammal species across all major clades in CT scans and dry skeletons, revealing three character states ranging from rigidity to high flexibility: a synostosis (fused), a symphysis (cartilage), and a syndesmosis (spanned by a hyperflexible ligament). Monotremes and marsupials (both with tiny neonates) only possess synostoses, whereas placentals exhibit all three states. High-impact locomotion, such as running and digging, favors a synostosis (e.g. in large cats, bovids, aardvarks). Flying and aquatic lifestyles alleviate constraints associated with terrestriality, particularly under strong obstetric selection. Syndesmoses are widespread phylogenetically (i.e. evolutionarily labile), strongly sexually dimorphic, associated with either single large neonates or large litters of small neonates, but constrained to species < 1.5 kg. A syndesmosis is thus a non-starter for humans given our body size. Nonetheless, our strong terrestriality, obligatory bipedalism, and

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

propensity for long-distance running predicts a pubic *synostosis,* suggesting that the human pubic symphysis is a compromise solution between opposing demands.

Revisiting linear enamel hypoplasia in Cayo Santiago rhesus monkeys (*Macaca mulatta*): Is there a matriline effect?

DEBBIE GUATELLI-STEINBERG[1], TAYLOR GUERRIERI[1], LIYA SAMUEL[1], TERRY KENSLER[2], LUCI KOHN[3], MARTIN ZHAO[4], GEORGE FRANCIS[5] and QIAN WANG[5]

[1]Anthropology, The Ohio State University, [2]Caribbean Primate Research Center, University of Puerto Rico Medical Sciences, [3]Department of Biological Sciences, Southern Illinois University, [4]Department of Computer Science, Mercer University, [5]Department of Biomedical Sciences, Texas A&M University School of Dentistry

Linear enamel hypoplasia (LEH) is an enamel defect that forms in response to physiological stress, such as malnutrition or disease, occurring during enamel formation periods. Such stresses can disrupt enamel secretion, resulting in linear bands of thin enamel. Previous study of these defects in Cayo Santiago rhesus monkeys demonstrated that LEHs were most often expressed on their lower P3s, occurred at higher frequency during the period of irregular provisioning during the colony's history, and were less numerous (though not significantly so) in individuals belonging to high as opposed to middle- and low-ranking matrilines. The present study explores whether some matrilines are more likely than others to exhibit LEH. Here, dental impressions of lower premolars, lower canines, and upper first incisors of 82 young individuals with unworn enamel surfaces were made from seven matrilines. Observation of LEH on dental replicas occurred without reference to matriline, using a Leica digital microscope in which lighting and magnification were systemically varied. Generalized estimating equations with a negative binomial distribution were used to evaluate defect counts per tooth type, side, and matriline. Lower premolars and lower canines had significantly greater defect counts than upper incisors, while side was not significant. Individuals from matriline 22 had the greatest number of defects per tooth, differing significantly from individuals of two of the remaining six matrilines. Because sample sizes per matriline were small, these results require additional testing on larger samples, but we tentatively suggest that some matrilines may be more likely to exhibit LEH than others.

Funding Sources: The Cayo Santiago colony is supported by NIH 5P40OD012217. This project is supported by NSF grants to DG-S., LK., MZ, and QW (NSF #1926528, 1926481, 1926402, and 1926601).

Epigenetic correlates of language training in chimpanzee brains

ELAINE E. GUEVARA[1,2], WILLIAM D. HOPKINS[3], PATRICK R. HOF[4,5], JOHN J. ELY[2,6], BRENDA J. BRADLEY[2] and CHET C. SHERWOOD[2]

[1]Evolutionary Anthropology, Duke University, [2]Department of Anthropology and Center for the Advanced Study of Human Paleobiology, The George Washington University, [3]Keeling Center for Comparative Medicine and Research, University of Texas MD Anderson Cancer Center, [4]Nash Family Department of Neuroscience and Friedman Brain Institute, Icahn School of Medicine at Mount Sinai, [5]New York Consortium in Evolutionary Primatology, [6]MAEBIOS

Human language is a hallmark of our species and, although progress has been made in understanding the genetic basis of this distinctive trait (e.g., comparative genomics and functional analysis of the brain developmental regulator *FOXP2*), much remains to be learned. Here, we leveraged rare frozen brain tissue from language-trained chimpanzees to assess whether these individuals show epigenetic differences from non-language-trained conspecifics. Specifically, we generated genome-wide CpG methylation data for the dorsolateral prefrontal cortex (DLPFC) and cerebellum of eight chimpanzees, two of whom, Sherman and Lana, received language training using lexigrams from around age two. We found only two differentially methylated regions in the DLPFC but ten in the cerebellum. Notably, two of these differentially methylated regions spanned regulatory regions of the gene *OTX2*, which encodes a homeodomain-containing transcription factor OTX2 (Orthodenticle homeobox 2) that is involved in cerebrum, cerebellar, pineal gland, and retina development. Moreover, OTX2 is a known postnatal master regulator of critical periods of neuroplasticity and has been proposed to play a crucial role in language development. Methylation levels are significantly lower in the language-trained chimpanzees, which is consistent with increased expression–and perhaps prolonged activity–of this gene. Although tentative due to the necessarily small sample size, our results a) provide further support to highlight the vital role of the cerebellum in language and, perhaps in non-verbal as well as verbal language production, and b) identify a gene, *OTX2*, that warrants further study in relation to language acquisition.

This work was supported by The George Washington University, the James S. McDonnell Foundation (220020293), the National Science Foundation (SMA-1542848, BSC-2127961, EF-2021785), and the National Institutes of Health (R24NS092988, R01AG067419).

Daytime Foraging Behavior of Semi-Free Ranging *Lemur catta* at the Lemur Conservation Foundation in Myakka City, Florida

ETHAN GULLEDGE[1], LYDIA E.O. LIGHT[1], ERIK PATEL[2], TIMOTHY BRANSFORD[3] and TAYLOR FISHER[3]

[1]Anthropology, The University of North Carolina at Charlotte, [2]The Lemur Conservation Foundation, [3]Animal Studies, Eckerd College

Semi-free ranging lemur species are found in places outside their native habitat and, thus, are often foraging for plant species that are not common to the diets of their wild Madagascan counterparts. The Lemur Conservation Foundation located in Myakka City, Florida houses such a population of ring-tailed lemurs (*Lemur catta*) divided into two semi-free ranging groups with 24 hour forest access. I hypothesized that the *L.catta* would be primarily ingesting immature foliage. I also hypothesized that the lemurs would forage within close proximity to their provisioned feeding locations. My final hypothesis was that the individuals would be foraging for food items primarily <1 meter above ground level. I observed the two lemur groups over a twelve week period from May-August 2022. Out of the total data collected, the vast majority of ingested items were mature leaves (55.9%) with detritus (12.6%) following after. The ingested items were also entirely within the home range for both lemur groups, with one group unable to forage near the building where their provisioned meals were provided. An overwhelming majority of ingested items were found <1 meter above ground level (87.4%). I conclude that mature leaves are not the primary foraging source of semi-free ranging *L. catta* and that the lemurs will forage primarily within their home range in close proximity to their provisioned feeding environments while selecting items within 1 meter above ground level.

Funding for this project was provided by the Lemur Conservation Foundation, and UNCC Department of Anthropology.

Reassessment of accentuated striae counts in deciduous tooth enamel in two Ohio populations of disparate socioeconomic status

KAITA N. GURIAN[1], DOUGLAS CREWS[1], SARAH HOLT[1], MARK HUBBE[1,2], PATRICK MAHONEY[3], GINA MCFARLANE[3], ALESSIA NAVA[4] and DEBBIE GUATELLI-STEINBERG[1]

[1]Anthropology, The Ohio State University, [2]Instituto de Arqueología y Antropología, Universidad Católice del Norte, Chile, [3]School of Anthropology and Conservation, University of Kent, Canterbury, UK, [4]Institute of Geological Sciences, Polish Academy of Sciences, Kraków, Poland

Accentuated striae (AS) reflect developmental disruptions of enamel visible in thin sections as thick dark lines paralleling regular growth lines

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

(striae of Retzius). AS have been used as non-specific indicators of stress in bioarchaeology, forensics, and primatology. Previous research has not definitively assessed whether AS are associated with socioeconomic status (SES), which itself is linked to childhood stress experience. This research reassesses AS in enamel thin sections examined in a preliminary study by further grinding and polishing of the slide sample to correct uneven slide thickness. The preliminary study suggested that SES was a significant predictor of AS formation. Here we ask whether data collected from these slides using more refined slide preparation yields the same result.

Histological slides of deciduous teeth (N=48) derived from two populations in Central Ohio, one high-income (A=affluent Central Ohio), the other low-income (B=rural Appalachian Ohio). Slides were re-ground and polished and counts of AS were taken in each tooth using a Motic BA 310 Microscope fitted with a Moticam camera. Presence of AS was compared between samples. Other variables--gestation length, birth mode, sex of the infant, gestational diabetes, anterior/posterior tooth type--were also examined.

AS were observed in both populations (A=16%, B=48%) but the presence of AS in the low-SES population is significantly higher than that observed in the high-SES population (p=0.02137). There are no significant associations between AS and any other variables. This reassessment of AS counts yields the same result as the initial study, supporting a link between AS and SES.

The effect of artificial light on a nocturnal primate

SHARON GURSKY[1] and NANDA B. GROW[2]

[1]Anthropology, Texas A&M University,
[2]Anthropology, Washington State University

An anthropogenic disturbance that is rarely addressed for nonhuman primates is the effect of artificial light at night (ALAN), thereby eliminating natural darkness. ALAN can be caused directly by a light source (e.g., streetlights), or indirectly from sky glow (artificial light that is scattered and reflected back to earth). The introduction of light at night can alter the perception of the passage of time as indicated by lunar cycles. Research has demonstrated that artificial lighting causes changes in animal behavior (e.g., disruption of seasonal behaviors, altered composition of communities), which can ultimately affect reproductive success and survivorship. The goal of this research project is to explore how the behavior of wild nocturnal spectral tarsiers, *Tarsius spectrumgurskyae,* is modified in response to artificial light. This study was conducted at Tangkoko Nature Reserve on the easternmost tip of the northern arm of Sulawesi in Indonesia from May-August 2022. The results of this preliminary study suggest that in response to artificial light tarsiers extend their daily activity time by increasing time spent travelling and foraging, leaving sleeping sites earlier, and returned to sleeping sites later. The tarsiers also left their sleeping trees at lower heights, and gave fewer vocalizations and fewer alarm calls each night in response to the addition of artificial light. The tarsier's lengthened night could increase interspecific competition for food as well as increase predation risk. Additional research on the long-term effects of ALAN on primates will clarify how light pollution should be considered in conservation plans.

Funds were graciously provided by WILD, Primate Conservation Inc., Mohammed bin Zayed Species Conservation Fund and Texas A&M University.

An anatomical reconstruction of KNM-WT 15000 (*Homo erectus*)

MARTIN HAEUSLER[1] and CHRISTOPHER B. RUFF[2]

[1]Institute of Evolutionary Medicine, University of Zürich, Switzerland, [2]Center for Functional Anatomy and Evolution, Johns Hopkins University, USA

Despite the completeness of the 1.47 Ma old KNM-WT 15000 skeleton of the Nariokotome *Homo erectus* youth it is still unclear whether differences in body shape and growth pattern relative to modern humans existed and how they affected stature and body mass. Remarkably, estimates of his stature-at-death diverge widely, with predictions based on lower limb length centering at 157 cm, while a body size of only 141–146 cm was suggested when also vertebral dimensions were considered. Part of this discrepancy might be owing to the paucity of similarly aged juveniles in the modern human reference samples, as well as the reported divergence in KNM-WT 15000's chronological age of 7.6–8.8 years based on tooth microanatomy and skeletal age of 11–15 years relative to modern human standards of epiphyseal fusion. We therefore performed a complete virtual anatomical reconstruction of the KNM-WT 15000 skeleton using high-resolution 3D surface scans of the original fossil. The vertebrae and the reconstructed epiphyses of the knee joint of KNM-WT 15000 were then registered to CT-generated 3D models of modern human juveniles aged 8–15 years while foot height was reconstructed from upright standing radiographs of similarly aged children. We found an almost perfect match in vertebral dimensions with the CT scan of a 9.4-year-old boy but not with the older juveniles. This indicated a stature-at-death intermediate between previous estimates. Further research needs to show whether the axial skeleton had a different growth trajectory than the limb skeleton in *Homo erectus* compared to modern humans.

This project was financially supported by the Swiss National Science Foundation (grant 31003A_176319).

Metabolome Analyses of Ancient Bison Dental Calculus

JACOB J. HAFFNER[1], SARAH J. JOHNSON[1], LELAND BEMENT[1,2], BRANDI BETHKE[1,2], CAITLYN MIDDLETON[3], LAURA-ISOBEL MCCALL[3,4] and CECIL M. LEWIS[1]

[1]Department of Anthropology, University of Oklahoma, [2]Oklahoma Archaeological Survey, University of Oklahoma, [3]Department of Chemistry and Biochemistry, University of Oklahoma, [4]Department of Microbiology and Plant Biology, University of Oklahoma

The metabolome represents the sum of all small molecules in a biological system and is shaped by lifestyles, behavior, and the environment. The archaeological application of metabolomics is burgeoning, particularly for human dental calculus, but few studies have applied metabolomics to non-human samples. ere, we used untargeted liquid chromatography-tandem mass spectrometry to examine dental calculus metabolomes from five historical bison samples approximately dated to 12,000 years ago. Our two primary research goals were: develop extraction methods for broad ranges of molecules from these ancient samples and determine whether evidence of past behavior such as diet or historical human-bison interactions can be gleaned from these molecules. We present our extraction method. Despite the significant time depth of our samples, 540 total metabolite features were detected. Annotation of these molecules was challenged by the current state of annotation within relevant databases, yet annotated data reveal the promise of metabolomics in reporting biocultural data and modern contamination challenges, which appear distinct from ancient DNA. Examples include palmitamide and taurocholic acid, which are common natural products. Other compounds such as diphenylamine, a plant biomarker, suggest possible dietary sources for these bison, but raises contamination questions. Additionally, the detection of human-associated molecules like DEET, a pesticide component, also highlight modern contamination concerns, despite conforming to contamination protocols common to ancient DNA studies. Nonetheless, this study presents novel methods for examining molecular components of human-animal interactions in historical contexts and highlight potential pathways for investigating the impact of modern human behavior on ancient molecular taphonomy.

Small, Odd, and Old: Sulawesi mountain tarsiers (*Tarsius pumilus*) represent an ancient lineage

LAURA HAGEMANN[2], NANDA GROW[1], YVONNE BOHR[3,4], DYAH PERWITASARI-FARAJALLAH[5,6],

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

YULIUS DUMA[7], SHARON GURSKY[8] and STEFAN MERKER[2]

[1]Department of Anthropology, Washington State University, [2]Department of Zoology, State Museum of Natural History Stuttgart, [3]Institute of Ecology, Diversity and Evolution, Goethe-Universität Frankfurt am Main, [4]Institute of Zoology, Universität Hamburg, [5]Primate Research Center, IPB University, [6]Department of Biology, IPB University, [7]Faculty of Animal Husbandry and Fisheries, Universitas Tadulako, [8]Department of Anthropology, Texas A&M University

Sulawesi is a biodiversity hotspot located in a collision zone of major tectonic plates. The region's geological past is linked to the evolutionary history of twelve known tarsier species that exclusively occur on Sulawesi and small surrounding islands. Tarsiers, small nocturnal haplorhine primates, arrived in southern Sulawesi in the early Miocene and split into two lineages in the early Pleistocene. Here we present results of the first genetic analyses to include the enigmatic *Tarsius pumilus,* whose role in the evolution of tarsiers was previously unclear. For a long time, the mountain (pygmy) tarsier was known only from a few museum specimens. The species is significantly smaller than lowland tarsiers, occurs exclusively in mountain forests above 2000 m asl, and exhibits unique behaviors, including extreme crypsis. Our results show that *T. pumilus* is the sister taxon to all other Sulawesi tarsiers. Its ancestors split from the predecessor of the remaining species approximately 10 MYA, 7 MY before they split into two lineages. Paleogeographic maps suggest that this event predates the presence of mountains on the western part of islands, suggesting that displacement into a mountain environment was likely not the underlying mechanism for speciation. The timing, however, coincides with the rise in sea level between the western and eastern parts of proto-Sulawesi, presumably forming a substantial barrier to dispersal. Given that *T. pumilus* underwent 10 MY of independent evolution, further research is necessary to clarify whether its small size and distinctive features are retained primitive traits or derived features.

Field research conducted by NG was funded by NSF Doctoral Dissertation Improvement grant #BCS-1028885 and Primate Conservation, Inc. grant #99-425691-00001. Lab analyses were partially funded by Conservation International Primate Action Fund.

Cultural transformations, migration and possible dietary shift during the 2nd Millennia BC in Eastern Central Europe - a bioarchaeological approach

TAMÁS HAJDU[1], ANETT GÉMES[1], TAMÁS SZENICZEY[1], KATALIN ÉVA GYENESEI[1], KRISZTIÁN KISS[1,2], KRISTÓF FÜLÖP[3], JÁNOS GÁBOR TARBAY[4], ASHLEY MCCALL[5], MAGDOLNA VICZE[6], ANIKÓ HORVÁTH[7], LÁSZLÓ PALCSU[7], ISTVÁN MAJOR[7], MIHÁLY MOLNÁR[7], ERIKA MOLNÁR[8], ANTÓNIA MARCSIK[8], KLÁRA P. FISCHL[3,9], GÉZA SZABÓ[10], EDIT MESTER[11], VAJK SZEVERÉNYI[12], GABRIELLA KULCSÁR[3], ILDIKÓ PAP[1,2,8], JÁNOS DANI[12] and VIKTÓRIA KISS[3]

[1]Department of Biological Anthropology, Eötvös Loránd University, Budapest, Hungary, [2]Department of Anthropology, Hungarian Natural History Museum, Budapest, Hungary, [3]Institute of Archaeology, Research Centre for the Humanities, Eötvös Loránd Research Network Budapest, Hungary, [4]Department of Archaeology, Scientific Directorate, National Institute of Archaeology, Hungarian National Museum, Budapest, Hungary, [5]Independent researcher, [6]Department of Experimental Archaeology and Innovation, SAX Project, Scientific Directorate, National Institute of Archaeology, Hungarian National Museum, Budapest, Hungary, [7]Isotope Climatology and Environmental Research Centre (ICER), Institute for Nuclear Research, Debrecen, Hungary, [8]Department of Biological Anthropology, Szeged University, Szeged, Hungary, [9]Department of Archaeology, Miskolc University, [10]Wosinsky Mór Museum, Szekszárd, Hungary, [11]Kiss Pál Museum, Tiszafüred, Hungary, [12]Déri Museum, Debrecen, Hungary

Archaeological investigation of the material culture of the 2nd Millennium BC in the Carpathian Basin has revealed several examples of cultural changes. The appearance of the Tumulus Grave Culture (TGC;1500-1300BC) is particularly important, since in this period almost in the territory of present-day-Hungary a relatively unified archaeological culture can be observed. It is not yet entirely clear whether the appearance of the TGC is a consequence of immigration, or it is a cultural transition of the local groups. The appearance of the TGC, however, resulted in the abandonment of the tell-settlements as well as a gradual increase in the number of horizontal settlements. It is still unclear whether there was a shift from farming to animal husbandry or the changes of settlements are unrelated to the transformation of subsistence strategy. The aim of our study is to present the results of our bioarchaeological project for chronology, mobility and diet on BA populations from present-day Hungary. Our results showed that:(1)The diet of population of Middle BA(MBA) groups lived in the 1st-2nd and 3rd part of MBA do not differ significantly from each other; (2) We observed a wide distribution of values for N isotope-ratio, indicating a variable protein intake throughout the populations; (3)We observed a tendency to a decrease in protein intake in the transition to the TGC period; (4)The C isotope values show the shift towards a C4-plant-based diet during the TGC period; (5)The earliest burial that shows a significant consumption of C4 plant (broomcorn millet?) is dated to 1530-1430BC.

Hungarian Scientific Research Fund (FK128013); Momentum Mobility project (Project Nr. LP 2015-3), Bolyai Scholarship granted by the HAS; ÚNKP-22-5 New Nat.Exc.Progr. of the Ministry for Culture and Innovation

Differentials in Morbidity and Mortality in Medieval Ireland

ALLISON C. HAM

Anthropology, University of South Carolina

Previous bioarchaeological studies of medieval Ireland have demonstrated differences in the frequency of stress markers and age-at-death based on sex, time period, and region. This study expands upon this research by inferring temporal- (Early, CE 500-1550 v. Late, CE 1150-1550), regional- (East v. West), and sex-based differences in morbidity and mortality using paleodemographic analyses that can address the Osteological Paradox and reveal patterns of selective mortality and heterogenous frailty. Kaplan-Meier survival analysis with a log rank test was used to assess temporal, regional, and sex-based trends in survivorship for individuals aged 15+ years (N=352). Chi-squared tests were used to assess the relationship between 1) dental calculus frequency and sex for individuals aged 15+ years (N=166) and 2) time period and region for individuals aged 5+ years (N=250). Preliminary analyses revealed no significant sex-based differences in survivorship; individuals from Late Medieval sites had reduced survivorship compared Early Medieval sites; individuals from Eastern sites had significantly reduced survivorship compared to those from Western sites. Chi-squared tests revealed no sex-based differences in dental calculus frequency; individuals from Late Medieval and Eastern sites had significantly higher frequencies of dental calculus than those from Early Medieval and Western sites. These results demonstrate a lack of sex-based differences in survival, which differs from previous results, but demonstrate similar regional and temporal patterns in survivorship. This study improves our understanding of the effect of sociodemographic, temporal, and regional variables on survivorship in the past through the use of skeletal markers of morbidity and mortality.

Funding for this project was provided by the National Science Foundation (#2120102) and the University of South Carolina Office of the Vice President for Research.

Digitization of the cast collection of *Homo erectus* remains from Zhoukoudian, China

ASHLEY S. HAMMOND[1,2], ALESSANDRA VECINO GAZABÓN[1,2,7], NATALIE TOEWS[3], EVA-MERCE FUENTES[3], BRUNO MAUREILLE[4], SONG XING[5,6] and CLÉMENT ZANOLLI[4]

[1]Anthropology, American Museum of Natural History, [2]New York Consortium of Evolutionary Primatology (NYCEP), [3]Yaghjian Internship Program, Division of Anthropology, American Museum of Natural History, [4]PACEA Laboratory, Université de Bordeaux, [5]Key Laboratory of Vertebrate Evolution and Human Origins, Institute of Vertebrate Paleontology and Paleoanthropology, [6]CAS Center for Excellence in Life and

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Paleoenvironment, [7]Richard Gilder Graduate School, American Museum of Natural History

The Middle Pleistocene hominin assemblage from Zhoukoudian includes nearly 200 skeletal and dental remains belonging to a minimum of 45 individuals (representing children and adults). The assemblage is exceptional for its anatomical diversity (with four crania, 11 mandibles, 147 teeth and 11 postcranial elements). The vast majority of the hominin remains were found between 1921 and 1937, during the excavation of the sediments of Locality 1, dated to 780–680 ka. Originally attributed to *Sinanthropus pekinensis* and dubbed 'Peking Man', the fossils were later lumped within the *Homo erectus* hypodigm. In 1941, during World War II, the collection was lost during transport from the Peking Union Medical College (Beijing) to the American Museum of Natural History (AMNH, New York). Today, the only evidence of the lost assemblage includes the detailed description of the fossils with pictures and radiographs published by Black and Weidenreich, and a series of 130 first-generation, high-resolution plaster casts of crania, teeth and post-crania curated at the AMNH. We present here the preliminary results of our work aiming to create a virtual archive that will be published online and accessible to the scientific community. We obtained high-resolution surfaces of the post-cranial and large cranial elements using Einscan Pro scanners. We scanned dental casts with both laser-based and microCT (GE Phoenix) scanners, and we found that microCT scans were more adapted to investigate teeth. Moving forward, these surface data will be published online and accompanied by key archival records, and measurements from original casts and surface models.

Funding provided by Région Nouvelle Aquitaine (project Zhoukoudian revival)

Oxygen transport phenotypes and the adaptive modes of Andean versus Tibetan highland native populations

TAYLOR S. HARMAN[1], PONTUS K. HOLMSTRÖM[2], KELSEY C. JORGENSEN[3], ANNE KALKER[4], MELISA KIYAMU[5], KIMBERLY T. ZHU[3], TREVOR A. DAY[6], ABIGAIL W. BIGHAM[3] and TOM D. BRUTSAERT[7]

[1]Department of Anthropology, Syracuse University, [2]Department of Health Sciences, Mid-Sweden University, [3]Department of Anthropology, University of California, Los Angeles, [4]Department of Anesthesiology, Raboud Medical Center, [5]Departamento de Ciencias Biológicas y Fisiológicas, Universidad Peruana Cayetano Heredia, [6]Department of Biology, Mount Royal University, [7]Department of Exercise Science, Syracuse University

High altitude native populations exhibit physiological adaptations to environmental hypoxia. It has been hypothesized that two of these populations, Andeans and Tibetans, demonstrate distinct adaptive modes with the former characterized by increased blood oxygen content, and the latter characterized by increased blood flow. To investigate this hypothesis, we recruited two groups of healthy adults (ages 18-35) with highland ancestry who were born and currently reside at high altitude. The groups were: Andean Quechuas recruited in Cerro de Pasco, Peru (AND, n = 301) and Tibetan Sherpas recruited in Pheriche, Nepal (SHP, n = 64). Participants were tested in field laboratories using identical equipment and protocols, at nearly identical altitudes (4,330m and 4,371m, respectively). We assessed a wide variety of physiological variables at rest, submaximal exercise, and maximal exercise. We found that although some phenotypes aligned with the above hypothesis, the majority did not. For example, as predicted, AND displayed significantly lower ($p<0.001$) ventilatory equivalents for oxygen (V_E/VO_2) at rest. However, this trend reversed at maximal exercise, with AND displaying significantly higher ($p<0.001$) V_E/VO_2 than SHP. Further, contrary to the above hypothesis, we found no statistically significant differences in flow-mediated dilation between the groups. These results suggest that the adaptive modes of these populations are perhaps not as distinct as previously supposed. Given that this hypothesis was formulated on the basis of data taken at rest, our data highlights the importance of assessing physiology both at rest and exercise, to gain a more complete understanding of adaptation to high altitude.

This work was supported by the National Science Foundation (BCS, Award Number 2141893).

The relationship between handedness and facial asymmetry in adults

KATARÍNA HARNÁDKOVÁ, LENKA KOŽEJOVÁ JAKLOVÁ, KAROLINA KOČANDRLOVÁ, JÁN DUPEJ and JANA VELEMÍNSKÁ

Department of Anthropology and Human Genetics, Charles University

Introduction: Facial asymmetry is often associated with manifestation of brain laterality - handedness. Deeper knowledge of this relationship could clarify the formation of asymmetry during the life. Most studies agree that (1) the right half of face (right hemiface) is more protrusive – forward arched (2) the facial asymmetry of left-handed subjects manifest reversed like on the right-handed.

Material and Methods: The sample of healthy adults consisted of 84 3D facial scans (self-reported, 31 right-handed, 53 left-handed) with neutral facial expression. Shape asymmetry was assessed by geometrics morphometry and described by colour and significance maps. Colour maps provide an information about protrusive/retrusive direction of shape changes.

Results: The results showed that the asymmetry of faces in right-handed subjects was manifested with more protrusive areas – forehead, nose, mouth, and chin with exception of the zygomatic area on the right hemiface. The difference between right and left-handed subjects was in right eyebrow and zygomatic area, which were more protrusive in left-handed subjects.

Conclusion: The first hypothesis was confirmed, thus right-handed subjects on the right hemiface had more protrusive forehead, nose, and chin areas with exception of zygomatic area. The second hypothesis was partially rejected. The results showed that the difference between right and left-handed was small and was in the eyebrow and zygomatic area, while the left-handed had these areas more protrusive. Also, the left-handed subjects were a little more asymmetrical than the right-handed. For more precise description, it would be appropriate to combine methodology of colour maps and landmarks.

This study was supported by Charles University Grant Agency – GAUK 372221.

Implications of variability in triceps surae muscle volume on joint reaction forces at the knee and ankle

CHRISTINE M. HARPER[1], ADAM D. SYLVESTER[2] and PATRICIA ANN. KRAMER[3]

[1]Department of Biomedical Sciences, Cooper Medical School of Rowan University, [2]Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine, [3]Department of Anthropology, University of Washington

Musculoskeletal modeling is a powerful tool for determining forces during locomotion. These models, however, are dependent on underlying assumptions, such as muscle parameters. Within triceps surae, muscle volume distribution across gastrocnemius lateralis, gastrocnemius medialis, and soleus vary when measurements are collected from young, healthy individuals or cadaveric specimens. Here we test if relative distributions of triceps surae muscle volumes (i.e., percentage of triceps surae volume apportioned to each muscle) impact maximum knee and ankle joint reaction forces (JRF).

Using kinematics and kinetics of two healthy individuals (one male, one female) walking at three speeds, three triceps surae muscle volume distributions (standard cadaveric model, average of 21 young adults, average of 21 cadavers) were evaluated in a standard musculoskeletal model. Maximum anteroposterior, mediolateral, and vertical forces of knee and ankle JRF were calculated using inverse dynamics and an algorithm to solve for forces in redundant muscles. Kruskal-Wallis tests were used to test for significant differences among the three distributions at each speed/within each subject.

Muscle volume distribution significantly affects maximum anteroposterior knee JRF at all speeds and vertical knee JRF at faster speeds in both individuals, with significant differences between

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

the standard cadaveric model and young adults ($p<0.03$), and anteroposterior and vertical ankle JRF at the self-selected normal speed in the male ($p<0.035$). This suggests that researchers utilizing knee JRF should pay careful attention to triceps surae muscle parameters; however, this is a less critical consideration for ankle JRF, likely because triceps surae force is distally transmitted through a common tendon.

Impact of high temperatures on leptin enzyme-linked immunoassay (ELISA) results

VICTORIA HARRIES[1], MARGARET CORLEY[1,2], GARY ARONSEN[1] and RICHARD G. BRIBIESCAS[1]

[1]Reproductive Ecology Laboratory, Anthropology, Yale University, [2]Ecology and Evolutionary Biology, Yale University

Ambient temperature conditions are a common concern during laboratory analysis. Due to an unexpected heatwave during transportation from the manufacturer, a shipment of two leptin ELISA kits (Leptin Ultrasensitive, ALPCO USA; Catalog #22-LEPHUU-E01) arrived at the university laboratory in a warm condition (76.3°F/24.6°C). The instruction manual advises the kits be kept at a temperature of 2-8°C, however, no validation is presented as to the results of transportation or storage at high temperature exposure on the assay results. This created the conditions to opportunistically test the impact of temperature above the recommended ELISA leptin kit maximum. Surplus human milk samples that were part of an experiment to test thaw periods in human milk sample analysis were assayed using the high temperature exposed assay kits. 100 mL samples of human milk were collected from four participants and aliquoted into twenty 5 mL vials. Samples were subjected to increasing hours of thawing outside of freezer conditions to test levels of hormonal degradation across extended periods of potential thawing. This thawing experiment gave us the opportunity to compare results from the warmed assay kits with kits that had remained within the temperature range recommended by the manufacturer. We found that exposure to high temperature resulted in the ELISA results being inconsistent and unable to accurately measure leptin concentration in the samples. In conclusion, when this particular ELISA is exposed to high temperatures the kit should not be used to run samples. Exposure to heat may render the assay kit unreliable.

Social Control and Cooperation: A bioarchaeological approach to understanding how communities react to periods of stress in the U.S. Southwest

RYAN P. HARROD[1,2] and KATHRYN M. BAUSTIAN[3]

[1]Dean of Academic Affairs, Garrett College, [2]Affiliate Professor, University of Alaska Anchorage, [3]Assistant Professor, Skidmore College

Using indicators of nutrition, activity, stress, and trauma, this paper compares human skeletal remains from two regions of the pre-contact southwest United States to identify patterned markers on the bone that reveal how shifting sociopolitical complexity was embodied differently on individuals and how societies adapted and persisted during periodic droughts. In Chaco Canyon and sites in the La Plata River and Red Mesa valleys (AD 850-1350) 271 human skeletal remains were examined. From Late Pithouse and Pueblo sites in the Mimbres region (AD 550-1350) there were 247 human skeletal remains analyzed. The authors reconstructed the bioarchaeological profile and biocultural identity of each individual from the remains. Comparisons of the two regions noted differences in sex demographics, entheseal changes, and trauma rates. For example, at one Chaco site there were more males 8/13 (61.5%) than females 5/13 (38.5%), and in contrast at all Mimbres sites sex distributions were similar with 116/247 (47.0%) males and 108/247 (43.7%) females. Additionally, at Chaco there were differences in activity-related development of the extremities between sexes, while Mimbres had similar development between males and females. Analysis of pathology among adults and children at the Chaco sites suggests that stress was a concern for individuals, but individuals affected at each site varied significantly. In contrast, Mimbres individuals had far less indicators of stress. Finally, the analysis of traumatic injuries among the populations indicated that nonlethal, and to a lesser extent, lethal injures were present among the Chaco people but not the people from Mimbres.

What morphological and genetic data can tell us about hybridization in Late Pleistocene Eurasia

KATERINA HARVATI[1,2] and REBECCA R. ACKERMANN[2,3,4]

[1]Paleoanthropology, Institute for Archaeological Sciences, University of Tübingen, [2]DFG Centre for Advanced Studies 'Words, Bones, Genes, Tools', University of Tübingen, [3]Human Evolution Research Institute, University of Cape Town, [4]Department of Archaeology, University of Cape Town

Recent paleogenomic research indicates that gene exchange between distinct lineages occurred multiple times during the Pleistocene, highlighting the potential significance of hybridisation in human origins. However, the effects of admixture on the phenotypic variation observed in the human fossil record are poorly understood. We investigated how cranial shape variation and developmental abnormalities in Late Pleistocene Eurasian modern humans correspond with Neanderthal genetic ancestry, in the framework of predictions from model taxa. Three 3D coordinate datasets were used (mandible, face, posterior cranial midsagittal profile), collected from late-Middle and Late Pleistocene (approximately MIS 7-2) fossil humans from Europe, Africa and the Middle East assigned to Neanderthals and H. sapiens, including individuals that are genetically identified hybrids. Data on skeletal abnormalities and percentages of Neanderthal genetic ancestry were compiled from the literature. 3D data were processed with Procrustes superimposition, semilandmark sliding and Principal Components Analysis. We compared cranial variation seen in the fossil record of Late Pleistocene hominins from Western Eurasia to representative Neanderthal and H. sapiens "parental" samples. The results showed some correspondence between different lines of evidence (see Harvati & Ackermann 2022). Here, we further discuss the implications of these results for future studies, especially for hypothesis generation and testing. In particular, we advocate for investigating hybridisation signals in a more fine-grained manner, exploring why different cranial regions may preserve hybridisation signals differentially. We also discuss individuals that we potentially flagged as having hybrid ancestry (but not previously identified as such) in the broader context of the Late Pleistocene record.

Supported by the European Research Council (ERC-AdG-101019659) and German Research Foundation (DFG-FOR-2237) awarded to KH and the National Research Foundation of South Africa (117670) awarded to RRA.

Hormonal and morphological changes during the flanging process in male orangutans

FAYE S. HARWELL[1] and CHERYL D. KNOTT[1,2]

[1]Anthropology, Boston University, [2]Biology, Boston University

The presence of two male morphs (unflanged and flanged) is one of the most fascinating aspects of orangutan biology, yet the measurable components of flanging are not well documented. Flanging results in changes in sexual and social behaviors and development of secondary sexual characteristics including cheek pads (flanges), a throat sac, and larger body size. To study this process, we collected weekly urine samples and facial photographs of two unflanged males of similar ages, Budi and Kembali, at the Toronto Zoo for three years. Body weights were recorded regularly as well as forearm lengths, which were measured using string. During the study, Budi underwent flanging while Kembali remained unflanged. On average, Kembali had higher log-transformed cortisol levels compared to Budi

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

(*T*(167)= -2.20, p= 0.029). Budi's testosterone levels fluctuated greatly, peaked in the middle of flanging, and ranged from 16.6- 508.6 ng/mg Cr. Regardless of flanging stage, Budi had higher log- transformed testosterone levels compared to Kembali, whose testosterone ranged from 7.6-69.9 ng/mg Cr (*T*(163)= 20.11, p <0.0001). Budi increased in body weight by 95.9% over the 3-year timespan. His face increased in width by 112.2%, or approximately 12cm. Both males experienced similar long bone growth with Budi having a marginally longer forearm (<1cm) compared to Kembali. Lastly, Budi became more aggressive and started to long call during the study period. This case study demonstrates the extent of physiological, morphological, and behavioral changes that occur during flanging along with providing insight into the timeline of these changes.

This project was funded by the NSF award BCS-2118082.

Microstructural properties of bone and the effect of pixel size

SHYAM F. HASSAN[1], LUIS DIEGO LUNA CENTENO[1], TAUTIS SKORKA[2], PETER S. CONTI[2,3], ADAM K. HUTTENLOCKER[1], BIREN A. PATEL[1] and TEA JASHASHVILI[1,4]

[1]Department of Integrative Anatomical Sciences, Keck School of Medicine, [2]Molecular Imaging Center, Department of Radiology, Keck School of Medicine, [3]Department of Biomedical Engineering and Pharmaceutical Sciences, University of Southern California, [4]Department of Geology and Paleontology, Georgian National Museum

Studying trabecular bone microstructural properties (TBMP) is essential in biological research. High-resolution micro-computed tomography (Hr-μCT) imaging is a standard method to study TBMP in the context of variation and effects on bone development and remodeling. Methodical examination of pixel size (PS) dependency, reproducibility, and sensitivity require detailed studies on TBMP for small and medium size research animals. This study aims to determine whether the PS difference of same-size structures affects the morphological outcome of TBMP when all other Hr-μCT parameters (i.e., acquisition, reconstruction, region of interest, thresholding, and Tb. Th) remain the same. We also evaluate how TBMP varies among different skeletal sites (e.g., humerus, femora, vertebra) in the same animal (e.g., human, pig, rat, and mouse) and what constitutes an acceptable PS of Hr-μCT images for effectively calculating TBMP without encountering PS effect on the results.

Our study demonstrates a significant effect of PS on TBMP. The PS effect significantly increases if the structure size is close to the PS used. This is due to fewer pixels covering the trabecular strut thickness, which increases the partial-volume effect. Results demonstrated that the lack of uniformity in image acquisition makes it challenging to compare and interpret the results of different studies and might yield conflicting results, not because of trabecular bone biology but because of PS differences. A well-defined plateau of continuous measurement of TBMP at different PSs or well-established histological measurements is recommended as a guiding factor during Hr-μCT scanning for the given animal model for given skeletal sites.

We thank the Department of IAS and MIC, Keck School of Medicine, USC. NSF BCS-1719140, USC Provost grant for Nikon Metrology XTS225ST micro-CT.

Analysis of Fluctuating Asymmetry of mandibular morphology using interlandmark distances and landmark-based-3DGM: A study on 3D mesh models of Japanese human remains from the 19th and 20th centuries.

NORIKO HASUDA[1] and NORIKO SEGUCHI[1,2]

[1]Integrated Sciences for Global Society, Kyushu University, [2]Department of Anthropology, University of Montana

Fluctuating Asymmetry (FA), the deviation from perfect bilateral symmetry in the developmental process, can be created by poor nutrition, stress, and poor health conditions. We analyzed human remains from the late 19th to the first half of the 20th century in the anatomical collection housed at Kyushu University. The skeletal human remains were collected without consent from marginalized groups, such as criminals and the poor. Therefore, they might be from individuals impacted by poor living circumstances. This study tries to shed light on the unwritten history of an aspect of the life of socially marginalized people in Japan.

In this study, mandibular 3D data were captured by EinScan scanning, and landmark coordinates were acquired by the Checkpoint program.

The following two methods were used to analyze mandibular FA. One method utilized landmark-based Geometric Morphometrics (GM), which removed the size factor by Procrustes fit. Package "Geomorph" in R was used for this procedure. The other method utilized the calculations of interlandmark distances and two-way ANOVA was performed.

The statistically significant results in FA of the mandibular were obtained by both methods. The results suggest that the GM method is an effective approach for FA, although it is crucial to perform interlandmark distances analysis with shape ANOVA preserving size factors. Our study also found that mandibular FA did not correlate to tooth wear asymmetry. Further studies must examine the relationships between stress, health, nutrition, and mandibular FA. We also discuss ethical protocols for the collection of samples from socially marginalized people.

A new, early Pleistocene hominin footprint site from Koobi Fora, Kenya

KEVIN G. HATALA[1], NEIL T. ROACH[2], CYPRIOT NYETE[3], APOLO A. LONGAYE[3] and LOUISE N. LEAKEY[3,4]

[1]Department of Biology, Chatham University, [2]Department of Human Evolutionary Biology, Harvard University, [3]Koobi Fora Research Project, Turkana Basin Institute, [4]Department of Anthropology, Stony Brook University

In 2019, members of the Koobi Fora Research Project identified a track surface while excavating a hominin skeletal fossil site within Area 103 of the Koobi Fora Formation. In 2022, targeted excavations and detailed study revealed that the surface includes a large assemblage of footprints from hominins and other animals. Based on available geological and geochemical evidence, the track surface lies in lake margin facies over 10 meters below the 1.52 Ma Elomaling'a Tuff. This inferred stratigraphic position makes this the oldest track surface currently known from the Koobi Fora Formation.

The hominin tracks are attributed to four individuals. One trackway includes 12 tracks from the same individual. Three isolated hominin tracks are oriented in perpendicular directions. Estimates of stature and body mass from track dimensions overlap the ranges of skeletally-derived estimates from early *Homo* and *P. boisei*. Analyses of relative stride length from the 12-step trackway, and the consistency of step lengths and widths, show that this individual was moving at a steady walking speed without evidence of slipping or other substrate-induced gait disturbances. Analyses of track morphology included comparisons with ~1.4-1.5 Ma tracks from nearby sites at Koobi Fora and Ileret. The expanded fossil dataset revealed a degree of variation in track morphology that exceeds that observed in large datasets from modern humans. Comparisons with experimental and fossil tracks suggest the potential presence of multiple forms of foot morphology and/or bipedal mechanics among the abundant sample of hominin tracks now known from the Koobi Fora Formation.

This work was supported by the National Geographic Society (to LNL).

Virtual reconstruction of crania of Homo naledi from the Rising Star cave system, South Africa

JOHN HAWKS

Department of Anthropology, University of Wisconsin–Madison, Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand

Excavation work has recovered partial remains of more than 19 individuals of Homo naledi from the Rising Star cave system. The LES1 partial skeleton from the Lesedi Chamber is the most complete

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

individual, including cranial fragments that represent most of the vault and part of the face. Cranial remains from the Dinaledi Chamber are less complete and include commingled elements of multiple individuals. In this study, I report new refits and associations of four fossil crania from the Dinaledi Chamber. Virtual reconstruction of these remains, including mirroring of elements, enables the comparison of overall cranial vault form of five H. naledi individuals, including LES1. These expand the known sample of H. naledi individuals with endocranial volume estimates. These five individuals are compared to a sample of 149 modern humans, extant primates, and fossil hominins. Using a phylogenetic comparative framework, the study estimates the landmark configuration expected for the ancestral node linking H. naledi and its sister clade including species of Homo with large endocranial volumes. This comparison suggests that the cranial shape of the last common ancestor of extant humans and H. naledi had a more humanlike configuration than early Homo erectus populations like that from Dmanisi.

Primate Ecotourism in Madagascar: The Effect of COVID-19 on Human Occupancy in Andasibe's Forests

LAURA K. HAYNES[1], CAITLYNN FILLA[2], DOMINIC MAYO[3], JHOANNY RASOJIVOLA[4], RADONIAINA RAFALIARISON[5], ZACHARY J. FARRIS[6] and KIM VALENTA[2]

[1]Department of Anthropology, University of Massachusetts Amherst, [2]Department of Anthropology, University of Florida, [3]Department of Anthropology, University of Michigan, [4]Department of Anthropology, University of Antananarivo, [5]Mad Dog Initiative, Antananarivo, Madagascar, [6]Department of Public Health and Exercise Science, Appalachian State University

Madagascar, the world's fourth-largest island, has among the highest rates of endemism and some of the most endangered species on Earth. Ecotourism has been proposed as a method to enhance and fund conservation efforts to protect this biodiversity, and lemurs are a particular ecotourism draw. During the COVID-19 pandemic (March 2020-November 2021), the Malagasy government shut down all tourism, leaving many protected areas and ecotourist-reliant communities without a source of revenue. Prior to this shutdown, Andasibe-Mantadia National Park and its surrounding protected areas were one of the most visited ecotourist destinations in Madagascar. At 3 sites in this region (12 camera stations total), we conducted 4 camera trap surveys from 2017–2021 to compare patterns of human occupancy for both tourists and local Malagasy people. We found that several trails that were previously occupied largely by tourists, with little Malagasy presence, became popular among Malagasy during the pandemic. This has implications for the displacement of local people as a result of ecotourism. Additionally, without consistent income, there is potentially a greater need to hunt, and the habituated animals along these trails would make easy targets. It is vital to understand these patterns in human behavior in relation to ecotourism in order to develop community-based strategies to rebuild livelihoods impacted by the pandemic and improve conservation.

From Traditional Models to Post-Colonial Partnership: 30 years of Craniometry in Museum and University Labs

GARY M. HEATHCOTE

Anthropology, Saint Thomas University

Participation in a poster symposium dedicated to sharing craniofacial data has prompted reflection on the profound changes that older generation osteologists have experienced in accessing and studying collections of human skeletal remains. In my case, from 1978 to 2018, benchwork in 15 different North American and Western Pacific museums and laboratories was enabled through compliance with a range of institutional procedures and policies that varied from no to full consultation, involvement, and approval of descendant communities whose ancestors I proposed to study.

The outcome of this research is a comparative, mostly caliper-produced, craniometric database (of up to 98 measurements) that describes the craniofacial form of over 600 anatomically-modern individuals, representing archaeological populations from the Arctic and Western Pacific, as well as Iceland and southern Ontario. Six waves of intermittent but intensive periods of research in university laboratories and museums (in 1978, 1979, 1990, 1991-92, 1997 and 2008) account for most of the database. During that period seismic policy shifts occurred, coincident with the repatriation movement. My poster presentation outlines conflicted concerns about the use of the "legacy data" produced during times when traditional models prevailed in institutions that housed skeletal collections. Also presented are personal turning points that led to my eventual decision to restrict involvement in human osteological research to projects that are requested by descendant communities and in full partnership with Indigenized or otherwise local institutions.

1990 research tour was supported by Social Sciences and Humanities Research Council of Canada Award No. 410-89-0667.

Early Origins of the Genus *Homo:* Taxonomic and Phylogenetic Assessment of KNM-ER 5431

BRI HEISLER

Anthropology, University of Nevada Las Vegas

The scarcity of hominin fossils discovered in east Africa from 2.0 - 3.0 million years ago (Ma) is a significant barrier to the study of the origins of our genus, *Homo*. Despite this, resolving the evolution of our ancestors is not out of reach. Even very incomplete specimens, for which comparable finds may be unavailable, are potentially informative. This is especially so in cases where analytical methods were not sufficiently developed at the time of their discoveries.

This study reexamines the KNM-ER 5431 fossil from the Koobi Fora Formation of Kenya. It is a well-preserved set of associated but isolated teeth from 2.7 - 3.0 Ma. Originally, it was categorized only as *Hominidae sp. et. gen. indet.* (more closely related to us than to chimpanzees, but of unknown taxonomy otherwise); thus, it has not been sufficiently considered despite being excavated decades ago.

By using geometric morphometric techniques together with cladistics analysis, the fossil is now taxonomically attributable at the genus level and can be coarsely situated phylogenetically among other archaic hominins. These results support the inclusion of KNM-ER 5431 within the *Homo* hypodigm.

Partial funding for this project was provided by the Angela Peterson Memorial Scholarship.

Morphological and molecular identification of helminths reveals species diversity in the gastrointestinal parasite communities of white-faced capuchin monkeys (*Cebus imitator*)

MEGAN C. HENRIQUEZ[1,2,3,4], HADJIRA HAMOU[1], JESSICA CHURCHER[1], JOELLE HASS[1], SUHEIDY ROMERO MORALES[6], LARISSA SWEDELL[2,3,4,5] and AMANDA D. MELIN[1,6,7]

[1]Anthropology and Archaeology, The University of Calgary, [2]Anthropology, The Graduate Center, CUNY, [3]-, The New York Consortium in Evolutionary Primatology (NYCEP), [4]Anthropology, Queens College, CUNY, [5]Archaeology, University of Cape Town, [6]-, Sector Santa Rosa Monkey Project, [7]Medical Genetics and Alberta Children's Hospital Research Institute, Cumming School of Medicine, University of Calgary

The analysis of patterns of parasitic infection in nonhuman primates is a valuable tool to help understand how infectious disease has shaped the evolution of our own lineage. White-faced capuchins (*Cebus imitator*) are excellent models in which to explore these questions due to their complex dietary and social behavior, which exposes them to a variety of gastrointestinal parasites. Here, we explore the gastrointestinal parasite community in a wild population of capuchin monkeys to identify the factors that affect infection. We collected ethanol-fixed fecal samples from 96 monkeys in the Sector Santa Rosa of the área de Conservación Guanacaste, Costa Rica from August 2020 to

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

August 2021. We developed and employed a 'morphology to molecular' pipeline to identify the parasites in those samples morphologically, using traditional microscopic methods, and molecularly using the ITS-2 genetic marker. We morphologically identified 9 suspected parasite morphotypes, including *Strongyloides sp., Necator americanus,* and various sublurids and spirurids, and we present the first known genetic information from the understudied but highly prevalent lungworm *Filariopsis barretoi*. Our data suggest that host social group membership affects parasite diversity and infection intensity, while individual characteristics, such as host age and sex, do not. Our results highlight the role of host social proximity in host-parasite interactions and suggest the utility of further investigation into the behavioral and ecological factors shaping parasite transmission among hosts. We hope our continued development of the parasite identification pipeline can serve as a resource for researchers interested in studying gastrointestinal parasites in other wild mammals.

Fat and lean body mass change following weight cycling in mice, a model for humans in energetically unstable environments

ISABEL D.K. HERMSMEYER, MIRANDA N. COSMAN, RACHEL HURWITZ, ALEXIS STOKEL and MAUREEN J. DEVLIN

Anthropology, University of Michigan

Weight loss reduces the masses of adipose tissue, bone, and muscle, but less is known about how weight loss impacts other organ tissues, or how these changes might persist after weight regain. Sustained body composition change following weight cycling (weight loss followed by regain) may indicate an adaptive shift in body composition to optimize energy allocation in an unstable environment. In this study, we test the hypotheses that (1) with weight loss, organs involved in costly but non-vital systems such as immune and reproductive function will decrease more in size compared to more vital tissues, and (2) altered body composition will persist after weight regain. To test these hypotheses, we individually housed female C57BL/6J mice from 9-15 weeks of age, with groups undergoing either a three week calorie restriction (70% of ad lib intake), or three weeks of calorie restriction followed by three weeks of ad-lib refeeding, each with paired control groups. Organ weights at euthanasia included the spleen and uterus. Results demonstrate insignificant differences in spleen mass but a highly significant difference in uterine mass (80.7%, $p < .001$) between calorie restricted and control mice, and a non-significant but still large difference after a complete weight cycle (39.1%, $p = .10$) while their overall body mass returned to control average. This finding potentially indicates an adaptive shift in tissue mass to reduce energy needs in the face of resource unreliability, supporting our hypothesis that expensive, but non-vital tissues, may adaptively reduce in size during energy restriction.

Funding was provided by the University of Michigan Anthropology Department to IDKH.

Dental Microwear Texture Analysis between occlusal and buccal surfaces

RAQUEL HERNANDO[1,2], MARINA LOZANO[1,2], ANTOINE SOURON[3] and JOHN C. WILLMAN[4]

[1]Palaeoanthropology unit, Catalan Institute of Human Paleoecology and Social Evolution (IPHES), [2]Department of History and Art History, University Rovira i Virgili, [3]UMR CNRS 5199, PACEA - Laboratoire de la Préhistoire à l'Actuel: Culture, Environnement et Anthropologie, University of Bordeaux, [4]Laboratory of Prehistory, CIAS – Research Centre for Anthropology and Health, Department of Life Sciences, University of Coimbra

The quantification of dental microwear is an effective and non-destructive method for dietary reconstruction. Dental microwear is generally analyzed on either the buccal or occlusal surfaces, but both surfaces are rarely examined in the same study. This may be explained by a difference in image acquisition technology and associated difficulties of data comparison. The aim of this study is to analyze and compare dental microwear textures on occlusal and buccal surfaces from the same tooth to determine whether using these surfaces in tandem can provide complementary data for dietary reconstructions. The results show no correlation between surfaces for any variable. Furthermore, we observed higher complexity values on occlusal surfaces than on buccal surfaces and the opposite for anisotropy values. Our findings support the assertion that the lack of "pitting" tends to produce lower complexity values on buccal surfaces. We propose that the higher anisotropy values found on buccal surfaces, compared to those on the occlusal ones, are attributed to the specific mechanisms of microwear formation for each surface. This means that abrasive particles, that would create pits on the occlusal surface, behave differently on the buccal surface where they are dragged and pushed across this surface. Future studies, with greater intergroup sampling, will help to understand.

2017SGR0011, 2017SGR1040; 2014/100482, CLT009/18/00024; H2020-MSCA-IF-2016 749188; ANR- 10-LABX-52; CEX2019-000945-M; PID2021-122355NB-C32; HAR2017-86509-P; 2019PFR-URV-91; URV 2019PMF-PIPF-59

Four potential cases of hyperostosis frontalis interna in a California historic population

BRIANNA E. HERNDON

Anthropology, University of California, Riverside

Hyperostosis frontalis interna (HFI) is a pathology of unknown etiology that presents in a variety of types, but primarily consists of thick, undulating bony deposition on the endocranial portion of the frontal bone. HFI commonly presents with diffuse idiopathic skeletal hyperostosis (DISH) and osteoporosis, likely indicating a link between these conditions. HFI overwhelmingly occurs in older female individuals, perhaps pointing even more specifically towards a relationship with changing hormone levels. Documentation of HFI in historic populations is relatively rare but prevalence levels can reach up to 50% in modern populations. Current hypotheses suggest that increased longevity – and thus overall prolonged exposure to estrogen – made possible by industrialization may be a strong explanatory factor.

This research presents four potential cases of HFI in the historic University of Iowa-Stanford Collection (UISC), which is comprised of 230 documented individuals born between the years of 1842 and 1907. All affected individuals fit the known risk group for HFI – elderly females. All four females were over the age of 60 at time of death. Out of individuals with the frontal bone present, HFI prevalence among females in the UISC is 16.00% (n=25) and 2.16% overall (n=184). Differential diagnoses include Caffey's hyperostosis, acromegaly, meningioma, Paget's disease, fibrous dysplasia, and Van Buchem's disease, all of which were ruled out in these instances. Given the relatively scant documentation of HFI in historic populations, it is the goal of this research to contribute: (1) information about prevalence, and (2) reference photographs to aid in future diagnoses.

Funding provided by the Center for Ideas and Society (Humanities Graduate Student Research Grant) and the Graduate Division of UC Riverside (Earle C. Anthony Travel Award).

Evaluation of entheseal changes in horticultural groups from Central Chile (0-1400 CE) from a materialist approach

MARIA JOSE HERRERA-SOTO[1,2], LORENA SANHUEZA[3] and LEANDRO LUNA[1,4,5,6]

[1]Facultad de Filosofía y Letras, Universidad de Buenos Aires, [2]Matrida Fundacion, Estudios de Patrimonio y Biantropología, Valparaiso, Chile, [3]Facultad de Ciencias Sociales, Departamento de Antropología, Universidad de Chile, [4]Instituto Multidisciplinario de Historia y Ciencias Humanas (IMHICIHU), CONICET, [5]Facultad de Odontología, Cátedra de Endodoncia e Instituto de Investigaciones en Salud Pública (IISAP), Universidad de Buenos aires, [6]Unidad de Investigación en Bioarqueología y Antropología Forense (UIBAF), Universidad de Buenos Aires

The current territory of Central Chile was occupied by non-hierarchical societies during the period ca. 0-1400 years CE. The Bato and Llolleo cultural complexes inhabited that region during the Early Ceramic Period (ECP, ca. 0-1000/1200 CE); these

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

contemporary groups display marked differences between them: Llolleo show a higher emphasis on horticulture and pottery production, while the mobility and use of space by Bato groups are similar to a hunter-gatherer lifestyle. Then, the Aconcagua culture (Late Intermediate Period, LIP, ca. 1000-1400 CE) is characterized by a greater dependence on food production. Different lines of evidence proposed higher differences by sex in Aconcagua (e.g., a greater consumption of maize by men). Considering these changes, we wonder if a sexual division of labor regulated the organization of daily life during LIP. We analyze the entheseal changes (Coimbra Method) to evaluate the biomechanical stress in adult skeletons of the ECP (N=25) and LIP (N=31). Although no statistically significant differences were identified when comparing the scores by sex and periods, several differences between women and men for both periods are evident, pointing to a decrease in male variability and an increase in female variability. This scenario may suggest a diversification of physical activities by women during the LIP related to food production and a rise of reproductive and offspring care works. A demographic growth during LIP is suggested, which is consistent with previous models that show a greater permanence in housing areas and a greater number of individuals in the residential units.

National Agency for Research and Development, Grant/ Award Number: 2018-72190531

Early growth and adult epigenetic age acceleration

MILAN HILDE-JONES[1], CALEN P. RYAN[2] and CHRISTOPHER W. KUZAWA[3]

[1]Anthropology, Northwestern University, [2]Mailman School of Public Health, Columbia University, [3]Institute for Policy Research, Northwestern University

Previous work has connected small size at birth, postnatal growth, and the timing of growth acceleration to risk of cardiovascular diseases and related conditions of aging. Evidence suggests that rapid infant growth is protective, while accelerated childhood growth predicts elevated long-term risk. With data from the Cebu Longitudinal Health and Nutrition Survey, we used conditional growth models to explore infant and childhood growth as predictors of DNA methylation-based epigenetic aging (DNAm age) for 840 males and 694 females. Analysis was conducted with six DNAm based clocks: Hannum, Horvath, PhenoAge, DNAm GrimAge, DNAmTL, and Dunedin PoAm. Hannum was run three ways: as the standard model (AgeAccelHannum), adjusted for cell composition (IEAAHannum), and upweighted for cell composition (EEAA). Results show a consistent negative relationship between rapid growth in infancy and DNAm age for girls. This suggests that rapid growth during specific developmental periods might be protective against multiple measures of epigenetic age acceleration (AA) and the long-term negative health outcomes with which AA is associated. Conditional height and weight for girls between birth and 2 years old was significantly associated with all indices of aging except IEAAHannum, which suggests that early growth might slow the adoption of age-related immune changes. There do appear to be sex differences in the degree of protection afforded by this particular pattern of growth, as evidence for a protective effect in boys is more mixed and depends on the specific clock. The results suggest possible life-history trade-offs between growth and maintenance for girls.

Bioarchaeology of Care in Individuals from a San Francisco Bay Area Muwekma Ohlone Ancestral Site

BRITTANY E. HILL[1], LAUREL ENGBRING[1], DAVE GRANT[2], DIANE DIGIUSEPPE[2], MONICA V. ARELLANO[3], ALAN LEVENTHAL[3,4], BRIAN F. BYRD[1] and BETH MABIE[2]

[1]NA, Far Western Anthropological Research Group, Inc., Davis, CA, [2]NA, D&D Osteological Services, San Jose, CA, [3]NA, Muwekma Ohlone Tribe of the San Francisco Bay Area, Castro Valley, CA, [4]Department of Anthropology, San Jose State University, San Jose, CA

This presentation applies Tilley and Cameron's 2014 Index of Care to the mortuary population of an ancestral Muwekma Ohlone site that was excavated alongside two others in the San Francisco Bay Area between 2016-2022 (CA-ALA-565/H, CA-ALA-677/H, and CA-ALA-704/H). These sites include the remains of 147 individuals dating between approximately 2200-110 cal BP. Specifically, five individuals from CA-ALA-565/H will be examined in greater detail and provide the main focal point for inter-site comparison. This analysis begins by describing the interred individuals and providing differential diagnoses of pathological conditions that were observed during osteological analysis of remains from this site. These individuals possess the most extreme evidence of congenital or acquired pathological conditions which certainly impacted their ability to care for themselves and would have relied on assistance from others inorder to survive. Stand out pathologies include tuberculosis, differentially diagnosed hydrocephalus, and septic arthritis. With the diagnoses described, we attempt to categorize and assess associated disability and models of care, seeking to illuminate how care given to these individuals in life reflects the agency of these people. In particular, notice is given regarding their memorialization in death by inclusion in the community's burial ground. By evaluating this assemblage through the Index of Care, we aim to highlight the unique challenges that individuals from these sites faced, and the way that compassion is evidenced in the bioarchaeological record.

Ditch the Gravitas and Build the Communitas: Adaptive Approaches to Public Engagement

KATIE HINDE

School of Human Evolution & Social Change, Arizona State University

Public engagement is an essential pillar of 21st century scholarship, in part because public funds are instrumental for empirical research and research infrastructure. Movements toward Open Science are important for inclusive scholarly access, but given the conventional format of academic products, these resources are typically "behind a paywall of jargon." Creative, atypical approaches to science communication, knowledge translation, and public engagement demonstrate important contributions academics may contribute to the public good. The evolutionary social sciences have explored human cognitive adaptations for stories, games, and communitas that can inform better practices in public engagement. Leveraging lessons learned from the annual tournament March Mammal Madness, the game show What's That Science?! and other public engagement models, I will highlight key adaptations that play a role in successfully engaging myriad publics in science dialogues. Here we will actively consider the ways in which gamified learning often improves learner attitude, emotion, and performance while affective collective experiences encourage repeat participation. Indeed, ongoing educator surveys reveal that MMM tournament participation has grown annually since 2013, reaching >600,000 players in 2022. Importantly, our professional activities are influenced by our individually manifested philosophies, cultural values, and lived experiences. Recognition of diversified scholarly portfolios that include unconventional professional activities is an instrumental element of dismantling the structures of exclusion within academia.

Primate Basal Metabolic Rates Diverge from Values Predicted from Organ Size

ELENA HINZ, HERMAN PONTZER and AMANDA MCGROSKY

Evolutionary Anthropology, Duke University

Basal metabolic rates (BMR, kcal/d) among mammals reflect the energy requirements of the organs at rest. Energetically "expensive" organs, including the brain, liver, and kidneys, have high tissue-specific metabolic rates (kcal/g/d) and therefore account for a large portion of BMR. It is unclear, however, whether tissue specific metabolic rates are similar across mammals or differ between clades. To investigate this question, we compiled organ size and body composition data for primates, other mammals, reptiles and aves. Clade-specific allometries for each organ or compartment (brain, liver, kidneys, heart, and total other) were combined with published

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

tissue-specific metabolic rates to estimate BMRs for primates, carnivores, rodents, marsupials, mammals, reptiles, and aves. We then compared these organ-based estimates of BMR to measured BMRs for each group. At 10 kg body mass, primates have the highest organ-based estimate of BMR (422 kcal/d). In contrast, observed BMR for primates in this size range (323 kcal/d) are lower than those of carnivores (360 kcal/d) and aves (362 kcal/d). The divergence between organ-based estimates of BMR and observed BMR suggest tissue-specific metabolic rates may differ between mammalian groups. This has implications for understanding how metabolic rates scale across taxa and how individual organs contribute to an organism's energy balance.

Pleiotropy: What tooth morphology may reveal about the human immune system

LESLEA J. HLUSKO[1], DORI E. KENESSEY[2], MADELINE G. MCNELIS[3] and G. RICHARD SCOTT[2]

[1]Paleobiology, CENIEH, [2]Anthropology, University of Nevada Reno, [3]Ecology and Evolutionary Biology, University of California Santa Cruz

This presentation highlights the dentition in the symposium "Toward a holistic approach - Investigating the genetic underpinnings of phenotypic variation." Recent research indicates that significant pleiotropy shapes the genetic architecture of the dentition. Here, we present evidence linking dental variation with a surprising non-dental trait: immune response.

Human incisor shoveling is influenced by the V370A variant of the *EDAR* gene. Expression of incisor shoveling across 5,333 people from 54 archaeological populations reveals that selection during the last ice age favored V370A in populations living in the Artic, an extreme environment because of very low ultraviolet radiation exposure and consequently reduced biosynthesis of vitamin D.

EDAR is a major gene in the ectodysplasin pathway. This pathway co-opted NF-κB signaling, an important modulator of the immune system's pro-inflammatory response. *EDAR V370A* increases the activity of the ectodysplasin pathway perhaps by as much as 100%. Through an extensive literature review, we found evidence that variants of the *FADS* and *Vitamin D Receptor* genes also experienced selection in these same Arctic populations. The *FADS* variant slows production of the most bioactive form of omega-3 that suppresses inflammation. The *VDR* variant enhances breast milk calcium content and intestinal calcium absorption but also inhibits a proinflammatory response. We hypothesize that the selection on the counter-acting variants of *EDAR* (pro-inflammatory) compared with *FADS*, and *VDR* (anti-inflammatory) may result from balancing the immune system's inflammatory response through NF-κB signaling in the omega-3-rich diet and low vitamin D availability of the Arctic.

Funding for this research is supported in part by the European Research Council Advanced Grant Project 101054659—Tied2Teeth.

The ecological and social context of women's hunting in small-scale societies

JORDAN HOFFMAN, KYLE FARQUHARSON and VIVEK VENKATARAMAN

Anthropology & Archaeology, University of Calgary

Women hunt in some societies but not in others. Recent archaeological work has suggested that women's hunting may have been more widespread in the past. However, there is insufficient synthesis on this issue among modern small-scale societies to evaluate these claims. Theoretical considerations from human behavioural ecology predict that women should engage in hunting under the following socioecological conditions: i) there are few cultural restrictions on access to hunting technology, ii) it is performed largely by pre- or post-reproductive individuals, iii) there is minimal conflict with childcare, iv) they pursue low-risk game within range of camp with the aid of dogs and/or in groups, and v) they fulfill key logistical or informational roles. We systematically reviewed 30 ethnographic reports across 18 modern hunter-gatherer societies and coded the ecological and social context in which women's hunting occurred. The data largely support theoretical expectations. Women tend to use technology such as nets, dogs, or traps instead of firearms, which were commonly used by men. There was little evidence to suggest that women only participated in hunting during non-reproductive years, but instead they utilized cooperative and care-giving networks to manage childcare responsibilities. Women commonly performed tracking or assistance roles during hunting excursions. In some societies, women aided hunting by carrying items and relaying information for the larger hunting party. These results clarify the conditions that promote women's hunting.

Space invaders: a reassessment and detailed histology of hyperostosis frontalis interna

RUSSELL T. HOGG[1] and TIMOTHY D. SMITH[2]

[1]Rehabilitation Sciences, Florida Gulf Coast University, [2]School of Physical Therapy, Slippery Rock University

Hyperostosis frontalis interna (HFI) is a human skeletal lesion characterized by nodules of hyperplastic bone and thickening of the frontal bone's inner surface. Despite its prevalence in the general population and its long history of observation – it is one of the most frequently observed pathologies in gross anatomy laboratories – HFI's etiology and pathogenesis remain poorly understood. This is largely due to the lack of a thorough survey of its histology across the various stages of its development. Our study has three major aims: 1) assess HFI histology from incipient to advanced lesions; 2) elucidate lamellar and trabecular structure in HFI; and 3) clarify impacts/roles of the dura mater in HFI. We hypothesize that: 1) HFI lesions begin as irregular appositional deposits of lamellar bone, rather than as "diploization" of cortical bone as suggested by prior studies; 2) as lesions progress, the lamellar bone is subsequently remodeled by cancellous or woven bone; 3) HFI nodules may erode through the meningeal dura mater and expand laterally, causing the frontal bone and its periosteum to directly contact the arachnoid mater. Results support all our hypotheses: sections of nondecalcified bone reveal that HFI growths begin as deposits of lamellar bone; as lesions progress, this lamellar bone is remodeled into woven bone deposits. Trichrome-stained sections reveal that growing lesions do erode through the dura mater, and effectively destroy this tissue layer as they grow laterally and inwardly. Our results suggest possible avenues of research to better understand the root causes of this disorder.

Evaluating the effect of using enhanced-contrast microCT imaging to measure in situ cervical morphology: a tamarin case study

NATASHA HOLDEN[1], THIERRA K. NALLEY[1], ELLEN FRICANO[1] and NEYSA GRIDER-POTTER[2]

[1]College of Osteopathic Medicine of the Pacific, Western University of Health Sciences, [2]Cell Systems and Anatomy, University of Texas Health at San Antonio

Previous research investigating the functional morphology of the tarsier neck using contrast-enhanced microCT imaging has identified possible vascular adaptations for extreme axial rotation of the cervical vertebral column. Relative to other primates, cross-sectional areas for the vertebral arteries of tarsiers are much smaller relative to the size of the bony foramina through which they pass. In this study, we examine whether this result is an artifact of measuring the vasculature from microCT images, given that vascular cross-sectional areas in other primates have been estimated using bony proxies or directly measured during dissection. Using the same methodological approach applied to the tarsier, we measured the areas of the vertebral artery and the transverse foramina of the cervical vertebrae from an adult male golden-headed lion tamarin (Leontopithecus chrysomelas). Tamarins are small-bodied primates that do not exhibit the derived positional behaviors observed in tarsiers and are thus not expected to demonstrate the same relationship between vascular and foramen cross-sectional areas. We compared the values for the tamarin to

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

those reported from a sample of Euarchontoglires. Results demonstrate that the tamarin is similar to other primates in having vertebral arteries that fill more of the transverse foramina than is the case for the tarsier. This finding supports the general comparability of measurements taken from contrast-enhanced microCT scans to other types of data. The contrast between the tamarin and tarsier is consistent with the hypothesis that tarsiers have relatively small vertebral arteries to avoid impingement and occlusion of the arteries during extreme neck rotation.

3D anatomy of otomandibular connections and their significance for cranial evolution in primates and other mammals

CASEY M. HOLLIDAY, EMMA COONEY and KALA FRAZIER

Integrative Anatomy, University of Missouri

The origin of the mammalian middle ear remains one of the great examples of innovations in vertebrate evolution resulting in new sound transmission structures as well as a novel craniomandibular joint, the temporomandibular joint (TMJ). Developmental biology and fossils offer many details on the cooption of ear ossicles from the primitive, quadrate-articular jaw joint bones. However, we know little about concatenate changes in jaw musculature that may have led to the origins of the articular disc and otomandibular ligaments in humans and other mammals. Comorbidities of middle ear and TMJ dysfunction in humans further suggests these patent, persistent ligaments hold functional significance. While the anterior mallear ligament is known to be a rudiment of Meckel's cartilage, the discomallear ligament's (DML) origin remains contentious. Here we test if the DML is a vestige of the pterygoideus lateralis attachment to the articular bone, or malleus, in humans and other mammals. We use DiceCT (Diffusible Iodine Contrast Enhanced CT), 3D soft tissue reconstruction and new 3D muscle fiber architecture modeling approaches to identify and visualize the jaw muscles, ligaments, TMJ and ear ossicles in a sample of human, pig and Virginia opossum heads. We found connections between the pterygoideus muscle, TMJ disc, DML and the malleus, further supporting an ancient connection between these structures. These new data will help clarify patterns of form, function and pathology in the feeding and hearing apparatus of primates and other mammals.

NSF IOS PMB 1457319 University of Missouri Research Council

Modeling mechanical advantage from fossils: What are we missing?

MEGAN A. HOLMES[1] and ANDREA B. TAYLOR[2]

[1]Department of Family Medicine and Community Health, Duke University School of Medicine,
[2]Department of Basic Science, Touro University California

Reconstructing hominin feeding behavior remains of paramount importance to paleoanthropologists. Modeling bite force potential has long factored in this effort but is hampered by the lack of preservation of the chewing muscles, which are responsible for generating the muscle forces that are converted into bite force. Extant primates serve as proxies for estimating bite force in extinct taxa but jaw-adductor muscle force in extant species has often been approximated from bony measurements. While jaw-muscle forces estimated from muscle physiologic cross-sectional areas (PCSAs) have recently been used to estimate bite force, these estimates have ignored variation in muscle fiber types by treating the jaw adductors as either homogeneously slow or fast muscles. Here we combined muscle mechanical advantage (MA) and PCSAs adjusted for fiber-type proportions and their specific tensions (P_o) in the masseter, temporalis, and medial pterygoid in extant primate samples that have served as models for interpreting hominin feeding ecology (tufted capuchins, *n*=3; baboons, *n*=4; sooty mangabeys, *n*=4). We used these data to estimate bite force using a static lever model and compared our results with traditional bite force calculation methods in the same specimens. Traditional bite force estimates assuming homogeneous muscle fiber-type were 33–77% larger than those combining MA with fiber-type adjusted PCSAs. This difference is due largely to the ubiquitous expression of the alpha-cardiac myosin, which was only recently identified in primates and has low P_o. These findings underscore the potential of this approach to improve our bite force models in extant and extinct taxa.

Funded in part by the Yerkes National Primate Research Center Grants No. ORIP/OD P51OD011132 and No. U42PDP11023, and a grant from the National Science Foundation (BCS-1719743).

Heel-striking reduces the lower limb joint work required for human walking

NICHOLAS B. HOLOWKA[1], ZACCHARIAH M. APOLITO[1], RONAK K. FANSIWALA[1], CALEB A. MASSIMI[1], KEVIN G. PALMISANO[1] and MATTHEW C. O'NEILL[2]

[1]Department of Anthropology, University at Buffalo,
[2]Department of Anatomy, Midwestern University

Human walking is characterized by a distinctive heel strike that incurs high impact forces but is hypothesized to have been selected in hominin evolution to reduce the energetic cost of walking. Several energy-saving mechanisms have been proposed for heel-strike walking, but so far no study has reported the effects of this walking style on lower limb joint work. Here we used high-speed motion capture to collect three-dimensional kinetic and kinematic data, as well as electromyographic data from 10 human subjects (6 male, 4 female; 26±5 yrs, 68±14 kg) who walked at similar speeds (0.18 Froude; v=1.25±0.04 m/s) using two different walking styles: heel strikes and forefoot strikes, where the ball of the foot contacts the ground before the heel is brought down in a manner similar to foot strike postures observed in chimpanzees. Our results indicate that heel-striking reduces negative ankle work by 46% on average compared to forefoot-striking ($p<0.001$), which coincides with 43% and 18% reductions in average gastrocnemius medialis and soleus muscle activations during heel-striking, respectively (both $p<0.001$). Further, these ankle work reductions during heel-striking appear to be related to 37% average reductions in positive hip work during transitions between single-support periods ($p<0.001$). These results suggest that heel-strike walking in fossil hominins may have reduced the hip and ankle work performed by the hip and triceps surae muscles, which could have made bipedal walking less energetically expensive at the cost of subjecting the body to higher impact forces.

Understanding childhood growth: A pilot study of facial soft tissue thicknesses and body mass relationships in children aged 13 – 17 years

TE WAI POUNAMU T. HONA and CARL N. STEPHAN

Laboratory for Human Craniofacial and Skeletal Identification (HuCS-ID Lab), School of Biomedical Sciences, The University of Queensland

Variations in facial soft tissue thicknesses (FSTTs) have largely been attributed to changes in the underlying cranial morphology. However, unlike craniometric dimensions, FSTTs do not necessarily increase with age and may, more consistently, vary dependent on an individual's body mass and distribution of adipose tissue with age. In this study, we use a mixed-longitudinal radiographic sample from the Bolton-Brush growth series to explore the relationship between FSTTs, body mass, and craniometric dimensions in children aged 13 to 17 years. A total of 102 lateral cephalometric radiographs from 42 individuals were assessed. FSTTs were measured at 15 cephalometric landmarks and craniometric dimensions were measured for head length (g-op) and height (g-pg). Corresponding body mass data were extracted from historical collection records for participants. Overall, the average facial soft tissue changes between 13 to 17 years of age were small (<2 mm). Multivariate analysis of variance (MANOVA) indicated that FSTTs are statistically different by body mass and age ($p < 0.05$). Body mass explained a greater percentage of total variation (partial eta-squared = 80%) than age (partial eta-squared = 70%). Correlations between craniometric dimensions and FSTTs were generally weak (head length [g-op] and height [g-pg] had R-values in the range of 0.06 to 0.38 and -0.11 to 0.44, respectively). Body mass typically

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

revealed stronger correlations with FSTTs, for example, yielding R values ranging from 0.5 to 0.7 at subnasale (sn-sn'), opisthocranion (op-op') and mid-philtrum (mp-mp'). These findings suggest that body mass has a larger and stronger impact on FSTTs than craniometric dimensions.

This research was supported by an Australian Government Research Training Program (RTP) Scholarship awarded to Te Wai Pounamu T. Hona.

Oral metagenomes of ancestral Maya individuals from Belize reveal insights into strain diversity and evolutionary histories of oral microbes

TANVI P. HONAP[1,2], SARAH J. JOHNSON[1,2], PAIGE A. LYNCH[3], DOUGLAS J. KENNETT[4], KEITH M. PRUFER[3,5] and CECIL M. LEWIS, JR.[1,2]

[1]Laboratories of Molecular Anthropology and Microbiome Research (LMAMR), University of Oklahoma, [2]Department of Anthropology, University of Oklahoma, [3]Department of Anthropology, University of New Mexico, [4]Department of Anthropology, University of California Santa Barbara, [5]Center for Stable Isotopes, University of New Mexico

Oral diseases, which are caused by dysbiosis in the oral microbiome, are thought to have increased in prevalence as human populations transitioned to an agricultural lifestyle. However, it remains unclear how such dietary transitions impacted the oral microbiome composition. As part of a consortium of community-focused studies, we aimed to characterize changes in the oral microbiomes of ancestral Maya individuals accompanying transitions from a foraging to a staple maize diet. We acquired dental calculus samples from directly-dated individuals from two rock-shelter sites in the Maya Mountains of Belize. DNA was extracted and double-stranded libraries were shotgun-sequenced using Illumina technology. We recovered oral metagenomes with minimal extraneous contamination from 24 individuals across three dietary categories: pre-maize (9600-4700 BP, n=9), transitional-maize (4700-4000 BP, n=1), and staple-maize (4000-1000 BP, n=14). Statistical analyses showed that bacterial abundances did not differ significantly between the dietary categories. We reconstructed genomes of oral commensals, Anaerolineaceae bacterium oral taxon 439 and *Pseudoramibacter alactolyticus*, and opportunistic oral pathogens, *Tannerella forsythia* and *Treponema denticola*. Strain-based analyses revealed examples of temporal/lifestyle continuity and discontinuity. The ancestral Maya individuals carried *P. alactolyticus* strains that persist in modern Americans even today, whereas they carried Anaerolineaceae bacterium oral taxon 439 strains found in other pre-contact Native Americans but absent from modern-day individuals. Our results suggest that different oral microbes show distinct evolutionary histories. Further analyses will focus on strain diversity of the opportunistic oral pathogens reconstructed from these individuals, with an emphasis on detecting virulence-associated genes which may have impacted oral health.

This work was funded by a National Science Foundation grant titled "Hominid Dental Metagenomes for Pathogen Evolution Research" (NSF BCS-2045308).

Muscle activity during walking at three degrees of crouch: Implications for approach hunting

MARTIN HORA[1], MICHAL STRUŠKA[1], ZUZANA MATĚJOVSKÁ[1], PETR KUBOVÝ[2] and VLADIMÍR SLÁDEK[1]

[1]Anthropology and Human Genetics, Faculty of Science, Charles University, [2]Anatomy and Biomechanics, Faculty of Physical Education and Sport, Charles University

Muscle activity during crouched walking has been previously studied in the context of the evolution of hominin bipedalism and human movement disorders. However, crouched walking is also used in approach hunting where postural height is often the limiting factor. Here, we aim to analyze the relationship between crouch degree and lower limb muscle activity (activation and force) during walking in humans who can freely adjust their posture to a desired postural height.

Adult males (n = 19) walked normally and at three degrees of crouch while their kinematics and muscle activation were recorded using 3D motion capture system and electromyography. We measured activation of tibialis anterior, soleus, gastrocnemius medialis, gastrocnemius lateralis, vastus lateralis, rectus femoris, biceps femoris, and gluteus maximus. We estimated total lower limb muscle force in our living participants and Late Pleistocene humans.

Muscle activation was greater during crouched walking compared to normal walking and increased with crouch degree in all measured muscles except for medial gastrocnemius. Total lower limb muscle force increased with crouch degree. Neandertals required less relative muscle force during crouched walking than Paleolithic modern humans.

General increase in lower limb muscle activity with crouch degree detected here contrasts with findings of previous studies in healthy individuals (limited by lower number of crouch degrees and smaller differences between them) and cerebral palsy patients. Our results suggest a positive relationship between crouch degree and energetic cost in healthy humans and may indicate a possible mechanism by which short stature could benefit the hunter in approach hunting.

This work was supported by the Czech Science Foundation, grant number 18-16287S. M.H. has been supported by Charles University Research Centre program No. 204069.

Once an outlier always an outlier? Limb joint articulations' relative distances from the morphological centroid

HALEY HORBALY[1,2] and MARK HUBBE[3]

[1]Department of Exercise Science, High Point University, [2]Department of Medical Sciences, High Point University, [3]Department of Anthropology, The Ohio State University

Prior work has established distinctive associations among human limb joint morphologies, particularly when articulating joint surfaces are compared. However, it is still unclear if individuals who occupy the extreme ends of the morphological distribution do so systematically across all their joints, or only within a subset of their joints. To test the degree of systemic differentiation of joint morphologies, 3D landmark data was collected on left and right-side articulations comprising the shoulder, elbow, hip, and knee joints for 200 adult skeletons. For each articulation, each individual's distance from the morphological centroid was determined, and distances were rank-ordered to measure their relative divergence from the centroid. The ranks for each of the eight articulations comprising four joints were tested for association using Spearman correlations. Results indicate no significant associations between the ranks of complementary articulations (e.g., between acetabulum and femoral head; $p > 0.05$), despite their functional co-dependency. However, significant associations were found between the ranks attributed to the left and right sides of the same articulation (r-values ranging from 0.16 to 0.53; $p < 0.05$ for all cases), suggesting that bilateral development has a significant impact in overall morphological deviations from centroid. Collectively, these results indicate that there is no systemic pattern of differentiation from centroid at the populational level, but there is evidence of bilateral consistency in the proximity to the morphological average. The association between left and right articulations provides additional support for the limited effects of activity on joint variation, which would otherwise yield asymmetrical patterns.

Reconstructing rodent locomotor behaviours using semicircular canal morphology

LILY HOU[1], ORNELLA C. BERTRAND[2], HIRUNI MUDANNAYAKE[1], CAMPBELL ROLIAN[3,4] and SUSANNE COTE[1]

[1]Anthropology and Archaeology, University of Calgary, [2]School of Geosciences, University of Edinburgh, [3]Anatomy and Cell Biology, McGill University, [4]Comparative Biology and Experimental Medicine, University of Calgary

Anatomical structures vary among mammals with different locomotor behaviours, including sensory structures such as the semicircular canals (SCCs) in the inner ear. Recent research suggests that SCC morphology correlates with different locomotor behaviours in various extant

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

and extinct mammalian taxa, but there is a lack of research on rodents, the most speciose and diverse mammalian group. Fossil rodents are frequently found in association with fossil primates and may be useful environmental indicators. Fossil rodent material consists mostly of craniodental remains; hence reconstructing fossil locomotion has been challenging. Understanding the correlation between SCC morphology and locomotor behaviours may be useful for 1) inferring locomotor modes in extant and extinct rodent species, and 2) providing context for paleoenvironment reconstructions.

We collected micro-computed tomography scans of a taxonomically diverse sample of 65 extant rodent species across 23 families, covering fossorial, semifossorial, semiaquatic, terrestrial, jumping, arboreal, and gliding taxa. We collected morphometric measurements (height, width, length, radius, and angles between canals) of digitally segmented SCCs. Principal component and discriminant function analyses suggest that SCCs of rodents with different locomotor behaviours occupy different morphospaces, although there is some overlap in morphospaces between terrestrial and semiaquatic locomotion, and between arboreal and gliding locomotion. Fossorial, semifossorial, and jumping morphospaces are distinct from each other, and from terrestrial/semiaquatic and arboreal/gliding morphospaces. The differences observed suggest that using SCC morphology in rodents is a viable tool for inferring probable locomotor repertoires. Applying this comparative sample to reconstruct fossil rodent locomotion can provide environmental and evolutionary context for fossil primates.

This research was supported by the Natural Sciences and Engineering Council of Canada, Leakey Foundation, and the University of Calgary.

A comparative primate organoid system for examining evolutionarily divergent patterns of gene expression during chondrogenesis

GENEVIEVE HOUSMAN[1,2], EMAAN MOHSIN[3] and YOAV GILAD[1,4]

[1]Section of Genetic Medicine, University of Chicago, [2]Department of Primate Behavior and Evolution, Max Planck Institute for Evolutionary Anthropology, [3]Department of Biochemistry and Molecular Biology, University of Chicago, [4]Department of Human Genetics, University of Chicago

Characterizing the contribution of gene regulation variation to the development and evolution of primate skeletal traits is challenging. Relevant tissues are difficult to obtain, with ethical and experimental considerations, and when available, samples often have preservation issues that limit the measurement of molecular patterns. Alternatively, cell culture systems utilizing primate induced pluripotent stem cells (iPSCs) provide a more accessible way of studying functional genomics in the skeleton. Specifically, to identify gene expression variation relevant for cartilage development and evolution, we established a comparative primate chondrogenic organoid model. Four human and four chimpanzee iPSC lines were differentiated into mesenchymal stem cells, aggregated into 3-dimensional spheroids, and further differentiated into chondrogenic cells. Single-cell RNA-seq data were collected at different timepoints throughout the course of chondrogenesis – day 0, day 7, and day 14 of spheroid differentiation. Gene expression levels were recovered from over 38,000 cells, and these data reveal patterns of differential expression between humans and chimpanzees within and across stages of differentiation. Comparing these data to regulatory patterns in other skeletal cell types and in similar iPSC-derived chondrogenic cells exposed to tissue-relevant mechanical and cytokine perturbations will provide further insight into the molecular mechanisms that may contribute to evolutionary differences in skeletal development, maintenance, and disease susceptibility. Altogether, this comparative primate chondrogenic organoid model serves as a novel way to examine functional genomics of primate skeletons.

Research was supported by the NIH NIGMS under award number R01GM122930 to Y.G. and the NIH NIAMS under award number F32AR075397 to G.H.

The impact anthropogenic deforestation on the behavior of mantled howler monkeys (*Alouatta palliata palliata*) at La Selva Biological Station, Costa Rica

SUE M. HOWELL[1], ORLANDO VARGAS RAMIREZ[2] and ENRIQUE ALONSO CASTRO FONSECA[2]

[1]Anthropology, University of Colorado Colorado Springs, [2]Organization for Tropical Studies, La Selva Biological Station, Costa Rica

This study considered the influence of varied forest zones on howler monkey behavior to better understand how howler monkeys cope with anthropogenic deforestation. From past research, we know howler monkeys are folivorous, forest generalists. Here we aimed to consider how howler monkeys adapt, not just to secondary edge forests, but also to abandoned agroforests with considerable anthropogenic change. We studied the impact of three forest zones (old growth forest, secondary forests, and abandoned agroforestry) on the behavior of six troops of howler monkeys (each with 2 males and 7 to 11 total individuals) at the La Selva Biological Station, Costa Rica. A group scan method was used to record behavior at 5-minute intervals between 5:30 AM and 5:00 PM. Six social groups were observed for 317 hours across three forest zones (Old Growth Forest, Secondary Forests, Abandoned Agroforestry) between 2020 and 2022. Behaviors recorded included feeding, resting, travelling, grooming, calling, and other or out of view. An arcsine-square root transformation and one-way ANOVA and Tukey Pairwise Multiple Comparison tests were used to consider the influence of forest types on behavior ($p<0.05$). We found no statistically significant differences between forest types and behaviors ($p>0.05$). We can report a trend ($p=0.08$) to be investigated in future studies. Howler monkeys in abandoned agroforest zones spent more time feeding in comparison to monkeys in old growth or secondary forests. Data collection is ongoing but promising and illustrate the ability of this forest generalist to cope with considerable anthropogenic deforestation.

Travel funding was provided by the University of Colorado Colorado Springs.

Cortical bone strength properties in the hindlimb of saltatory primates, rodents, and marsupials

KAITLIN C. HSU[1,2], CHLOE A. KNITT[1,2] and KRISTI L. LEWTON[2]

[1]Department of Biological Sciences, University of Southern California, [2]Department of Integrative Anatomical Sciences, University of Southern California

Leaping primates experience relatively large locomotor forces and exhibit greater hindlimb bone elongation compared to their quadrupedal sister taxa. Using a broad, comparative sample of primates, marsupials, and rodents, we use a convergence approach to examine the relationship between bipedal leaping/hopping locomotion and cortical bone strength properties in the hindlimb. We predicted that saltatory species would exhibit relatively stronger tibiae and femora in bending, torsion, and compression and evidence of stereotyped loading patterns compared to quadrupedal species. We micro-CT scanned 136 femora and 89 tibiae from 42 mammalian species, virtually reoriented each scan, and extracted the following cross-sectional properties from the midshaft: polar section modulus (Z_p, an estimate of bending strength), I_{max}/I_{min} (representing cortical bone distribution), polar second moment of area (an estimate of torsional strength), and cortical area (an estimate of compressive strength). For each bone, analyses of variance were performed to compare scaled cross-sectional properties between saltatory and quadrupedal species. Femoral and tibial measures were compared using linear regression and correlation. Some, but not all, of our predictions were supported. As predicted, tibial scaled Z_p and femoral I_{max}/I_{min} were greater in the saltatory species compared to quadrupeds ($p<0.0005$ and $p<0.0002$, respectively). However, other cross-sectional properties were greater in quadrupeds. Our results suggest that primates and other saltatory mammals

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

may not consistently exhibit relatively stronger hindlimb bones than quadrupedal species; more research is necessary to clarify complex patterns within and among taxa.

This study was funded by the National Science Foundation BCS-1944571.

The effect of admixture on heritability underlying complex traits

JINGUO HUANG[1,2], MARK D. SHRIVER[1] and ARSLAN A. ZAIDI[3,4]

[1]Department of Anthropology, Penn State University, [2]Huck Institutes of Life Sciences, Penn State University, [3]Department of Genetics, Cell, and Developmental Biology, University of Minnesota, [4]Institute of Health Informatics, University of Minnesota

Admixed populations are useful for variant discovery and polygenic prediction. Both variant discovery and polygenic prediction depend on the amount of genetic variation underlying complex traits – a quantity that is not well defined in admixed populations. Here, using theory and simulation, we quantitatively describe the behavior of the heritability of complex traits in admixed populations.

We show that the heritability in admixed populations depends on the degree of linkage disequilibrium (LD) across genetic loci. Admixture LD in turn depends on the degree and dynamics of admixture and on the degree of assortative mating after admixture. To make these results more interpretable, we took the example of skin pigmentation – a trait that varies considerably across populations. We described the heritability under such a trait in two extreme models of admixture: (i) where admixture occurs in a single generation, and (ii) where gene flow occurs continuously between the parental populations. In the first model, the heritability is maximum at the time of admixture and decays in subsequent generations as admixture LD breaks down due to recombination. The rate of decay is slower in the presence of assortative mating. In the second model, the heritability increases rapidly at first with every generation as continuing gene flow increases admixture LD, eventually plateauing.

Our results emphasize the importance of demographic history, particularly admixture, on complex traits architecture. These results are not only relevant for understanding the behavior of complex trait variation in contemporary populations but also for understanding the impact of archaic introgression.

The development of selective information-seeking in macaques

YIYUN HUANG[1] and ALEXANDRA G. ROSATI[1,2]

[1]Department of Psychology, University of Michigan, [2]Department of Anthropology, University of Michigan

Metacognition is the ability to think about one's own knowledge state, an ability that is crucial for flexible learning and adaptive behavior. While humans regulate and control their metacognitive processes by seeking out information when they lack knowledge, a skill that improves over our long juvenile period, the evolutionary origins of this ability are unclear. In this current study, we used a comparative developmental approach to test whether rhesus macaques (*Macaca mulatta*) understand when information-seeking is necessary and show human-like developmental changes in this skill. Monkeys ranging from juvenility to adulthood (n = 80) were tested in one of two conditions where they observed a food reward being hidden in one of two tubes behind a barrier. In one condition, monkeys received direct information about the location of the food reward, and thus information seeking was not necessary. In the other, monkeys did not receive any direct information about the location of the hidden food reward, but could engage in information-seeking by peering into a central vantage location to locate it. Monkeys searched at the correct side location when information-seeking was not necessary, but correctly approached the center vantage point when it was necessary [x^2 = 52.20, p < 0.001]. Yet younger and older monkeys showed similar abilities [x^2 = 0.68, p = 0.41], indicating a different developmental trajectory in monkeys with faster life history characteristics than in humans. These results show that macaques understand when metacognitive information-seeking is necessary even early in development.

This research is funded by NSF #1944881 to AR.

Bone modeling variability in the human mandible

MADISON L. HUBBART[1], ALEXANDRA SCHUH[2] and SARAH E. FREIDLINE[1]

[1]Anthropology, University of Central Florida, [2]CNRS, MC, PACEA, UMR 5199, Université de Bordeaux

Bone growth through bone modeling involves the uncoupled activity of osteoblasts forming bone and osteoclasts resorbing bone. Limited understanding of bone modeling patterns in humans can be attributed to a lack of quantitative data and small sample sizes. This study quantifies mandibular bone modeling patterns in a sample of *Homo sapiens* to assess variability and identify a shared or divergent pattern of growth. A sample of 12 mandibles were collected from three geographically diverse regions: Western Europe (France, Germany, and Portugal), Greenland (Inuit), and South Africa (Khoekhoe and San), and divided into four dental age groups ranging from birth to adulthood. Bone formation and resorption data were collected from casts of bone surface molds and quantified for both the anterior and posterior periosteal surface of the mandible. This information was utilized to create digital maps of bone modeling patterns for each individual. The results of this study suggest limited variability in bone modeling patterns for each age group. Mandibles with deciduous dentition are largely represented by bone formation. When the first and second permanent molar are in occlusion, mandibular surfaces are resorptive from the mandibular ramus to the body, with highly resorptive areas running posterior from the mandibular condyle to the gonial angle. Upon the eruption of the second molar, resorption in the same areas decrease, leaving behind a bone surface at rest. Although appearance of muted population differences in bone modeling patterns are seen, a general bone modeling pattern persists and may be a trademark of all *Homo sapiens*.

The role of stabilizing selection on the evolution of *Homo* cranial morphology

MARK HUBBE[1,3] and KATERINA HARVATI[2,3]

[1]Department of Anthropology, Ohio State University, [2]Paleoanthropology, Institute for Archaeological Sciences and Senckenberg Center for Human Evolution and Paleoenvironment, Eberhard Karls University of Tübingen, [3]DFG Centre for Advanced Studies 'Words, Bones, Genes, Tools: Tracking Linguistic, Cultural and Biological Trajectories of the Human Past', Eberhard Karls University of Tübingen

The complex evolution of our lineage is clearly observed in the great diversity of cranial morphology in the fossil record of the genus *Homo*. This evolution was the outcome of a balance between maintaining the functionality of anatomical and developmental modules that define the skull and external environmental pressures acting on individuals' fitness over time. Therefore, the myriad of intrinsic and extrinsic evolutionary forces acting on cranial morphology can result in several different outcomes, which ultimately produced the speciation events in our lineage. Despite the complex nature of the evolution of cranial morphology, few studies have explored the possible evolutionary pathways that led to the diversity of shapes seen in the genus *Homo*, especially when it comes to the role of stabilizing selection and non-linear evolutionary forces like punctuated equilibrium. In this study we evaluate the maximum likelihood estimates of several competing evolutionary models (diversifying selection, stabilizing selection, random walks, punctuated equilibria) to explain the cranial morphological changes across *Homo*. Twenty-nine linear craniometric variables and indices were analyzed from 74 fossil and 105 modern human skulls grouped into 8 Operational Taxonomic Units. The maximum likelihood

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

estimates show that 19 variables fit more strongly stabilizing selection, nine show highest likelihood when explained through random walk, and only one variable shows strong fit with diversifying selection. These results suggest that, despite the changes observed in the genus *Homo*, the constraints acting on the accumulation of variance are possibly the most important baseline in the evolution of the cranial morphology of *Homo*.

This research was supported by the Deutsche Forschungsgemeinschaft (DFG-FOR-2237). KH is supported by the European Research Council (ERC-AdG-101019659)

Investigating identification disparities in forensic anthropology casework

CRIS E. HUGHES[1,2], AN-DI YIM[3,4], CHELSEY A. JUAREZ[5], JOHN SERVELLO[6], RICHARD THOMAS[7], NICHOLAS PASSALACQUA[8] and ANGELA SOLER[9]

[1]Anthropology, University of Illinois at Urbana-Champaign, [2]Carl R. Woese Institute for Genomic Biology, University of Illinois at Champaign-Urbana, [3]Health and Exercise Sciences, Truman State University, [4]Biology, Truman State University, [5]Anthropology, California State University Fresno, [6]Forensic Anthropology Unit, UNT Center for Human Identification, [7]Trace Evidence Unit, Federal Bureau of Investigation, Laboratory Division, [8]Anthropology and Sociology, Western Carolina University, [9]Forensic Anthropology, New York City Office of Chief Medical Examiner

Forensic anthropology is shifting to self-reflect on the impact of its practices within the criminal justice context in important ways. This study contributes to such work by examining how decedent demographics and biological profile estimations are related to identification trends in forensic anthropology cases. The study uses data from more than 1,200 identified and unidentified persons forensic anthropology cases from three U.S. agencies (together representing a nation-wide sample). The results are as follows: i) multivariate analyses indicated that decedent sex, age, and race and/or ethnicity are not related to case identification rates in the pooled United States sample, ii) when identification rate differences do occur, they appear to be smaller effects and/or related to the context of a particular agency, iii) for agency with available data, there was no consistent evidence for a discrepancy in the duration of an identification investigation based on a decedent's sex, age, or race and/or ethnicity, and iv) estimations of sex, age, and ancestry can improve the odds of identification for decedents. Although previous studies have identified bias in other areas of the criminal justice system, the results suggest that decedent demographic estimation practices by forensic anthropologists in general do not appear to contribute to bias in identification trends. Contextual factors and practices specific to U.S. investigative agencies likely contribute to identification trends. More research is needed to infer whether the identified trends hold true in other agencies.

Long lost cousins or distant neighbours? The dental morphology of early South-East Asian migration

TOBY HUGHES[1], SANJIT SURESH[1], MICHELLE BOCKMANN[1], KYLIE DAVIS[1] and ALAN BROOK[1,2]

[1]Adelaide Dental School, The University of Adelaide, [2]Barts and the London Dental Institute, Queen Mary University of London

The efflux theory of migration in early South East Asia (SEA) suggests outward movement of a SEA ancestor (Sunda-Pacific dentition) into East Asia, with directional dental adaptation. The influx theory suggests inward movement of East Asians into SEA, with gene flow between East Asians and an Australian Aboriginal-like SEA ancestor (Sahul-Pacific dentition).

This study investigated dental morphology of modern Australasian populations to derive estimates of population distance, comparing indigenous Malaysian Orang Asli to populations of ethnic Malaysians, Chinese Malaysians, Indian Malaysians and Australian Aboriginals from the Warlpiri people.

Dental casts were selected from cohort samples located at the University of Adelaide. Eighty (40F/40M) young individuals with a full adult dentition (excluding M3) were chosen from each population. Crown traits were scored using ASUDAS. Trait frequencies underwent reliability analysis, external validation, and UPGMA population clustering. Trait frequencies were compared to established dental complexes.

Shovelling, double-shovelling (DS) and lower second molar cusp number (LM2CN), dictated most population clustering. Traits were scored reliably aside from DS, Bushman's canine (BC), cusp 5, and protostylid. BC and cusp 5 were omitted from further analysis and breakpoints of DS and protostylid were adjusted.

Clustering was sensitive to the presence of LM2CN; inclusion provided support for efflux. Exclusion, and comparison to established dental complexes, provided support for influx. Analyses were sensitive to traits which had both high leverage and were challenging to score, explaining previous conflicting results. The dental morphology of the indigenous SEA population may be the result of complex interactions arising from both migration pathways.

Dental casts from the Yuendumu growth study used in this research were originally collected with the support of funding from the NIH.

Examining Temporal Bones for Evidence of Pearl Diving in Prehistoric Arabia

MADISON HULL[1], CADEN RIJAL[2], LESLEY A. GREGORICKA[3] and JAIME ULLINGER[4]

[1]Anthropology, Dickinson College, [2]Anthropology, Wellesley College, [3]Sociology, Anthropology, and Social Work, University of South Alabama, [4]Sociology and Anthropology, Quinnipiac University

During the Umm an-Nar period (2700-2000 BCE), pearls from the Arabian Peninsula were traded throughout the surrounding area. We examined temporal bones from two tombs (Unar 1 and 2) located at the Shimal Necropolis in the Emirate of Ras al-Khaimah (UAE) for signs of external auditory exostosis (EAE) and otitis media (OM), both associated with water exposure, for evidence of pearl diving. We hypothesized that there may be a significant difference between males and females and that EAE and OM may be associated. We scored temporal bones on EAE presence and severity (0-3), and the mastoid process (1-5) to estimate sex. We used a digital microscope to examine the cochlear promontory surface for remodeling and resorption, which are both signs of OM. Differences were tested with Fisher's Exact (FE) tests and Odds Ratios (OR).

Four Unar 1 (9%, n=46) and three Unar 2 (2%, n=145) individuals had EAE. This difference is not statistically significant (FE p=0.059). We estimated 55 individuals to be female and 20 to be male. Four males and one female had EAE, a statistically significant difference (FE p=0.016). Combined, 74% (n=94) of individuals from both tombs had evidence of OM. There was no association between EAE and OM (OR=0.50, CI [0.078 - 3.190]). A small portion of these individuals may have been spending a significant amount of time in the water, perhaps to collect pearls. Males were more likely to participate in these maritime activities, consistent with the literature on sex-based differences in diving practices.

This research was funded by a National Science Foundation Research Experiences for Undergraduates Award (#1852426).

Assessing morphological correlates of knuckle-walking behavior in hominid taxa based on carpals

LAURA E. HUNTER, PETER A. STAMOS and ZERESENAY ALEMSEGED

Department of Organismal Biology and Anatomy, University of Chicago

The uniqueness of bipedalism in *Homo sapiens*, among living primates, has made it difficult for researchers to determine what locomotor behavior preceded it. The prominence of knuckle-walking in *Pan* and *Gorilla* has led some researchers to hypothesize that early hominins may have included knuckle-walking in their locomotor repertoire. This has been challenged by evidence from the forelimb of *Ardipithecus*

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

ramidus, whose locomotion is reconstructed to have included substantial palmigrady. Carpal morphology is central to examining these claims, but carpal shape and its relationship to locomotor behavior remain poorly understood due to the carpals' complex shapes making them challenging to quantify. We collected 3D scan data of each carpal (excluding pisiforms) from a sample of hominid taxa (*Homo* = 24, *Pan* = 14, *Gorilla* = 20, *Pongo* = 9) and represented their morphologies using global point signature shape decomposition analysis. With these data, we trained a support vector machine on each carpal element to detect whether the individual it belonged to was a "knuckle-walker" or "non-knuckle-walker". These algorithms correctly categorized above chance for all carpals analyzed, suggesting that overall carpal morphology predicts knuckle-walking, or lack thereof. Carpal elements related to limiting wrist extension (e.g. capitate) more reliably predicted knuckle-walking than others (e.g. triquetrum). Future research will expand this sample to include more taxa to test whether these algorithms can differentiate between other locomotor behaviors. These methods may also shed light on the locomotor behavior of extinct taxa and inform our understanding of the evolution of bipedalism and tool use in hominins.

The spread of genes and culture in the Late Holocene of South America

TÁBITA HÜNEMEIER

Population Genetics, Institute of Evolutionary Biology (IBE/CSIC-UPF), Genetics and Evolutionary Biology, University of Sao Paulo

Agriculture and sedentarization led to higher rates of population growth in South America, resulting in demic expansion events and restructuring the genetic landscape and cultural diversity in the Late Holocene. Cultural variables relating to subsistence strategies are likely to be the primary determinants affecting the broader patterns of genetic structure, particularly after the enormous population dispersals of agriculturalists during the Holocene. In eastern South America, populations with agriculturalist subsistence strategies expanded out of the Amazon. The Tupí expansion was one of the most significant human movements of the Holocene, dispersing thousands of individuals in search of fertile lands for more than four thousand kilometers starting from the west of the Amazon to southern and eastern South America. Here we analyzed genomic data from the Tupi population from different regions of South America to understand the impact of the Tupi expansion on the present-day genetic diversity of South America. We found that this demic movement led to a complex process of linguistic dispersion, giving rise to different groups, genetically structured. Furthermore, a unique linguistic substitution event occurred due to the Tupi demographic expansion, where an Arawak group was likely conquest and adopted the Tupi language. Our results showed this single demographic event's significant impact on South American Indigenous cultural and biological diversity.

FAPESP 15/26875-9 and 21/06860-8 (Brazil)

Stw 573 fibula suggests a human-like popliteus muscle

ALEXANDRA C. IDSO[1,2] and ASHLEY S. HAMMOND[1,2,3]

[1]Department of Anthropology, The Graduate Center, City University of New York, [2]New York Consortium in Evolutionary Primatology, [3]Division of Anthropology, American Museum of Natural History

The human popliteus muscle allows the medial thigh rotators to transmit torque to the ground by preventing internal rotation of the femur and unlocks a fully extended knee, making this muscle integral to hominin bipedal locomotion. It has been previously observed that African great apes have an unusual Y-shaped popliteus tendon, with arms originating from the femur and the fibula. The fibular origin in African apes was marked by a distinctive pit for tendon attachment. This diverges from the human condition, wherein the popliteus originates from a single tendon from the femur. Importantly, Stw 573 ("Little Foot") retains a well-preserved proximal fibula that allows us to test whether early *Australopithecus* had an African ape-like or human-like configuration. Our study aims to (1) comparatively investigate the occurrence and frequency of the pit on the proximal fibula associated with the popliteus, and (2) characterize the configuration in Stw 573. Our comparative osteological sample includes fibulae of *Pan*, *Gorilla*, and *Pongo*. The feature was observed in 95% of *Pan* outside *Pan troglodytes verus,* where it was highly variable, and in 94% of *Gorilla*. A pit for the popliteus muscle tendon was not observed in *Pongo* fibulae. Although it must be confirmed by dissection studies, this result suggests that a fibular origin for the popliteus tendon is specific to African great apes. Interestingly, the Stw 573 fibula is unlike the African ape morphology (i.e., lacking a pit for the popliteus tendon), suggesting this early biped may have had fairly human-like knee function.

Reconstructing the Mobility Pattern in the Center of the Iranian Plateau during the Bronze Age, Kafarved-Varzaneh

TABASOM ILKHAN[1], BABAK RAFI'I-ALAVI[2] and ARKADIUSZ SOŁTYSIAK[3]

[1]Department of Archaeology, Simon Fraser University, [2]Department of Archaeology, Art University of Isfahan, [3]Department of Bioarchaeology, University of Warsaw

A significant depopulation and abandonment occurred on important archaeological sites in the Iranian Plateau during the 3rd millennium BC, which has been explained by several theories, including mass migration, climate and ecological changes. The Kafarved-Varzaneh area is home to more than two hundred Early Bronze Age sites (dated by radiocarbon to the mid-3rd millennium BCE), which contradicts the traditional views that human settlements declined entirely in the Iranian Plateau during the Bronze Age. This study is based on human skeletal remains retrieved from the Kafarved-Varzaneh area, located in the heartland of the Central Plateau, in the Zāyandeh-rūd river basin near Esfahan province, Iran. To investigate the mobility pattern in this region, 87Sr/86Sr values in enamel of 42 individuals were measured and compared with the strontium values of 19 plant samples collected across the neighboring regions (East-West and South-North) and Zāyandeh-rūd river basin. The results show a large overlap between areas and a wide range of 87Sr/86Sr values in all defined subsets. The Mann-Whitney test showed that although 87Sr/86Sr values of the eastern regions are lower than the western areas, the difference is not statistically significant. The isotope values in human enamel mainly matched the local range, and there are only four possible immigrants with very low Sr isotopic values from site 051. The consumption of non-local and local resources in Kafarved-Varzaneh might also explain these differences in isotopic values of human enamel.

Keywords: Isotope Analysis, 87Sr/86Sr, Bronze Age, Kafarved-Varzaneh, Iran

Dental and genomic data in recent global population samples yield corresponding evidence for the Late Pleistocene population diffusion out of Africa

JOEL D. IRISH[1,2], ADELINE MOREZ[1], LINUS GIRDLAND FLINK[3] and G. RICHARD SCOTT[4]

[1]School of Biological and Environmental Sciences, Liverpool John Moores University, [2]The Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand, [3]Department of Archaeology, University of Aberdeen, [4]Anthropology Department, University of Nevada, Reno

We previously demonstrated that Arizona State University Dental Anthropology System (ASUDAS) traits are reliable proxies for genetic data in assessing population relatedness. Correlations between distance matrices from 25 ASUDAS traits [mean measure of divergence (MMD)] and >350,000 SNPs (Hudson's F_{ST}) in matched recent samples are *rm*>0.8 in Africa (*n*=12 samples) and >0.7 globally (*n*=32). These matrices also correlate with spatial distances (km), notably at the global level, >0.7, and yield geographic patterning in MDS plots—suggesting isolation by distance. Explicitly, beginning with southern African San, both dental and genomic samples 'proceed' out of Africa and around the world, to America and Australia/Melanesia.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Here, to further assess data comparability, all 32 dental and 32 genomic samples were placed at the origins of separate scatterplots comparing MMD/F_{ST} by geographic distances. Thirty-two regression coefficients subsequently calculated between matched samples again suggest concordance (r=0.68). Unsurprisingly, large R^2-values are associated with sub-Saharan Africans, including one from East Africa (R^2=0.62 dental; R^2=0.75 genomic)—commonly promoted as the source of Late Pleistocene out-of-Africa diffusion. However, R^2-values from the abovementioned San are greater, i.e., two dental samples R^2=0.83 and 0.85, and matched genomic pairs, R^2=0.88 and 0.87 (all r>0.9). Samples of southern African 'Bantu' populations with significant Khoesan admixture, e.g., Tswana (0.82 and 0.83), also have higher R^2-values than the East Africans. The takeaway message, then, is that like genomic, dental data are reliable for identifying past population movement. Additionally, as some maintain, South Africa cannot be ruled out as the ultimate source of the diffusion.

Data collection by the first author was funded by the National Science Foundation (BNS-9013942, BNS-0104731, BCS-0840674), the ASU Research Development Program, and the American Museum of Natural History.

Correlating leaping frequency with primate hip and knee morphology

SPENCER W. IRVINE[1], ALICE L. ZHANG[1] and ERIC J. SARGIS[1,2]

[1]Anthropology, Yale University, [2]Vertebrate Zoology, Yale Peabody Museum

Many primates leap to cross gaps in the canopy in search of food and mates or to avoid predators. Across primates, leaping frequency varies from 0% to 65%. These locomotor differences are reflected in their skeletal morphology; several features of the hip and knee have been associated with leaping performance, including a longer ilium, shorter ischium, deeper femoral condyles and patellar groove, and more proximal positions of the lesser and third trochanters. To determine which features are correlated with degree of leaping in primates, we analyzed 47 Yale Peabody Museum specimens comprising 23 species with a broad range of locomotor behaviors. We recorded 32 linear measurements of the innominate, proximal femur, distal femur, and proximal tibia for each specimen. We standardized these measurements with a body size proxy, conducted principal component analyses (PCA) for each element, and performed correlation analyses and linear regressions to assess the relationship between morphology and leaping frequency. Seven linear measurements are strongly and significantly correlated with leaping frequency, with femoral condyle depth having the strongest correlation. PC1 is significantly correlated with leaping frequency for all elements except the innominate, with overall distal femoral morphology most strongly correlated (R^2 = 0.65). These results reaffirm the importance of primate hip and knee functional morphology to leaping ability. The correlations can be applied to better predict leaping frequency in primates that lack behavioral data, including fossils, beyond assigning them to broad locomotor categories. This can ultimately help test the grasp-leaping hypothesis for primate origins.

Research was supported by the Yale Institute for Biospheric Studies (YIBS) Small Grants Program, YIBS Graduate Research Fund, Yale Peabody Museum Summer Internship Program, and the Alan H. Smith Fund.

Seasonality in activity budgets and cathemerality across the 24-hour cycle in two Malagasy lemurs, and the impact of methodological choices on interspecific comparisons

MITCHELL T. IRWIN[1,4], VOLOLONIRINA RAHALINARIVO[2], HAJA F. RAKOTOMANANA[3], JEANNOT RANDRIANASY[2], JEAN-FREDDY RANAIVOARISOA[2], BRUNO RAMORASATA[4], JEAN-LUC F. RAHARISON[4] and KAREN E. SAMONDS[5]

[1]Anthropology, Northern Illinois University, [2]Anthropobiology and Sustainable Development, University of Antananarivo, [3]Zoology and Animal Biodiversity, University of Antananarivo, [4]Research, NGO Sadabe, [5]Biological Sciences, Northern Illinois University

A species' overall activity pattern includes both its activity budget, and the timing of activity in the 24-hour cycle (diurnal/nocturnal/cathemeral). Interspecific and inter-season comparisons can reveal aspects of adaptive strategies, including responses to pressures like predation, competition, thermoregulation, digestive constraints and sociality, yet comparisons are often hampered by differing methods. We documented 24-hour activity for two lemurs (the frugivorous *Eulemur fulvus* and the folivorous *Propithecus diadema*) across 17 months at Tsinjoarivo, Madagascar, using instantaneous sampling. Activity budgets were dominated by resting (*E. fulvus*: 73.3%; *P. diadema*: 85.2%), followed by feeding (16.9%, 12.4%) and travel (9.03%, 1.74%). The lower feeding but higher resting in *P. diadema* likely reflects slower gastrointestinal transit, allowing fermentation of fibrous food. *E. fulvus* showed a strong lean season shift (more feeding, less travel; "energy maximizing") while *P. diadema* showed a trend in the opposite direction ("time minimizing"). *E. fulvus* was cathemeral (4.9x more activity in daylight/twilight than in nighttime); seasonal variation was complex, but nocturnality decreased with increasing frugivory, suggesting that non-fruits promote night feeding. Both species' strategies pivot around fruit: for *E. fulvus*, activity level (mainly travel) increased with fruit availability. For *P. diadema*, activity increased with percent frugivory but not fruit availability (perhaps only few fruits are suitable). Comparisons between the species were only possible by extrapolating nighttime rest in the *P. diadema* dataset. Primatologists traditionally calculate time budgets by expressing time as a percentage of observed/active time; only by using a 24-hour period can we make meaningful comparisons among species, populations and seasons.

Funding from National Geographic CRE, Eppley Foundation for Research, Northern Illinois University, IdeaWild.

Futures of Bioarchaeology and Personhood: Osteobiography of Two Individuals from the Hamann-Todd Collection

KENDRA B. ISABLE and MARIN PILLOUD

Anthropology, University of Nevada, Reno

As bioarchaeologists imagine new futures of the discipline, we can also image new ways of engaging with the dead. A reimagining of this future may include acknowledging the full personhood of the individual with respect to their life history and lived experiences. As researchers we can embrace the documented resources of these individuals to better tell their stories. Therefore, this research aims to present osteobiographies of two individuals from the Hamann-Todd Human Osteological collection with this agenda in mind.

These two individuals were chosen as they both have severe linear enamel hypoplasia and extensive antemortem fracturing with areas of active healing. Their osteobiographies highlight the number of fractures, location of the fractures, types of fractures, and the degree of healing in each individual. These are then interpreted in conjunction with the linear enamel hypoplastic defects that are an indicator of childhood stress and may have increased their disease vulnerability, survivability, and overall quality of life. Thereby, the Developmental Origins of Health and Disease (or DOHaD) is employed as a framework to interpret these pathological conditions. The records of these individuals are also consulted to more broadly tell the stories of these men. Ultimately, this research will try to move past mere description and quantification of pathological conditions within populations as a sign of frailty and/or poor health, but rather move towards a praxis that incorporates lived experiences to understand resilience within marginalized populations.

Big Brain Energy: The Metabolic Contributions of the Gut Microbiome and its Implications for Encephalization in Early Homo

HANNAH C. JACOBSON

Department of Anthropology, Northwestern University

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Homo sapiens remain atypical within the primate lineage due to their large brain to body size ratio and unique life history traits. Previous literature has suggested that an increasingly high-quality diet and bipedal movement around 2 MA provided the energy increase necessary for encephalization, but the archaeological record shows that encephalization, high-quality diet, and bipedalism do not coincide with one another. This suggests other factors were important in reorganizing or increasing the energy budgets of early *Homo,* such as the gut microbiome.

The gut microbiome has coevolved with their hominin hosts and contributes to host metabolism and energy supply, which is often overlooked in paleoanthropology and has not yet been codified into theories of hominin evolution. The metabolic contributions of the gut microbiome may have played an important role in producing the energy surplus needed to support encephalization in early *Homo*.

Here, I present results from a secondary statistical analysis of human fecal microbiome data from 2 KA in the U.S. midwest to clarify the structure of microbes and their function in the host's energy economy prior to the industrialization process of agriculture that significantly altered modern gut flora. Results show that the ancient samples were enriched with bacteria specialized for short-chain fatty acid production, an important metabolite that contributes to host energy supply. This finding indicates that ancient human microbiomes contributed to their host's energy economy differently than in contemporary times, allowing predictions to be made for how ancestral gut structure and function impacted hominin evolution.

Influence of substrate variation on limb joint kinematics in wild primates

JUDITH JANISCH[1], ALLISON MCNAMARA[2], NOAH T. DUNHAM[3], TAYLOR PHELPS[1], LYDIA C. MYERS[2], NICOLE SCHAPKER[1,4], TYLER WILLARD[1], LIZA J. SHAPIRO[2] and JESSE W. YOUNG[1]

[1]Department of Anatomy and Neurobiology, Northeast Ohio Medical University, [2]Department of Anthropology, University of Texas at Austin, [3]Conservation and Science Department, Cleveland Metroparks Zoo, [4]School of Biomedical Sciences, Kent State University

The arboreal environment places multiple challenges on primates when moving over narrow, compliant, angled, and disparate supports. Previous research has shown that captive primates often respond to narrower and steeper supports by flexing limb joints (thereby lowering the center of mass) and adopting a compliant gait, marked by increased proximal joint excursions and increased yield at distal joints (thereby flattening the center of mass trajectory). In this study we tested if these strategies are also adopted by wild primates – including four species of platyrrhines, three species of catarrhines and three species strepsirrhines – freely ranging over a variety of supports in their natural habitats. We used ImageJ to measure the angular kinematics of forelimb and hindlimb joints from high-speed videos of quadrupedal locomotion on a variety of arboreal supports. Pearson product-moment correlations were used to test for associations between joint posture and support diameter/inclination (measured using a forestry-grade rangefinder). Preliminary results confirm previous kinematic studies of captive primates and suggest that in *Papio anubis*, *Cercopithecus l'hoesti* as well in *Saimiri sciureus,* variation in support orientation as well as diameter influence quadrupedal gait kinematics when moving in their natural habitat. Substrate properties were not significantly related to kinematic variation in any of the other species. This suggests that there might be other locomotor adaptations in place to overcome the challenges of the precarious environment.

Supported by NSF BCS-1921135, BCS-1921314, BCS-1640552 and BCS-1640453.

Neolithic human remains from Ljubićeva pećina (Istria, Croatia)

IVOR JANKOVIĆ[1,2], JAMES CM. AHERN[2], VALENTINA MARTINOIA[3], MARIO NOVAK[1], RORY BECKER[4] and SANJIN MIHELIĆ[5]

[1]Centre for Applied Bioanthropology, Institute for Anthropological Research, Zagreb, Croatia, [2]Department of Anthropology, University of Wyoming, Laramie, USA, [3]Department of Archaeology,, Simon Fraser University, Canada, [4]Department of Anthropology and Sociology, Eastern Oregon University, USA, [5]Archaeological Museum in Zagreb, Croatia

Excavations at Ljubićeva pećina (Istria, Croatia) site yielded archaeological material from various prehistoric periods (Paleolithic to Iron Age), including human skeletal remains. Here we report preliminary results of the bioarchaeological and stable isotope analysis of Neolithic human sample from the site.

Nine, and possibly 13 skeletal elements can securely be ascribed to the Neolithic. Based on the morphological characteristics, including the duplication of skeletal elements and age assessment, the MNI is 5. Three of the bones were directly dated to between 6938 and 6621 cal BP (1 σ), which corresponds to the Early Neolithic in the region. Random spatial distribution and fragmentary state of the remains, make it unclear if the remains were accumulated as a result of burial practices.

Stable isotope results (carbon and nitrogen) for the three individuals of different ages have been compared to the Early Neolithic data from eastern Adriatic sites (Kargadur, Vela Spilja on Lošinj, Crno Vrilo, and Vela Spila on Korčula). The adult from Ljubićeva pećina displays similar $d^{13}C$ and $d^{15}N$ values to the individuals from the comparative samples, suggesting a terrestrial based diet. The relatively high $d^{15}N$ levels displayed by the infant from Ljubićeva pećina are similar to those observed for the individual from Vela Spilja on Lošinj, and are consistent with breastfeeding. Conversely, the juvenile from Ljubićeva pećina displays the lowest $d^{15}N$ values of all the comparative specimens, suggesting a purely C_3 diet with either a very little intake of terrestrial protein or the consumption of very low trophic level foods.

This work was supported by the Croatian Science Foundation [grant number HRZZ IP-2019-04-7821]. Stable isotope analysis was done at Dr. Michael Richards' Stable Isotope Lab (Simon Fraser University, Burnaby, Canada)

Kin availability and mortality among older adults in nineteenth and early twentieth century Utah and North Orkney, Scotland

JULIA A. JENNINGS[1] and KEN R. SMITH[2,3]

[1]Anthropology, University at Albany, [2]Family and Consumer Studies, University of Utah, [3]Population Sciences, Huntsman Cancer Institute, University of Utah

Kin are important sources of support for older adults, and a rich literature focused on contemporary populations demonstrates that support is associated with improved health for this group. Less is known about whether these associations existed in the past, either before or during the demographic transition, when mortality and morbidity patterns were changing along with the size and structure of families. Few contemporary datasets include full genealogical information, limiting the measurement of kin networks. We examine kin availability and its association with mortality among older adults in historical Utah (N=90,582) and North Orkney, Scotland (N=3,339). These regions were predominantly agrarian, yet they provide contrasting contexts that may affect the role of kin support for older adults. Utah was a frontier region with high land availability, high nuptiality, and high fertility while Orkney was near demographic saturation with low land availability, lower nuptiality, and early fertility decline. Using discrete-time event history models of mortality, we find differences in relationships between counts of kin types and mortality within and between populations. Effects of kin are pronounced for closer kin, with effect sizes decreasing as genetic distance increases. In Utah, siblings were associated with lower mortality for most sociodemographic groups. In Orkney, siblings were associated with elevated mortality for some groups. These differences may reflect the social and economic challenges faced by

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

unmarried siblings who did not inherit land and were often not housed by relatives as they aged in Orkney and patterns of familism and religious adherence in Utah.

National Institute on Aging (K01AG055664), University at Albany Faculty Research Award Program (FRAP-A), University of Utah Huntsman Cancer Institute, National Cancer Institute (P30CA2014)

The mosaic framework of sex/gender

DAPHNA JOEL

Psychology, Tel Aviv University

The suggested talk is part of an invited symposium: Born Which Way? Biological and Genetic Engagement in Sex, Gender, and Sexuality Research.

In it, I will review my work in the past decade on the brain and gender mosaic. The mosaic hypothesis builds on animal studies which showed that the effects of sex on the brain may be opposite under different conditions, and holds that as a result of these complex interactions, sex effects do not add-up consistently in individuals to create 'male' and 'female' brains or 'natures'. Instead, each brain is comprised of a unique mosaic of both female-typical and male-typical features. Analyses of the structure of over 20,000 human brains support the mosaic framework and further reveal that the brain architectures typical of women are also typical of men, and vice versa, and that sex category provides very little information regarding how one brain will differ from or resemble another brain. Similarly, analyses of attitudes, preferences, and behaviors of over 15,000 individuals reveal that each individual possesses a unique mix of both feminine and masculine psychological traits.

The mosaic framework is orthogonal to the question of nature versus nurture and defies the mainstream binary understanding of sex, brain, and gender. In particular, it refutes the common binary interpretation of sex/gender differences in brain and behavior as evidence that men and women belong to different "kinds" – an interpretation which promotes a *biological-essentialist* approach to gender and perpetuates non-egalitarian gender ideology.

This work was partly supported by the Israel Science Foundation (grant No. 217/16) and by an ERC Advanced grant 101054741 BeyondGenderBinary

Comparison of field methods to estimate number of howler monkey (*Alouatta palliata*) groups at La Selva Research Station, Costa Rica

CHRISTOPHER E. JOHNSON[1], AMY L. SCHREIER[2], ISABEL PACHECO[3], ORLANDO VARGAS[4] and MICHAEL D. WASSERMAN[1]

[1]Anthropology, Indiana University, [2]Biology, Regis University, [3]Environmental Science & Policy, St. Edward's University, [4]La Selva Research Station, Organization for Tropical Studies

Globally, 60% of primate populations are threatened with extinction, indicating how imperative it is to understand current population numbers to inform conservation efforts. A howler monkey (*Alouatta palliata*) census was last conducted at La Selva Research Station, Costa Rica, in 1992 by Kathryn Stoner using a standard triangulation method to estimate the minimum number of howler groups. We conducted a follow-up census in May 2022 at La Selva to collect location and distance data of howler monkey calls. Located across the 16ha forest, 24 volunteer pairs recorded when a call was heard, the direction angle (degrees) it was coming from, and a distance category of the call (close: 0-100m, middle: 100-1000m, and far: 1km+). Data from this census were visualized and analyzed using GIS in three ways: 1. Displaying calls from self-mapped locations, 2. Generating points using angle and distance category data, and 3. Displaying vectors using angle and distance category data. Preliminary analysis estimated 28, 27, and 27 groups, respectively, and a point cluster analysis of the distance category map estimated 27 groups. A broad census primate survey of 1km line transects from the summer of 2022 yielded a howler group encounter rate of 0.14 ±0.06 (SE), predicting total group numbers to be 13 – 32 (average: 22.5). While there is variation across these field methods and analyses, results suggest that current howler group numbers are higher than Stoner's 15 groups in 1992, further highlighting the importance of conserving an old-growth tropical forest to protect a vulnerable primate species.

Oral microbiomes of ancestral Native American individuals reveal bacterial diversity in the pre-Colonial era

SARAH J. JOHNSON[1,2], CARA MONROE[1,2,3], TANVI P. HONAP[1,2], ALAN LEVENTHAL[4,5], MONICA V. ARELLANO[5] and CECIL M. LEWIS[1,2,3]

[1]Department of Anthropology, University of Oklahoma, [2]Laboratories of Molecular Anthropology and Microbiome Research (LMAMR), University of Oklahoma, [3]Center for the Ethics of Indigenous Genomic Research (CEIGR), University of Oklahoma, [4]Department of Anthropology, San Jose State University, [5]Muwekma Ohlone Tribe

Periodontal pathogens are a perpetual threat requiring daily intervention to reduce the risk of disease. Surprisingly, we know little about the microbiome dynamics, biogeography, and history of these organisms. As part of a consortium of community-focused studies, and in partnership with the Muwekma Ohlone Tribe, the Native American Heritage Commission's Most Likely Descendant Tribe, we studied the oral microbiomes and putative oral pathogens of Ancestors (n=38) from twelve ancestral heritage cemetery sites dating to approximately 3670-650 YBP. These hunter-gatherers had a diet heavy in starch from acorn and seed consumption. With permission from the tribal leadership, DNA was extracted from dental calculus and partially treated with uracil deglycosylase. Double-stranded DNA libraries were prepared and shotgun-sequenced with Illumina technology. Samples from 36 individuals displayed an oral signature, of which 34 were authenticated to be of ancient origin. To the best of our knowledge, this represents the largest oral metagenome dataset from a single geographic area pre-dating European contact in the Americas. Opportunistic oral pathogens were identified at sufficient coverage for reconstruction and phylogenetic analysis in some individuals, including *Tannerella forsythia* and *Pseudoramibacter alactolyticus*. Commensal oral microbes were also identified, including Anaerolineaceae bacterium oral taxon 439 and *Methanobrevibacter oralis*. Situating these organisms within an ancestral Native American community contributes to the understanding of factors that have contributed to devastating oral diseases. Adding to the compendium of oral microbial communities prior to agricultural transitions and colonial expansion provides an additional layer to the investigation of how such major events can impact oral health.

This work was funded by a National Science Foundation grant titled "Hominid Dental Metagenomes for Pathogen Evolution Research" (NSF BCS-2045308)

Variation in the flexor sheath ridge morphology of primates

SARAH N. JOHNSON and JOHN HAWKS

Anthropology, University of Wisconsin-Madison

Primate hands are often in direct contact with the substrate during movement and are well-adapted to their locomotor role. Longitudinal curvature of manual phalanges correlates with arboreal versus terrestrial substrate use. Less attention has been focused on other aspects of phalangeal shape. A recent study suggests that flexor sheath ridge morphology has biomechanical importance for reducing strain, but variation in flexor ridge morphology has not been fully documented. Here we examine the variation in flexor sheath ridge morphology across 30 species of extant primates, using both linear measurements and a landmark-based approach. We analyze this variation within a phylogenetic comparative framework to find the relationship between these morphological variables with curvature and locomotion. Locomotor strategies are considered not only on arboreal and terrestrial substrates but also in terms of their actual hand positioning such as digitigrade and palmigrade positioning and suspension, brachiation, and other climbing grips. The results indicate that the arboreal-terrestrial contrast in locomotor strategies does not capture all relevant correlations between phalangeal

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

morphology and locomotor use of the hands. The phylogenetic relationships of species also inform the manner in which morphology reflects locomotion. The three broad categories observed in flexor sheath ridge morphology include dorsoventrally tall ridges with a concave palmar surface, mediolaterally flared ridges with a convex palmar surface, and primates that do not exhibit any notable ridge development with a flat palmar surface along the entire shaft.

Leveraging genomic signals of natural selection to identify genotype-phenotype associations in Andean highlanders

KELSEY C. JORGENSEN[1], MELISA KIYAMU[2], GIANPIETRO ELÍAS[3], JENNA ISHERWOOD[4], OBED A. GARCIA[5], KATARINA EVANS[6,7], MARIA INCLAN[8], FRANK S. LEE[9], MARIA RIVERA-CHIRA[2], FABIOLA LEON-VELARDE[2], MARK SHRIVER[10], LAUREL PEARSON[10], TOM D. BRUTSAERT[3] and ABIGAIL W. BIGHAM[1]

[1]Department of Anthropology, University of California, Los Angeles, [2]Departamento de Ciencias Biológicas y Fisiológicas, Universidad Peruana Cayetano Heredia, [3]Department of Exercise Science, Syracuse University, [4]Department of Anthropology, University of Michigan, [5]Department of Biomedical Data Science, Stanford University, [6]Department of Anthropology, City University of New York (CUNY), [7](NYCEP), New York Consortium in Evolutionary Primatology, [8]Department of Political Studies, Centro de Investigación y Docencia Económicas, [9]Department of Pathology and Laboratory Medicine, The University of Pennsylvania, [10]Department of Anthropology, The Pennsylvania State University

For part of the symposium: Toward a holistic approach - Investigating the genetic underpinnings of phenotypic variation. Human populations in the Andean highlands have thrived at high elevations for thousands of years despite the environmental challenge of low oxygen, or hypoxia. Recent research has demonstrated evidence of genetic adaptation to high altitude. However, the precise genetic variant(s) contributing to the functional physiological responses to hypoxia remain elusive. We leveraged the power of whole-genome sequencing to identify genotype to phenotype associations in Andean highlanders related to adaptive hypoxic regulation. We recruited (n=48) Peruvian Andean participants from Cerro de Pasco, Peru (4,330m) and (n=48) lowland Mexican Maya speakers from Palenque, Chiapas, Mexico (71m). After applying several standard statistical tests to detect signatures of natural selection among Peruvian Andeans, we discovered novel variation in regions associated with oxygen sensing and metabolism including transcriptional regulation of oxygen homeostasis. We then characterized the functional impact of the significant SNPs using a combination of tools including Encode data, the GTEx database, and an in silico functional analysis. From these results, we then tested the top significant genetic regions predicted to have functional protein consequences for association with altitude-adapted phenotypes including arterial oxygen saturation, hemoglobin concentration, and maximal oxygen consumption during exercise (VO2max). Through these genotype to phenotype association analyses, our research expands current understandings of how genetic variation drives phenotypic responses to high-altitude hypoxia in Andeans.

Data collection for this project was funded by the National Science Foundation grant BCS-1132310 (T.D.B., F.L., and A.W.B.).

Evidence for positive selection in relation to tuberculosis in Ecuadorian high-altitude populations before European contact

SOPHIE K. JOSEPH[1], ALESSANDRO ACHILLI[2], NICOLA RAMBALDI MIGLIORE[2], ANNA OLIVIERI[2], ANTONIO TORRONI[2], AMANDA OWINGS[3], MICHAEL DEGIORGIO[4], WLADIMIR GALARZA ORDÓÑEZ[5], J.J. ORTIZ AGUILÚ[6], FABRICIO GONZÁLEZ-ANDRADE[7] and JOHN LINDO[1]

[1]Department of Anthropology, Emory University, [2]Department of Biology and Biotechnology "L. Spallanzani", University of Pavia, [3]Department of Biology, University of Iowa, [4]Department of Electrical Engineering and Computer Science, Florida Atlantic University, [5]Centro de Estudios, Investigaciones y Trabajos Arqueológicos (CEITA), [6]Universidad Técnica de Manabí, [7]Translational Medicine Unit, Central University of Ecuador, Faculty of Medical Sciences

Despite ongoing genomic studies from the Andean highlands of Peru, high-altitude adaptation in the region is still poorly understood from a genetic perspective. To grasp a more diverse perspective on how this adaptation occurred, we present whole genomes from high-altitude Indigenous populations from Ecuador. Utilizing haplotype, allele-frequency, and admixture-aware methods, we scanned the genomes for putative signals of selection that may correlate with the hypoxia adaptation. We identified regions of the genome that show signals of strong selection to both cardiovascular and hypoxia pathways, which are distinct from those uncovered in Peruvian populations. However, the strongest signals of selection were not related to these pathways, but instead to regions of the genome that are involved in immune function related to tuberculosis. We further present evidence that the timing of the selection event occurred thousands of years before the arrival of Europeans, suggesting that *M. tuberculosis* was not only present in the region, but the Indigenous people of Ecuador have also adapted to this bacterium.

This work was funded by National Geographic Society GR-000043627, NSF BCS-1926075, BCS-1945046, BCS-2001063, DEB-1949268, and DBI-2130666, NIH R35GM128590, and Italian Ministry of Education, University and Research (MIUR) for PRIN2017 20174BTC4R.

Analyzing interrater reliability using the Refined Classification system for Thermally Damaged Human Remains by Body segment

CHELSEY JUAREZ[1], ELAYNE POPE[2] and ALISON GALLOWAY[3]

[1]Anthropology, Cal State Fresno, [2]Forensic Anthropology, SLO FIST inc., [3]Anthropology, University of California Santa Cruz

Eight forensic anthropologists each participated in scoring a series of twenty photos of burned human remains using the Pope et al., (2022) Refined Classification System for Thermally Damaged Human remains by body segment method. The goal of the project was to test the ease of use of the method, and to assess the interrater reliability of the method. All eight participants held PhD level education and seven were Diplomats of the ABFA. Participants were asked to use the six-stage scoring system with illustrations to consider and score the changes the body and body position. Study participants were able to indicate a number (1-6) and letter score denoting early or late-stage changes for each body segment.

Interrater reliability- the level of agreement between judges- was assessed using Interclass correlation in JMP PRO 16 for Mac OES assuming absolute agreement. In total, there were 160 scores provided over four body segments for twenty photos. The interclass correlation coefficient calculated for all 160 scores assuming absolute agreement was 0.907 indicating excellent reliability between study participants using the classification system.

Study participant notes indicated that certain body portions had differing levels of scoring difficulty. An investigation of ICC for each body segment individually revealed variation in reliability ranging from 0.80 for the head to 0.966 for the lower limb. An ANOVA indicated that the variation between the study participants scores was not statistically significant (p=0.06). The largest variance found between participants (0.78) was found in scoring the torso.

Pastoral subsistence among Jordanian nomads during the Ottoman Period (1299-1922 CE), Jordan

MARGARET A. JUDD[1], CLAIRE E. EBERT[1] and LESLEY A. GREGORICKA[2]

[1]Anthropology, University of Pittsburgh, [2]Sociology, Anthropology, & Social Work, University of South Alabama

Scholars propose a multi-resource subsistence among nomadic groups and a symbiotic product exchange with sedentary communities likely, resulting in similar diets. Using stable carbon and nitrogen isotope analysis we test the hypothesis that multiple-resource subsistence and product exchange is supported for Ottoman (1299-1922 CE) adult nomads interred at Khirbet al-Mudayna

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

(KM) and Tall Jawa (TJ) (n=18) in Jordan, when compared to Iron Age II (~1000-539 BCE) townsfolk recovered from a KM burial chamber (n=9) and presumably sedentary individuals recovered from a rural Ottoman cemetery at Tall er-Rumeith (TR) (n=3).

Nomads had similar mean $\delta^{13}C$ values (KM = −16.2 ± 1.5‰; TJ = −16.1 ± 0.1‰), which were statistically significant compared to mean $\delta^{13}C$ values for the Iron Age II (−18.7 ± 0.2‰, $t = 2.4$, $p < .05$) and TR (−18.7 ± 0.8‰, $t = 5.3$, $p < .05$) people. Nomads had a higher mean $\delta^{15}N$ value (+11.8 ± 1.4‰) and a broader spread of $\delta^{15}N$ values (+9.9 to 15.2‰), but the mean $\delta^{15}N$ values were not significantly different between the groups. The nomadic diet represents a mixed C3/C4 diet with higher C4 foods compared to the Iron Age II and TR individuals. The narrow range of $\delta^{13}C$ values (−19.3 to −18.1‰) suggests a homogenous diet for non-nomads. Multi-resource subsistence with agricultural product exchange is not supported for the Ottoman nomads when compared to Iron Age II and rural Ottoman groups. This work adds to the limited bioarchaeological knowledge of marginalized Jordanian nomads.

Wenner-Gren Grant #9786

Testing hypothesis about modularity related to chewing biomechanics in the hominine skull

HYUNWOO JUNG[1], DAVID STRAIT[2,3], CAMPBELL ROLIAN[4] and KAREN L. BAAB[1]

[1]Department of Anatomy, Midwestern University, [2]Department of Anthropology, Washington University in St. Louis, [3]Palaeo-Research Institute, University of Johannesburg, [4]Department of Anatomy and Cell Biology, McGill University

Testing hypotheses about functional modules is a crucial step in understanding how functional integration potentially constrains or facilitates morphological evolution in hominines (African apes and humans). Here, we test the hypothesis that functional modularity is altered in *Homo sapiens* compared to the two African ape species. This hypothesis applies whether stabilizing selection or phenotypic plasticity is the primary driver of functional modularity. Stabilizing selection may be weaker in *H. sapiens* given the evolutionary shift toward a more processed and less mechanically-resistant diet. Moreover, the agricultural diet of the Nubian population studied here results in a different loading environment compared to apes.

26 linear dimensions of the cranium and 17 linear dimensions of the mandible were obtained from 3D coordinates in *Homo sapiens* (n=119 cranium, 89 mandible), *Pan troglodytes* (n=81 cranium, 79 mandible), and *Gorilla gorilla* (n=101 cranium, 92 mandible). Dimensions were grouped into five and four functional modules in the cranium and mandible, respectively, reflecting jaw adductor size, jaw lever mechanics, jaw gape, bony reinforcement, and tooth crown mechanics. We used the covariance ratio effect size (Z_{CR}) to directly compare the strength of modular signal across species.

Results were inconsistent with the hypothesis insofar as the strength of modularity did not differ significantly ($p > 0.05$) across taxa for any module in the cranium or mandible. The general congruence across species suggests that functional modules were already present in hominine ancestors and may have been important factors shaping the tempo and direction of morphological evolution in the hominine skull.

This study was supported by the National Science Foundation under grant BCS-2019669.

How does heat affect cut-marks? An Experimental study of cooked and uncooked bones for taphonomic signatures

PENINA E. KADALIDA

Anthropology, University of Minnesota, Twin cities

How can researchers solve the problem of "equifinality" (*i.e.,* different processes resulting in identical or near identical outcomes) in the study of bone surface modification? Studying the present to understand the past is fundamental to taphonomy. This often involves making experimental observations of how faunal remains are modified to infer analogous past scenarios. For some years, experimentations on the cut-marks have played a significant role to researchers interested in butchery, tools use, the meaning of surface modifications, and how environmental factors affect faunal remains. However, little attention has been paid to how heat affects cut-marks, and how this can hinder taphonomic interpretations.

Here we present results from an experimental study on cut-marks' morphology on cooked and uncooked bones to understand how heat can affect taphonomic signatures. Ten cow bones were defleshed using lithic tools, thirty cut-marks were made, dry roasted for six hours under 232.2,ÑÉ., and images were captured before and after heating using the Reflectance Transformation Imaging (RTI) technique. Observations were made on attributes including the presence of shoulders, grooves, microstriation, cut-mark shape and dimensions, and bone color.

Results show that after heating, the walls of the cut-marks remained slightly smooth and recognized, groove depth and shape were reduced, and slightly changed from V to U-shaped, and microstriation was removed. This research serves as a basis for reasoning by analogy to better understand the meaning of modifications on faunal remains after the invention of fire and highlights the need for care to be taken when interpreting ancient bones.

This conference will be funded by the Department of Anthropology from the University of Minnesota and the Wenner-Gren Foundation.

Culture as an added value metric for chimpanzee conservation

AMMIE K. KALAN

Department of Anthropology, University of Victoria

Recent calls in the academic literature have highlighted the potential utility of animal cultures for the conservation of wild populations. However these appeals have elicited more questions than answers, especially regarding the practical implications of applying a concept such as culture in a field where conservation metrics such as population viability and genetic diversity are considered essential. Here, I first review the underlying arguments and common tenets of multiple researchers advocating for the importance of behavioural or cultural diversity for animal conservation, drawing particular attention to examples relevant to wild chimpanzees, *Pan troglodytes*. Second, I summarize recent international efforts by multiple organizations to highlight the significance of culture for applied wildlife conservation, again focussing on chimpanzees. Finally, I evaluate the strengths and challenges associated with including culture as an additional conservation metric, relying on my personal experience as a current member of multiple chimpanzee conservation initiatives. Overall, by presenting the myriad of ways in which culture has been operationalized and described in the context of wildlife conservation, I draw attention to how a single approach to this issue is untenable and flexible solutions must be sought. Ultimately, I aim to stimulate a broader discussion in the primatological community on the ways in which culture may contribute to current conservation efforts to facilitate the incorporation of behavioural and cultural diversity into primate conservation more widely.

Collaboration and Exchange: Generating reference datasets.

KELLY R. KAMNIKAR[1], DANIEL JIMÉNEZ[2] and JOSEPH T. HEFNER[3]

[1]Department of Anthropology, University of New Mexico, [2]Tantologia Forense, Instituto Nacional de Ciencias Forenses de Guatemala, [3]Department of Anthropology, Michigan State University

Research on craniofacial variation requires reference datasets. Modern reference datasets from the recently deceased (i.e., forensic cases) or living populations are especially pertinent to forensic anthropological research and analysis. Reference datasets often form the backbone

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

of analytical tools used to calculate population affinity estimates for unknown skeletal material. Gaps in reference datasets produce low likelihood statistics or unclear results, complicating analysis.

The dataset presented here comes from forensic casework in Guatemala developed through collaborative research between the Instituto Nacional de Ciencias Forenses (INACIF) de Guatemala and Michigan State University. Anthropologists at the INACIF receive casework from all over the country. These individuals are typically decomposed, skeletonized, and/or exhibit traumatic injury, thus requiring a more specialized examination by anthropologists. Cranial macromorphoscopic (MMS) trait data are collected from deidentified skeletal remains by the first author and later INACIF anthropologists. The goals of data collection are 1) to fill in a gap in cranial MMS trait data for Latin American populations outside the U.S.; 2) capture human variation pertinent to the U.S. forensic system and the migration crisis; and 3) test hypotheses related to violent deaths and the Guatemalan medico-legal system.

Collaboration between institutions for data collection, data sharing, and research illustrates the benefit of partnerships. Cranial MMS data will be added to the Macromorphoscopic Databank, housed at MSU, which holds cranial MMS data from geographically and temporally diverse populations. Data from the MaMD are freely provided to interested researchers.

Application of the auricular surface osteometric method for subadult sex estimation on a Medieval sex identified skeletal collection from Austria

FABIAN KANZ[1], CHRISTOPH REISINGER[1], SANDRA LÖSCH[2] and MARLON BAS[1]

[1]Center for Forensic Medicine, Medical University of Vienna, [2]Institute of Forensic Medicine, University of Bern

This study applied subadult osteometric sex assessment on the auricular surface of the ilium as originally proposed by Luna and co-workers in 2017 on a medieval sample from Austria.

The sample comprised 55 female and 48 male individuals, aged 0-18 years, retrieved from a 13th century mass-grave from St. Pölten (Lower-Austria), all previously molecular biologically sexed. Following the Luna protocol the dimensions DE, AD, FI and CF were measured on the auricular surface, DE/AD, FI/CF ratios were calculated, and sex estimated by discriminant function (DF) and logistic regression (LR). To identify significant sexual dimorphism Mann Whitney (U) and Kolmogorov Smirnov (Z) tests, as well as Pearson correlation (*r*) for the evaluation of the influence of age at death were performed with SPSS 26. Finally DF and LR sex predictions were counterchecked with molecular sexes to get accuracy rates for the applied method.

Both ratios for both sexes revealed similar means and standard deviations (DE/AD: female=0.893±0.278, male=0.884±0.257; FI/CF: female=1.152±0.457, male=1.110±0.459). Therefore unsurprisingly both ratios didn't present any significant dimorphic results but DE/AD showed age at death dependency (DE/AD: U=1269, p=0.736; Z=0.715, p=0.686; r=-0.340, p<0.001 and FI/CF: U=1261, p=0.696; Z=0.919, p=0.368; r=-0.131, p=0.187). Both sex predictors revealed an overall accuracy of 51.5% for DF (female=47.3%; male=56.3%) and only 44.6% for LR (female=25.5%; male=66.7%), low precision, far from reaching the minimum accuracy requirements of 75%.

The applied osteometric sex estimation method could not replicate the accuracy values for Medieval Austrian subadult skeletons that Luna and co-workers achieved with a modern Portuguese sample.

Howling for taller trees: Mantled howler monkeys (*Alouatta palliata*) howl more in forest interior than edge in Costa Rica

FRANCESCA V.E. KASER[1], C. ERIC JOHNSON[2], MICHAEL ENNIS[1], NYLA PETE[3], ISABEL PACHECO[3], MICHAEL WASSERMAN[2], LAURA M. BOLT[4,5] and AMY L. SCHREIER[1,5]

[1]Department of Biology, Regis University, [2]Department of Anthropology, Indiana University, [3]Department of Environmental Science and Policy, St. Edwards University, [4]Department of Anthropology, University of Toronto Mississauga, [5]Maderas Rainforest Conservancy

Howler monkeys rely on large trees for their folivorous-frugivorous diet, and males produce loud calls, at least in part, to defend valuable food resources. At La Selva Biological Station, a protected forest zone in Costa Rica, we explored the relationship between tree size and howling behavior in the forest interior and edge (defined as 100m from forest perimeter). Because forest interior typically has higher resource abundance than edge, we predicted that trees would be larger and taller in forest interior than in the edge, and that number of howls per bout, howl duration, and howl rate would be higher in the interior than edge because there are more fruit resources to defend in the former. We measured tree height and DBH along vegetation transects across both interior and edge zones (May-July 2022) and conducted all-occurrences sampling of howling behavior (November 2018-February-2019; May-June 2022). Tree height was greater in forest interior (16.0m) than edge (15.3m), but DBH was not (interior: 28.3m; edge: 31.3m). Number of howls per bout was significantly higher in the forest interior (39.9) than edge (23.4; p = 0.031). However, there were no significant differences in howl duration (interior: 140.6sec; edge: 148.7sec) and rate (interior: 0.6howl/hour; edge: 0.7howl/hour). Our results suggest that howler monkeys emit more howls per bout in forest interior to defend the taller trees there. Tree height, rather than DBH, may be a more salient indicator of fruit abundance for howler monkeys at La Selva.

Form and Function in the Neandertal Mandible

BRIAN A. KEELING[1] and ROLF QUAM[1,2,3,4]

[1]Department of Anthropology, Binghamton University (SUNY), Binghamton, NY 13902-6000 (USA), [2]Department of Human Evolution, Centro de Investigación UCM-ISCIII sobre la Evolución y Comportamiento Humanos, Avda. Monforte de Lemos 5, 28029 Madrid (Spain), [3]Division of Anthropology, American Museum of Natural History, Central Park West at 79th St., New York, NY 10024-5192 (USA), [4]Cátedra de Otoacústica Evolutiva y Paleoantropología (HM Hospitales-Universidad de Alcalá), Área de Antropología Física, Departamento de Ciencias de la Vida, Universidad de Alcalá, 28871 Alcalá de Henares, Madrid, Spain

The mandible in Neandertals and modern humans show several morphological differences, including the presence of derived features. We conducted a joint biomechanical and geometric morphometric shape analysis of the mandibular symphysis and corpus at the M_1/M_2 interdental septum on two-dimensional cross-sectional slices generated from μCT scans in 10 Neandertals, 9 Pleistocene *Homo sapiens* and 10 recent *Homo sapiens*. We found that Neandertals on average had significantly ($p < 0.05$) greater bending rigidity (J) and breaking strength (Zp) in the symphysis, but not the M_1/M_2, compared to *Homo sapiens* even when adjusting for size. We also found that these variables and the orientation of the largest bending resistance (theta) were also useful in taxonomically classifying these groups (92.9% for symphysis; 100% for M_1/M_2). Only size-adjusted cortical area and the ratio between the maximum and minimum bending rigidity significantly covaried ($p < 0.01$) with symphysis shape ($r = 0.722$), but not at the M_1/M_2. Further, canonical variate analyses of the Procrustes residuals for both the symphysis and M_1/M_2 demonstrated a high group classification accuracy (93%), while principal components analysis revealed some degree of shape variation. When evaluating the allometric influence on shape, we found no significant influence based on the Procrustes residuals. We also found that the symphysis and M_1/M_2 shapes significantly covaried (r-pls = 0.99, p = <0.01). This study represents a novel approach to elucidating the potential underlying adaptive basis for shape differences in the mandible of Neandertals and modern humans.

This research was partially funded by (SUNY) Binghamton University.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Investigating mummy bundles found at the Wari imperial site of Huaca del Loro, Nasca, Peru (650-1000 CE)

CORINA M. KELLNER, ETHAN BRAUNSTEIN and SUSAN BRAUNSTEIN

Anthropology, Northern Arizona University

Encountering elaborate archaeological mummy bundles or fardos in situ in Nasca, Peru is rare, but these remains help us better understand burial practices during a time of imperial conquest. Two recent field seasons at the Wari site of Huaca del Loro revealed new information on the relationship between Nasca and Wari during the Middle Horizon (650-1000 CE). We uncovered a D-shaped temple and an associated compound indicative of Wari presence and evidence of habitation areas to the east. Four individuals buried in a seated, flexed position wrapped in layers of textiles and cotton batting (mummy bundles or fardos) were encountered in the associated compound to the north. Elite individuals were usually treated in this way on the coast during the Middle Horizon. Two individuals were buried together in a small circular tomb marked by three posts, while two were outside this round structure and possibly associated with young camelid offerings. One individual buried outside the structure is a child, while the others are likely adults. Each has different textiles and offerings included with them. Radiography using X-ray analysis was used to examine the fardos. We found no evidence of the typical Nasca cranial vault modification or any major pathological lesions. However, one adult's burial treatment is smaller than the rest, with some indication that they may have been a secondary burial. We hypothesize that the compounds associated with this D-shaped temple were devoted to Wari ancestor worship.

Funding provided by the National Science Foundation #1758084

Testing the Respiratory-Energetics Hypothesis: An investigation of metabolic demands and nasal size across human populations

ALEXA P. KELLY and SCOTT D. MADDUX

Center for Anatomical Sciences, University of North Texas Health Science Center

While ecogeographic variation in nasal shape has long been attributed to climatic pressures, recent studies have hypothesized that variation in overall nasal size may be more strongly linked to metabolic demand. This "respiratory-energetics hypothesis" posits that larger individuals with greater metabolic requirements need larger nasal passages to ensure a sufficient intake of oxygen during normal breathing (eupnea). To test this hypothesis, we assessed nasal morphology in conjunction with body mass and basal metabolic rate (BMR) estimates derived from associated postcranial elements for 21 European, 43 Iranian, and 80 Arctic modern human adults. Sixty-six 3D-coordinate landmarks were collected from CT scans of each cranium, while postcranial measurements were physically collected from skeletal elements directly associated with each cranium. Body mass and climate-specific BMR were estimated from the postcranial skeleton using established formulae. These data were then employed in multivariate regression analyses to test for statistical associations between nasal morphology and metabolic factors. Results indicate that overall nasal size is significantly correlated with both body mass (Iran $p=0.035$; Europe $p=0.013$; Arctic $p<0.001$) and BMR (Iran $p<0.001$; Europe $p=0.006$; Arctic $p<0.001$) in each of the 3 groups. Subsequent analyses indicate significant correlations between metabolic variables and linear measurements of nasal height/length dimensions, but not breadth dimensions, in each group. These results support the basic tenets of the respiratory-energetics hypothesis and suggest that metabolic pressures on overall nasal size are primarily meditated by nasal height and length dimensions, while breadth dimensions are likely associated with climatic pressures for intranasal heat and moisture exchange.

National Science Foundation (BSC #2050253) to APK & SDM and the Wenner-Gren Foundation (#10009) to APK.

Enamel stable oxygen isotopes reconstruct precipitation changes and depositional environment variation in the Turkana Basin

MADELEINE KELLY[1], KRYSTAL KOSKI[2], SILINDOKUHLE MAVUSO[3,4], DAVID R. BRAUN[5] and ZERESENAY ALEMSEGED[1]

[1]Department of Organismal Biology and Anatomy, University of Chicago, [2]Department of Anthropology, University of Michigan, [3]Department of Geology, Rhodes University, [4]School of Geosciences, University of the Witwatersrand, [5]Center for Advanced Study of Human Paleobiology, The George Washington University

In the Plio-Pleistocene Turkana Basin, a paleoenvironmental trend of increasing aridification and expansion of open grassland habitats is commonly cited as influencing the emergence of morphological and behavioral adaptations that define the hominin lineage. These environmental changes were likely closely linked to variations in water availability, including precipitation changes and tectonically-mediated paleogeographic shifts between river- and lake-controlled systems. To investigate how these variations in paleohydrology are reflected by the mammalian community, we examine published stable oxygen isotope values ($\delta^{18}O$) of mammalian herbivore tooth enamel from the Shungura and Koobi Fora Formations. Given the complexities associated with interpreting $\delta^{18}O$ signals, we focus on community-scale variations in median $\delta^{18}O$ values. Grouped by geological member, median enamel $\delta^{18}O$ increases over time, potentially reflecting a trend toward greater aridity. This is interrupted by a period of increased precipitation around 2.0 Ma, inferred from a decrease in median $\delta^{18}O$. To explore how non-climatic shifts in hydrological systems are reflected in enamel $\delta^{18}O$, data were grouped by depositional environment using published stratigraphic descriptions and lithofacies analyses conducted in the field. Median $\delta^{18}O$ is greatest in fossil assemblages from lacustrine contexts, followed by those from fluvial and deltaic settings. However, this inferred association between enamel $\delta^{18}O$ and drinking water source is not necessarily consistent at the sub-member scale and may be confounded by time-averaging and altered precipitation patterns. These results indicate that comparing enamel $\delta^{18}O$ among fossil assemblages can reveal the ways in which hydrological variations facilitated paleoenvironmental heterogeneity at various spatial and temporal scales.

This research was supported by National Science Foundation Grant 1852441 Research Experiences for Undergraduates, Archaeology Program award BCS-1624398, University of Chicago Graduate Council, and U.S. Department of Education GAANN #P200A220020.

Methodological Advances in Cementochronology (TCA) for Taphonomically Altered Samples

SAIGE KELMELIS[1], THOMAS COLARD[2,3], STEPHAN NAJI[4], ERIC PUBERT[2], JULIE HOGGARTH[5] and JAIME AWE[6]

[1]Department of Anthropology and Sociology, University of South Dakota, [2]PACEA, University of Bordeaux, [3]Department of Oral and Maxillofacial Radiology, University of Lille, [4]Recovery Unit, Commonwealth War Graves Commission, [5]Department of Anthropology, Baylor University, [6]Department of Anthropology, Northern Arizona University

Taphonomic alteration to bone is a major source of variation/error for age estimation of archaeological samples. Dental tissues, especially tooth cementum annulations (TCA), are potentially more reliable to provide age estimation for highly altered skeletons. While TCA protocol exists for modern and well-preserved archaeological skeletons, there is no standard approach to creating TCA thin sections from archaeological teeth with severe taphonomic damage. For this study, we adapted a protocol for creating TCA thin-sections for monoradicular teeth from taphonomically damaged skeletons from four archaeological sites in the Belize (c. 250-900 CE). Twenty-seven permanent teeth were selected from 15 adults of unknown age of death. Thin-section preparation consisted of four main steps: (1) embedding the tooth in resin, (2) cutting-low-speed Isomet Buehler saw, (3) gluing the embedded tooth to slides, (4) finishing by coating each cut with resin to strengthen it and polishing. Results of this adapted protocol

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

suggests that taphonomically-altered teeth lack the same structural integrity as preserved teeth and requires a dedicated protocol. Observed variation in cementum preservation resulted from fungus and bacterial invasion of the cementum layers; however, many regions of interest were still preserved and visible enough to estimate a minimum number of TCA for age estimation. This new protocol demonstrates that it is possible to yield usable regions of interest from highly taphonomically altered teeth for age reconstruction from archaeological remains.

Funding for this research was provided by the first author through their research start-up.

Comparative perspective on gaze during naturalistic locomotion in humans

ADDISON D. KEMP and KRISTI L. LEWTON

Integrative Anatomical Sciences, University of Southern California Keck School of Medicine

Human gaze behaviors are proposed to facilitate efficient striding bipedalism, minimizing the additional energy required to cross uneven terrain by targeting future footholds that approximate an individual's preferred stride length and timing. Whether these gaze behaviors evolved because of the shift to bipedal locomotion in hominins, evolved in basal primates along with other locomotor and visual adaptations, or are shared more broadly across mammals is impossible to determine without comparative data. Cats are the only non-human mammal with existing data on gaze during naturalistic locomotion, and research into their gaze during locomotion has demonstrated temporal correlations between stride cycle events and gaze behaviors like fixations. This study evaluates temporal correlations of human gaze during locomotion to provide comparative context for the evolution of human gaze behaviors.

Gaze and kinematic data were simultaneously collected as subjects crossed terrain of variable complexity (n = 20 strides). Gaze data were collected using a calibrated wireless infrared optical gaze-tracking system. A 90 millisecond (6 frame) threshold was used to identify fixations, a gaze behavior in which the subject's gaze remains stationary within their surroundings, allowing the collection of detailed visual information. Like cats, humans spent more time fixated on the substrate when crossing more complex terrain ($p < 0.01$). Unlike cats, humans showed no significant correlation between stride cycle events and fixations ($p > 0.05$), suggesting that the patterns of gaze during locomotion seen in humans is not broadly shared across mammals, though it may have evolved either in hominins or earlier primates.

Morphological differences in the macaque upper limb

BRITTANY KENYON-FLATT[1,2] and NOREEN VON CRAMON-TAUBADEL[2]

[1]Department of Molecular Biomedical Sciences, North Carolina State University, [2]Department of Anthropology, University at Buffalo

Currently, there are 23 recognized macaque species throughout Asia and northern Africa. Previous research has suggested that some species are taxonomically distinct morphologically, however, the specific ways in which they differ is currently unknown. As such, we explored which morphological aspects of the macaque upper limb contributed to their taxonomic differences.

Data included 3D surface scans from eight macaque species (*M. arctoides, M. fascicularis, M. fuscata, M. mulatta, M. nemestrina, M. nigra, M. radiata, M. sylvanus*) representing different geographic locations for 257 individuals. Fixed anatomical and semilandmarks were applied to three skeletal elements from the upper limb for each individual (scapula=66; humerus=38; radius=33), and a regression analysis was performed to minimize the effects of sexual dimorphism. Between-groups principal components analyses were employed to visualize the average morphological differences among species, distance matrices describing morphological and genetic differences were compared using Mantel tests, and least-squares Procrustes rotations based on 2D multi-dimensional scaling plots helped visualize whether morphology tracked genetic centroids for a given species.

Results suggested that different macaque species have unique morphology, which correlated with genetic distances. Some species like *M. sylvanus* and *M. fuscata* tended to be more morphologically unique for all three upper limb bones. *M. radiata* had a particularly distinct radius, while *M. fascicularis, M. mulatta,* and *M. nemestrina* tended to exhibit a more general macaque form. These results may be useful for paleoanthropological studies when fossils belonging to unknown taxa are discovered, as this work supports taxonomic distinction in the upper limb among closely related species.

This research is supported by the National Science Foundation Grants (BCS-1945735, BCS-1830745, DBI-2010844), Field Museum Visiting Researcher Fellowship, Primate Research Institute Cooperative Research Grant, and the Mark Diamond Research Fund (SP-18-13).

Evaluating cortical bone speed of sound (SOS) measured by a non-invasive ultrasound bone sonometer as an alternative age-at-death indicator for elderly: a pilot study

JIEUN KIM[1], ERIN R. LESLIE[1], HADIAH KEDWAII[2] and RYAN ALLEN[2]

[1]Anatomy, Midwestern University, [2]Chicago College of Osteopathic Medicine, Midwestern University

Age-at-death estimation of the adult skeleton suffers from inaccuracy and bias due to decreasing predictability of traditional macroscopic age indicators past midlife. Of age-related changes in bone microstructures, the loss of cortical bone density is known to have onset past the 5th-6th decade of life which suggests its potential utility as an age-at-death estimator for the elderly. This study introduces the use of portable, medical quantitative ultrasound (QUS) that indirectly assesses BMD via the speed of soundwaves (speed of sound, SOS) traveling through radial and tibial cortical bone. The use of SOS as an objective metric to capture age-related bone loss on human remains is evaluated.

First, the applicability of QUS to human remains is assessed by comparing SOS values collected from intact anatomical cadavers and exposed bones of the same cadavers. Second, the study hypothesizes that the decrease in cortical bone density with increasing age is detected by SOS. A preliminary analysis on a pooled-sex sample (n=26) with ages ranging from 56 to 97 years indicates no significant difference between the intact-cadaver and exposed-bone SOS (p=0.5), suggesting its applicability to skeletonized remains. Piecewise regression indicates an accelerated decrease in the radial SOS past 91.5 years whereas the tibial SOS shows a steady decrease until 66 years followed by a gradual increase. Although SOS captures general age-related bone loss (and possible gain) in the oldest group, the study requires a larger, sex-specific sample representing more diverse age groups to fully evaluate the potential utility of QUS for age-at-death estimation.

More flex, more stress: Female stress responses to male social instability in wild *Colobus vellerosus*

ALLYSON G. KING[1], RUDY BOONSTRA[2,3], SUSANNE COTE[1], PHOEBE D. EDWARDS[2,3,4], RUPERT PALME[5], LORI SANDE[1] and PASCALE SICOTTE[1,6]

[1]Anthropology & Archaeology, University of Calgary, [2]Biological Sciences, University of Toronto Scarborough, [3]Ecology & Evolution, University of Toronto, [4]Psychology, University of Toronto Mississauga, [5]Biomedical Sciences, University of Veterinary Medicine Vienna, [6]Biology, Concordia University

Success for female primates necessitates an ability to appropriately assess dynamic environments and scale maternal investment accordingly.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Colobus vellerosus reside in groups of varying social structures and experience frequent male takeovers that can result in infanticide. When cues of social instability are present, we predict higher stress levels in females. We assess whether female fecal glucocorticoid metabolite (FGM) concentrations are associated with the number of males, the frequency of subordinate male presence in the group, and/or rates of agonistic male displays, vocalizations, and behaviors. From August-November 2019, we collected daily fecal (n=658), focal behavior (n=564), and *ad libitum* samples from ten adult females and three alpha males from three groups of wild *C. vellerosus* at Boabeng-Fiema Monkey Sanctuary, Ghana. We extracted fecal samples in the field and analysed FGMs with an enzyme immunoassay at the University of Toronto. Using AIC model selection, we compared the fit of competing GLMM models: female FGMs were best explained by models including group type, frequency of male presence, and male vocalizations. Females had lower FGMs if residing in unimale groups (estimate = -0.25, SE = 0.08) and when male vocalizations occurred more frequently (estimate = -0.77, SE = 0.23). More subordinate male presence was associated with higher female FGMs (estimate = 0.14, SE = 0.05). Our findings indicate that females actively monitor cues of alpha male strength and are stressed by unstable male social dynamics. Glucocorticoids may play a mechanistic role, enabling females to responsively invest in long-term reproduction despite fluctuating social environments.

Funding was provided by the Natural Sciences and Engineering Research Council of Canada (NSERC) and the University of Calgary.

Diving into dimensionality: Using multivariate methods to explore variation in intracortical bone area in a multi-scalar perspective

KATHERINE M. KINKOPF[1], TRENT M. TROMBLEY[2], SABRINA C. AGARWAL[2], JEFFREY A. SECKINGER[2], GIULIA RICCOMI[3], SIMONA MINOZZI[3], STEFANO CAMPANA[4] and VALENTINA GIUFFRA[3]

[1]Department of Geography and Anthropology, Cal Poly Pomona, [2]Department of Anthropology, UC Berkeley, [3]Paleopathology Division, University of Pisa, [4]Department of History and Cultural Heritage, University of Siena

Life-course approaches in bioarchaeology rely on deep and meaningful understandings of skeletal heterochronicity—the differential rates and timing of growth, development, and maintenance processes. However, comparisons of different bone tissue regions proves challenging precisely because of the heterogeneous quantity and quality of cortical bone throughout the skeleton. We analyzed matched rib, metacarpal, and femoral cortical bone quantity indicators from a subset of individuals with excellent preservation in each of these three skeletal regions (n=70) from the medieval Italian site Pieve di Pava (10th-12th centuries AD). Previous results from this rural site suggest a complex underlying population substructure in cross-sectional properties with highly dispersed variation in most cross-sectional properties. Variation in relative cortical bone was assessed intraskeletally using standardized *z*-scores in order to normalize values across differing elements, alongside descriptive and multivariate statistics. Results show stochastic trends in the relationship between rib, metacarpal, and femora relative cortical bone quantity, but a general correspondence between femoral and metacarpal cortical bone values. However, on closer inspection we found that by examining the dimensionality in our dataset there were intersectional age- and sex-related trends that likely reflect confounding influences of the biocultural context, local mechanical environment, and genetics. We approach dimensionality in our dataset as a potential avenue for intervention and knowledge production, rather than a mere hindrance that needs to be reduced to understand central tendencies in the data. Our approach contextualizes these findings in terms of larger anthropological narratives of normalcy and disability studies.

University of California Berkeley, Archaeological Research Facility Stahl Grant; University of Pisa School of Medicine and Surgery Visiting Fellows Programme

Prevalence of antimicrobial resistance in the human gut microbiome among diverse populations lifestyles

HANDE A. KIRIT[2], AHMED HUSSAN[1], SAADIA NAZIR[1], DAVID JACOBSON[2], THÉRÈSE S. KAGONE[3], ANDREW OZGA[4], ALEXANDRA J. OBREGON-TITO[2], RAUL Y. TITO[2], CECIL M. LEWIS JR.[2] and KRITHIVASAN SANKARANARAYANAN[1]

[1]Microbiology and Plant Biology, University of Oklahoma, [2]Anthropology, University of Oklahoma, [3]Department of Biological Sciences, Centre MURAZ Research Institute, [4]College of Natural Sciences and Oceanography, Nova Southeastern University

Antimicrobial resistance (AMR) is an emerging global public health and economic threat, requiring active surveillance of various ecological reservoirs of AMR bacteria, including clinical, environmental, and food production/distribution sources. However, the role of host (human) associated microbial ecologies in the development, maintenance, and spread of AMR bacteria remains underexplored. Among host-associated ecologies, the human gut microbiome (GM) serves as the primary ecological niche for several taxa including *Escherichia/Shigella*, *Klebsiella*, and *Enterococcus*, commonly associated with acute AMR infections. Here we report the recovery and quantification of ampicillin, ceftriaxone, and ciprofloxacin resistant *Escherichia coli* from the GM of individuals (n=10 each) from three populations: remote hunter-gatherers from Peru, subsistence farmers from Burkina Faso, and an urban community from Oklahoma. Overall, *E. coli* harboring resistance to ampicillin were the most prevalent in all three populations (Peru: 40%, Burkina Faso and Oklahoma: 90% of individuals). Further, the subsistence farmers with under-regulated access to antibiotics had a higher prevalence of resistance against ceftriaxone (90%) and ciprofloxacin (30%) compared to the population from Oklahoma (ceftriaxone: 10%, ciprofloxacin: 20%) with regulated access to these antibiotic medicines. Finally, the hunter-gatherer population with limited exposure to therapeutic antibiotics had a high prevalence of resistance against ceftriaxone (70%) and ciprofloxacin (40%) highlighting the resistance potential of the pre-industrial human GM. Globally, traditional lifeways are rapidly being replaced and communities are transitioning into environments with increasing and under-regulated antibiotic use. Monitoring AMR diversity in the GM would thus be critical to help mitigate the health risks associated with these lifestyle transitions.

This work was supported by OCAST (HF20-032-1) funds awarded to CML and KS

The Evolution of Technology: the evidence from "tools for other tools"

MARC KISSEL[1] and JENNIFER FRENCH[2]

[1]Anthropology, Appalachian State University, [2]Archaeology, Classics and Egyptology, University of Liverpool

How does technology shape both social processes (cultural evolution) as well as individuals' development? As part of a larger project on the role of concepts in human evolution, we examined how technology influences, imposes limitations on, and offers affordances for "the possible" in the dynamics of the human niche. Technology has deep evolutionary roots and is the instrument by which, and within which, we conduct most of our social lives. It also plays a key role in co-creating the human body as technologies have shrunk time and space. In this project we ask how technology has affected the human cultural niche.

We look at tools that are *tools for other tools*, such as shelters & containers. We first used the D-Place and HRAF databases to collect archaeological data on early manifestations of these technologies and ethnographic data on their role in recent small-scale societies. We then asked how these technologies are both influenced *by* human biology as well as influence *our* biology via the concept of embodiment. Our results indicate that our biology might have been more influenced by these technologies than previously suggested and that a feedback loop between brain size (and other aspects of human biology) and technology might help to explain some recent findings. We

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

present these data as a fully illustrated comic poster, showing the interaction between and among these two technologies and changes in human biology over time

John Templeton Foundation Grant ID# 61924: Concepts as a Dynamic Assemblage

Myokine secretion during low-intensity physical activity: dose response of interluekin 6 to walking duration

TIMOTHY M. KISTNER and DANIEL E. LIEBERMAN

Human Evolutionary Biology, Harvard University

Chronic low-grade inflammation is rising worldwide, fueling increasing incidence of non-communicable diseases. While the sources of chronic inflammation are varied, lack of physical activity is a key risk factor. During physical activity, contracting muscles secrete a variety of immunomodulatory and metabolic factors called myokines that reduce chronic inflammation. Foremost among these is interleukin 6 (IL-6), which increases fatty acid mobilization and stimulates anti-inflammatory cytokine release. Since IL-6 release has traditionally been linked with muscle glycogen depletion, the majority of previous studies have focused on modern high intensity exercise contexts such as marathon running. Few studies have assessed IL-6 secretion during evolutionarily normal contexts such as walking and the majority of those studies use relatively short exercise protocols (<1 hour) and high intensities (50-60% VO_{2max}). To test the hypothesis that IL-6 release occurs during evolutionarily normal contexts like long distance walking, we performed a dose response experiment to test the effect of walking duration on IL-6 secretion. 13 participants completed four moderate intensity walking trials (55% HR_{max}) for 30min, 1hr, 2hrs, and 3hrs with intervening washout periods of at least one week. Capillary blood samples were taken before and after each exercise bout to evaluate changes in IL-6. Using a linear mixed effects model, we found that IL-6 levels increased significantly only during the two- and three-hour walking trials. These results demonstrate that myokine secretion occurs even during low intensity physical activities, supporting the hypothesis that decreased time walking in modern environments is a mismatch that contributes to chronic inflammation.

This research was supported by the American School of Prehistoric Research at Harvard University.

Does hair length or number explain variation in primate hair microbiome diversity?

CATHERINE E. KITRINOS[1], RACHEL B. BELL[2], SNEHA MAGESH[3], BRENDA J. BRADLEY[4,5] and JASON M. KAMILAR[1,2]

[1]Department of Anthropology, University of Massachusetts, Amherst, [2]Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts, Amherst, [3]Department of Biology, University of Massachusetts, Amherst, [4]Department of Anthropology, The George Washington University, [5]Center for the Advanced Study of Human Paleobiology, The George Washington University

Microbiome diversity plays a critical role in host biology and is influenced by both environmental and evolutionary factors. For nonhuman primate hair, microbiome diversity is associated with several factors including sex, environmental conditions, and species identity. In addition, human hair microbiome studies suggest that hair length and number may explain variation in hair microbiome diversity, but this has been unexplored for other primate species. Therefore, in this study, we investigated the strength of hair number and hair length as predictors of primate hair microbiome diversity using a comparative dataset of 12 species sampled across several body regions. We used linear models to test the association between alpha diversity and several predictors including hair length, hair number (as a proxy for density), host species identity, sex, housing institution, and body site. We quantified the strength of each predictor using the sum of AICc weights. We found that both hair length and number were weak predictors of alpha diversity when accounting for other factors. Host species identity was the strongest predictor. We suggest that primate hair microbiome diversity is explained by other factors related to primate host biology, such as sweat or scent gland morphology and density. In addition, our results indicate that a relatively small number of hairs (averaging 35 hairs in our study) can accurately quantify primate hair microbial communities.

Funded by the Leakey Foundation and UMass Amherst

Life among the trees? Sir Arthur Keith's 'plantigrade stage' in the *Homo habilis* hand (OH 7) and foot (OH 8) remains

TRACY L. KIVELL[1,2], ZEWDI J. TSEGAI[1,3], EMMA E. BIRD[4], CHRISTOPHER J. DUNMORE[1], SAMAR M. SYEDA[1] and MATTHEW M. SKINNER[1,2]

[1]School of Anthropology and Conservation, University of Kent, [2]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand, [3]Department of Organismal Biology and Anatomy, University of Chicago, [4]Centre for Human Evolution Research, Natural History Museum London

Building upon the insights of Lamarck and Darwin, Sir Arthur Keith proposed three stages in hominoid evolution, involving an initial shift from forelimbs specialised for an arboreal environment ('hylobatian') to 'equalised' limbs adapted to both arboreal and terrestrial settings ('troglodytian'), and finally specialisation of the lower limbs for terrestrialism ('plantigrade'). In the absence of 'transitional' fossils, Keith recognised that human gait and posture is a culmination of a series of evolutionary phases acting on the orthograde ape body plan. Here, we shed light on the 'plantigrade stage' of *Homo habilis,* focusing on functional signals derived from the internal bone structure of the hand (OH 7) and foot (OH 8). Cortical thickness mapping and cross-sectional geometry (CSG) show that the OH 7 manual phalanges are most similar to non-human apes, the scaphoid's internal cortical and trabecular structure shows an intermediate pattern, while the external shapes of the carpals are human-like. Despite primitive features of the OH 8 talus shape, both talar trabecular distribution and CSG across the metatarsals suggest human-like loading of the ankle and forefoot. Internal structure of the metatarsals indicates the OH 8 foot belongs to an adult individual and thus OH 8 and OH 7 should be attributed to different individuals. The functional signals of the fingers indicate powerful grasping while the foot suggests human-like load distributions. Despite their discovery only ~40 years after Keith's proposal, the *H. habilis* fossils continue to offer novel information about the diversity of 'plantigrade' and 'troglodytian' behaviours in Pliocene-Pleistocene hominins.

Research is supported by European Research Council under the European Union's Horizon 2020 research and innovation programme (No. 819960) and Marie Sklodowska-Curie Postdoctoral Fellowship (No. 101025719).

Differential gene expression between the proximal and distal developing calcaneus: Implications for primate evolution

KELSEY M. KJOSNESS[1], SUNGDAE PARK[2], LAUREN N. WILSON[1], DOUGLAS B. MENKE[2] and PHILIP L. RENO[1]

[1]Bio-Medical Sciences, Philadelphia College of Osteopathic Medicine, [2]Genetics, University of Georgia

Calcaneus morphological changes are important to our understanding of human and non-human primate locomotor evolution, including increased size and cross-sectional area of the calcaneal tuberosity in humans and distal end elongation in tarsiers and galagos. The calcaneus is the only tarsal to form a growth plate and associated secondary ossification center, which is located at the proximal end of the calcaneal tuberosity. Thus, distal elongation likely occurs independent of the growth plate and suggests at least two independent development modules define the calcaneus. While calcaneus morphology and evolution is frequently discussed, little is known about the genes underlying the development and morphology of this bone and its single growth plate. To address this deficiency, we used RNA sequencing to determine differentially expressed genes (DEGs) between the proximal (growth plate forming) and distal (non-growth plate forming) ends of the calcaneus in 0, 4, and 9 day old mice. On the proximal end, 27 DEG were expressed

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

in at least 2 of the 3 ages. Gene ontology (GO) analysis found these to be associated with embryonic development and the retinoic acid signaling pathway. For the distal end, 148 DEGs were similarly identified and were surprisingly associated with functions related to muscle development, ion channels, and actin binding. However, genes known to affect skeletal development including *Sall1* and *Hoxa13* were also differentially expressed. This analysis identifies potential genetic targets with downstream morphological effects that can be targeted by natural selection to produce region-specific evolutionary changes.

Funding provided by NSF grants IOS-1656315 & BCS-1638812.

A Preliminary Investigation into the Effects of *Lucilia sericata* (Meigen) Blow Fly Larval Feeding on Sharp Force Trauma (SFT) Wound Patterns in Decomposing Bones of *Sus scrofa domesticus*

ERICA L. KLAFEHN[1,2], ANGELIQUE CORTHALS[2] and JENNIFER ROSATI[2]

[1]Anthropology, University of Nevada, Reno, [2]Sciences, John Jay College of Criminal Justice - City University of New York (CUNY)

An important aspect of forensic anthropological investigations involves the analysis of skeletal trauma as it can provide valuable information regarding the cause and manner of death. Research on Sharp Force Trauma (SFT) on soft and skeletal tissue typically applies a variety of analytical microscopic methods to explore trauma variation. Thus far, minimal research has integrated a forensic entomology approach with forensic anthropology. This study aims to bridge that gap by considering anthropological and entomological effects in examining SFT.

Using Scanning Electron Microscopy (SEM), this study examined the relationship between *Lucilia sericata* blow fly larval feeding and the nature of SFT an individual may encounter in a forensic case. This research observed two types of traumatic injuries in ribs using a porcine model (n=45). The SFT observed included cutmarks caused by a saw blade and punctures caused by a flathead screwdriver . Based on the SEM imaging results, blow fly larval feeding had an effect on bone morphology in sites of SFT after 24, 48, and 72 hours of decomposition. More specifically, bones with SFT lost integrity of the periosteum and trabecular bone structure, particularly the spacing of the trabecular bone after larval feeding. These results demonstrate a need to further explore this interdisciplinary research, as insect feeding may have an effect on trauma or interpretation of pathological conditions more broadly.

Medicolegal Death Investigation: Medical Examiners/Coroners, Forensic Pathology, and Collaboration with Forensic Anthropology

LAURA D. KNIGHT[1,2] and MARIN A. PILLOUD[3]

[1]Forensic Pathology, Washoe County Regional Medical Examiner's Office, [2]Pathology, University of Nevada - Reno School of Medicine, [3]Anthropology, University of Nevada - Reno

Medical Examiners and Coroners are responsible for the medicolegal investigation of sudden, unexpected, unexplained, or violent deaths. Unexpected discovery of skeletal remains requires investigation, and examination of the remains by a forensic pathologist (Medical Examiner) is necessary, usually in conjunction with a forensic anthropologist. A qualified forensic anthropologist can make prompt assessment for critical initial considerations, such as human vs. non-human, and contemporary (forensic) vs. archeological/historical. Once skeletal remains are determined to be of forensic interest, the forensic anthropologist may be asked to undertake examinations to: generate a biological profile leading to tentative identification; estimate the postmortem interval; analyze for trauma; and/or analyze tool marks present on the skeletal elements.

The resolution of medicolegal death investigations is a complex process requiring expertise of the forensic pathologist who works with law enforcement, death investigators, and other forensic scientists. This presentation will provide an overview of medicolegal death investigations with a particular focus on the Washoe County Regional Medical Examiner's Office (WCRMEO). This office regularly consults with a forensic anthropologist who conducts on average 15 cases per year. While highlighting the investigation process, various case studies will be presented that demonstrate the utility of forensic anthropology. These include differentiating among multiple types of skeletal trauma present in a single case, identifying blunt trauma in the presence of severe thermal damage, determining the type/class of implement used in a case of decapitation, and resolving commingled cases serving to identify additional missing decedents.

No funding was received for this project.

Scaling of femoral and tibial cross-sectional properties with body size in prosimian primates

CHLOE A. KNITT[1,2], KAITLIN C. HSU[1,2] and KRISTI L. LEWTON[2]

[1]Department of Biological Sciences, University of Southern California, [2]Department of Integrative Anatomical Sciences, University of Southern California

Hindlimb bone cross-sectional geometric properties (CSP) differ according to locomotion among strepsirrhine primates, a group that exhibits large variation in body size. However, the potential influences of body size on CSP are less well understood. We examined the relationships between body size and CSP of the femur (n=91) and tibia (n=75) in a sample of 28 species of prosimians that use leaping and quadrupedal modes of locomotion. We collected micro-CT scans of each bone, virtually reoriented the scans, and obtained midshaft slices. The following midshaft CSP were calculated: polar section modulus (an estimate of bending strength), cortical area (an estimate of compressive strength), and polar second moment of area (an estimate of torsional strength). CSP were ln-transformed and regressed on ln-body mass to test scaling hypotheses; analyses of variance were conducted on scaled CSP to compare small- and large-bodied species (i.e., those <1 kg vs >1 kg); and the relationships between femoral and tibial CSP were assessed using correlations. Femoral and tibial CSP scaled isometrically or with slight positive allometry. Small-bodied species tend to have significantly stronger/more rigid femora relative to size than large-bodied species, and this trend is amplified within the leaping taxa; this pattern was less clear in tibial comparisons. Correlations between femoral and tibial CSP were significant, but no clear size-related patterns emerged. Our results suggest that intralimb patterns of CSP may relate to functional differences in postural and locomotor kinematics between small- and large-bodied leapers.

This study was funded by the National Science Foundation BCS-1944571.

Comparing oral pathology in the Imperial Roman period and Late Antiquity in Dyrrachium/Dyrrachion (modern-day Albania)

MARLON KOCI[1], BRITNEY KYLE[2], LAURIE J. REITSEMA[3] and ULSI TOTA[4]

[1]Department of Anthropology, University of Central Florida, [2]Department of Anthropology, University of Northern Colorado, [3]Department of Anthropology, University of Georgia Athens, [4]Department of Prehistory, Institute of Archaeology, Albania

Sociopolitical conditions present in different historical periods may influence the health of communities differently. The Imperial Roman period (I-IV AD) and Late Antiquity (IV-VII AD) were periods when historical events and factors changed the organization of societies and the lifestyle of individuals. Dyrrachium/Dyrrachion (modern-day Durres) was the most prosperous city in Illyria (ancient Albania). Historical sources and archaeological remains indicate how historical changes impacted the city's political origination and social life. However, we do not have information about how social-political changes were reflected in health and lifestyle. We test the hypothesis that oral pathologies deteriorate from the Roman period to Late Antiquity, a transitional period associated with conflicts and

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

regression. We assess 60 skeletons from the two periods from Durres that show dental pathology, including caries, periodontal disease (including abscesses), and antemortem tooth loss AMTL. The pathological prevalence is: 52%/40% (p=0.438) for dental caries; 24%/37% (p=0.285) for periodontal disease, and 32%/34 (p=0.591) for AMTL. Oral health is not statistically different between these two periods, which indicates that sociopolitical changes did not affect key aspects of the individual's oral health. Considering the etiology of oral pathology, we may infer that carbohydrate and sugar consumption linked with caries, and oral hygiene, masticatory loading, nutritional status, and psychological stress linked with periodontal disease did not meaningfully differ in these periods. We contextualize our findings by examining the oral health of other Mediterranean sites, analyze variation by age/sex categories, and consider the limitations of the sample.

Funding citation: This research was supported by the University of Georgia Sarah Moss Fellowship, the University of Northern Colorado, Institute of Archaeology, Albania.

Japan's COVID 19 Infection Rate: How demographic factors affect infection rates

LAUREN M. KOERNER and LORENA MADRIGAL

Anthropology, University Of South Florida

The emergence of COVID19 exposed latent inequalities in access to health care, dignified housing, healthy nutrition, and general well-being throughout the world. Biomedical/applied anthropology is suited to assess barriers to healthcare access and its causes. The aims of this paper are to assess what demographic factors explain differences in COVID-19 infection rates in different neighborhoods in the prefecture of Tokyo. Basic demographic data were obtained from the Tokyo 2015 population Census and general mortality data were obtained from the 2019 vital statistics survey.

To account for differences in district sample sizes, all data were standardized to a common population size (Preston et al. 2001). The main demographic variable analyzed is the type of family structure found in different districts in the prefecture, as family is an intersection of culture, biology, and environment. Families were divided into the following groups: Nuclear, Multigenerational, Single, Aged, and Unknown. Districts were divided into three levels of urbanization. The level of urbanization affects the standardized infection rate (X^2= 52.7192, df=2, p<.0001), and the distribution of people by age category is not independent from level of urbanization (X^2 = 14.1457, df = 6, p < 0.0281). Using Japan's meticulous census, we quantified the frequency of different family structures by area of urbanization. Through regression analysis we identified demographic variables that were either positively or negatively associated with COVID19 infections in Tokyo (R^2 =0.41, df=1, p<.0001). In Japan, just as in the USA, the distribution of COVID was not blind to the demographic characteristics of neighborhoods.

Dental Dimensions As Indicators of Genetic and Environmental Factors Influencing Cayo Santiago Rhesus Macaques

LUCI ANN P. KOHN[1], KATELYN BAKER[1], TERRY B. KENSLER[2], DEBBIE GUATELLI-STEINBERG[1,3], MARTIN Q. ZHAO[4], GEORGE FRANCIS[5] and QIAN WANG[5]

[1]Biological Sciences, Southern Illinois University Edwardsville, [2]Caribbean Primate Research Center, University of Puerto Rico Medical Sciences Campus, [3]Anthropology, The Ohio State University, [4]Computer Science, Mercer University, [5]Biomedical Sciences, Texas A&M University School of Dentistry

Dental development is influenced by many factors, both genetic and environmental, and may serve as an indicator of developmental stress. Crown development, and resultant crown dimensions, may be influenced by environmental stresses, including malnutrition and disease. This study examines maxillary dental dimensions in rhesus macaques (*Macaca mulatta*) from Cayo Santiago. We test for dental differences associated with improved care (food provisioning, reduction in tetanus), natal social group, and matriline. Maxillary mesiodistal and buccolingual lengths of permanent teeth were measured on 107 individuals, derived from ten matrilines and seven social groups. While dental dimensions exhibited sexual dimorphism, individual teeth showed limited differences across time, natal social group, and matriline. Significant dimensional differences were found within tooth type associated with sex, improved care, and natal social group. Developmental stress influences multiple teeth developing at the time of impact, resulting in a complex effect on dental dimensions. A larger sample is needed to test further matrilineal and genetic differences.

The Cayo Santiago colony is supported by NIH 5P40OD012217. This project is supported by NSF grants to DG-S., LK., MZ, and QW (NSF #1926528, 1926481, 1926402, and 1926601).

Profile likelihood estimation of stature from humerus and radius length

LYLE W. KONIGSBERG[1], SUSAN R. FRANKENBERG[1] and CHRISTOPHER B. RUFF[2]

[1]Anthropology, University of Illinois at Urbana-Champaign, [2]Center for Functional Anatomy and Evolution, Johns Hopkins School of Medicine

Stature estimation using the Fully (1956) method as revised by Raxter et al. (2006) can provide accurate and unbiased estimates, but it requires relatively complete skeletons. For incomplete skeletons there is a long history of using long bone lengths and regression analysis to estimate stature. When using two or more long bones most of these methods have used multiple regression of stature on the bone lengths. This amounts to using the reference sample stature distribution as an informative prior and has consequently led to the development of population and sex specific equations. Classical calibration circumvents this problem but leads to the unfortunate side effect that prediction intervals shrink when the predicted long bone lengths given estimated stature depart from the actual long bone lengths. This can produce prediction intervals that shrink to a point and then disappear. Brown (1982) has shown that profile likelihood estimation, where all but the estimated stature are treated as nuisance parameters, solves this prediction interval problem. Ruff's (2018) European dataset provides a large sample with anatomically estimated stature and long bone lengths. We use the Italian female sample (N=37) and summary statistics from a large dataset (N=2015) published in Konigsberg and Jantz (2018) to estimate stature from humerus and radius lengths. Our results show that the profile likelihood method produces coverage which matches the nominal rates. In contrast, multiple regression produces coverage that is below the nominal rates because the estimates are biased and the prediction intervals are too narrow.

Psychological Distress and Dietary Outcomes among Resource Insecure University Students

MIRIAM C. KOPELS[1], CASEY J. ROULETTE[1] and ERIC C. SHATTUCK[2]

[1]Anthropology, San Diego State University, [2]Public Health, University of Texas, San Antonio

This paper utilizes 24-hour food recall and interview data among n=51 resource insecure university students to investigate how food insecurity (FI), psychological distress, and emotional disruptions to diet are associated with diet. Utilizing standards from the USDA, we tested the following: 1) do resource insecure students eat in accordance with recommendations; 2) do mental health variables impact diet; 3) does FI impact diet; and 4) how are mental health and FI related. We found that students eat more saturated fat and processed sugar, and less fruit, vegetables, lean protein, and unsaturated fat than is recommended. Additionally, psychological distress (as opposed to FI) was a far greater predictor of diet-related outcomes. We found that those with serious psychological distress were more likely to: 1) eat fewer fruit calories (p=0.0327, df=49); 2) consume more alcohol calories (p=0.0445, df=49); 3) eat less lean protein (p=0.0332, df=49); and 4) those reporting psychological and financial disruptions to diet were more likely to consume calories below USDA recommendations (mean = 1047.74, p=0.0274, df=49). Additionally, we found a linear relationship between psychological distress and

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

FI (p=0.003, R-squared=0.2015). These results are supported by our ongoing research with another student population (n=105) demonstrating initial associations between psychological distress and self-reported dietary quality (p=0.003, df=83). This work contributes to our understandings of the intersectional relationship of mental and physical health and demonstrates that poor mental health may be a factor contributing to susceptibility to diet-related disease. These results can be used to identify health vulnerabilities and design targeted interventions.

This work was funded the Social and Economic Vulnerabilities Initiative of San Diego State University and the Economic Crisis Response Team of San Diego State University

Faunal community composition across varied paleoenvironmental contexts.

KRYSTAL L. KOSKI[1], MADELEINE KELLY[2], SILINDOKUHLE MAVUSO[3,4], FRANCES FORREST[5], DAVID R. BRAUN[6] and EMMANUEL NDIEMA[7]

[1]Department of Anthropology, University of Michigan, [2]Department of Organismal Biology and Anatomy, University of Chicago, [3]Department of Geology, Rhodes University, [4]School of Geosciences, University of Witwatersrand, [5]Department of Sociology and Anthropology, Fairfield University, [6]Center for Advanced Study of Human Paleobiology, The George Washington University, [7]Department of Archeology, National Museums of Kenya

The Koobi Fora Formation in the northeastern Turkana Basin is a fluvio-lacustrine sequence preserving evidence of Plio-Pleistocene ecosystems. After a trend towards increasingly arid environments began as early as 2.7 million years ago (Ma), additional expansion of open habitats occurred around 2.0-1.4 Ma. However, faunal abundance and dental enamel stable isotopes indicate these changes varied spatially. This suggests that diverse factors influenced the ecosystems that hominins inhabited. Standing water availability is hypothesized as an important influence on habitat due to its impact on vegetation structure. This aspect of paleoenvironmental context can be inferred through the exploration of faunal community composition contextualized by sedimentology. We combine these methods to investigate diverse influences of habitat heterogeneity by characterizing differences in faunal community composition related to depositional environment variability in the upper Burgi Member (~1.98-1.87 Ma). Using published faunal data and new collections (n=204), we calculated 1) relative family abundances and 2) relative bovid tribe abundances for each depositional environment. Depositional environments were characterized with lithofacies analysis. Results show higher relative abundances of families associated with more closed habitats (e.g., Suidae, Giraffidae) in fluvial and deltaic contexts than lacustrine. Families associated with more open habitats (e.g., Bovidae, Equidae) demonstrate the opposite pattern. Bovid tribes associated with open habitats (e.g., Antilopini) are most abundant in lacustrine contexts, while tribes associated with closed habitats (e.g., Reduncini) are more prevalent in fluvial and deltaic contexts. These distinctions among faunal communities across depositional contexts may reflect heterogeneity in Plio-Pleistocene vegetation structure in the Koobi Fora Formation.

Multiple cranial pathological conditions: A complex case using a bioarchaeology of care framework

DANIËL KOTZE[1], GENEY D. GUNSTON[1], LETIAN HE[2] and VICTORIA E. GIBBON[1]

[1]Department of Human Biology, University of Cape Town, [2]Department of Archaeology and Museology, Lanzhou University

In this individual-centred case study, we focused on the skeletal remains of a San woman from 19th century, Northern Cape, South Africa. Her cranium showcased a complex pathology suggesting a potential context for care. No previous research has conclusively diagnosed the pathology or sought to understand how the individual may have been affected by it. Therefore, we aimed to apply the first two steps of the bioarchaeology of care framework to diagnose the pathology and infer the likely impact (if any) it may have imposed on the individual during her life. The cranium was examined morphologically, morphometrically and radiographically (CT and Lodox technology) to provide a comprehensive report on the pathology. CT data were used to generate two-dimensional and three-dimensional reconstructed images of the skull and conduct measurements for assessing various anomalies. A differential diagnosis was conducted to identify present pathological conditions, and the clinical literature was consulted to infer how these may have impacted the individual. Multiple pathological conditions were diagnosed from the skull, including generalised osteoporosis, biparietal thinning, platybasia and basilar invagination. Basilar invagination may have impacted this woman during life, possibly causing neurological and/or musculoskeletal complications. This may have rendered her reliant on others in her community to some degree. Our research demonstrates the value of radiographic technology for evaluating and diagnosing pathological conditions in bioarchaeology. It contributes to our understanding of rare and poorly characterised conditions documented in archaeological human remains and reveals aspects of this woman's life story that were previously unknown.

This research was supported through A/Prof. Gibbon by the National Research Foundation, South Africa (Grant No. 115357 and 120816), the Department of Human Biology, UCT.

Intergroup encounters in wild white-faced capuchins of the Taboga Forest Reserve

SARAH A. KOVALASKAS[1,2], AGOSTINA COLOSIMO[2,3], JACINTA C. BEEHNER[2,4,5], THORE J. BERGMAN[2,4,6] and MARCELA E. BENÍTEZ[1,2]

[1]Biological Anthropology, Emory University, [2]Capuchins at Taboga Research Project, Taboga Forest Reserve, [3]Tropical Biodiversity and Ecosystems, Free University Brussels, [4]Psychology, University of Michigan, [5]Anthropology, University of Michigan, [6]Ecology and Evolutionary Biology, University of Michigan

Conflict between social groups is a common facet of many primate societies. In wild white-faced capuchins (*Cebus imitator*), intergroup encounters (IGEs) are typically hostile and appear to function as a long-term reproductive strategy for dispersing males to assess the composition of neighboring groups. Here, we investigate the causes and consequences of intergroup encounters at the Taboga Forest Reserve in Guanacaste, Costa Rica. The reserve is composed of fragmented tropical dry forest that experiences anthropogenic disturbance and has 2-6 times the density of capuchins as other long-term field sites. We sought to determine: a) How rates of IGEs at Taboga compared to other white-faced capuchin field sites and b) whether patterns found in other capuchin populations (i.e. factors that impact participation in IGEs; relationships between interaction location, group size/composition, and IGE outcomes) also characterize IGEs at Taboga. Between May 2018 and May 2022, we observed 274 intergroups across 5 groups. The rate of intergroup encounters was 0.043 IGEs/contact hour, higher than published rates at neighboring capuchin sites. We observed higher rates of IGEs in the wet season (0.054 IGEs/contact hour) than in the dry season (0.032 IGEs/contact hour). At Taboga, the average number of participants in an IGE is 3.7 and this number increased as meetings escalated in physical intensity (i.e. contact aggression). Furthermore, the group that experienced the highest IGE rates also experienced many demographic changes (dispersal, takeover, immigration) supporting the idea that IGEs function as reconnaissance opportunities.

Facial Asymmetry in Children with and without Orofacial Clefts Aged 3 Months to 2 Years: 3D Landmarks-based Method Study

LENKA KOZEJOVA JAKLOVA, KATARINA HARNADKOVA, KAROLINA KOCANDRLOVA, JAN DUPEJ and JANA VELEMINSKA

Deparment of Anthropology and Human Genetics, Charles University

Introduction: Research on facial asymmetry in early childhood is crucial to the effectiveness of surgical treatment related to perceptions of attractiveness and other psychosocial matters. The objective was to compare facial asymmetry

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

in children with complete unilateral cleft lip/palate (CL, UCLP) with controls and to demonstrate changes in asymmetry during the follow-up period.

Materials and Methods: The 3D facial scans of 35 cleft patients (20 CL, 15 UCLP) and 65 age-matched healthy children were analyzed between the 1.1–1.5 years (T2) and 1.6–2.0 years (T3). The shape asymmetry of 9 landmarks was evaluated by geometric morphometrics and multivariate statistics.

Results: Facial asymmetry was evident in almost all cleft groups (CL T3; UCLP T2, T3), with the greatest variability occurring in the UCLP group. Asymmetry in the UCLP group was manifested by the location of exocanthions upper than endocanthions and right cheilions were upper than the left ones. The midline area was more symmetrical after 1.6 years of age. Groups of CL had similar pattern of asymmetry in eye area, but the cheilions were on the right side lower than on the left side. In healthy control, asymmetry was insignificant.

Conclusions: Our results suggest the following conclusions: (1) the UCLP patients exhibited the most asymmetrical features, mainly in the oral region, where the right corner was located higher; (2) the UCLP and CL patients had similar pattern of facial asymmetry except the oral region, where the mouth corners were oriented oppositely; (3) the directional asymmetry was not significant in controls.

This study was supported by the Charles University project GA UK No 266522.

Queering Primate Osteology: Orangutan Skeletons Challenge Normative Assumptions of Binary Sex and Gendered Behavior

ALEXANDRA E. KRALICK

Department of Anthropology, University of Pennsylvania

Queer theoretical approaches challenge binary and gendered interpretations of biological sex in human skeletons but seemingly have yet to be similarly applied to the study of non-human primate skeletons. Orangutans are an ideal primate taxon to begin such conversations because, while they are described as a highly sexually dimorphic genus, their biological sex is more complicated than only large males and small females. Orangutan males exhibit a plastic polymorphism whereby some develop into flanged males shortly after reaching sexual maturity and others delay the development of flanges up to 20 years or may never flange. Adult unflanged males have been argued to fill a niche in response to increasing ecological stress for a discreet female-sized "sexual predator." This claim is examined by measuring orangutan skeletons in museum collections for osteological correlates to body size (e.g. long bone length, cross-sectional area, femoral head diameter), reported weight, and markers of stress events in dentition. Data on adult unflanged male body size range between that of adult flanged males and adult females, complicating binary depictions of biological sex. Further, flanged males show evidence of more severe stress events in early life than adult unflanged males, suggesting flanged males are more likely to have experienced stressful conditions compared to adult unflanged males. These results defy the normatively gendered expectation that large-bodied "preferred" males exhibit the ancestral condition and run counter to the idea that smaller-bodied adult unflanged males are the ones whose presence requires an evolutionary explanation and who exhibit an "alternative reproductive strategy."

This research was supported by the National Science Foundation, Leakey Foundation, and University of Pennsylvania.

Hip width and metabolic energy expenditure of abductor muscles

PATRICIA ANN. KRAMER[1] and ADAM D. SYLVESTER[2]

[1]Anthropology, University of Washington, [2]Center for Functional Anatomy and Evolution School of Medicine, The Johns Hopkins University

Despite a paucity of physiological support, simplistic biomechanical analyses have led researchers to assume that humans who have wider hips use more energy to walk. Pitting biomechanical first principles against physiological data has led to little deepening of our understanding of bipedalism and its evolution. Both approaches, however, use proxies for the energy used by muscles. We decided to approach the question directly.

Using a musculoskeletal model of the human body that estimates the metabolic energy expenditure of muscle activation for 48 people (25 men, 23 women), 752 trials were evaluated. Metabolic energy consumption for the abductor muscles was summed over a stride to create total abductor energy expenditure. We calculated the maximum hip joint moment acting in the coronal plane. We hypothesized that wider hips would be correlated with increased total abductor energy expenditure when mass and velocity were controlled.

Using least squares multiple regression with adjustment for repeated measures, we found that hip width does not predict total abductor energy expenditure ($p=0.74$), although mass and velocity combine to predict 61% of the variation (both $p<0.001$). Maximum hip joint coronal plane moment is predicted by hip width ($p<0.001$) and, in combination with mass and velocity (both $p<0.001$), explains 79% of the variation. Our results indicate that people use their morphology in ways that limit differences in energy expenditure. Consistent with recent discussion, intraspecific variation might not be useful to understand differences among species.

Differences in elemental composition within enamel suggest differences in wear

KRISTIN L. KRUEGER[1], LUZ CASTREJON[1], ALEX FOK[2], CHRISTOPHER SCHMIDT[3], REID ELLERBRAKE[1] and GRETA KELLER[1]

[1]Anthropology, Loyola University Chicago, [2]Minnesota Research Center for Biomaterials and Biomechanics, University of Minnesota, [3]Anthropology, University of Indianapolis

Understanding the factors that influence dental wear is crucial to interpreting the paleoanthropological and bioarchaeological records. Specifically, recent debates have called into question how enamel is worn, and how that might affect microwear formation and interpretation. Here we attempt a novel approach to understanding enamel wear: using scanning electron microscopy (SEM) and energy dispersive x-ray spectroscopy (EDS) to analyze elemental composition.

A sample of surgically extracted third molars (n=11) and archaeological molars (n=10) were analyzed. The fresh molars were kept hydrated in 10% neutral buffered formalin, while the archaeological teeth were kept in standard collection bags since excavation. Occlusal surfaces of the fresh molars were twice analyzed for oxygen, carbon, calcium and phosphorous using a Hitachi TM 3000 SEM/EDS at the University of Minnesota: once while unworn and again after grinding with a Buehler grinder/polisher. The archaeological molars were once analyzed for elemental composition since the occlusal surfaces were already worn.

Elemental analyses of the fresh molar sample revealed significant differences in elemental levels before and after grinding. After grinding, the worn occlusal surfaces had higher levels of calcium and phosphorous, and lower levels of carbon. The archaeological sample had levels consistent with the fresh sample after grinding. The ratio of calcium to phosphorous remained stable in all three samples. These data suggest that unworn occlusal surfaces have less calcium and phosphorus than worn occlusal surfaces, providing possible insight into differences in wear properties across the lifespan of a tooth.

We thank the LUC-INSPIRED microgrant program and Loyola University Chicago Research Support Grant for funds to complete this research.

The evolution of primate gestation

CHRISANDRA KUFELDT[1] and MARK GRABOWSKI[2]

[1]Sociology and Anthropology, James Madison University, [2]Research Centre in Evolutionary

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Anthropology and Palaeoecology, Liverpool John Moores University

Gestation length is an important component to understanding a species life history and is broadly correlated with brain size and body size in mammals, and this generally holds true for primates. Humans have a distinct suite of life history traits, thus how and why gestation length evolves has important implications for exploring growth and development in fossil hominins. To address these questions, we tested the relationship between published primate gestation length and predictors such as body size, brain size, diet, and sociality in 74 species of living primates using phylogenetic comparative methods that account for adaptation and ancestry. Our preliminary results suggest gestation length evolves towards niche-dependent adaptive trends with longer gestation lengths in haplorrhines than strepsirrhines, which may be related to increased brain size and larger bodies. However, no other predictors had an effect when body size was included in the model. We then estimated gestation length based on the amount of prenatal enamel quantified from histological sections of the M_1 from a subset of the living primates and fossil primates from the Eocene (e.g, *Cantius*) and Miocene (e.g., *Proconsul*) epochs and used this data to reconstruct the adaptive landscape of gestation length evolution. Our larger analysis reveals specific adaptive trends in gestation length may be related to shifts in body size, maternal investment, or longevity, and provides new insight into when an ape-like pattern of growth arose. Our results add complexity to the growing body of research on primate life history evolution.

Dietary reconstruction after the fall of the Huari Empire in the Andean Highlands: Further studies of stable isotopes from human dental calculus

SUSAN C. KUZMINSKY[1,2], SIMON R. POULSON[3], G. RICHARD SCOTT[4] and TIFFINY A. TUNG[5]

[1]Department of Anthropology, California State University, Channel Islands, [2]Anthropology Department, University of California, Santa Cruz, [3]Department of Geological Sciences and Engineering, University of Nevada, Reno, [4]Department of Anthropology, University of Nevada, Reno, [5]Department of Anthropology, Vanderbilt University

Paleodietary research traditionally utilizes a combination of either collagen from bone and/or dentin and dental apatite carbonates to obtain carbon and nitrogen isotope signatures that aid in reconstructing life histories in bioarchaeological research. However, destructive analyses that remove bone and/or teeth alter the integrity of human skeletal remains and may not be permitted in some cases. Alternatively, the use of dental calculus as a less destructive biomaterial than bone or teeth can serve as a proxy since it is minimally invasive, requires small samples, and may complement collagen or enamel apatite signatures. To gain a better understanding of using dental calculus for reconstructing diet, we sampled 35 individuals from the post-Huari Late Intermediate Period (1100-1400AD) in the central Peruvian highlands. Results show $\delta^{13}C$ values from -19.7‰ up to -12.3‰, consistent with the use of C4 plants (maize) as a major component of the diet and isotope signatures derived from collagen, while nitrogen values ranged up to +18.8‰. Since marine foods were not part of the typical diet in the Peruvian highlands, heavier values may be explained by isotope enrichment from aridity or crop fertilization (camelid dung) given that the LIP was a time of social disruption coupled with a severe drought. Although calculus signatures are isotopically lighter, we reached the same conclusions as studies that utilized traditional proxies to reconstruct diet in the region. Moreover, an emphasis on less invasive and sustainable methods for reconstructing behavior using human skeletal remains warrant its use as a complementary biomaterial for paleodietary research.

This work was funded by the National Science Foundation Grant (#1335302) and the University of Nevada, Reno.

3D data from South Africa to meet the challenges of forensic identification

ERICKA NOELLE N. L'ABBE[1], GABRIELE C. KRUGER[1], MICHAEL W. KENYHERCZ[2], LEANDI LIEBENBERG[1], OKUHLE SAPO[1] and KYRA E. STULL[3]

[1]Anatomy, University of Pretoria, [2]Defense POW/MIA Accounting Agency, US Department of Defense, [3]Anthropology, University of Nevada, Reno

In South Africa, an estimated 60,000 non-natural deaths occur each year, accounting for approximately 12% of the country's mortality. Additionally, several hundred unidentified remains are retrieved each year, requiring osteobiographical profiles. The demographic structure of South Africa is highly heterogeneous and has been, both historically and socially, divided into four self-defined social groups, namely black, white, coloured and Indian South Africans. The aim of this poster is to highlight the current data available on these South African groups and its current applications in establishing presumptive identifications in South Africa. Craniometric data on three socially defined South African groups, namely black, white and coloured South Africans was acquired from three cadaveric skeletal collections from two geographic regions in the country, including the Pretoria Bone Collection, the Raymond A. Dart Collection and the Kirsten Collection. All crania were digitized with a MicroScribe G25. Ethical approval was obtained from the Research Ethics Committee within the Faculty of Health Sciences at the University of Pretoria for all craniofacial projects. A total of 768 crania are available and are divided into 482 black South Africans (430 male, 52 female), 109 white South Africans (60 male, 49 female), and 177 coloured South Africans (115 male, 62 female). An analysis of size and shape has been performed and published in international journals, with groups statistically separating from each other. The data is currently used via the import function in Fordisc 3.1 for estimating population affinity and sex on unidentified persons.

Investigating alternative approaches to ancestry (sic) National Research Foundation (NRF) Project 71002 (2010-2012)

Dietary variation in young Neandertals from France, Pech de l'Azé 1 and Hortus II, using dental microwear texture analysis

FRANK L'ENGLE WILLIAMS[1], CHRISTOPHER W. SCHMIDT[2], JESSICA L. DROKE[3], GAËL BECAM[4] and MARIE-ANTOINETTE DE LUMLEY[5]

[1]Anthropology, Georgia State University, [2]Anthropology, University of Indianapolis, [3]Anthropology, University of Wyoming, [4]History of Art and Archaeology, Université de Perpignan, [5]Paléoanthropologie, Centre Européen de Recherches Préhistoriques de Tautavel

The dietary proclivities of Neandertal adults are known to have varied with respect to climate and paleoecology. We examine whether these dietary distinctions are evident in Neandertal children of MIS 3 in southern France by comparing Pech de l'Azé 1, from a temperate interval, to Hortus II, from a particularly cold-arid phase. To reconstruct the diet of Pech de l'Azé 1 and Hortus II, dental microwear texture analysis is performed using epoxy replicas of the fossil mandibular deciduous second molars. The differences between Pech de l'Azé 1 and Hortus II are compared to deciduous molars from two Neolithic cave burials of Belgium, Caverne de la Cave at Maurenne (n = 6) and Bois Madame (n = 6), radiocarbon dated to circa 4.6-4.0 ka. The variation within and between the two Neolithic groups contextualizes the differences present in the Neandertal children. The elevated complexity of Pech de l'Azé 1, indicating the consumption of hard foods, or foods that were poorly processed or grit-laden, is distinct from Hortus II with a low value, and from most of the Neolithic children from Belgium. However, Pech de l'Azé 1 and Hortus II both exhibit low anisotropy, suggesting they masticated foods with multiple and varied movements of the jaws typical of subadult Paleoamerican foragers from Brazil. The chewing mechanics of very young people can differ from that of adults; nonetheless, the microwear texture data indicate these Neandertal children had diets that aligned with geography and climate in a manner similar to that of Neandertal adults.

Funding for this research was received from Fulbright-Belgium and the National Science Foundation (BCS 0922930).

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Prolonged cyclical loading, dietary properties, and the saturation response in growing jaws

SUSAN E. LAD[1,2], HUI DING[3], CARMEN E. ALVAREZ[4], REBECCA J. ANDERSON[3], JENNA M. MCKINNON[3], OLIVIA P. HEMING[3], DANIEL F. LIGGIO[3], JONATHAN C. COURI[3], WILLIAM W. ABERGER[3], TALIA J. THORNTON[5], HANNAH M. MORRIS[3], FREDERICK T. LOCKIE[3] and MATTHEW J. RAVOSA[6]

[1]Exercise Science, High Point University, [2]Physical Therapy, High Point University, [3]Biological Sciences, University of Notre Dame, [4]Population Biology, Ecology, and Evolution, Emory University, [5]Health and Human Sciences, Purdue University, [6]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

The magnitude of bone growth in mammalian jaws is dependent on the number of daily load cycles, with more chews resulting in more osteogenesis. However, we previously reported that rabbits raised in a bimodal feeding pattern (access to food for 2.25 hrs twice daily with an intervening rest period of 5 hours) from weaning through adulthood had greater bone growth in the mandibular corpus, symphysis, and condyle than rabbits fed in a unimodal pattern (continuous access for 9.5 hrs). This finding supported the hypothesis that cyclical loading can cause a 'saturation response', such that bone cells become desensitized and cease to respond after prolonged and unabated cyclical loading. Here we test the prediction that increasing the number of load cycles renders the 5-hour rest period insufficient for avoiding the saturation response. 20 male rabbits (*Oryctolagus cuniculus*) were raised in the same experimental protocol, except this cohort consumed hay cubes in addition to rabbit pellets. Hay is stiffer (3335.6 vs. 29.2 MPa) and tougher (2759.8 vs. 1030.6 Jm^{-2}) than pellets, requiring higher chewing investment and duration. Cortical area was measured at multiple sites along the corpus, symphysis, condyle, and maxillary alveolus via microCT. The resulting pattern was similar to the previous pellets-only cohort: bimodal rabbits had a greater osteogenic response than unimodal rabbits in the corpus and symphysis (T-test, $P<0.005$). Thus, our prediction that overloading the jaws requires a longer rest period to avoid saturation response was not supported, which has implications for the interpretation of phenotypic variation vis-à-vis feeding behavior.

Supported by NSF grant BCS-1749453 to MJR.

Celts down the Alps. New isotopic data on territorial mobility among the Late Iron Age *Cenomani* of Verona (NE Italy, 3rd -1st c. BCE)

ZITA LAFFRANCHI[1], STEFANIA ZINGALE[2], DOMINGO C. SALAZAR-GARCÍA[3,4], SANDRA LÖSCH[1], MANUELA DE LA CRUZ CÓRDOBA[3], GABRIELE ARENZ[1], VALENTINA COIA[2], ALICE PALADIN[2], LUCIANO SALZANI[5], SÖNKE SZIDAT[6], UMBERTO TECCHIATI[7], ALFONSINA AMATO[7], IRENE DORI[8], ALBERT ZINK[2] and MARCO MILELLA[1]

[1]Department of Physical Anthropology, Institute of Forensic Medicine, University of Bern, Switzerland, [2]Institute for Mummy Studies, Eurac Research, Bolzano, Italy, [3]Department of Prehistory, Archaeology and Ancient History, University of Valencia, Spain, [4]Department of Geological Sciences, University of Cape Town, South Africa, [5]Soprintendenza per i Beni Archeologici del Veneto, Settore territorio, Sede di Padova-Nucleo di Verona, Italy, [6]Department of Chemistry, Biochemistry and Pharmaceutical Sciences, University of Bern, Switzerland, [7]Department of Cultural and Environmental Heritage, PrEcLab - Laboratory of Prehistory, Protohistory and Prehistoric Ecology, University of Milano, Italy, [8]Soprintendenza Archeologia, Belle Arti e Paesaggio per le province di Verona, Rovigo e Vicenza, Italy.

The Late Iron Age (4th -1st centuries BCE) was characterized by frequent movements of people and goods across the Alpine range resulting in the settlement of "Celtic" groups in the Italian peninsula. Explorative stable isotope data of oxygen and carbon of the *Cenomani* of Seminario Vescovile (SV-Verona, Italy 3rd -1st c. BCE) suggested the presence of few non-local individuals in this community. Here, we build on these preliminary results and expand them by analyzing a larger sample from SV and additional isotopic ratios. Our aim is to clarify the degree of mobility in this group, the potential origin of non-locals, and the correlation between mobility, sex, and funerary treatment. We analyze the ratios of sulfur ($\delta^{34}S$; N=127) and strontium ($^{87}Sr/^{86}Sr$; N=57) from bone collagen and dental enamel respectively. We establish the local isotopic range based on published soil, plants and water values, as well as on the human and animal variability by using as criterion the median ± 3MAD (three times the median absolute deviation). We check for differences between sexes and funerary features in $\delta^{34}S$ and $^{87}Sr/^{86}Sr$ by means of Mann-Whitney tests. The highest frequency of non-locals (10/57: 17.5%) is found when considering $^{87}Sr/^{86}Sr$, with at least two individuals showing values consistent with an alpine/transalpine origin. No trend characterizes isotopic values based on sex or funerary treatment. Our data allow revising previous estimates about a reduced mobility at SV, while supporting at the same time a link between this population and both alpine and transalpine contexts.

This research was supported by a Swiss National Science Foundation grant to Marco Milella and Albert Zink (grant number: 10531FL_197103/1).

Dental microwear complexity as a defining feature of early agriculturalists in the American Midwest

EMMA M. LAGAN[1], CHRIS W. SCHMIDT[2], LUCA FIORENZA[3], ROBERT A. COOK[1], MARK HUBBE[1] and DEBBIE GUATELLI-STEINBERG[1]

[1]Anthropology, The Ohio State University, [2]Anthropology, University of Indianapolis, [3]Anatomy and Devleopmental Biology, Monash University

Dental microwear texture analysis (DMTA) provides a means for identifying dietary groups through measures of anisotropy (epLsar) and complexity (asfc). Previous analyses of worldwide samples demonstrated a decrease in complexity from foragers (1.47) to farmers (1.36) to pastoralists (0.89), as diets become softer and less abrasive. Concomitantly, there is an increase in anisotropy from foragers (0.0027) to pastoralists (0.0034) to farmers (0.0035). The present study analyzes two transitional farming Fort Ancient sites in the Middle Ohio River Valley (c.1000-1250 CE) to determine whether their DMTA signatures reflect their presumed diets. We found that the two sites, Guard and Turpin, have average complexity values comparable to or greater than those of foragers (2.145 n=9, 1.474 n=20, respectively), which does not reflect a transitional diet. We note, however, that early farmers in the American Midwest, spanning consistently exhibit higher complexity than either foragers or farmers worldwide. Guard's average anisotropy is similar to that of foragers (0.00285, n=9), while Turpin's is similar to that of farmers (0.0032), indicative of dietary variation that might be expected during Fort Ancient's dietary transition. To explore why complexity in the American Midwest is higher than average, Guard and Turpin are further compared using additional sources of dietary information (e.g., isotopic and ethnographic data) to Late Woodland, Fort Ancient, and Mississippian sites as well as to farmers from a variety of regions. Plausible explanations include consumption of wild foods, particularly nuts and seeds, and/or eating dried corn kernel fragments that may have persisted in food preparations as hominy.

This research was supported by the Department of Anthropology and the Graduate School (Alumni Grant, Presidential Fellowship) at The Ohio State University.

Morphometric variation among Plio-Pleistocene hominin proximal radii

MICHAEL R. LAGUE

Biology Program, Stockton University

Although the proximal radius is relatively common in the Plio-Pleistocene hominin fossil record, previous studies of this element have each included a different small subset of available specimens. A more complete comparative analysis is needed to determine the extent to which the radii generally attributed to *Homo* are similar to one another and whether they possess

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

a consistent set of features that differentiates them from australopith radii. This study evaluates a large sample (n = 16) of early hominin proximal radii in the context of variation among extant hominoids to improve our understanding of radial shape variation and to clarify the taxonomic status of disputed/uncertain specimens. The fossils include representatives of at least three genera (*Australopithecus*, *Paranthropus*, *Homo*). Landmark data of the radial head were collected along with measurements of radial neck width from 3D surface scans. Multivariate ordination techniques were used to explore morphometric affinities among specimens and resampling procedures were used to assess the magnitude of variation within fossil groups and between specimen pairs. The results indicate two morphotypes (*Homo* vs. australopiths) among the fossils, with australopith radii exhibiting more chimpanzee-like radial head morphology. Contrary to previous suggestions, early *Homo* is more similar to australopiths than to modern humans with respect to medial beveling of the radial head. *P. boisei* differs somewhat from other australopiths in head morphology and in its unusual degree of mediolateral neck constriction. The radial (and humeral) morphology of the KNM-ER 1500 skeleton is inconsistent with its conventional attribution to *P. boisei*.

Supported by grants from the Leakey Foundation and the Wenner-Gren Foundation to J.M. Plavcan & C.V. Ward.

The primate feeding system does not optimize energetic expenditure

MYRA F. LAIRD[1,2], MICHAEL C. GRANATOSKY[3], CLÁUDIA MISUE KANNO[4], CHRISTINE E. WALL[5], JOSÉ AMÉRICO DE OLIVEIRA[6] and CALLUM F. ROSS[7]

[1]Basic and Translational Sciences, University of Pennsylvania, [2]Integrative Anatomical Sciences, University of Southern California, [3]Department of Anatomy, New York Institute of Technology College of Osteopathic Medicine, [4]Emergency Department, Araçatuba Dental School, Universidade Estadual Paulista, Araçatuba, [5]Department of Evolutionary Anthropology and Duke Lemur Center, Duke University, [6]Department of Basic Sciences, Araçatuba Dental School, Universidade Estadual Paulista, Araçatuba, [7]Department of Organismal Biology and Anatomy, University of Chicago

Increasing body size is associated with sweeping anatomical, ecological, and behavioral changes: across species, larger body sizes are accompanied by higher metabolic energy budgets and increased performance demands. Most studies have focused on explaining inter-specific allometric relationships within separate biomechanical systems; however, direct, intra-specific comparisons between biomechanical systems promise insight into general principles of musculoskeletal design and scaling performance demands. The energetic costs of cyclical chewing are poorly understood, and these costs have not been studied across different body sizes or compared to the locomotor system. We directly compared the metabolic costs of cyclic locomotion and chewing to test the assumption that biomechanical systems are optimized to reduce energetic expenditure.

We collected energetic data from twenty-nine semi-wild tufted capuchins at the Araçatuba Dental School, Universidade Estadual Paulista, Brazil ranging in body mass from 1.2 – 4.2 kg. Open flow respirometry was used to measure CO_2 production, O_2 consumption, water vapor pressure, barometric pressure, room temperature, and air flow rates while each animal chewed tea biscuit or locomoted on a moving treadmill. The mass-specific incremental costs of locomotion and cost per cycle decreased significantly as animals increased in size, which is consistent with most mammals. In contrast, mass-specific incremental costs of cyclical chewing and cost per cycle increased significantly with body mass. These data suggest divergent relationships of feeding and locomotor systems with body mass in tufted capuchins. In the feeding system, energetic efÔ¨Åciency may be a less important performance criterion than control of bite force and displacement.

Funding was provided by NSF BCS-1062239.

Core competencies, certification, and licensure: the future of forensic anthropology practice and education

NATALIE R. LANGLEY[1], MARIATERESA A. TERSIGNI-TARRANT[2,3], NICHOLAS V. PASSALACQUA[4], CHRISTIAN M. CROWDER[5,6], HEATHER M. GARVIN[7], WENDY MCQUADE[8], MIRIAM SOTO MARTINEZ[9] and MARIN A. PILLOUD[10]

[1]Department of Laboratory Medicine and Pathology, Mayo Clinic, [2]Department of Pathology, Saint Louis University School of Medicine, [3]SNA International, in support of Defense POW-MIA Accounting Agency, [4]Anthropology and Sociology Department, Western Carolina University, [5]Tarrant County Medical Examiner and Forensic Science Laboratories, Fort Worth, TX, [6]Department of Sociology and Anthropology, University of Texas at Arlington, [7]Department of Anatomy, Des Moines University, [8]Center for Human Identification, University of North Texas Health Science Center at Fort Worth, [9]Harris County Institute of Forensic Sciences, Houston, TX, [10]Department of Anthropology, University of Nevada, Reno

Forensic anthropologists assist decedent identifications, medicolegal investigations and court proceedings; however, no requirements exist for practice. An American Board of Forensic Anthropology (ABFA) survey of agencies employing forensic anthropologists indicated only 37% of respondents have a forensic anthropologist on staff; of these, 57% are ABFA certified. Unqualified practitioners may make errors that affect case outcomes, potentially harming the public and impeding investigations. This presentation discusses changes in ABFA certification and implications for education, training, and practice.

The ABFA was accredited by the Forensic Specialties Accreditation Board as a Conformity Assessment Body in 2004 and has offered certification (Diplomate) for forensic anthropologists with a PhD since 1977. Diplomates are qualified, vetted, adherent to a code of ethics, and maintain certification through continued professional development. The ABFA recently approved the development of a new tier of certification (Analyst) for applicants with a minimum of a Master's degree. This expansion advances the ABFA's goals of strengthening forensic anthropology, serving the public, and discouraging practice by unqualified individuals.

The ABFA has defined core competencies for each certification level (Analyst and Diplomate) and aligned certification processes with these competencies. These core competencies will be disseminated to stakeholders (educators, students, practitioners, and employers), providing an understanding of the knowledge and skills required to practice forensic anthropology. Such information should be used to structure education and training, and possibly create an accreditation for forensic anthropology programs. Finally, the ABFA is exploring licensure to ensure qualified individuals are practicing.

A new three-dimensional musculoskeletal model of the chimpanzee upper body and forelimb

SUSAN G. LARSON[1], ARAVIND SUNDARARAJAN[2], AVERY WILLIAMS[3], NICOLE MAHMOOD[4], BRIAN R. UMBERGER[5] and MATTHEW C. O'NEILL[2]

[1]Anatomical Sciences, Stony Brook University School of Medicine, [2]Anatomy, Midwestern University, [3]College of Medicine, University of Arizona, [4]College of Veterinary Medicine, Midwestern University, [5]School of Kinesiology, University of Michigan

Musculoskeletal modeling and simulation are robust methods for integrating complex morphological and experimental data, and permit estimation of quantities that are difficult or impossible to measure in vivo. Modeling studies of chimpanzees have provided important insights into the mechanics, energetics and control of their locomotor behavior, facilitating the functional interpretation of early hominin fossils. In this study, we develop a model of the chimpanzee upper body and forelimb in order to expand the computational analysis of chimpanzee behaviors.

A new generic model of the chimpanzee upper body and forelimb was created in SIMM and OpenSIM. The model includes geometric representations of the torso, scapula, clavicle, arm, forearm and hand. Kinematic descriptions

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

of the forelimb joints, and Hill-type models of 30 forelimb muscles represented via 49 muscle-tendon elements, were parameterized based on cadaveric measurements. The model allows calculation of muscle-tendon lengths and moment arms, as well as force and moment generation capabilities of the shoulder, elbow, wrist, metacarpophalangeal and interphalangeal joints of digits 2-5, as well as the carpometacarpal joint of digit 1. To evaluate model robustness, we compare the model-predicted and experimentally-measured muscle moment arms. Inverse kinematics of the forelimb in bipedal walking and knucklewalking were generated to further assess model robustness.

In general, our model reproduced both the direction and magnitude of the measured moment arm functions, and coupled with the initial inverse kinematic results, indicate that our musculoskeletal model is suitable for inverse and forward dynamics analyses of chimpanzee forelimb function during knucklewalking, climbing and other movement tasks.

Supported by NSF BCS-0935321, NSF BCS-0935327

Rethinking genotype-phenotype mapping: hair as a case study

TINA LASISI[1], ARSLAN ZAIDI[2,3], NINA G. JABLONSKI[4] and MARK D. SHRIVER[4]

[1]Quantitative & Computational Biology, University of Southern California, [2]Department of Genetics, Cell, and Developmental Biology, University of Minnesota, [3]Institute of Health Informatics, University of Minnesota, [4]Department of Anthropology, The Pennsylvania State

This abstract is being submitted as part of the symposium: "Toward a holistic approach - Investigating the genetic underpinnings of phenotypic variation."

The study of hair morphology has long been hampered by the use of subjective typologies to measure variation and by the absence of data on African and African-descendant populations among other groups with tightly curled hair.

Here, we present results from the application of novel high-throughput methods to measure various hair characteristics in admixed US participants with African and European ancestry. By conducting a GWAS and cross-referencing our significant SNPs against previously reported loci, we identified 24 replicated variants at a nominal significance level of P = 0.05 or lower. Moreover, we were able to replicate the direction of effect sizes for previously reported hair-linked loci. Additionally, we find that certain replications are more difficult to interpret, pointing to complex relationships between different hair characteristics. Lastly, we demonstrate the usefulness of using continuous quantitative phenotypic data over classification through the replication of certain previously reported hair loci using a categorical phenotyping method and others with quantitative methods.

Complex phenotypes, like hair morphology, may not be accurately mapped using conventional methods because they are multi-dimensional and which dimension best defines a "phenotype" is subjective. Our results suggest that we may benefit from rethinking genotype-phenotype maps by exploring connections between different definitions of the same phenotype. By re-analyzing existing data with this approach, we might be able to obtain a more in-depth understanding of the genetic architecture of complex traits.

This research is supported by The Wenner-Gren Foundation (Gr. 9911) and the National Science Foundation (No. 1847845).

Clavicular length, growth, and dimorphism in hominin evolution

NATALIE M. LAUDICINA[1,2] and MATT CARTMILL[2,3]

[1]Biomedical Sciences, Grand Valley State University, [2]Anthropology, Boston University, [3]Evolutionary Anthropology, Duke University

The broad shoulders of human newborns often present serious difficulties in traversing the birth canal during labor. Evolutionary theory would lead us to expect selection for shorter clavicles to alleviate the risk of shoulder dystocia during human childbirth. However, such selection pressures may have been countered by competing pressures favoring broad shoulders (in throwing, fighting, and/or intersexual selection) in adults. How these competing factors have combined to influence clavicle length throughout hominin evolution is unclear. We find that modern human clavicles are average in relative length for large hominoids. Clavicle length in great-ape species and modern humans varies isometrically with body mass, so that intersex differences in clavicle length simply reflect body-size dimorphism. This pattern conforms to H. Dunsworth's thesis that such differences are commonly not products of natural selection, but merely incidental byproducts of low estrogen levels that delay post-pubescent epiphyseal fusion in males. However, prolonged male growth and the sexual dimorphism resulting therefrom are neither inevitable (cf. gibbons) nor selectively neutral. These male growth patterns are attained at a considerable cost in both metabolic-resource allotment and postponement of reproduction, and will not be preserved unless they confer a selective advantage. The distinction between proximate and ultimate causes, disputed by Dunsworth, must still be drawn in explaining sexual dimorphism. Neandertals and Upper Paleolithic humans exhibit significantly greater dimorphism (positive clavicle-length allometry) than modern humans. Selection favoring broader male shoulders may have been relaxed in recent human populations, resulting in reduced sexual dimorphism.

Habitual physical activity levels and foot strength and stiffness

CHLOÉ LAUER[1], NICHOLAS B. HOLOWKA[2], THOMAS S. KRAFT[3] and IAN J. WALLACE[1]

[1]Department of Anthropology, University of New Mexico, [2]Department of Anthropology, University at Buffalo, [3]Department of Anthropology, University of Utah

Many people in post-industrial societies have weaker foot muscles and lower foot arch stiffness compared to people in non-industrial societies. The most common explanation for this phenomenon relates to footwear: people in post-industrial societies are thought to develop weaker, less stiff feet due to their use of shoes with features that restrict foot motion (e.g., arch supports, toe boxes), while people in non-industrial societies are more likely to be habitually barefoot or minimally shod. Here, we propose a different but complementary hypothesis: risk of developing weak, pliable feet may be related to the increasingly sedentary lifestyles of people in post-industrial societies. That is, we hypothesize that people who do not use their feet much for physical activity are less likely to develop strong, stiff feet. To test this hypothesis, we collected data on physical activity levels and foot strength and stiffness among a sample of adults in the United States who normally wear restrictive footwear. We measured daily step counts and time spent in moderate-to-vigorous physical activities using accelerometry, cross-sectional areas of foot muscles using ultrasound, longitudinal arch height and stiffness while standing using photography, and dynamic longitudinal arch stiffness during walking using kinematic and kinetic data. Data collection is ongoing, but preliminary results from 13 individuals (n=7 females) suggest that physical activity levels are not significantly associated with foot strength or stiffness. If similar findings are obtained from a larger sample, the results of this study underscore the key role of footwear type in determining foot strength and stiffness.

Funding was provided by a Maxine Graves Undergraduate Award (to C.L.) and NSF BCS-2142091 (to T.S.K. and I.J.W.).

Influences of turning on muscle forces of the foot and ankle

STEVEN G. LAUTZENHEISER[1], ADAM D. SYLVESTER[2] and PATRICIA ANN. KRAMER[3,4]

[1]Department of Anthropology, University of Tennessee Knoxville, [2]Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine, [3]Department of Anthropology, University of Washington,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

[4]Department of Orthopaedics and Sports Medicine, University of Washington

Musculoskeletal models estimate muscle forces and have been commonly used to understand differences among people and gaits, but little research exists regarding how the body produces a directional change, a ubiquitous activity in human locomotion. Understanding how turning forces are produced by and affect the elements of foot and ankle complex (FAC) is important because the foot is the interface between the rest of the body and the substrate. In this work, we ask: do turning FAC muscle forces differ from those of straight path walking?

Kinematic and kinetic data were collected using a Qualisys motion capture with four Kistler force plates. Five adults (ages 19-55) walked unshod at their self-selected normal velocity in four conditions: straight line, 45° turn with and without a crossover-event, and 90° turn. A musculoskeletal model was used to calculate muscle forces in the lower limb (42 muscles; 169 muscle elements in each limb). Maximum muscle forces for the foot evertor and invertor muscles were examined via Students *t*-test to determine if differences exist between turning and straight path walking.

Maximum forces produced by *fibularis brevis*, *tibialis anterior*, and *tibialis posterior* are different between straight path and all turning conditions during braking (all p's<0.05) but not propulsion. Our results suggest that these FAC muscle forces stabilize the body as it brakes to make a turn. Given that bones and soft tissues adapt ontologically and in evolutionary time to applied forces, turning conditions should be included in efforts to understand human locomotion.

Dental wear in wild chimpanzees (*Pan troglodytes)* : Using *in vivo* photographs to assess molar enamel

ADAM J. LAW[1], BEN J. FINKEL[1] and MÁIRE A. MALONE[2,3]

[1]Anthropology, University of Michigan, [2]Institute of Human Origins, Arizona State University, [3]School of Human Evolution and Social Change, Arizona State University

Tooth wear accumulates over the lifespan, yet whether dental senescence diminishes chewing performance in great apes remains uncertain. Studies of primate dentition rely on data from postmortem specimens, precluding the examination of wear ontology, or from invasive measurement in field captures. To address these challenges, we adapted a technique from Scott (1979) to measure teeth from *in vivo* photographs. We scored molars on an ordinal scale based on the degree of secondary dentine exposure, as enamel is a key indicator of the functional life of the tooth. We applied these methods to photographs of wild chimpanzees (*Pan troglodytes*) and coded 87 image-series from 36 adult males in the Ngogo community from 2003- 2019. To validate methods, we built cumulative link mixed models to examine correlates of wear and assess inter-observer reliability. Researcher ID was not a top predictor (AIC <10% ω) although one coder had higher wear scores (Beta=0.75±0.31). Further, molar number (Beta=-1.39±0.14) and subject age (Beta=-1.9±0.02) were positive predictors of wear score, although there was no difference between the wear of the second and third molars. We also matched five post-mortem photo-series to corresponding *in vivo* subjects for which wear scores did not vary significantly. These findings match most predicted patterns of wear and support our measures. We discuss ways to improve this method for future studies that may incorporate this approach to measure dental wear in wild primates.

Funding statement: The Leakey Foundation (N025458), National Science Foundation (BCS-1927384), American Philosophical Society, International Primatological Society, University of Michigan.

A novel workflow for quantifying 3D skeletal anatomy of living humans for morpho-functional analysis

AUSTIN B. LAWRENCE[1], KEVIN M. MIDDLETON[2], JAMIE B. HALL[3], JACOB THOMAS[4], TRENT M. GUESS[3,5] and CAROL V. WARD[1]

[1]Department of Pathology and Anatomical Sciences, University of Missouri, Columbia, [2]Division of Biological Sciences, University of Missouri, Columbia, [3]Department of Physical Therapy, University of Missouri, Columbia, [4]School of Health Professions, University of Missouri, Columbia, [5]Department of Orthopaedic Surgery, University of Missouri, Columbia

Accurate and repeatable assessments of three-dimensional (3D) skeletal morphology are critical to interpretations of functional anatomy, and, therefore, reconstructions of behavior and ecology in the fossil and archaeological records. In skeletal specimens, these goals can be accomplished using *in-silico* models derived from 3D laser scan, photogrammetry, or computed tomography (CT) data. Assessments of skeletal morphology in living subjects, especially humans, are more challenging and are often either cost-prohibitive (e.g., magnetic resonance imaging) or expose subjects to high doses of ionizing radiation (e.g., CT). Here, we present a new, open-source method for assessing 3D skeletal morphology of living human subjects using ultra-low dose biplanar radiographs. Biplanar radiographs are obtained using an EOS Imaging System (EOS Imaging, Inc.) with the subject standing so that the relative positions of skeletal elements are captured in a loaded, functional position. Landmarks are manually placed on features of interest in radiographs using the StereoMorph package for R. Landmark coordinate data are then processed, undistorted, and scaled using custom R scripts. We combine this workflow for quantifying 3D skeletal morphology with established tools for 3D motion analysis to directly test hypothesized form-function relationships in the human post-cranial skeleton. We demonstrate this workflow with an analysis of lower-limb skeleton torsional alignment and walking biomechanics in a sample of healthy adult humans (n=30). This approach provides a safe (i.e., lower radiation) and lower cost solution for *in-vivo* analyses of musculoskeletal form and function applicable to multiple human cohorts, as well as to other biplanar radiograph platforms and study organisms.

This study is funded by the National Science Foundation (BCS Award #2217844), the Leakey Foundation, Sigma Xi, and the Universirty of Missouri.

"The best scanners you'll ever have": how 3D technology can complement what we see with our own eyes, and where nothing but the fossil will do

JULIE LAWRENCE

Human Evolutionary Biology, Harvard University, Institute of Human Origins, Arizona State University, School of Human Evolution and Social Change, Arizona State University

Computed Tomography has allowed us to study the internal structures of fossil material that would otherwise only be accessible through destructive methods. This paper evaluates the advantages of 3D scanning equipment, image analysis, and geometric morphometric methods (GMM) in elucidating the already visible macromorphology of fossil specimens with surface scans. Through examples from the study of craniofacial morphology (browridge, dental arcade, midface) in australopiths, early *Homo* and comparative extant apes, I demonstrate where GMM highlight holistic morphological patterns. I compare the effect of using of standard landmarks, semi-landmarks, and linear measurements to study taxonomic variation in different regions of the face.

Paleoanthropology is a science of fossils, but access to fossil material and the manner by which such data are shared remain contentious issues for the discipline. In theory, greater use of scans could protect fossils from the hazards of handling, and allow more scientists to perform additional analyses that further the discipline. Despite the increasing use of 3D imaging techniques in paleoanthropology, there has been very little discussion of the cumulative error during scan acquisition and post-processing. This paper will comment on these issues, and on how far paleoanthropology has come in making fossil data more visible to a broader audience, where it is lacking, and what the future may hold.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

ABSTRACTS

Natural selection of immune and metabolic genes associated with health in two lowland Bolivian populations

AMANDA J. LEA[1,2], ANGELA GARCIA[3], JESUSA AREVALO[4], JULIEN F. AYROLES[5,6], KENNETH BUETOW[3], STEVEN W. COLE[4], DANIEL EID RODRIGUEZ[11], MAGUIN GUTIERREZ[7], HEATHER M. HIGHLAND[8], PAUL L. HOOPER[9], ANNE JUSTICE[8], THOMAS S. KRAFT[10], KARI E. NORTH[8], JONATHAN STIEGLITZ[12], HILLARD KAPLAN[13], BENJAMIN C. TRUMBLE[14,3] and MICHAEL D. GURVEN[15]

[1]Department of Biological Sciences, Vanderbilt University, [2]Child and Brain Development Program, Canadian Institute for Advanced Research, [3]Center for Evolution and Medicine, Arizona State University, [4]Department of Medicine, University of California: Los Angeles, [5]Department of Ecology and Evolution, Princeton University, [6]Lewis Sigler Institute for Integrative Genomics, Princeton University, [7]Gran Consejo, Tsimane, [8]Department of Epidemiology, University of North Carolina: Chapel Hill, [9]Economic Science Institute, Chapman University, [10]Department of Anthropology, University of Utah, [11]Institute of Biomedical Research, Faculty of Medicine, San Simon University, [12]Institute for Advanced Study, Toulouse, [13]Institute for Economics and Society, Chapman University, [14]School of Human Evolution and Social Change, Arizona State University, [15]Department of Anthropology, University of California: Santa Barbara

A growing body of work has addressed human adaptations to diverse environments, but few studies have connected putatively selected alleles to phenotypes. Studies of natural selection and genotype-phenotype relationships in under-represented populations hold potential to uncover previously undescribed loci underlying evolutionarily- and biomedically-relevant traits. Here, we worked with the Tsimane and the Moseten, two Amerindian populations inhabiting the Bolivian lowlands. We focused most intensively on the Tsimane, because long-term anthropological work with this group has shown that they have a high burden of both macro and microparasites, as well as minimal cardiometabolic disease or dementia. We therefore generated genome-wide genotype data for Tsimane individuals to study natural selection, and paired this with blood mRNA-seq as well as cardiometabolic and immune biomarker data generated from a larger sample that included both populations. In the Tsimane, we identified 21 non-overlapping regions that are candidates for selective sweeps, as well as 5 immune traits that show evidence for polygenic selection (e.g., CRP levels and the response to coronaviruses). Genes overlapping candidate regions were enriched for known involvement in immune-related traits, such as abundance of lymphocytes and eosinophils. Importantly, we were also able to draw on extensive phenotype information for the Tsimane and Moseten and link five regions (containing the *PSD4*, *MUC21* and *MUC22*, *TOX2*, *ANXA6*, and *ABCA1* genes) with biomarkers of immune and metabolic function. Together, our work highlights the utility of combining long-term anthropological study with evolutionary analyses to gain new insight into the genetic basis of health-related traits.

This work was supported by the Helen Hay Whitney Foundation, the Canadian Institute for Advanced Research, and the National Institute on Aging (R01AG024119, R56AG024119, RF1AG054442).

An examination of changes in nationwide preterm birth rates during the early COVID-19 pandemic

ZAIRA P. LEAL, SHEILY LIM and AMY L. NON

Anthropology, University of California San Diego

Black and Latina women in the United States (U.S.) have historically experienced disproportionately higher preterm birth rates than White women. The causes of preterm births are largely unknown, but are more common among women with less access to medical care and education, and women with high levels of stress. The COVID-19 pandemic exacerbated stressors, particularly around the nationwide lockdown in March 2020. Surprisingly, many studies report *reduced* preterm birth rates early in the pandemic, particularly in wealthier nations. However, few analyzed if changes varied by race/ethnicity, nativity, or socioeconomic status. We analyzed nationwide U.S. preterm birth data from the Center for Disease Control between 2016-2020. We observed changes in seasonal patterns in 2020 relative to prior years. Using Fisher exact tests, we compared singleton live preterm births in the months of April-June in 2019 versus 2020, to control for seasonal fluctuations and rising rates over time. Logistic regression models were adjusted for maternal age, sex of baby, nativity status, education, race/ethnicity, delivery type, and interactions among these factors. We hypothesized that more educated women and White women would experience the greatest reductions in preterm births post-COVID, as they may benefit most from working remotely. We found significant reductions in preterm births among both Hispanic and White women (OR=0.9607, OR=0.9712, both $p<0.001$), across all educational groups, among US-born women (OR=0.971, $p<0.0001$), among vaginal births (OR=0.9609, $p<0.0001$), but only marginally for C-section births (OR=0.9840, $p=0.0630$). Further research is needed to determine the causes of these varied changes early in the pandemic.

The Dogs of Krasnosamarskoe: The Use of a Novel Dentine Microsampling Technique to Investigate Canid and Human Diets

ALICE LEE[1,2], RICK SCHULTING[2] and DAVID ANTHONY[3]

[1]Laboratories of Molecular Anthropology and Microbiome Research, Department of Anthropology, University of Oklahoma, [2]School of Archaeology, University of Oxford, [3]Department of Anthropology, Hartwick College

In recent years a small number of studies have been published on the use of microsampling to analyze dog dentine, a material which through isotopic analysis can provide a wealth of information on the diet of humans and canids. However, there is currently no systematic method to sample this material. The canid assemblage at Krasnosamarskoe, a Bronze Age site in the Samara Valley, was used to test the first use of a systematic dentine micro sampling technique developed specifically for canine dentition. This technique allows for the analysis of a finer temporal range than has been possible previously in canid dentine analysis due to the utilization of information on the timetable of dog dentition development. The isotopic results of this analysis has provided information on the canids diet during a very narrow window of time and, through comparison with previously collected isotopic data from humans in the Samara Valley further emphasizes the use of dog dietary analysis as a proxy for that of humans. Additionally some evidence of seasonal shifts in food availability may have been found but the narrow window provided by dentine microsampling restricts the ability to fully explore this possibility, a downside of this technique. However we can conclude that further uses of this canid dentine micro sampling technique may be insightful in other cases, such as where very few if any human samples are available for analysis, providing a more finely tuned timeframe through which human and canid diets can be analyzed than was previously possible.

Absolute, Relative, and Conditional Sociality Metrics

KEVIN C. LEE[1,2] and KEVIN E. LANGERGRABER[1,2]

[1]School of Human Evolution and Social Change, Arizona State University, [2]Institute of Human Origins, Arizona State University

Students of animal sociality are faced with many choices when it comes to methods in data collection and analyses. While the assumptions and implications of some of these choices have been explored in greater detail, others have not. Using real-world data from a large study population of wild chimpanzees, we examined potential impacts of two classes of analytical choices commonly utilized in studies on social bonding in non-human animals: 1) standardizing metrics by group and 2) controlling for differences in opportunity. We demonstrate that although the overall impact of these choices may appear small—as indicated by high positive correlations in results with and without the respective analytical controls—the differences are often concentrated in a predictable, biased subset of the data. These differences can substantially alter perceptions of the relative sociality between individuals/dyads,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

especially if subjects are categorized based on the common practice of rank-ordering thresholds. Additionally, these choices have the potential to affect downstream analyses—linking sociality to fitness outcomes, for example—again in a predictable, biased manner, though the significance of the impact will be context-dependent. The appropriate analytical choices are ultimately driven by the data and questions at hand, but we encourage analysts to carefully consider the assumptions and implications of these choices, and further suggest that their choices may be guided by the theorized mechanisms linking sociality and outcomes of interest.

Funding support from The Leakey Foundation, National Geographic Society, International Society for Human Ethology, Arizona State University

Investigating Prehistoric Migration into the Japanese Archipelago through Phylogenic Networks

SOL LEE[1], MIGUEL G. VILAR[1,2], NINA J. ST. HILLAIRE[1,3] and NICK COSTELLO[3]

[1]Anthropology, University of Maryland, College Park, [2]Research and Development, Family Tree DNA, [3]Biology, University of Maryland, College Park

Archaeologists have suggested early migration into the Japanese archipelago occurred through the Korean peninsula as early as 30,000 BCE. While geographic distance likely provided subsequent isolation, genomic analyses indicate that Japanese today maintain a closer affinity to Koreans than to other Asian populations. Investigating the phylogenetic relationships between the two regions will shed light on population origins and inter-population interactions.

To assess population interactions and directionality of migration between Japan and Korea, we researched mitochondrial DNA (mtDNA) from more than 400 individuals from various publications and public databases. Genomes from mtDNA haplogroups D4a1, M9a1a, M7b1a1a1, and A5a were further characterized using Median-Joining Network phylogenies.

The older and geographically-dispersed D4a1 and M9a1a showed patterns associated with Pleistocene migration through east Asia to the Korean peninsula and the islands. In contrast, M7b1a1a1 and A5a displayed patterns informing on more recent population interactions, possibly associated with the introduction of wet rice cultivation to Japan in the last 3,000 years.

Neither haplogroup D4a1 or A5a showed an ancestor-descendant relationship between Korea and Japan, yet showed the Japanese types to be younger. In contrast, M7b1a1a1 and M9a1a phylogenies suggested an ancestor-descendant relationship between the two regions, supporting the hypothesis that the Korean peninsula likely served as the entryway to Japanese archipelago. M9a1a and D4a1 also showed lineage sharing between Japan and China associated with gene flow from recent interaction between the countries. Future autosomal and Y-chromosome DNA would inform this research and clarify the directionality of gene flow.

New hominin fossils from Drimolen Cave and their bearing on microevolution in *Paranthropus robustus*

ANGELINE LEECE[1], JESSE MARTIN[1], DAVID STRAIT[2], GARY SCHWARTZ[3] and ANDY HERRIES[1]

[1]Archaeology and History, La Trobe University, [2]Anthropology, Washington University in St. Louis, [3]Human Evolution and Social Change, Arizona State University

Martin and Leece et al (2021) argued that morphological differences between different samples of *Paranthropus robustus* represented microevolution in a hominin lineage. The study presented by Martin and Leece et al (2021) demonstrated that the Drimolen Main Quarry (DMQ) *P. robustus* sample is likely ancestral to the Swartkrans Member 1 *P. robustus* sample. However, phylogenies based solely or predominately on cranial traits can differ from studies based solely or predominately on dental traits. The study presented here has assessed the DMQ *P. robustus* dentitions in an effort to further investigate the newly presented microevolution hypothesis as compared to the long-standing hypothesis that such morphological differences can be attributed to marked sexual dimorphism in the species. Quantitative assessment of permanent *P. robustus* dentitions has been conducted and found to be parsimonious with either hypothesis. However, given that the morphology of deciduous dentitions is thought to be of high phyletic weight, qualitative assessment of these specimens has also been conducted. Cladistic analyses of deciduous dental character traits, both independently and in conjunction with the trait matrix presented by Martin et al (2021), were found to support the microevolution hypothesis.

Australian Research Council Discovery Grant no. DP170100056

Tooth enamel nitrogen isotope ratios as a novel proxy for diet reconstruction in the archaeological record: a case study from Central America

JENNIFER N. LEICHLITER[1,2,7], ASHLEY E. SHARPE[3], JONATHAN D. CYBULSKI[4,5], MARISSA VINK[1,2,6,7], ALFREDO MARTINEZ-GARCIA[2,7] and TINA LÜDECKE[1,2,7]

[1]Emmy Noether Group for Hominin Meat Consumtion, Max Planck Institute for Chemistry, [2]Organic Geochemistry Group, Max Planck Institute for Chemistry, [3]Center for Tropical Paleoecology and Archaeology, Smithsonian Tropical Research Institute, [4]Marine Studies, Smithsonian Tropical Research Institute, [5]Swire Institute of Marine Science (SWIMS), and Stable Isotope Ratio Mass Spectrometry Laboratory (SIRMS), The University of Hong Kong, [6]Department of Archaeological Sciences, Leiden University, [7]Department for Climate Geochemistry, Max Planck Institute for Chemistry

Nitrogen isotope ratios ($\delta^{15}N$ values) are a well-established geochemical tool for investigating diet. However, the application of this tool in the archaeological record can be limited by poor preservation of organic matter (collagen) in skeletal material (bone/dentine), particularly in tropical regions and in samples older than 100 kya. This study represents the first measurements $\delta^{15}N$ of organic matter preserved in tooth enamel ($\delta^{15}N_{enamel}$) in the archaeological record of Central America.

We present $\delta^{15}N_{enamel}$ values for fauna from one lowland (Ceibal) and one highland (Kaminaljuyu) Maya archaeological site in Guatemala (~ 1000 BCE – 1000 CE). We measured $\delta^{15}N_{enamel}$ values of 43 individuals belonging to six mammalian taxa. Herbivores (white-tailed deer, tapir, paca) have lower mean $\delta^{15}N_{enamel}$ values (= 4.6 ± 1.1 ‰) than both omnivores (peccary; = 4.7 ± 1.0 ‰), and carnivores (jaguar, domestic dog; = 7.4 ± 1.7 ‰). These data show that $\delta^{15}N_{enamel}$ values for archaeological specimens record clear trophic differences between herbivores and carnivores. Additionally, bulk and compound specific amino acid $\delta^{15}N$ values were measured for the same taxa from these sites, permitting direct comparison of enamel and collagen isotope values. Our results indicate that diagenetically resistant tooth enamel records dietary information in a manner similar to collagen. This data highlights the potential of $\delta^{15}N_{enamel}$ as a new proxy for exploring diet in the archaeological record, particularly when used in combination with existing stable isotope data ($\delta^{13}C$, $\delta^{18}O$, $^{87}Sr/^{86}Sr$).

Funded by the American Association of Biological Anthropologists Cobb Professional Development Award (to J.L.); German Research Foundation Emmy Noether Fellowship LU 2199/2-1 (to T.L.) and the Max Planck Society (MPG).

Calibrating primate body mass growth spurts

STEVEN R. LEIGH, JULIE M. THOMAS, and YUTING GAO

Anthropology, University of Colorado Boulder

Body mass growth spurts influence primate adult body mass and mass dimorphism. Both the timing and intensity of growth spurts are correlated with adult body size, diet, and sexual selection. Here, we compare different quantitative approaches to calibrating anthropoid primate growth spurts to enhance our understanding of this key feature of ontogeny.

We use SITAR (Superimposition by Translation and Rotation [in R]) to investigate body mass growth patterns in a small sample of anthropoid primate species, comparing results to earlier

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

nonparametric investigations of anthropoid growth spurts. Repeated measures for individual animals derive from large captive samples available from the Primate Aging Database (*Callithrix jacchus*, *Chlorocebus aethiops*, *Cercocebus atys*, *Pan troglodytes*, *Gorilla gorilla*). Preliminary analyses investigate the timing, duration, and peak velocity of growth spurts for these species, comparing SITAR results to results from nonparametric approaches.

SITAR growth spurt estimates generally match parameters calibrated in earlier studies. Males of all these species (except common marmosets) exhibit growth spurts, concurring with earlier research. Female data match less closely, with lower magnitude growth spurts. Methods concur in showing correlations between spurts and species size. SITAR consistently measures greater peak velocities than nonparametric approaches.

High SITAR peak velocities are plausible, given that previous studies treat data cross-sectionally, which can dampen spurts. SITAR could increase objectivity by reducing judgements and steps needed for nonparametric analyses. SITAR also generates clear parameters with which to compare groups. However, underlying parametric foundations of SITAR need to be explored in interspecies comparisons.

Yerkes National Primate Research Center Grants (No. ORIP/OD P51OD011132 and U42PDP11023) supported data analyzed.

The Evolution of microRNA-regulated Gene Expression Networks in Ancient and Modern Humans

NATHAN H. LENTS[1], HUNTER R. JOHNSON[2] and JOSÉ A. GALVÁN[3]

[1]Sciences, John Jay College, [2]Mathematics and Computer Science, John Jay College, [3]Biology, New York University

The more we explore ancient hominin genomes, the more it becomes clear that subtle changes to gene expression networks played a major role in the diversification of hominins and our unique evolutionary trajectory over the last million years. Our laboratory recently reported the *de novo* evolution of microRNA genes in the human lineage, highlighting an underappreciated role of microRNAs in human evolution. In the present study, we have examined the entire pool of microRNA genes – and their siRNA products – in the genomes of Neanderthals, Denisovans, and modern humans. While the vast majority of these siRNAs are identical across these closely related species, each lineage harbors around two dozen unique siRNAs. Each unique siRNA regulates hundreds of gene targets throughout the body through binding to the 3'-UTR of the target mRNA. However, the target sequences themselves are also subject to co-evolution, which uncovered additional unique siRNA-mRNA relationships in each lineage. Using these unique siRNAs and their mRNA targets, we have reconstructed the gene expression networks whose regulation have evolved in unique ways in each of the hominin lineages. Interestingly, the gene expression networks most altered by recent evolution are those involved in embryonic development, specifically of the central nervous system, the heart, and the immune system. In addition, genes involved in cognitive functions, synaptic transmission, learning, memory, and sensation/perception are especially affected. The emerging picture is that microRNA gene evolution has had a direct and underappreciated role in the unique evolution of humans and our close relatives.

This project was funded by the PSC-CUNY Research Awards Program, #TRADB-51-502. Support for student research provided by the PRISM program at John Jay College, funded by USDOE, NSF, and NYSDOE.

"People with disabilities are left with another layer of complexity": Inclusive design and science communication in college paleobiology and paleoanthropology courses

TAORMINA LEPORE[1,2], JENNY LU[1,2], LAURA ARMSTRONG[4] and LESLEA J. HLUSKO[1,2,3]

[1]Integrative Biology, University of California Berkeley, [2]University of California Museum of Paleontology, (UCMP), [3]Centro Nacional de Investigación sobre la Evolución Humana, (CENIEH), [4]School of Pharmacy, University of California San Francisco

Research shows that inclusive learning environments are vital to building more inclusive science communities. We developed a project to equip undergraduate students with inclusive design methods in a class assignment, hypothesizing this would increase their awareness of and appreciation for disability accessibility, and increase accessibility for all.

During fall 2020 and spring 2022, we designed and implemented a 6-week-long digital media project in four U.S. college courses centered in paleobiology or paleoanthropology. Students produced a digital product that explained aspects of a peer-reviewed scientific article related to the course material. In addition to their science communication goals, students incorporated aspects of inclusive design, such as closed captioning, audio narration, colorblind accessible palettes, or alt text. Students were provided with pedagogical scaffolding and low-stakes formative assessments throughout.

From the combined post-course survey data, a majority of students (N=399) agreed that this project increased their awareness of disability accessibility (93%) and they considered disability to be a component of human diversity (96%) more than before. Between 82-85% of students also agreed that they felt more included in science as a result of this project. We used reflexive thematic analysis of student written responses to develop four overarching themes - including meaning-making around disability and accessibility, effort of noticing accessibility, and the privilege of knowledge access.

Having more frequent dialogue about disability accessibility in our courses can make a tangible difference in creating a more just and equitable learning experience for each of our students.

Funding provided by the Human Evolution Research Center and the SURF SMART undergraduate-graduate student mentorship program at UC Berkeley

Daubert: Advancing or constraining forensic anthropology research?

KATE M. LESCIOTTO[1] and ANGI M. CHRISTENSEN[2]

[1]Physiology & Anatomy, University of North Texas Health Science Center, [2]Laboratory Division, Federal Bureau of Investigation

The 1993 US Supreme Court decision of *Daubert v. Merrell Dow Pharmaceuticals, Inc*. set forth guidelines for judicial evaluation of the admissibility of scientific expert witness evidence and testimony, including assessments of whether the expert's methods were validated, had known error rates, and were generally accepted within the relevant field. In the aftermath, forensic anthropologists predicted a paradigm shift, urging researchers to pursue objective methods that would more strictly meet the *Daubert* criteria. This bibliometric study evaluated 1142 forensic anthropology articles published in the *Journal of Forensic Sciences* from 1972-2020 to examine how researchers had addressed issues of evidentiary admissibility. Over 10% of these articles referred to an evidentiary legal standard, including 85 articles specifically citing *Daubert*. A significant increasing trend in the proportion of articles that discussed legal standards since 1972 was identified (tau = 0.519; $p < 0.001$), and qualitative thematic analyses found that articles often placed the reported results within the framework of *Daubert* (n=43) or cited *Daubert* to justify the research (n=13). The data show a persistent and growing preoccupation with ensuring that forensic anthropology research is framed within the *Daubert* context. In practice, however, *Daubert* was intended as a flexible framework for judges to evaluate admissibility and was never intended to set standards for scientific research. Moreover, judicial precedent shows that it is extremely unlikely for forensic anthropological evidence to be excluded. Therefore, a new perspective is warranted, in which *Daubert* is not viewed as a rigid prescription for forensic anthropologists to constrain research design.

National Science Foundation (SES Award No. 2214747; co-funded by National Institute of Justice)

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

The metabolic allostatic response to stress (MARS) hypothesis: patterns from studies of human and non-human primate metabolic adaptation to cold stress and other stressors

STEPHANIE B. LEVY

Anthropology, CUNY Hunter College, New York Consortium in Evolutionary Primatology

Metabolic responses to environmental stressors are highly variable across individuals. The metabolic allostatic response to stress (MARS) hypothesis builds on studies of multiple stressor types across humans and non-human primates and provides a framework for testing the possible evolutionary origins of variation in metabolic responses to stress. The hypothesis proposes that, based on previous experience of the stressor, the body will predict that it is adaptive to accelerate energy use in response to a stressor (i.e. hypermetabolic response) when resources are likely to be sufficient and decelerate energy use (i.e. hypometabolic response) when resources are likely to be insufficient due to the individual's a) life stage; b) energy status; c) severity of the stressor; and d) duration of the stressor. Evidence from a study of metabolic responses to mild cold stress among the Yakut, a population indigenous to northeastern Siberia, provides preliminary support for this hypothesis. Data were collected from 57 young adults (32 women; 25 men; mean age 24.5 + 7.1 years old) during the early fall of 2015. Multiple regression analyses revealed that adults that reported spending more time outside during the previous week exhibited significantly smaller changes in cold-induced energy expenditure ($p=0.04$) and less evidence of BAT thermogenesis ($p=0.006$) in response to acute, mild cold stress, suggesting a hypometabolic response. These results will be contextualized within other studies of metabolic adaptation to stress among human and non-human primates, and the evolutionary significance of this hypothesis will be explored.

Northwestern University; Leakey Foundation; National Science Foundation DDRIG-1455804

Complicating categories: How historical documents can impact osteological interpretations

ALYSHA LIEURANCE[1], CHRISTINE BAILEY[2] and AMANDA WISSLER[3]

[1]Department of Anthropology, University of Pittsburgh, [2]Physical Anthropology, Cleveland Museum of Natural History, [3]Department of Anthropology, University of South Carolina

The Hamann-Todd Osteological Collection (HTOC), housed at the Cleveland Museum of Natural History, has been extensively used in anthropological and medical research due to its size and known demographic composition of 3,018 individuals who died between 1911-1939. While the collection has been widely used for method development and validation studies, a recent trend has been to incorporate historical documents with osteological data to better understand individuals, their lived experiences, and the implications this has on skeletal research. Although ancestry designations in the HTOC are limited to "Black" and "white" in the collection's database, archival records establish ancestral heterogeneity even within the "white" cohort, which contains approximately 37 foreign countries/territories. Birthplace data of 773 white males in the HTOC who died between 1911-1938 were collected from public death records and reviewed for this pilot study. The results show that 33% of the individuals were born in the US (with only 7.5% recorded as born in Ohio), while 67% were born outside of and immigrated to the US. Archival documentation can both be used to better understand broader populational trends such as immigration patterns and capture an individual's biohistorical, environmental, and health history which may impact their skeleton and our interpretations of it. The utility of combining skeletal data with historical records is demonstrated through a case study of individual HTH 1684, whose skeleton has characteristics of rickets which might be better explained by their lived experience in Switzerland rather than their identification as "US white" within the Hamann-Todd collection.

Analyzing vertebral pathologies on individuals from the 8-B-5.A cemetery on Saï Island, Sudan

AMANDA O. LIMA[1], STEPHANIE M. FUEHR[1], ANELIS DIAZ[1], TOSHA L. DUPRAS[2] and VINCENT FRANCIGNY[3]

[1]Department of Anthropology, University of Central Florida, Orlando, FL, [2]College of Arts and Sciences, Texas Tech University, Lubbock, TX, [3]CNRS, UMR 8167, Orient & Méditerranée, Sorbonne Université, Paris, France

This research examines vertebral pathological conditions of adult individuals from the Meroitic Period cemetery, 8-B-5.A, on Saï Island, in modern-day Sudan. Minimal osteological analyses from this site have been conducted and published, thus preventing Saï Island from being included in comparisons and interpretations for the region. Vertebrae from 11 individuals excavated from three tombs were macroscopically analyzed to observe vertebral pathological conditions of individuals living in ancient Nubia. These individuals' age categories ranged from young to old adults, with most of the pathological conditions observed on the lower thoracic and lumbar vertebrae. The comparison of sex estimation during osteological analysis was not possible due to numerous individuals only being represented by their vertebral elements. Evidence of osteoarthritis, diffuse idiopathic skeletal hyperostosis (DISH), ankylosing spondylitis (AS), osteophytosis, and spondylolysis were differentially diagnosed. Features of these observed conditions include apparent sliding of the articular facets that indicate possible spondylolisthesis, fusion of the vertebral bodies and articular processes, enthesophytes, osteophytes, vertebral body compression, and microporosities. These findings, along with supplemental analyses from Meroitic Period sites, are consistent with conditions due to the rigorous activity associated with an agricultural society; despite these individuals being considered religious elite. While skeletal analyses have not been conducted for individuals from other cemeteries at the site, this research provides preliminary post-cranial pathological interpretations that can be utilized to assess other Saï Island cemeteries in the future. This research is the initial step to understanding the lived experiences of individuals from Meroitic Saï Island.

Deep learning empowers fine-grained population affinity estimation with craniometric data

XIAOMING LIU[1,2] and JINYONG PANG[2]

[1]USF Genomics, University of South Florida, [2]College of Public Health, University of South Florida

Estimating population affinity from skeletal remains is one of the most crucial tasks of forensic anthropology. Craniometric data is the most commonly used data source for this task. Multiple statistical and computational methods have been developed for craniometric population affinity estimation, including but not limited to linear discriminant analysis (LDA), geometric morphometrics, mixture model-based clustering, and Artificial Intelligence (AI). While LDA remains the most commonly used method, AI or machine learning-based methods often outperform traditional statistical methods (e.g., LDA) as to the accuracy of the predictions. The recent debate on the practice of ancestry estimation in forensic anthropology has demanded methods with good performance with fine-grained population definitions. We hypothesize that deep learning (DL) models can be potential candidates for such practices. DL is a recent breakthrough in AI that has surpassed traditional machine learning methods in many areas. We developed several deep feed-forward neural network models for population affinity estimation using Howells' main craniometric data set, which consists of 82 craniometric measurements from 2,524 human crania from 30 populations collected globally. We obtained average accuracies of 96% for six-group (Europe, Africa, Austro-Melanesia, Polynesia-Micronesia, America, and East Asia) affinity estimation, 95% for 11-group (East Africa, West Africa, South Africa, Greenland, Siberia, East-Southeast Asia, Andaman, America, Polynesia-Micronesia, Australia-Melanesia, Central-North Europe) affinity estimation, and 82% for all 30-population

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

affinity estimation. The results suggest that deep learning models can help to obtain decent to good accuracy for fine-grained population affinity estimation.

Dearly De-Parted: Using Stable Isotopic Data to Assess the Role of Maya Ancestors in Making Place

ANGELINA J. LOCKER

Sociology & Anthropology, George Mason University, Anthropology, Vanderbilt University

For the ancient Maya, close proximity interments of Ancestors linked past peoples with the living, thus generating a "genealogy of place" (McAnany 2013: 65). However, less attention has been given to secondary burials and their role in Maya social memory and placemaking. Given these ties between ancestors, the living, and the landscape, ancestors may have been brought when descendants moved from place to place. I applied biogeochemical methods to address questions about mobility, and in this paper, I present data from a Late Preclassic (300 BCE – 250 CE), simple co-burial at the urban center of Dos Hombres. This burial consisted of a primary, articulated individual with two disarticulated secondary individuals. Archaeological evidence indicates multiple ancestral veneration practices were associated with this burial event. Approval for this research was granted by the Institute of Archaeology under the National Institute of Culture and History in Belmopan, Belize. I measured stable oxygen and strontium isotopes to assess whether or not individuals were born where they were buried and to gauge how bodies may have been moved to make and claim place. $\delta^{18}O$ values suggest the primary individual is local to the site of Dos Hombres; however, the two secondary individuals have $\delta^{18}O$ values which fall outside the established local range, indicating these individuals were non-local to the region. In this paper, I argue that bodies, and pieces of bodies, were used as heirlooms, such that the practice of removing and reburying pieces of ancestors' bodies was used to claim and make place.

This research was funded by an Early Career Grant to AJL from the National Geographic Society and an Archaeology Grant to AJL from the Rust Family Foundation.

A preliminary study of normalized metacarpal length in terrestrial baboons and mixed-locomotion chimpanzees

VICTORIA A. LOCKWOOD

Center for the Advanced Study of Human Paleobiology, The George Washington University

While most previous studies of hand morphology and locomotion have considered the relationship between locomotor mode and ray length or hand proportions, some have focused on specific skeletal elements (e.g., metacarpals). Chimpanzees knuckle-walk during both arboreal and terrestrial locomotion, and similar metacarpal positioning and morphology have been noted in digitigrade and knuckle-walking primate species. Understanding how the metacarpals differ between a mostly terrestrial primate species and a species with more locomotor flexibility, may help researchers interpret the functional significance of hominin metacarpal morphology. I measured maximum metacarpal length of digits 2-5 in a sample of adult baboons (*Papio anubis*, *cynocephalus*, *hamadryas*, *ursinus*, N=16) and chimpanzees (*Pan troglodytes*, N=17). Measurements were normalized using tibial proximal mediolateral breadth as a proxy for body mass, and then analyzed in a linear mixed model to investigate the effects of digit, species, and sex. Normalized metacarpal lengths were significantly longer in *Pan troglodytes* compared to *Papio anubis* and *Papio hamadryas*, however, the difference is slight. Sex had no effect. This suggests that whilst the inclusion of arboreality in the locomotor repertoire may increase normalized metacarpal length, the degree of lengthening may be constrained by the position of the metacarpals relative to the other skeletal elements in the hand during locomotion. Future work will investigate a broader range of arboreal hand positions alongside additional morphological aspects of the skeletal elements in the hand.

The Postmortem Agency of Undocumented Migrants: Potential Risks with Applying a Structural Vulnerability Framework

DAYANIRA LOPEZ and JENNIFER F. BYRNES

Anthropology, University of Nevada, Las Vegas

The present discourse concerning the estimation of "ancestry" in forensic anthropological casework continues to garner much attention as disagreement among practitioners persists. Recognizing that established methods have historically categorized individuals into defined groups — a form of structural violence that contributes to systemic erasure of social identity and lived experiences of minorities — we argue that individuals of Latin American and Caribbean (LAC) descent are at greater risk of becoming unidentified decedents in medical examiner/coroner offices as a contributing factor of this social identity. According to the National Missing and Unidentified Persons System (NamUS), there are approximately 4,660 unidentified decedents labeled "Hispanic/Latino, Black/African American, or Uncertain" between Florida, California, Arizona, and Texas combined, composing 59% of all decedents from these ancestry groups across the nation. Consequently, we argue that the proposed application of a Structural Vulnerability Profile (SVP) in forensic anthropology casework that supports "ancestry" estimations have the potential to hinder the accuracy of our analyses by producing inaccurate representations of diverse human groups that are then mirrored as "unidentified" in forensic databases. Specifically, this can occur when making estimations of group identity based on nonspecific skeletal biomarkers, like those associated with nutritional deficiencies or developmental stress. This approach may lead to inadvertently promoting continued structural violence, harm, and marginalization of minorities of LAC descent. As such, we caution against the application of methods that support ancestry estimations via SVPs in forensic anthropological casework and rather recommend alternative intersectional methods that will promote postmortem agency to these individuals.

Application of 3D digital microscopy to the study of non-alimentary dental wear

MARINA LOZANO[1,2], RAQUEL HERNANDO[1,2], JOSE-MARIA BERMUDEZ DE CASTRO[3,4], EUDALD CARBONELL[1,2], JUAN-LUIS ARSUAGA[5,6] and ALEJANDRO ROMERO[7]

[1]Paleoanthropology, Institut Catala de Paleoecologia Humana i Evolució Social (IPHES-CERCA)., [2]History and Art History, Universitat Rovira i Virgili, [3]Paleoanthropology, Centro Nacional de Investigación sobre la Evolución Humana (CENIEH), [4]Anthropology, University College London, [5]Paleoanthropology, Centro Mixto UCM-ISCIII de Evolución y Comportamiento Humanos, Instituto de Salud Carlos III, [6]Paleontology, Facultad de Ciencias Geológicas, Universidad Complutense de Madrid, [7]Biotechnology, Facultad de Ciencias, Universidad de Alicante

Non-alimentary dental wear is the result of the use of teeth as tools. There is a great variety of patterns regarding different *Homo* species, chronologies and geographical areas. Methods for analyzing non-alimentary features have been focused on macroscopic observations and scanning electron microscopy. This work examines the suitability of 3D digital microscopy to assess non-alimentary features.

Our sample comes from Sima de los Huesos pre-neandertals and *Homo sapiens* from El Mirador cave site. Anterior dentition with evidence of non-alimentary wear has been selected and analyzed using a HIROX KH-8700 3D digital microscope.

We analyzed originals and casts under the low and middle-range lens with magnifications between 35x and 140x. 3D microscope provides high quality images of the largest features such as grooves and chipping, and detailed areas with multiple and superimposed labial striations (cutmarks). Measurements of width and a profile of the striations' depth were taken directly from the software associated with 3D digital microscope. Images of wider areas could be photographed using the 3D DM mosaic tool by tilling and stitching a variable number of images in few minutes.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Overall, 3D digital microscopy requires no sample preparation, offers fast processing yielding excellent color 3D images, digital models and accurate measurements. The data of these preliminary results will allow the comparison with non-alimentary dental wear in other fossil hominins and human populations increasing our knowledge about the use of teeth as tools.

PID2021-122355NB-C32 (MINECO/FEDER), and CERCA Programme/ Generalitat de Catalunya, AGAUR 2017 SGR 1040. URV Martí-Franquès Research Grant (URV 2019PMF- PIPF-59). "María de Maeztu" program for Units of Excellence (CEX2019-000945-M).

Implications of morphometric variation in the human fifth metatarsal for restoring functionality after fracture

LUIS DIEGO LUNA CENTENO[1], SHYAM F. HASSAN[1], AUDITI I. AUTHOY[2] and TEA JASHASHVILI[1,3]

[1]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [2]STAR/EHA, Francisco Bravo Medical Magnet High School, [3]Department of Geology and Paleontology, Georgian National Museum

Studying morphological variation and its impact on bone adaptation is essential for understanding human biological development and evolution. Accounting for this variation potentially benefits skeletal trauma research and treatment by individualizing protocols. Fifth metatarsals (MT5) are the most commonly injured bone of the human foot. Zone II fractures (ZIIF) are located at the proximal metaphyseal-diaphyseal junction and are associated with significant morbidity and long-term functional impediments due to delayed union, nonunion and elevated refracture rates. Nonunion of ZIIF, for example, is primarily related to poor vascularization and variations in medullary canal diameter, bone length and lateral curvature. When selecting intramedullary screw sizes, these factors pose challenges for operative management.

Since MT5 anatomical variations affect functionality after intramedullary screw fixation, this study aims to define a protocol for customizing screw size during operative care that accounts for morphological variation. Selecting surgical screw sizes based on correlated anatomical measurements promotes optimal healing and rehabilitation. Furthermore, comparing MT5 morphometric variation in diverse human populations (n~300 individuals) to hominin fossils may shed light on why MT5 fractures are not observed in hominin MT5s.

Our results confirm considerable MT5 morphometric variation among human populations, especially in medullary cavities and cortical bone distributions along their midshafts. Differences in these aspects of MT5s are also observed in hominin fossils and may be related to their low fracture incidence. The extent of variation documented in the present sample of MT5s confirms the merit of using the proposed protocol featuring customized screw sizing for successful operative management of ZIIF.

We thank the Department of Integrative Anatomical Sciences, Keck School of Medicine, USC. The free access human database is funded by the National Institute of Justice grant number 2016-DN-BX-0144.

Homosexualizing risk: Queer theory and human monkeypox infection

JUSTIN LUND

Anthropology, Northern Arizona University

Inaccurate framing and blatant misinformation have driven the creation of a narrative that human monkeypox infection is only transmissible among men who have sex with men. In fact, this observation relating sexual activity to disease transmission has yet to be tested. Monkeypox, like smallpox, is transmitted directly through close contact with a person carrying the infection and indirectly via contact with materials contaminated with the virus. Queer identity, as well as gay male identities, are structured in relation to a heteronormative society and often depend upon a society's ability to successfully enforce an expected performance of binary gender. Queer theorists view hetero/homosexual binaries as categories of knowledge that frame what we know about bodies, desires, and sexualities while shaping moral boundaries and political hierarchies. Applying queer theory to this outbreak can shed light on how this very contagious disease is being sexualized, and as a result risk is specifically being *homosexualized*. A scoping review of US top newspapers from January 2022 to September 2022 suggests that messaging often attempted to strike a delicate balance between stigmatizing gay men and warning them and the public of their potential risk. I argue that this can be seen as an attempt to assert a code of ethics to the behaviors of gay males, it further stigmatizes an historically outcast group, and potentially endangers other populations.

Differential tooth wear among extant primate dietary categories

RISA LUTHER[1] and RILEY C.W. O'NEILL[2]

[1]Anthropology, University of Minnesota, [2]Applied Mathematics, University of Minnesota

Many dental analyses require specimens that are slightly or moderately worn, limiting inferences about diet and function to a restricted period of an organism's life. This uses moderately to heavily worn teeth to explore relationships among tooth shape, function, and diet as they change during maturation. Dental topographic analysis variables (DNE, ariaDNE, OPCR, 3D-OPCR, RFI) were collected for 133 mandibular M2s representing all stages of wear in frugivorous, folivorous, and hard-object hominoid species. These variables and a composite computed using principal component analysis (PCA) were fit to a linear mixed-effects model with diet, wear stage, and the interaction terms as possible independent variables. Results show that within frugivores, RFI values accurately reflected diet across wear stages ($p < 0.0001$); as the teeth increased in wear the variable did not change, showing this is a consistent measure for diet even through moderate to heavy wear. DNE values, however, did change in every diet category, and therefore may not accurately reflect diet across wear stage. Additional results indicate that patterns of surface changes due to wear differ substantially according to diet, with significant values for the interaction term of DNE, OPCR, and the PCA variable ($p < 0.0001$). Thus patterns of wear *do* differentiate well among primates with different diets. However, the consistency of dietary signaling provided by the crown surface varies according to both wear stage and the variable. These results warrant further exploration using a larger sample, and indicate these methods provide important new information about diet and tooth function.

3D Analysis of Stress-Related Dental Defects in Neolithic Humans from Liguria, Italy

SABRINA MACCARON[1], JILLIAN CLARKE[1], ELIZA ORELLANA-GONZÁLEZ[2], IRENE DORI[3], VITALE SPARACELLO[4] and KATE MCGRATH[1,5]

[1]Anthropology, State University of New York at Oneonta, [2]CNRS, PACEA, University of Bordeaux, CNRS, PACEA, UMR 5199, France, [3]Soprintendenza Archeologia, Soprintendenza Archeologia, Belle Arti e Paesaggio per le province di Verona, Rovigo e Vicenza, Italy, [4]Department of Life and Environmental Sciences, University of Cagliari, Italy, [5]Center for the Advanced Study of Human Paleobiology, The George Washington University

Linear enamel hypoplasia (LEH) indicates that a tooth's normal growth was disrupted by a physiological stressor like malnutrition or disease. In this study, we examined the canines of people who lived before, during, and after the Neolithic Revolution in Liguria, Italy. 22 high-resolution epoxy replicas of canines from 16 individuals were analyzed, ranging from ~4-30 years of age at the time of death. 12/16 teeth were directly radiometrically dated from the Late Upper Paleolithic (10431-10039 BCE) to the Metal Ages (c. 3600-1280 BCE). One canine was selected per individual, visually evaluated for LEH defects, and scanned using a Sensofar confocal profilometer to obtain sub-micron resolution 3D digital elevation models of the enamel surface. Defect and perikymata (normal growth increment) width and depth were measured using Fiji ImageJ. We found significant differences in defect depth ($H(2)=7.10$, $p=0.029$) and width ($H(2)=7.10$, $p=0.029$) among the three time periods. The individual who lived during last ice age (Younger Dryas event, N=3 defects), has significantly deeper defects compared to those

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

from the Neolithic (N=41, p=0.014) and the Metal Ages (N=6, p=0.071). This adolescent presents a rare form of diffuse hypertrophic osteoarthropathy often associated with pulmonary or cardiac conditions. Relatedly, severe stressors including illness have previously been linked with deeper defects in apes and sheep. Ligurian perikymata are deeper than published values for Upper Paleolithic and medieval humans, but comparable to other Neolithic individuals. Future work will assess normal growth increments as they relate to dental growth rates in Liguria and compare defect metrics across sites.

SUNY Oneonta's Summer Research Fellowship Program, the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No 798117, and the SUNY PRODiG program.

Vertebral morphology in the primate post-transitional spine reflects locomotor pattern

ALLISON L. MACHNICKI[1], PHILIP L. RENO[2] and ADAM D. SYLVESTER[1]

[1]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, [2]Department of Bio-Medical Sciences, Philadelphia College of Osteopathic Medicine

Human bipedality and ateline brachiation both require orthograde postures and high levels of spine mobility. Therefore, we hypothesized that atelines and humans would have similar vertebral morphology to facilitate these locomotor patterns. To test this hypothesis, we analyzed articular facet, spinous process, and centrum shape.

The sample included humans, great apes, gibbons, and New World monkeys (n=21 total). Vertebral level was defined by the articular facet definition, and the sample included five vertebrae spanning and including the transitional vertebra. Landmarks were placed on surface models in 3D Slicer to capture the shape and orientation of the articular facets, spinous processes, and centrum. Landmarks were subjected to Procrustes analysis, and shape variation was summarized using principal components analysis.

In the pre-transitional spine and the transitional vertebra, spinous processes and articular facets had similar shape across species, although humans had a relatively large centrum and small spinous process. In the post-transitional vertebrae, centrum size and orientation of the spinous process accounted for most of the variation. Humans, gibbons, New World monkeys, and orangutans shared similar features, whereas chimpanzees and gorillas had vertebrae characterized by a narrow centrum and caudally oriented spinous process. At the second post-transitional vertebra, we observed similar patterns among the sample, except howler monkeys differentiated themselves from the other New World monkeys with a more cranially projecting spinous process. These data show that post-transitional vertebral morphology may reflect differences in spine mobility and locomotor behaviors, in particular the stiffness of the African ape spine.

Wenner-Gren (ALM); NSF GRFP DGE1255832 (ALM), NSF BCS-1650879 (ALM & PLR); NSF BCS-1638812 (PLR)

The effect of longitudinal femoral and tibial curvature on the kinematics of locomotion in steep terrain

MARLA MACKINNON[1], TESS CARSWELL[2], JOSH W. GILES[2] and ALISON MURRAY[1]

[1]Department of Anthropology, University of Victoria, [2]Department of Mechanical Engineering, University of Victoria

The biomechanics of limb bone curvature are complex, and though anterior curvature clearly exhibits some relationship with behaviour, the mechanisms shaping it and its biomechanical purpose remain unclear. Among both Neanderthals and humans, anterior limb bone curvature correlates strongly with other limb bone adaptations known to reflect high mobility, particularly in steep variable terrain. Here we investigate the extent to which anterior lower limb bone curvature affects kinematics when moving uphill in steep terrain, proxied by stair-climbing. Femoral and tibial laser scans were used from two archaeological individuals matched for estimated body mass and crural index but contrasting in anterior diaphyseal curvature. A default OpenSim musculoskeletal model was modified to each individual's muscle attachment coordinates and then put through a stair-climbing gait simulation using experimentally collected motion capture data. Results show that patterns of muscle activity across the gait cycle are similar between the two models, but differences are notable between the magnitude and activation of certain muscle groups at key timepoints. Femoral curvature constrains extension and requires greater force production by the knee extensors during the final stages of extension (~20-25% more force), and tibial curvature constrains excursion into ankle dorsiflexion and shifts a greater proportion of force production to the superficial ankle extensors (~30% greater force production). While the tissue-level mechanisms shaping anterior limb bone curvature remain poorly understood, results of the current study suggest that variation in that curvature could meaningfully impact kinematics and muscle forces during uphill locomotion.

The T allele of the MTHFR gene in Turkish populations is associated with negative fertility outcomes

CAROLINE MACLEAN[1], MIGUEL DIMANLIG[2] and LORENA MADRIGAL[1,3]

[1]Anthropology, University of South Florida, [2]Anthropology, University of South Florida, [3]Anthropology, University of South Florida

Background: The MTHFR C677T mutation deleteriously affects one-carbon metabolism and reproduction, with the highest frequencies found in Native Mesoamerican populations. Hypotheses explaining the continuation of high frequencies of the mutation are lacking.

Materials & Methods: These are secondary data including maternal genotype; maternal serum folate, serum B12, serum homocysteine values; and the fetal or birth outcome of each pregnancy assessed. Outcomes assessed include positive outcomes (a healthy birth) and negative outcomes (intrauterine death, miscarriage, and recurrent pregnancy loss).

Results: Negative outcomes were significantly more frequent amongst heterozygotes. 46% of all negative outcomes were experienced by CT women, 38% of negative outcomes were experienced by TT women, while only 14.93% of negative outcomes are experienced by CC women (X^2 = 54.88, df = 2, $p < 0.0001$). CT and TT women have high but similar incidences of intrauterine death and miscarriage compared to CC women, but CT women have much higher incidence of recurrent pregnancy loss (RPL) than TT and CC women. Of all women who experience RPL, 65% are CT, while 27.7% are TT and 7.23% are CC (X^2 = 15.56 df = 4, $p < 0.003$).

Conclusion: These data indicate that CT and TT women have a selective disadvantage. We currently cannot explain the high frequency of an allele (T= 0.47 and 0.58 in this subset) with such deleterious outcomes. Evolutionary theory leads us to propose that this is a case of evolutionary mismatch with the current environment. We will test this hypothesis further with additional populations.

Investigating relationships between immune activity, bone density, and bone turnover: a preliminary biomarker analysis among Indigenous Amazonian Shuar youth

FELICIA C. MADIMENOS[1,2], SAMUEL S. URLACHER[3,6], GEETA N. EICK[4], MELISSA A. LIEBERT[5], LAWRENCE S. SUGIYAMA[4] and J JOSH SNODGRASS[4,7]

[1]Anthropology, Queens College, [2]New York Consortium of Evolutionary Primatology, NYCEP, [3]Anthropology, Baylor University, [4]Anthropology, University of Oregon, [5]Anthropology, Northern Arizona University, [6]Child and Brain Development Program, CIFAR, [7]Global Station for Indigenous Studies and Cultural Diversity, Hokkaido University

Tradeoffs between immune activity and skeletal growth have primarily examined linear growth; less is known about tradeoffs between immunity and bone accretion (i.e., formation and resorptive processes) during stages of skeletal growth and puberty. Here we investigate the relationships between three biomarkers of immune defense

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

and inflammation (total immunoglobulins G and E [IgG, IgE]) and C-reactive protein [CRP]) and two biomarkers of bone turnover (osteocalcin [OC; marker of bone formation] and tartrate-resistant acid phosphatase-5b [TRACP-5b; marker of bone resorption]). Radial and tibial bone density (estimated using a MiniOmni Ultrasonometer) and Shuar-specific z-scores (height-for-age [HAZ], weight-for-age [WAZ], body mass index-for-age [BAZ]) were also included in the analyses. The participant population included 67 Indigenous Shuar children and young adults (ages 3-20 years; males: n = 33; females: n = 34). Biomarkers were analyzed from dried blood spots; concentrations were log-transformed due to non-normality. Relationships between anthropometric, skeletal, and immune markers were analyzed using linear regressions with OC and TRACP-5b as dependent variables; analyses were performed separately for males and females. Initial analyses show that among males, higher CRP and IgE predict higher TRACP-5b ($R2$ = .545; $p < 0.05$); among females, higher TRACP-5b predicts lower OC ($R2$ = .537; $p < 0.05$), while being taller and lighter for age predicts higher TRACP-5b ($R2$ = .446; $p < 0.05$). Results suggest that bone formation and resorption processes among youth may be associated with immune biomarkers that indicate acute (i.e., CRP) or chronic (i.e., IgE) activation of immune function, although these relationships remain complex.

PSC CUNY Award, NSF-SPRF #SMA1606852; CIFAR Global Scholars Program

100 Years of *Australopithecus*: Raymond Dart's Unpublished Manuscript on the Taung Child

PAIGE MADISON[1] and BERNARD WOOD[2]

[1]Applied Ecology, North Carolina State University, [2]CASHP, Department of Anthropology, George Washington University

In 1925, Raymond Dart declared a fossil skull recovered from South Africa the first genuinely ancient fossil human ancestor. Dart named the specimen *Australopithecus africanus* in a letter to *Nature*. Scientists requested a detailed description of the fossil, which was poised to reconfigure existing ideas about human origins. Over the next five years, Dart compiled a 300-page account of the fossil's significance titled "*Australopithecus africanus* and his place in human origins." But the manuscript has never seen the light of day. This poster focuses on a brainchild of Bill Kimbel's, which was to mark the centennial of Dart's *Nature* publication by publishing a book-length facsimile of the unpublished manuscript, including Grafton Elliot Smith's handwritten edits.

The manuscript provides historical context for the Taung child's discovery and immediate reception. We consider the theoretical commitments the Taung discovery challenged. As Dart recognized, "the investigation of fossils forces us to confront the question of what precisely should constitute a form ancestral to [hu]mankind," a "starting-point beset by controversy." Dart's unpublished manuscript, which illuminates a crucial and controversial moment in paleoanthropology, sits at what Kimbel called "the intersection of the science of prehistory and the history of science." Understanding current interpretations of the fossil record, Kimbel believed, requires examining how we have come to know what we think know.

The dental enamel proteome of *Paranthropus robustus*

PALESA P. MADUPE[1,2], PATRICK L. RÜTHER[4], CLAIRE KOENIG[4], IOANNIS PATRAMANIS[6], NOMAWETHU HLAZO[2,5], MEAGHAN MACKIE[1,4], ALBERTO TAUROZZI[1], MIRRIAM TAWANE[7], FRIDO WELKER[6], LAUREN SCHROEDER[3,8], CLÉMENT ZANOLLI[9], FERNANDO RACIMO[6], JESPER V. OLSEN[4], REBECCA R. ACKERMANN[2,5] and ENRICO CAPPELLINI[1]

[1]Geogenetics, Globe institute, University of Copenhagen, Denmark, [2]Human Evolution Research Institute (HERI), University of Cape Town, South Africa, [3]Human Evolution Research Institute, University of Cape Town, South Africa, [4]Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, Denmark, [5]Department of Archaeology, University of Cape Town, South Africa, [6]Section for Molecular Ecology and Evolution, Globe Institute, University of Copenhagen, Denmark, [7]Natural History department, Ditsong National Museum of Natural History, Pretoria, South Africa, [8]Department of Anthropology, University of Toronto Mississauga, Canada, [9]Prehistory to Present Time: Culture, Environment and Anthropology, CNRS Institute, University of Bordeaux, France

It has been consistently observed that protein fragments survive beyond the diagenetic limits of DNA, allowing for the recovery of biomolecular information deeper in time, even from temperate and sub-tropical climates. Phylogenetically informative dental enamel proteins have been recovered from *Gigantopithecus blacki* (~1.9 Ma) and *Homo antecessor* (~8-900 ka), clarifying the taxonomic position of these two species. Here, we report the recovery of dental enamel proteins from four *Paranthropus robustus* (*P. robustus*) specimens from Swartkrans, South Africa, dated to 2.2-1.8 Ma (SK830, SK835, SK850, SK14132). We employed a digestion-free extraction protocol and tandem mass spectrometry for peptide sequencing. To reconstruct protein sequences from MS/MS spectra a combination of different data search strategies was employed. Specimens SK835 and SK850 were identified as biological males, through the confident identification of amelogenin Y (AMELY)-specific peptides. This opens the possibility of reassessing our understanding of sexual dimorphism in *P. robustus* and potentially in other early hominins. The reconstructed enamel protein sequences from *P. robustus* were compared to their orthologous ones from all extant and some extinct hominid taxa. The multi sequence alignment enabled us to clarify the variation that exists within the hominid group. Although the coverage breath of the ancient enamel proteome sequence recovered is admittedly limited, we identified potentially informative single amino acid polymorphisms, which enabled the tentative phylogenetic placement of *P. robustus*. Extending this work to other African hominin species will provide a better understanding of the variation within and between these taxa in Africa.

This project has received funding from the European Union's Horizon 2020 Research and Innovation Programme under: Marie Sklodowska-Curie grant No. 861389, and European Research Council (ERC) grant No 101021361 "BACKWARD".

Temporal Changes in Childhood Exposure of Heavy Metals from Historic San Francisco

DIANA MALARCHIK[1], JELMER W. EERKENS[1] and TOM OSTRANDER[2]

[1]Department of Anthropology, University of California, Davis, [2]Archaeology, Environmental Science Associates

Modern medical studies show that prolonged and elevated exposure to heavy metals has negative physical and cognitive effects. These effects are not restricted to a person's bodily health. For example, childhood ingestion of mercury can affect one's ability to learn and enculturate into their family and society. This study examines trace element concentrations of heavy metals in dental enamel from individuals buried in the mid to late 1800s in San Francisco using Inductively Coupled Plasma-Mass Spectrometry (ICP-MS). Results suggest a shift from 1850s inhabitants, who display high levels of industrial metals (i.e. iron) to high concentrations of more medicinal metals (i.e. mercury) in the later 1800s. Early inhabitants of San Francisco show 10 to 100 times higher concentrations of iron than later residents. Interestingly, increased levels of lead were present among all individuals, with Historic samples showing 100 to 1000 times more lead exposure than Native San Francisco inhabitants. Cultural changes that increased metal exposure first came with industrialization, followed by an increase in advertising of medicines later, specifically those for children. These childhood exposure events may have caused lifelong changes to individuals mental and physical health, affecting both their well-being and enculturation into society.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Assessment of metrical mandibular and postcranial sex estimation parameters in southern African Holocene San and Khoekhoe populations

SADIYAH MALEK[1], JUDITH C. SEALY[2] and VICTORIA E. GIBBON[1]

[1]Department of Human Biology, University of Cape Town, [2]Department of Archaeology, University of Cape Town

Accurate population-specific sexing standards do not exist for southern African Holocene San and Khoekhoe populations. Due to their markedly small stature, skeletal gracility, and past physically active lifestyle, this population exhibits reduced sexual dimorphism, complicating application of traditional sexing standards.

The accuracies of eight common metrical sex estimation variables (six mandibular and two post-cranial epiphyseal) were assessed in 174 archaeological Holocene San and Khoekhoe adults. Sex estimates based on these metrics were compared with pelvic (Phenice) sex estimates, and measurements obtained were subjected to cross-validated discriminant function analysis. All parameters assessed were sexually dimorphic, with femoral and humeral vertical head diameter (FHD and HVHD) showing the largest differences: The most accurate discriminant function equations were for direct multivariate bicondylar breadth, FHD and HVHD (77%), univariate FHD (75%), and stepwise multivariate FHD and HVHD (73%). Minimal accuracy decreases were observed when equations were cross-validated, confirming their predictive accuracy. The least reliable measurements for estimating sex were found to be univariate bicoronoid breadth (62%) and coronoid height (65%).

Whilst all variables were sexually dimorphic, they produced lower accuracy rates than in other populations using the same skeletal parameters, illustrating this population's reduced range of sexual dimorphism. Notably, the equations produced are the first for archaeological San and Khoekhoe people. Application of these equations allows for sex estimation with considerable accuracy and a known error rate, previously not possible for this population.

UCT Ada & Bertie Levenstein Bursary, UCT Vice-chancellors scholarship, National Research Foundation: Innovative Master's scholarship (Malek), Grant no. 467192 (Gibbon) and South African Research Chairs Initiative Grant no. 84407 (Sealy).

Photogrammetric Documentation of Sheep Eater Writings in the Frank Church River of No Return Wilderness visualized in Virtual Reality

BLAINE MALEY[1], JASON HILL[2], WYATT BRUNETTE[3], BEN ZUCKERMAN[3] and MORGAN ZEDALIS[4]

[1]Anatomy, Idaho College of Osteopathic Medicine, [2]Emergency Medicine, Columbia University, [3]Anthropology, University of Alabama, [4]Heritage Management, US Forest Service

The history of anthropological site and object documentation and presentation has historically been limited to video and 2-D images. These modalities limit the resolution of site and object research and documentation, but also the ability to share remote site details for academic and public educational purposes. With the advent of 3-D digitization using photogrammetry technology, anthropological sites and objects can now be documented and visualized with ultra-high resolution 3-D color imaging.

The Frank Church Wilderness, specifically the tributaries of the Salmon River, hosts a long history of Native American occupations that are generally considered inhabited by the Sheep Eater or Tukudika people. These historic occupation sites are extremely remote, generally only accessible through back packing and river rafting through extremely challenging terrain.

One such site, PY-119, also known as Big Creek Gorge Rock Shelter, contains a number of painted panels spanning both sides of Big Creek, a tributary of the Middle Fork of the Salmon River. Photogrammetric data were collected with a Nikon D600 using 24 and 50 mm lenses. The images were then compiled in MetaShape Pro (Agisoft). The 3-D models of several or the panels were then uploaded into VR format for 3-D presentation.

The purpose of this work is to provide highly detailed and accurate site data that can be used for research, education, documentation, and preservation purposes. The VR presentation demonstrates the quality of this data as well as the application for utilizing these tools for sharing and studying anthropological sites.

The Time Has Come: Revisiting the South African Plio-Pleistocene faunal record

MEGAN G. MALHERBE[1,2], MARTIN HAEUSLER[1], DEANO STYNDER[2] and ROBYN PICKERING[3]

[1]Evolutionary Morphology, University of Zurich, [2]Archaeology, University of Cape Town, [3]Geology, University of Cape Town

South Africa's Cradle of Humankind contains some of the most important sites of human evolution, representing hominin fossils attributed to at least five species. However, lack of a detailed chronology for the sites has meant that these significant fossils are yet to be placed within a precise climatic framework, thus we could not hypothesize about how species responded to the dramatically changing environments that characterised the Plio-Pleistocene. Now, recent research has provided precise ages via uranium-lead dating for eight of the most vital fossil-bearing sites in the Cradle: Bolt's Farm, Cooper's Cave, Drimolen, Haasgat, Hoogland, Malapa, Sterkfontein, and Swartkrans. Therefore, the bovid assemblages – found in abundance and crucial palaeoenvironmental indicators – have established dates and can be interrogated without the hermeneutic constraints accompanying eastern African comparisons, which have previously been the only way to estimate South African chronology. We conduct ecomorphological analysis on bovid metapodials via 3D geometric morphometrics, providing the first direct comparison between eastern and southern African Plio-Pleistocene fauna and associated environments. Our results are two-fold: firstly, we do not see a progression in aridity in the Plio-Pleistocene, but rather stasis is observed with predominantly dry/open environments across all South African sites. This is in accordance with inferences from the cave site formation and uranium-lead analysis. Secondly, differences in landscape are seen between southern and eastern sites of corresponding ages, contrasting historical reports. These findings fundamentally advance understandings of both a pivotal period in hominin evolution, as well as species responses to climate change in the Quaternary.

This research was partly funded by the Western Interior Palaeontological Society (WIPS), the Swiss Society for Anthropology (SSA), and the Graduate Research Campus (GRC) of the University of Zurich.

Compromised growth: An examination of growth, stress, and health among a Late Antique infant and child cemetery in Roman Italy

SIERRA W. MALIS[1], MOLLY K. ZUCKERMAN[1], JORDAN A. WILSON[2], ANNA J. OSTERHOLTZ[1], JULIANNE PAIGE[3] and DAVID SOREN[4]

[1]Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Anthropology, Pennsylvania State University, [3]Anthropology, University of Nevada, Las Vegas, [4]Classics, University of Arizona

Developing perinates and infants are the most sensitive to external environmental stressors and, therefore, are sensitive barometers to their environmental surroundings. Combining research from infant and child development, public health, bioarchaeology, and history, this research examines the relationship between growth and skeletal indicators of chronic and/ or episodic physiological stress amongst 60 juveniles interred at the Late Antique infant and child cemetery at Poggio Gramignano (PG) (5th cent. CE) located near Lugnano in Teverina, Umbria, Italy, associated with a rural agricultural community. Growth disruption – evidenced by decreased long bone length compared to dental age – and stress experience – evidenced by skeletal stress indicators – amongst the individuals were compared to 66 juveniles from the Put Dragulina (PD) cemetery (1st–6th cent. CE), an urban, Roman-era cemetery located near Trogir, Croatia. Results indicate the individuals at PG had smaller long bone lengths-for-age than

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

those at PD (F(1,41)=16.108, p=0.0002), however, independence tests suggest the frequency of porotic hyperostosis (value=52.476; p<0.001) and cribra orbitalia (value=60.412; p<0.001) was higher among juveniles at PD, while periosteal new bone formation (value=5.884; p=0.051) and dental enamel hypoplasia (value=0.416, p=0.860) was not. These differences in growth and stress experience were likely a result of differing biosocial and ecological environments present in the different regions at the time, which may have included differential levels of nutrition, disease, and socioeconomic structures between urban and rural populations throughout the decline of the Western Roman Empire.

Cobb Institute of Archaeology, Mississippi State University.

The first occurrence of a Middle Pleistocene Hominin from the Central Highlands of Kenya

NASSER R. MALIT[1,8], KAREN L. BAAB[2], FRANCIS M. KIRERA[3,8], VERONICA WAWERU[4,8], DANIEL P. MIGGINS[5], JILLANI NGALLA[6], CHRISTINE OMUOMBO[7,8], RAHAB KINYANJUI[8,9], ARYEH GROSSMAN[10,11,12,2], FRANCIS NDERITU[13,8], LORNA N. CHEGE[14] and RICHARD KINYUA[15]

[1]Department of Anthropology, SUNY Potsdam, [2]Department of Anatomy, Midwestern University, [3]Department of Biomedical Sciences, Mercer University, [4]Council on African Studies at the MacMillan Center for International and Area Studies, Yale University, [5]The 40Ar/39Ar Geochronology Laboratory, Oregon State University, [6]Institute of Primate Research, National Museums of Kenya, [7]Department of Geosciences and the Environment, Technical University of Kenya, [8]Department of Earth Sciences, National Museums of Kenya, [9]Department of Archeology, Max Planck Institute for Geoanthropology, [10]Arizona College of Veterinary Medicine, Midwestern University, [11]Arizona College of Osteopathic Medicine, Midwestern University, [12]Arizona College of Optometry, Midwestern University, [13]Department of Geosciences, Georgia State University, [14]Unaffiliated Geologist, P. O. Box 12614-00100, Nairobi, [15]Unaffiliated Naturalist, Freelance Nature Enthusiast

We report the first fossil human KNM-GT 77377 discovered in Ngobit, a new site outside of the East African Rift System, in the Central Highlands of Kenya. The remains are radiometrically dated to 614-500 ka. This is a poorly sampled time interval but is key to when modern human and Neanderthal lineages diverged. Both nonmetric and metric data were collected on the Ngobit specimen and compared to various fossils belonging to the *Homo* lineage. The nonmetric data include the features of the parietal emissary foramen and the middle meningeal vessels. The metric comparisons include the parietal emissary foramen distances from lambda, the parietal chord dimensions, and cranial thickness at lambda and areas preserved. The KNM-GT 77377 parietal preserves a single emissary foramen and the reticulation of the middle meningeal vessels show anastomoses, a derived condition like modern humans. The distance from the parietal emissary foramen to lambda is longer than recorded in other Mid-Pleistocene *Homo* fossils, and a regression-based estimate of sagittal parietal chord length indicates a large parietal bone that groups the Ngobit specimen with archaic (e.g., Eliye Springs, Omo 2, BOU-VP-5/1, Narmada) and early modern humans (e.g., Omo 1, Herto, Skhul 5), and separates it from *H. erectus* and *H. naledi*. These findings place the Ngobit parietal among the large-brained Middle Pleistocene *Homo sp*. of unknown taxonomic affinity. The site of Ngobit is positioned to add crucial new insights about the morphological and taxonomic diversity of the hominins from the early to Mid-Pleistocene of Africa.

"All have had to be moved": Paleopathology and memory at the Old Burial Ground, Heuvelton, New York

MADELEINE MANT[1], MINDY C. PITRE[2], TIMOTHY ABEL[3] and LINDA JOHNSON WOOD[4]

[1]Anthropology, University of Toronto Mississauga, [2]Anthropology, St. Lawrence University, [3]Consulting Archaeologist, Carthage, NY, [4]Historian, Heuvelton Historical Association

In 2019, skeletal human remains were unexpectedly discovered during the construction of a new water tower in Heuvelton, New York. Historical maps revealed that the construction site was the previous location of the village's Old Burial Ground, which was closed in 1870. At the time, families were asked to retrieve their relatives' remains and move them to the newly consecrated Hillcrest Cemetery. Among those apparently left behind were five complete individuals (four subadults, one young adult) with a suite of pathological conditions including non-specific periosteal new bone growth, carious lesions, and tarsal coalition. Importantly, a 3-year (+/- 12 months) individual showed evidence of healed vitamin D deficiency rickets. This case is one of the few recognized from a bioarchaeological context in the Americas and assessed using updated paleopathological criteria. Contemporary data from the United States Census allows for a biocultural contextualization of this child's short life; we propose that a synergistic relationship between weaning, low immune function, and lack of sunlight during recuperation could explain their condition. Our analysis contributes to the growing literature demonstrating that rickets was not exclusive to urban groups in the past. This community-collaborative research reveals the care initially taken in burying (and reburying in 2022) these 'forgotten' individuals and sheds new light upon the settler experience in 19th-century northern New York.

X-linked variation in chimpanzees (*Pan troglodytes verus*) offers potential insights into sexual dimorphism of disease susceptibility

CLARA L. MARIENCHECK[1], CHET C. SHERWOOD[1], WILLIAM D. HOPKINS[2], JOHN J. ELY[1,3] and BRENDA J. BRADLEY[1]

[1]Center for the Advanced Study of Human Paleobiology, Department of Anthropology, George Washington University, [2]Keeling Center for Comparative Medicine and Research, University of Texas MD Anderson Center, Bastrop, TX 78602, [3]MAEBIOS, Alamogordo, NM 88310

In humans and other mammals, there is sexual dimorphism in immune response to infectious diseases, and in morbidity and mortality rates to viruses and other pathogens. Females generally demonstrate more immunocompetency than males, in part because of differences in reproductive life history trade-offs, and the immunosuppressive effect of androgens. The X chromosome has a high density of genes (e.g. *ACE2*, *TLR*s) that regulate disease susceptibility and immune response, and this could also impact sex-based differences. However, the role of sex chromosomes in shaping sexual dimorphism in immunity has been largely unexplored. This study examines variation in X-linked immunity genes within chimpanzees (*Pan troglodytes verus*) using published genomic data supplemented with exon sequencing using a panel of unrelated captive individuals (N=15). We identified previously unrecognized X-linked variation that could result in functional differences between the sexes. For example, we found coding variation in *ACE2*, which encodes the receptor for several respiratory viruses including SARS-CoV-2. This includes a T1425C variant resulting in an Isoleucine to Threonine substitution (frequencies in Hardy Weinberg equilibrium, $X2$=0.20, df=1, p=.691; derived minor allele frequency 0.10). Variation at this gene has been shown to affect COVID-19 susceptibility in humans, and impact predictors suggest this Ile421Thr variant would likely have a functional effect. Humans and chimpanzees show different patterns and sites of variation at these genes, likely reflecting different evolutionary histories of virus exposure. Understanding X-linked differences in immune biology could provide insight on sexual dimorphism as well as species-specific adaptations.

This research is funded by the International Primatological Society, The George Washington University, and the National Science Foundation Graduate Research Fellowship.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

A comparison of ethanol concentrations in chimpanzee consumed fruits at lowland and mid-altitude sites

ALEKSEY E. MARO[1], AARON SANDEL[2], ROMAN WITTIG[3,4], ALPHONSE B. BI ZAH[4,5], JOHN MITANI[6] and ROBERT DUDLEY[1]

[1]Integrative Biology, University of California, Berkeley, USA, [2]Anthropology, University of Texas, Austin, USA, [3]Institute for Cognitive Sciences, CNRS UMR 5229 University of Lyon 1, Bron, France, [4]Taï Chimpanzee Project, CSRS, Abidjan, Côte d'Iviore, [5]Systématique et Biodiversité Végétale, Université Félix Houphouët Boigny, Abidjan, Côte d'Iviore, [6]Anthropology, University of Michigan, Ann Arbor, USA

Human attraction to alcohol is hypothesized to have originated from an ancestral frugivorous diet, whereby low levels of dietary ethanol are chronically consumed and impose selection over evolutionary time. Whether levels of fruit-derived ethanol in primate diets vary geographically, however, is unknown. To investigate this issue, we compared ethanol levels between ripe fruits consumed by two subspecies of wild chimpanzees living at different altitudes, Ngogo in Uganda (*Pan troglodytes schweinfurthii*, 1400 m asl) and Taï in Cote d'Ivoire (*Pan troglodytes verus*, 200 m asl). Two Taï fruits, on which chimpanzees spend ~20% of their annual feeding time, exhibited average ethanol concentrations of 0.33% and 0.20% (n=149 and 63 fruits, respectively). At Ngogo, the most consumed fruit species (~18% annual feeding time) contained an average ethanol concentration of 0.45% (n=40). Analysis of 13 fruit species, representing ~75% of total chimpanzee feeding time at Ngogo, revealed that chimpanzees there typically consume fruit containing 0.30% ethanol, weighted by total annual feeding time. Considering absolute rates of fruit consumption, these ethanol concentrations suggest a daily consumption rate of 10–20 grams of ethanol. Fruit-ethanol concentrations were similar at Taï and Ngogo despite the lower air temperatures at Ngogo which might otherwise inhibit fermentative activity by yeast. Taken together, these data suggest chronic low-level dietary ingestion of ethanol by chimpanzees at both sites.

Biomolecular approaches to the ancestry, ecology and relatedness of the cannibalised human remains from Gough's Cave (UK)

WILLIAM A. MARSH[1,2], SILVIA M. BELLO[1], SELINA BRACE[1], OLIVER E. CRAIG[2] and IAN BARNES[1]

[1]Department of Earth Sciences, Natural History Museum, [2]BioArCh, University of York

Gough's Cave (UK) is among the most northern examples of the Magdalenian, an Upper Palaeolithic Western Europe culture (19-15kya) characterised by a complex behaviour that includes the production of specialised bone tools, the engraving of stones, faunal and human skeletal elements, as well as cannibalism. In order to better understand the ecology and ancestry of individuals from this cannibalised assemblage, we have generated both genetic and dietary isotope data. All members of the group are found to share a genetic affinity associated with the continental European Magdalenian culture (Goyet-Q2), and which is distinct from the Epigravettian (Villabruna), the other genetically recognisable Late Pleistocene human group that inhabited Europe at this time. We find evidence for a small effective population and biological kinship within the assemblage. Compound specific isotopic analyses shows a d15NGlu:d15NPhe ratio indicative of an omnivorous diet, mirroring similar work carried out on other Magdalenian sites and showing no marine or freshwater component to the diet.

Offspring sex ratios in two Bornean rainforest primate populations

ANDREW J. MARSHALL

Anthropology, University of Michigan, Ecology and Evolutionary Biology, University of Michigan, Program in the Environment, University of Michigan, School for Environment and Sustainability, University of Michigan

Evolutionary theory predicts that mammalian mothers that are in relatively good condition will disproportionately produce male offspring because high quality sons are expected to have higher lifetime reproductive success than high quality daughters. Although intuitively appealing, this prediction is frequently contradicted by empirical results, suggesting the existence of more subtle interactions between maternal condition, ecology, and offspring sex ratios– and demanding that we take seriously the possibility that many reported results reflect stochasticity, small sample sizes, and publication decisions that are biased towards significant findings. My team and I monitored populations of two Bornean rainforest primates inhabiting a mosaic of seven distinct forest types for 24 months (2000-2002). These habitats differed by more than an order of magnitude in the primate densities that they supported (an index of habitat quality), although which particular forest types were of highest quality differed between the two species. In both socially monogamous gibbons (*Hylobates albibarbis*, n = 33 groups) and polygynous leaf monkeys (*Presbytis rubicunda rubida,* n=13 groups) offspring sex ratio (proportion males) was strongly positively related to population density (model comparison of binomial regression models indicates that models including population density strongly outperform intercept-only models, bearing >99% of model weight). Monitoring of groups from 2007-2020 suggests that population densities and sex ratio biases were stable for two decades. Upon closer inspection, neither result readily conforms to theoretical predictions. I discuss various potential explanations for these perplexing results, including chance, differences in female condition among habitats, and the role of abiotic factors.

Harvard, UC Davis, University of Michigan, Victoria University Wellington, Hellman Foundation, Leakey Foundation, Fulbright Foundation, Mohamed bin Zayed Species Conservation Fund, AZA Ape TAG Initiative, Disney Conservation Fund.

Transgender Identification: Gender and Sex Estimation in Forensic Casework

BENJAMIN J. MARTIN and SEAN D. TALLMAN

Anatomy and Neurobiology, Boston University Aram V. Chobanian & Edward Avedisian School of Medicine

Societal knowledge about issues faced by transgender and gender-diverse individuals has increased; however, the field of forensic anthropology has struggled to keep abreast with ever-evolving perceptions of sex and gender. Specifically, forensic anthropology lacks a codified approach to identifying transgender decedents due to binary assigned sex estimation methods that lack a biocultural approach and divergent perspectives on the role of gender. Via an anonymous survey of forensic anthropologists (n=130), the present research explores the processes of biological profile deployment in forensic casework, along with current perspectives on sex and gender and associated methods, language, and reporting. Regarding the role of gender in casework, most (51.5%) believe identifying gender improves the odds of identification, and many (40.8%) would include such information in a forensic anthropological report, with 59.0% uncertain about testifying to gender. Additionally, 55.4% of respondents report that skeletal sex estimation does not represent a decedent's gender, and most would cite signs of gender-affirming surgery (59.2%) or material evidence (47.7%) for use in reporting gender despite uncertainties about Daubert compliance (38.5%). Regarding terminology, respondents prefer "sex" (52.3%) or "biological sex" (34.6%) over other arguably more apt descriptors such as "assigned sex" (19.2%). While forensic anthropologists acknowledge the need for clarity in gender-inclusive definitions and mostly maintain that skeletal sex is not equivalent to gender, further studies for a truly biocultural forensic anthropology should focus on the role of sequential evidentiary unmasking and material evidence alongside assigned skeletal sex analyses.

Maternal and infant SARS-CoV-2 antibody responses following maternal COVID-19 infection

MELANIE A. MARTIN[1,2], MONICA KEITH[1,2], RYAN M. PACE[3], JANET E. WILLIAMS[4], SYLVIA H. LEY[5], CELESTINA BARBOSA-LEIKER[6], BEATRICE

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

CAFFÉ[7], CAROLINE B. SMITH[7], AMANDA KUNKLE[1], KIMBERLY A. LACKEY[4], ALEXANDRA D. NAVARRETE[8], CHRISTINA DW. PACE[3], ALEXANDRA C. GOGEL[3], DAN TA. EISENBERG[1,2], BETHANEY D. FEHRENKAMP[4,9], MARK A. MCGUIRE[4], MICHELLE K. MCGUIRE[3], COURTNEY L. MEEHAN[7] and ELEANOR BRINDLE[10,2]

[1]Anthropology, University of Washington, [2]Center for Studies in Demography and Ecology, University of Washington, [3]Margaret Ritchie School of Family and Consumer Sciences, University of Idaho, [4]Department of Animal, Veterinary and Food Sciences, University of Idaho, [5]Department of Epidemiology, Tulane University School of Public Health, [6]College of Nursing, Washington State University Health Sciences, [7]Department of Anthropology, Washington State University, [8]Elson S. Floyd College of Medicine, Washington State University, [9]WWAMI Medical Education, University of Idaho, [10]Maternal, Newborn and Child Health & Nutrition, PATH

Infants exposed to caregivers infected with SARS-CoV-2 may have heightened infection risks due to their intensive care and feeding needs. However, there is limited research on COVID-19 outcomes in exposed infants beyond the neonatal period. Between June 2020 – March 2021, we conducted interviews and collected capillary dried blood spots from 46 mothers diagnosed with COVID-19 (COVID+ group) and their infants (aged 1-36 months old) for up to two months following maternal infection. Comparative maternal-infant data were also collected from a control group of mothers with no known SARS-CoV-2 infections or exposures (n = 26, control group), and from mothers who tested SARS-CoV-2 negative following suspected infection (n = 11, COVID- group). Most infants (87%) were breastfed during the study. Maternal and infant blood spots were self-collected with HemaSpot-HF devices and analyzed for anti-SARS-CoV-2 S-RBD IgG and IgA positivity and anti-SARS-CoV-2 S1 + S2 IgG concentrations.

Among COVID+ mothers and their infants, mean probability of seropositivity was lower for infants vs. mothers (0.54 vs. 0.87 for IgG; 0.33 vs. 0.85 for IgA), and likelihood of infant infection was positively associated with the number of maternal symptoms and total other household infections reported. Among the control group, 44% of mothers but none of their infants tested antibody positive. No samples returned by COVID- mothers or their infants tested antibody positive. Our results demonstrate minimal risk to infants following exposure to maternal COVID-19 infection, including for breastfeeding infants, and the utility of at-home biomarker collection for antibody monitoring.

Funded by NSF (IOS-BIO 2031753, 2031715, 2031888, 2031761), Bill and Melinda Gates Foundation (INV-016943), UW CSDE (NICHD P2C HD042828), US NIH (R01 HD092297-03), USDA NIFA (Hatch project IDA01643)

Employing the power of the Tooth Fairy or Ratón Pérez in developing a community-engaged scientific collection of deciduous teeth

MARINA MARTÍNEZ DE PINILLOS[1,2], LESLEA J. HLUSKO[1,3], MARIO MODESTO[1,4], IAN TOWLE[1], MARÍA MARTINÓN-TORRES[1], CHITINA MORENO-TORRES[1], PILAR FERNANDEZ[1] and LAURA MARTÍN-FRANCÉS[1]

[1]Paleobiology, CENIEH, [2]Laboratorio de Evolución Humana, Universidad de Burgos, [3]Integrative Biology, University of California Berkeley, [4]Human Evolution, Universidad Internacional de La Rioja

Tradition says that when children lose a baby tooth, they should place it underneath their pillow while they sleep and the *Tooth Fairy* will trade the lost tooth for a small gift. In Spain and other Hispanic-speaking countries, that little fairy takes the form of a mouse called *Ratón Pérez*. All of these baby teeth and the parents who carefully recorded when they were shed represent a tremendous opportunity to study in detail the deciduous dentition. Here, we introduce the *Ratón Pérez Collection* to the scientific community and invite collaborators to utilize the resource.

The Dental Anthropology Group of the National Research Centre on Human Evolution (CENIEH) organized the first campaign of the *Ratón Pérez Collection* in 2014. Since then, campaigns have been carried out every year, growing into a highly successful community-engaged project that teaches children about science and includes them in the endeavor. The collection currently comprises more than 4,000 teeth from children between the ages of 2 and 15 years. Each tooth is associated with basic information about the individuals, their parents, and grandparents (sex, date and place of birth, ancestry, country of residence), as well as important data about early life history (pregnancy duration, breast-feeding, bottle-feeding) and other relevant information provided by the donors. We present an overview of these demographic features and discuss this in context with published comparative data.

Given the scarcity of deciduous dental samples available, the *Ratón Pérez* collection is highly valuable for disciplines ranging from forensic, dental and anthropological fields.

European Research Council within the European Union's Horizon 2020 Research and Innovation Program (Grant Agreement 101054659); Fundación La Caixa; Fundación Caja de Burgos; Spanish Ministerio de Economía y Competitividad (CGL2015-65387-C3-3-P)

Female copulation calls of chimpanzees (*Pan troglodytes*) at Gombe National Park, Tanzania: advertisement and partner diversification

ANTHONY P. MASSARO[1], EMILY E. BOEHM[2], ELIZABETH V. LONSDORF[3], CARSON M. MURRAY[4], MARGARET A. STANTON[5] and MICHAEL L. WILSON[1,6]

[1]Ecology, Evolution, and Behavior, University of Minnesota- Twin Cites, [2]Center for Faculty Excellence, University of North Carolina-Chapel Hill, [3]Anthropology, Emory University, [4]Anthropology, George Washington University, [5]School of Social and Behavioral Sciences, University of New England, [6]Institute on the Environment, University of Minnesota- Twin Cities

In many different primate species, members of one or both sexes produce copulation calls: acoustically distinct vocalizations given during or immediately after mating. Researchers have proposed many potential explanations for the function of these signals. Here, we analyze a sample of 2632 mating events observed at Gombe National Park, Tanzania (1987–2015) to test predictions of these hypotheses using information-theoretic model selection methods. We found that female chimpanzees were more likely to produce copulation calls earlier in their reproductive cycles, closer to the onset of turgescence (model-averaged parameter = 0.22, 95% CI = 0.04–0.40). We also found that nulliparous females were more likely to produce copulation calls (model-averaged parameter = -1.00, 95% CI = -1.38– -0.62) and females produced copulation calls less frequently when higher-ranking females were present (model-averaged parameter = -0.11, 95% CI = -0.19– -0.03). Using a subset of well documented reproductive cycles, we found that females who had mated with a greater proportion of potential male partners were less likely to produce a copulation call during a mating event (logistic regression, β = -0.54, t=-3.84, p<0.01). Females who produced copulation calls were more likely to subsequently mate with a new copulation partner, as opposed to mating with the same partner (chi-squared test, x^2 = 13.63, df = 1, p < 0.01). These results suggest that female chimpanzees employ copulation calls to attract attention from additional males, promoting paternity confusion. They also appear to modulate call production in response to audience effects.

Preliminary Estimates of Maxillary Canine Sexual Dimorphism in Early Miocene Catarrhines using the Coefficient of Variation (CV) Method

ERIKA MATTHEWS

Anthropology, University of Arkansas

Sexual dimorphism is difficult to assess in the fossil record as determining the sex of a given specimen is impossible to know with certainty. As such, it is preferable to estimate sexual dimorphism in extinct primates without assigning sex to specimens, a task commonly accomplished by the coefficient of variation (CV) method (Plavcan and Cope, 2002). A preliminary analysis of maxillary canine sexual dimorphism for five early Miocene catarrhine species was carried out using

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

the CV method and the results were compared to extant hominoids. Early Miocene catarrhines display a broad range of sexual dimorphism much like the extant hominoids, with *Ekembo nyanzae* and *Dendropithecus macinessi* being most like the panins (*Pan)* and members of genus *Limnopithecus* and *Kalepithecus* being most like gibbons (*Hylobates*). These findings have implications for the characterization of Miocene catarrhines being highly sexually dimorphic, suggesting instead a broad diversity of sex differences or lack thereof.

The application of random forest modeling to histological age-at-death estimation of the human rib

SOPHIA R. MAVROUDAS and NICHOLAS P. HERRMANN

Anthropology, Texas State University

This study utilizes N=278 human rib samples from North American individuals with known demographic histories to examine the applicability of random forest modeling to histological age-at-death estimation of the human rib. The individuals were sampled from the Texas State Donated Skeletal Collection (n=105) in San Marcos, TX, identified individuals from forensic casework (n=82) in the United States, a known cemetery sample (n=41) from Missouri, and the Universidad Autónoma de Yucatán (n=50) in Merida, Mexico. The samples were prepared according to standard histological protocols and imaged on a light microscope. Data from each slide was collected using a combination of live-view microscopy and digital imaging utilizing Image J and a digitizing tablet. The following histomorphometric data was collected: number of intact osteons, number of fragmentary osteons, total rib area, medullary area, cortical area, number of drifting osteons, number of double zonal osteons, number of embedded osteons, number of primary osteons, osteon area (On.Ar), osteon circularity, Haversian canal area (H.Ar), and Haversian canal circularity. From this data the following variables were calculated: osteon population density (specific to each osteon type as well as total counts of intact and fragmentary osteons), average On.Ar, average H.Ar, percent osteonal bone, activation frequency, bone formation rate, and relative cortical area. The results show that random forest modeling is applicable to histological age estimation of the human rib and can provide improved age-at-death estimates over traditional linear regression modeling. The random forest models generated from this data can be used in applied contexts for age-at-death estimation.

The origin of hip fracture in modern humans: An evolutionary perspective

HILA MAY[1,2], HADAS LEAH. AVNI[1,2], NIR SHVALB[3], ARIEL POKHOJAEV[1,2,4], JEAN-JACQUES HUBLIN[5,6] and FRANK RÜHLI[7]

[1]Department of Anatomy and Anthropology, Sackler Faculty of Medicine, Tel Aviv University, [2]Dan David Center for Human Evolution and Biohistory Research, Tel Aviv University, [3]Mechanical Engineering Department, Ariel University, [4]Department of Oral Biology, The Maurice and Gabriela Goldschleger School of Dental Medicine, Tel Aviv University, [5]Chaire de Paléoanthropologie, Collège de France, [6]Human Evolution, Max-Planck Institute for Evolutionary Anthropology, [7]Institute of Evolutionary Medicine, University of Zurich

The transition to an erect stance and bipedal locomotion is among the most fundamental milestones in human evolution. This transition involved significant morphological adaptations to the human skeleton, including the femur. These modifications cause many of today's prevalent physical impairments, including hip fractures (HF). Recognizing the elementary risk factors for HF is valuable for improving our ability to predict the risk of fractures and develop new preventive measures. This study aimed to reveal the morphological changes in the proximal femur (PF) that increase the risk of HF in present-day populations. Using the landmark-based Geometric Morphometric method, we followed shape changes in the PF over time and examined their relationships with HF. The sample of this study included *Pan troglodytes*, early hominins, early *Homo*, Neanderthals, as well as archaic and recent *Homo sapiens* (with and without HF). Multivariate statistical analyses and visualization were carried out based on the 3D landmark configurations. We found changes in PF shape over time and between populations that practiced different lifestyles (e.g., hunter-gatherers and recent humans). We showed that the proximal femur morphology is a risk factor for HF, independent of osteoporosis. During human evolution, changes in the PF, such as shortening and an enlarged convexity of the femoral neck and an increased antero-lateral expansion of the greater trochanter, were associated with an increased risk for HF. We concluded that HF is a trade-off for efficient bipedal walking in modern humans and is exacerbated by reduced physical activity.

This study was funded by the Mäxi Foundation, Switzerland; the Broad-Israel Science Foundation (#2632/18); and the Dan David Foundation.

Islands of change: Zanzibar red colobus, climate change, & human-wildlife interactions

JENNECA MCCARTER[1], NELSON TING[1], ALEXANDER V. GEORGIEV[2] and TIM R. B. DAVENPORT[3]

[1]Anthropology, Institute of Ecology & Evolution, University of Oregon, [2]School of Natural Sciences, Bangor University, [3]Re:Wild

The Zanzibar red colobus (*Piliocolobus kirkii*) is an endemic, endangered primate found on the island of Unguja with a population of roughly 5,800 individuals. A 1,666 km^2 island, Unguja is one of the most densely populated regions in rural Africa, leading to high amounts of human-wildlife interactions. In addition, as a low-lying island with an agriculture and fishing driven economy, Unguja and all its inhabitants are seriously impacted by the effects of climate change. Quantifiable shifts in sea level, patterns of precipitation, and soil quality have already been recorded, with far-reaching impacts on agriculture and the overall economy. This research assesses how climate change may impact the geographic range of the red colobus, and thus the geographic distributions of human-wildlife interactions. To generate these data, we used correlative ecological niche modeling and subsequent climate modeling. We built ecological niche models via both a presence-background approach (Maxent) and a presence-pseudo-absence approach (generalized linear model) using red colobus census data from 2015 and publicly available environmental data. We examined the potential effects of climate change by modeling four climate change scenarios (SSP1-2.6, SSP2-4.5, SSP4-6.0, SSP5-8.5) across four timescales (2021-2040, 2041-2060, 2061-2080, 2081-2100). These models indicate range shifts of varying degrees can be expected for the Zanzibar red colobus, depending on the scenario modeled. These range shifts are likely to increase the overlap of humans and colobus, highlighting the need for climate change informed land-use planning as a preventative management tool for human-wildlife interactions and thus the conservation of Zanzibar red colobus.

This research is funded by a SYLFF (Sasakawa Young Leaders Fellowship Fund) Fellowship.

Better Defining the Uluzzian: Proteomics and Radiocarbon Dating on a Middle- to Upper-Paleolithic Faunal Assemblage from Grotta del Cavallo, Apulia, Italy

MAXINE MCCARTY[1,2], FRANCESCO BOSCHIN[3], ADRIANA MORONI[3], ANNETTE OERTLE[4], DAVID CHIVALL[5], LUKE SPINDLER[5], PETER DITCHFIELD[5], KATERINA DOUKA[4,6] and THOMAS HIGHAM[2,5,6]

[1]School of Life Sciences, Arizona State University, [2]Department of Archaeology, University of Oxford, [3]Department of Physical Sciences, Earth, and Environment, University of Siena, [4]Department of Archaeology, Max Plank Institute for Human

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

History, Jena, Germany, [5]Oxford University Radiocarbon Accelerator Unit, University of Oxford, [6]Department of Evolutionary Anthropology, University of Vienna

In Europe, a subset of occupation layers lies between known or assumed modern human and known or assumed Neanderthal techno-complexes. These so called "transitional techno-complexes" fall into a crucial period for understanding the transition from Neanderthals to modern humans as well as their interactions and material cultures. One such transitional techno-complex, the Uluzzian, stretching across Italy and into Greece, has provided much controversy into species authorship, an attribution that could have large implications into current understanding the adaptation of its makers into new environments. Here, we use Zooarchaeology by Mass Spectrometry (ZooMS) and radiocarbon dating on an assemblage of bone fragments from the Uluzzian type-site, Grotta del Cavallo. In addition to providing taxonomic information, ZooMS was used as a proxy for screening and choosing for further dating bones with good collagen preservation. These are the first radiocarbon dates on bones from the site and support the argument that the Uluzzian at Cavallo started at least by 42 ka cal BP and posit that changes in the faunal assemblage could reflect an anthropogenic change at the site.

FINDER Project funded by the European Research Council and The University of Oxford Department of Archaeology

The effect of commingling on skeletal preservation: Assessing postmortem alteration of human remains from human interference at the Graeco-Roman site of Kourion's Amathus Gate Cemetery

PHILLIP MCCHEYNE[1], DAWN BARI[2], MICHAEL GIVEN[3] and XENIA PAULA KYRIAKOU[4]

[1]Anthropology, Athabasca University, [2]Anthropology, Trent University, [3]Archaeology, University of Glasgow, [4]Justice Studies, Florida Gulf Coast University

Taphonomic processes are responsible for the degree of human bone preservation and could impact observations that deduce the demographic and health profile of a population. Postmortem human interference related to mortuary practices (intentional commingling, burial reuse) and looting have detrimental effect on the quality of bone. This study evaluates weathering and completeness of bone from Kourion's Amathus Gate Cemetery in Cyprus to determine the effect postmortem interference has on the remains. A total of 4840 bone fragments were evaluated from 24 cist graves and 10 trenches, containing commingled remains. The degree of completeness and weathering was scored using a modified version of Buikstra and Ubelaker (1994) (1 – 4) and the IFA (2004) system (0 – 5+) respectively. Stratigraphy determined the position of the remains (trenches, surface/topsoil, grave fill, burial level). Frequencies and statistical (ANOVA; MANCOVA) relationships were calculated using SPSS Version 28.0. A total 43% of all bone had poor preservation. Completeness was poor (47%), but degree of weathering was low (1.6%). Bone from the trenches had the highest frequency of good preservation (44.8%), followed by burial level (38.9%), grave fill (32.9%) and surface/topsoil (21.3%). Bone from the surface/topsoil had the highest frequency of poor preservation (57%). Statistical significance was found between stratigraphy and bone weathering (p=<.001) and bone completeness (p=.003). Stratigraphy was positively correlated with bone weathering and bone completeness (p=<.001). The results suggest that intentional commingling increases skeletal fragmentation but does not affect bone's surface preservation. This renders observations for perimortem trauma and biological profile data difficult.

Exploring the Evolution of Vocal Range in Non-Human Primates

KATHRYN M. E. MCCOLLUM, KEELY Q. MAYNARD and STEPHANIE A. POINDEXTER

Anthropology, University at Buffalo

Primate vocalizations vary from low frequency chirps in mouse lemurs to duetting songs in gibbon pairs. These sonic vocalizations are a way for primates to communicate information to conspecifics, such as territorial range, mating solicitation, and predator alarm calls. All primates have sonic vocalizations which are within the hearing range of humans (<0.020 kHz), but some can vocalize in the ultrasonic range which is outside the range of human hearing (>20 kHz). There is ongoing discourse among primate communication researchers as to how and why acoustic range is so diverse in non-human primates. Body size and acoustic variation has been linked to the acoustic allometry principle which states there is a negative relationship between body size and acoustic range. Here we sought to estimate the acoustic range of the primate most recent common ancestor (MRCA) through the creation of a dataset which included vocal range and body size for 72 extant primates. The results place the primate MRCA acoustic range closest to the families Lemuridae, and Cercopithecidae with an average vocal range of 10.82 kHz to 41.65 kHz (mean: 26.53 kHz). We can infer from the vocal range that the primate MRCA could have been a medium to small-sized primate. Our data did support the acoustic allometry principle but suggested that the MRCA had a vocal range typically seen in diurnal primates. This contributes to ongoing debates as to the diel pattern for the primate MRCA.

A Test of Identical Twin Mirroring in the Dentition

TESS MCCRARY[1], KATHLEEN S. PAUL[2], TOBY HUGHES[3] and ALAN H. BROOK[3,4]

[1]Department of Biological Sciences, University of Arkansas, [2]Department of Anthropology, University of Arkansas, [3]Adelaide Dental School, University of Adelaide, [4]Barts and the London Dental Institute, Queen Mary University of London

In bioarchaeology, fluctuating asymmetry data provide insight into experiences of developmental stress that inform broader investigations of past health events and structural violence. However, the biological foundations of dental asymmetry are complex, and other factors may influence the composition of associated datasets. This study explores one such phenomenon—*twin mirroring*—in which members of monozygotic (MZ) pairs express similar phenotypes, but on opposite sides (twin 1 left phenotype = twin 2 right phenotype). Mirroring occurs in approximately 25% of MZ twins when a single embryo splits after initiation of bilateral organization. This study examines whether mirroring explains patterns of asymmetry in tooth crown morphology within a sample of Australian twins. We referenced an existing longitudinal dataset comprising Arizona State University Dental Anthropology System scores for 57 MZ twin pairs, 35 same-sex dizygotic (DZ) twin pairs, and 12 opposite-sex dizygotic (OS) twin pairs. Cases of deciduous mirroring account for 5.3% of the MZ dataset, compared to ~5.6% of the DZ and OS datasets. For permanent morphology, cases of mirroring account for 7.8% of the MZ dataset, exceeding the DZ (7.6%) and OS (5.7%) results. Fisher's exact tests failed to detect any nonrandom association between mirroring and twin type, which suggests this embryological event does not explain the structure of the asymmetry dataset. Instead, mirroring is manifested in crown morphology to a minimal degree. The results provide support for traditional interpretations of fluctuating asymmetry data, even in small-scale bioarchaeological contexts that may contain twins, such as households or family cemeteries.

Data collected under NSF 2015 GROW, NSF DDRI Grant 1540313, Wenner-Gren Dissertation Fieldwork Grant (KSP)

Triple oxygen isotopes in modern African ungulates: Implications for paleoecology

ELIZABETH A. MCGUIRE[1], ILYA BINDEMAN[2], KENDRA L. CHRITZ[3] and SCOTT A. BLUMENTHAL[1,3]

[1]Department of Anthropology, University of Oregon, [2]Department of Earth Sciences, University of Oregon, [3]Department of Earth, Ocean and Atmospheric Sciences, University of British Columbia

Aridity has been a central component of theories attempting to explain human evolution for almost a century. Testing those hypothesized

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

connections requires ecology to be reconstructed at the local level, but generating site-scale environmental records is challenging. $\delta^{18}O$ approaches are limited because it is difficult to separate aridity from other environmental factors. Triple oxygen isotopes (,àÜ'^{17}O) in mammalian tooth enamel show promise as a new proxy for paleoaridity that is not subjected to the same shortcomings as $\delta^{18}O$; however, modern relationships between aridity and ,àÜ'^{17}O are not well understood. Before any fossil application, ,àÜ'^{17}O needs to be characterized across a range of modern African mammals: where isotopic variation can be directly related to local climatic conditions and behavioral context. We present preliminary results from ungulates (n=22) from arid to humid modern and historic environments, including bovids, elephantids, equids, giraffids, hippopotamids, and rhinocerotids. Triple oxygen isotope ratios were measured via laser fluorination of enamel phosphate, enabling small (1-2 mg) sample sizes. ,àÜ'^{17}O values span 159 per meg, ranging from -259 to -100 per meg (-0.259 to -0.100‰.) We find taxa that obtain most of their needed water from leaves, such as giraffids, have lower ,àÜ'^{17}O values compared to those with high drinking water requirements, including hippopotamids. We convert results to body water to combine with published data of African mammals and observe significant differences in ,àÜ'^{17}O values between families living in arid vs. humid environments. This suggests that triple oxygen isotopes are a promising tool for tracing paleoaridity in African ecosystems.

This research is supported by the American Society of Mammalogists Grant-in-Aid of research, NSF/GSA Graduate Student Geoscience Grant #13702-22 (funded by NSF award #1949901), and the University of Oregon.

Plumbing New Depths in Industrialization: Anthropogenic Lead Exposure Amongst Individuals from Two English Towns

SARA A. MCGUIRE[1,2], MARK HUBBE[2], WILLIAM J. PESTLE[3], ARASH SHARIFI[4,5] and ALI POURMAND[4]

[1]Museum Conservation Institute, Smithsonian Institution, [2]Department of Anthropology, The Ohio State University, [3]Department of Anthropology, University of Miami, [4]Department of Marine Geosciences, University of Miami, Rosenstiel School of Marine and Atmospheric Science, [5]Research and Development Department, Isobar Science

Lead is a commonly exploited resource, and has been mined in England since before Roman times. To explore the physiological manifestations of social and structural inequality experienced in unmitigated anthropogenic environments, we examined lead exposure among individuals who lived in England during the Industrial Revolution (c. 1760 AD to 1850 AD). In particular, we analyzed collections representing populations that inhabited positions midway along the spectrum ranging from agrarian/rural to industrialized urban societies, which allowed us to evaluate nuances in lead exposure. These collections are from the small, more agrarian town of Barton-upon-Humber (n = 40), and the larger, more industrial town of South Shields (n = 54). Skeletal lead concentrations were measured to assess anthropogenic versus geogenic exposure, and a suite of lead ($^{206}/_{204}$ Pb, $^{208}/_{206}$ Pb, $^{207}/_{206}$ Pb, and $^{206}/_{207}$ Pb) and radiogenic $^{87}Sr/^{86}Sr$ isotope ratios were measured to examine potential sources of exposure. Individuals' lead concentrations ranged between 1.17 μg g^{-1} and 128.18 μg g^{-1}, significantly greater than the concentration found in the geological background (0.7 μg g^{-1}). Individuals from Barton-upon-Humber had significantly higher concentrations of skeletal lead (mean 49.35 ± 39.01 μg g^{-1}) than individuals from South Shields (mean 27.02 ± 19.78 μg g^{-1}) ($p = 0.020$), and there were significant differences ($p < 0.001$) between collections with respect to lead and strontium isotopes. We identified several locations throughout England with overlapping lead isotope signatures, suggesting a far-reaching network in the sourcing of mined lead in the form of coal and used in industrial goods.

Exploring the relationship between perceived home and neighborhood safety and sleep in a sample of indigenous Wixárika living in Guadalajara, Mexico

LEELA MCKINNON[1,2], ERIC C. SHATTUCK[1,3,4], RENÉ CROCKER SAGASTUME[5], IGOR RAMOS H.[5], PARI TEMAI GONZÁLEZ[5], ADDY VILLASEÑOR[5], YARA MARTIN[5], PAOLA PÉREZ[5], SOFIA MUÑOZ[5], THANKAM S. SUNIL[6] and DAVID R. SAMSON[1,2]

[1]Department of Anthropology, University of Toronto Mississauga, [2]Centre for Urban Environments, University of Toronto Mississauga, [3]Institute for Health Disparities Research, University of Texas San Antonio, [4]Department of Public Health, University of Texas San Antonio, [5]Departamento de Salud Pública, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, [6]Department of Public Health, University of Tennessee Knoxville

Home and neighborhood safety are understood to influence sleep patterns. Cross-cultural studies have reported that individuals who perceive their neighborhoods and homes as less safe experience shorter, lower quality sleep. Here, we explore the influence of perceived safety on sleep patterns in a pilot study of indigenous Wixárika living in the Guadalajara Metropolitan Area of Jalisco, Mexico. Sleep was measured with actigraphs from 20 participants (65% females, mean age=33 years) in Summer 2022. We modeled the effect of perceived neighborhood and home safety on sleep duration, efficiency, and timing using linear mixed effects models, controlling for age, sex, and physical and mental health. Average nightly sleep duration was 6.49 hours and average sleep efficiency was 76.90%. Participants fell asleep at 23:53 and woke up at 8:08 on average. We found that female participants have significantly higher sleep efficiency (estimate=0.32, p=0.01), but this is not significant when including the interaction of sex and perceived safety. Interactions indicate that perceived safety is a more significant predictor of improved sleep efficiency for female participants than for males. The interaction of sex and perceived safety is also a significant predictor of time that participants fell asleep (estimate=0.99, p<0.001) and woke up (estimate=1.30, p<0.001), with perceived safety associated with later sleep and wake times for female participants and earlier sleep and wake times for male participants. These preliminary results point to sex differences in how safety affects sleep, and offer promising areas of future research to better understand sleep and health in Wixárika communities.

This research was supported by the Centre for Urban Environments Research Award and the Shelley R. Saunders Thesis Research Grant.

Nature of the early African hominin fossil record

RYAN T. MCRAE and BERNARD A. WOOD

Center for the Advanced Study of Human Paleobiology (CASHP), The George Washington University

Hypotheses about early hominin alpha taxonomy should focus on skeletal elements that are well-represented in the fossil record. Surprisingly, there is no open-access database that contains detailed information about skeletal element representation in the hypodigms of early hominin taxa, so we set out to assemble one. This presentation builds on our previous work, presenting skeletal element abundance data for 14 early hominin taxa prior to *Homo erectus s.l.* (*Sahelanthropus tchadensis*, *Orrorin tugenensis*, *Ardipithecus kadabba*, *Ardipithecus ramidus*, *Kenyanthropus platyops*, *Australopithecus anamensis*, *Australopithecus afarensis*, *Australopithecus africanus*, *Australopithecus garhi*, *Australopithecus sediba*, *Paranthropus aethiopicus*, *Paranthropus boisei*, *Paranthropus robustus*, and early *Homo s.l.* The 100 anatomical categories we use to quantify skeletal and dental element abundance maximize coverage, while reducing redundancies. We intend to make this database available on-line with detailed descriptions of our 100 element categories, links to papers from which we extracted the data, and additional information on provenience and dating. This presentation is an opportunity for the community to make suggestions about how we can maximize the database's utility.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Examining the effect of thermal alteration on histological structures: Implications for histotaphonomic interpretation of skeletal remains

LAUREN A. MECKEL[1], SOPHIA R. MAVROUDAS[2], JUSTIN Z. GOLDSTEIN[3], SHELBY L. GARZA[2] and TIMOTHY P. GOCHA[2]

[1]Cell Biology and Anatomy, Louisiana State University, [2]Anthropology, Texas State University, [3]New York City, Office of Chief Medical Examiner

The use of histotaphonomic indices to interpret postmortem treatment of human remains is increasing in bioarcheological investigations, however, little experimental research has been carried out to test the assumptions of researchers interpreting histotaphonomic changes. This project used willed body donations (N=6) from the Forensic Anthropology Center at Texas State (FACTS) in fire death scenarios to experimentally test the effect of thermal alteration on histological structures. Midshaft samples of the sixth rib, femur, and fifth metatarsal were taken from each donor pre- and post-burning when available. Thermocouples were used to record temperatures during burning. The average burning temperatures ranged from 25.8 ,ÑÉ to 1384.6 ,ÑÉ. Standard histological taphonomic alteration indices were applied to both pre- and post-burn samples including the General Histological Index (GHI), the Cracking Index (CI), and the Birefringence Index (BI) to quantify visible changes. Two-tailed t-tests were used to evaluate differences in index score between pre- and post-burn samples. In the femur, differences in BI were observed between pre- and post-burn samples ($p<.05$). In the metatarsal, differences in CI were observed between pre- and post-burn samples ($p<0.05$). No significant differences in taphonomic indices were observed in the ribs. When pooling all elements, differences in BI and GHI were observed between pre-burn ($p<.01$) and post-burn samples ($p<.05$). Previous research on the sample emphasized the utility of thermally altered remains for histological age at death estimation methods, however, the results of this study document the effects of thermal alteration on histotaphonomic interpretation of skeletal remains in applied context.

A call for incorporating conceptual tools from the extended evolutionary synthesis for discussing human expansions in South America

LUMILA P. MENÉNDEZ

Anthropology of the Americas, University of Bonn, Evolutionary Biology, University of Vienna

The question of the origin of the biological variation of the earliest Native Americans has been a subject of intense debate over the last two centuries. As a result, several models have been proposed, based on the analysis of morphological (dental, cranial) and molecular data (serologic, mtDNA, Y chromosome, full genomes) of contemporaneous and ancient individuals. Despite the flourishing of cutting-edge techniques and the massive obtention of data in the last decades, some classic questions such as how diverse were the early Native Americans remain a matter of debate. More importantly, there have been no efforts for trying to reconcile disparate results from the genetic history and morphological evolution of Native Americans. Here I argue that many of the inconsistencies are due to the use of different samples and methods, the distinctive influence of random (e.g., drift, mutation) and non-random factors (e.g., plasticity, selection), but also the dissimilar time scales and rates of change. I illustrate this by employing publicly available data sets to compare morphometric and genetic distances among South American populations. I propose a pluralist framework for combining and/or interpreting distinctive sources of data and argue that when studying evolutionary history, environmental factors and developmental plasticity should be considered. I conclude that morphological and molecular data could be analysed in the context of the Extended Evolutionary Synthesis, which provides conceptual tools for dealing with different trajectories of inheritance, diverse timescales, and allows considering multiple causal factors for interpreting biological evolution.

This project is funded by the German Research Fundation (DFG Project N° 415489479).

Differentiation of ecological niche patterns between sympatric *Eulemurs* spp. in NW Madagascar: Implications for their conservation

FERNANDO MERCADO MALABET[1], JEAN-CLAUDE RAZAFIMAMPIANDRA[2], FINARITRA T. RANDIMBIARISON[2], CORAL CHELL[1], MALCOLM S. RAMSAY[1], BERTRAND ANDRIATSITOHAINA[3,4], MAMY RAZAFITSALAMA[4], TRAVIS S. STEFFENS[4,5] and SHAWN M. LEHMAN[1]

[1]Department of Anthropology, University of Toronto, [2]Mention Zoologie et Biodiversité Animale, Université d'Antananarivo, [3]Faculté des Sciences, de Technologies et de l'Environnement, Université de Mahajanga, [4]Planet Madagascar, [5]Department of Sociology and Anthropology, University of Guelph

How species respond to habitat loss and fragmentation depends in part on the flexibility of their niche requirements. Species with specialized, narrower breadth of niche requirements relative to more generalized taxa are predicted to experience higher vulnerability for extirpation or even extinction. Empirical tests of this prediction between sympatric congenera allows us to examine the importance of niche requirements relative to their conservation risk. In this study, we compared the distribution and ecological niche patterns of sympatric common brown lemur (*Eulemur fulvus*) and mongoose lemur (*E. mongoz*) in northwestern Madagascar. We hypothesized that Critically Endangered *E. mongoz* would exhibit a narrower breadth of niche requirements resulting in a smaller distribution than Vulnerable *E. fulvus*. We used MaxEnt v3.4.4 to develop species distribution models (SDMs) using presence-only data collected between 2015 and 2020 and ten independent background covariates. The comparison of our two models (EF-AUC=0.87 and EM-AUC=0.95) provide strong support for our hypothesis. The top 10th percentile of the *E. mongoz* probability distribution estimates an effective habitat of 449.2ha – much smaller than the predicted effective habitat of *E. fulvus* (1,435.02ha). Although the two species exhibited some degree of niche overlap, our *E. mongoz* model predicts a narrower niche breadth when compared to the *E. fulvus* model. The association of our results with the conservation status of *E. fulvus* and *E.* mongoz suggest that a relatively more generalized niche breadth enables *E. fulvus* to better respond to habitat loss and fragmentation.

Schools of the Environment and Graduate Studies at the University of Toronto, Nottingham Trent University, The Ontario Government, NSERC, Primate Conservation, Inc., Global Wildlife Conservation LCAF, CEPF, and IUCN-SOS.

Prevalence of growth arrest lines and their relationship to burial goods in an Early Medieval juvenile skeletal sample from Germany

JANA VALESCA MEYER

Anthropology, University of New Mexico

In hierarchical societies, limited access to resources disproportionately exposes those with lower social status to physiological stressors, leading to adverse health consequences. The Merovingian period in Germany (5th-8th centuries AD) enforced a strict societal hierarchy, while maintaining the habit of interring the dead with burial goods (BG), presumably reflecting the wealth of an individual or their family. This allows for investigating the effects of social status on stress exposure and survival.

I am presenting findings on the prevalence of growth arrest lines, so called Harris Lines (HL), a non-specific stress indicator, in the Merovingian skeletal assemblage from Großvargula, Germany, using x-ray. The sample (n=12) consists of individuals aged 7 to 18 years and includes individuals with and without BG. Using Odds Ratio (OR), I compared the exposure to arrested growth between individuals with and without BG. Applying presence/absence categories, there was a reduced likelihood for individuals without BG to exhibit HL (OR=0.1). This could reflect higher survival rates (heterogeneity in frailty) among individuals with BG, presumably coming from wealthier families. Considering differences in HL-count, the relationship between HL and BG

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

reverses. Between individuals with and without BG, the likelihood for developing four HL is equal (OR=1), while the likelihood for developing five HL is increased for individuals without BG (OR=4).

This highlights the importance of considering stress not only in terms of presence/absence, but to assess burden of stress in a nuanced manner when trying to detect heterogeneity in exposure and survival of stress between subgroups of a population.

Separating signal from noise in *Sahelanthropus*

MARC R. MEYER[1], JASON P. JUNG[2], ISABELLA FX. ARAIZA[3,4] and SCOTT A. WILLIAMS[3,4]

[1]Anthropology, Chaffey College, [2]Biology, California State University, San Bernardino, [3]Center for the Study of Human Origins, Department of Anthropology, New York University, [4]New York Consortium in Evolutionary Primatology

Since its discovery two decades ago, claims for *Sahelanthropus tchadensis* representing a basal hominin have been met with skepticism. Its curious provenience is not often discussed, as the bones were not found in situ. Recently, two partial ulnae and a femoral shaft were published and suggested to represent postcrania associated with the TM 266 cranium. Analyses of the femur were contradictory, with one finding support for previous interpretations of the base of the skull that *Sahelanthropus* was a bipedal hominin, while a second analysis suggested quadrupedal locomotion.

Here we assess the attribution of the cranium with the postcranial elements and employ cross-sectional data and elliptical Fourier shape analyses to identify locomotor signals in the fossil remains. The comparative sample (n = 73) includes extant hominoids (including recent modern humans), Miocene apes, and Pliocene and Pleistocene hominins.

The term "signal" is an analogy for the patterns and meaning hidden in data that may be obscured by "noise," or confounding variability in the data. We identify robust locomotor signals from aspects of the forelimb and more noise in data from the hindlimb that contribute little to interpretive models of this fossil assemblage. Our results suggest that *Sahelanthropus* had not emancipated its forelimb from a significant role in terrestrial locomotion and was likely to have used its forelimb in a manner similar to extant knuckle-walkers. While facultative bipedality cannot be ruled out, the aggregate signal from the appendicular postcranium of *Sahelanthropus tchadensis* differs from hominins and is similar to knuckle-walking *Pan* and *Gorilla*.

Fossil pelves attributed to early *Homo*: variants and variation

EMILY R. MIDDLETON[1] and SUSAN C. ANTÓN[2]

[1]Department of Anthropology, University of Wisconsin-Milwaukee, [2]Center for the Study of Human Origins, Department of Anthropology, New York University

Recent analyses of long known and newly discovered fossils have suggested three different morphological variants, or morphs, among the pelvic material broadly attributed to early *Homo* (i.e., *Homo habilis*, *Homo rudolfensis*, and *Homo erectus*). Here we use qualitative observations and quantitative assessments of these fossil pelves to evaluate variation in size and shape, then to propose how many morphs are represented and which specimens are attributed to each morph. Using a diverse comparative sample of modern human 3D coordinate data collected using a Microscribe G2X that includes individuals from subtropical, temperate, and cold regions from both Africa/Eurasia and the Americas (n=460), we contextualize the range of variation observed in early *Homo* pelvis fossils and test hypotheses about size-related shape variation and inferred sex attributions. Linear metrics were extracted from the human dataset and collected from casts of KNM-ER 3228, OH 28, and KNM-WT 15000 using digital calipers and from 3D surface models of KNM-ER 5881 and KNM-ER 77072. Metrics were analyzed in R using principal components analysis and box plots. Our analyses suggest the presence of two, or possibly three, pelvic morphs for the early *Homo* fossils and highlight a key sexually dimorphic relationship in modern humans between greater sciatic notch morphology and position of the cristal tubercle/iliac pillar. Given the lack of secure taxonomic associations for most fossil pelves, evaluating ranges of variation for proposed postcranial morphs within a diverse comparative context is key in linking fossils to understand functional adaptations and histories of extinct taxa.

Comparative data collection was supported by LSB Leakey Foundation and Wenner-Gren Foundation for Anthropological Research grants to ERM/SCA.

As above, so below: deposition, modification, and reutilization of human remains at Marmoles cave (*Cueva de los Marmoles*: Southern Spain, 4000-1000 cal BCE)

MARCO MILELLA[1], RAFAEL M. MARTÍNEZ SÁNCHEZ[2], SANDRA PICHLER[3], JUAN CARLOS VERA RODRÍGUEZ[5], MARÍA JOSÉ MARTÍNEZ FERNÁNDEZ[6], JUAN ANTONIO CÁMARA SERRANO[4] and ZITA LAFFRANCHI[1]

[1]Department of Physical Anthropology, University of Bern - Institute of Forensic Medicine, [2]Department of History, University of Córdoba, [3]Integrative Prehistory and Archeological Science (IPAS), Department of Environmental Sciences, University of Basel, [4]Department of Prehistory and Archeology, University of Granada, [5]Department of History, Geography and Anthropology, University of Huelva, [6]Independent Researcher

The deposition, retrieval, and manipulation of human remains in natural caves are well known throughout Prehistory in the Iberian Peninsula. Although these practices are archaeologically documented from the 6th to the 2nd millennium BCE, their biocultural meaning is still largely unclear. Here we present and discuss new anthropological and taphonomic data from *Cueva de los Marmoles* (CM, Priego-Cordoba), a cave context from Southern Spain that returned a large number of commingled skeletal remains documenting its funerary use from ca. 4000 to 1000 cal BCE. Our aims are to: a) estimate the minimum number (MNI) and demographic distribution of the buried individuals; b) reconstruct the depositional and post depositional processes characterizing this assemblage. We analyzed macroscopically and microscopically all skeletal finds (410 bone fragments and 57 dental remains), and quantified the MNI and anatomical distribution of anthropic traces using the approach of Mack et al. (2016). We tested the statistical significance of these patterns using nonparametric tests and logistic models. Results highlight: a) a MNI of 12 (7 adults - including four females and one male - and 5 nonadults); b) cut marks and fresh fractures on 5 and 116 bone fragments respectively (1% and 28% of total), including one example of "skull cup"; c) no specific trend in the anatomical distribution of anthropic traces. These results suggest that CM was the focus of specific rituals centered on the human body and, when compared with similar contexts from Southern Iberia, the presence of shared funerary traditions and ideologies in this region.

Funding from "Archaeobiology of the Neolithic of the Southern Iberian Peninsula" (NeArqBioSI) A-HUM-460-UGR18 by Consejería de Economía, Conocimiento, Empresas y Universidad. FEDER Programme - Junta de Andalucía-Universidad de Granada. Call 2019.

Modeling Embodied Social Inequity from Skeletal and Dental Tissues: Presenting the Structural Vulnerability Profile (SVP) and Trait List

KATHERINE A. MILLER WOLF, ALLYSHA P. WINBURN, MEREDITH G. MARTEN, EMILY ROMDENNE, ALIANA SCHWARTZ and C KIRK

Anthropology, University of West Florida

Lived experiences of social marginalization leave traces on skeletal and dental tissues. The extent to which structural and social inequity is embodied can be modeled using criteria derived from traditional approaches utilized in biological anthropology, including the osteological paradox (Wood et al. 1992). Our research group recently proposed the Structural Vulnerability Profile (SVP; Winburn et al. 2022) as a means to augment biological profile information with data

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

on embodied experiences. In this presentation, we introduce a SVP biomarker trait list (n=40) that can be applied during osteological assessment to identify the degree of vulnerability, inequity, and resilience experienced by an individual during life. We present the results of an application of the SVP to 50 individuals from the New Mexico Decedent Image Database (NMDID; Edgar and Berry 2019). The anonymized medicolegal CT images were authorized for research purposes by next of kin and are thus contextualized with demographic data to further articulate skeletal data with lived experiences. The SVP effectively links skeletal and dental markers of inequity to social and economic stressors that are embodied during life such as sex, social race, poverty, and access to medical care. While our SVP is initially applied to a forensic sample, we argue it has major implications for research in biological anthropology, bioarchaeology, and medical anthropology.

Funding provided by a Wenner-Gren Post PhD Research Grant (#10277) and Anthropology Research Support at the University of West Florida.

A New Hominin Patella from Kromdraai, South Africa

CATHERINE K. MILLER[1,2], JEREMY M. DESILVA[1,2], BERNHARD ZIPFEL[3] and JOSÉ BRAGA[3,4]

[1]Ecology, Evolution, Environment, and Society, Dartmouth College, [2]Anthropology, Dartmouth College, [3]Evolutionary Studies Institute, University of the Witwatersrand, [4]Centre d'Anthropobiologie et de Génomique de Toulouse, Université Paul Sabatier Toulouse III

The Kromdraai B locality in South Africa has yielded a number of Pleistocene hominin fossils, including the type specimen of *Paranthropus robustus*. Recent excavations of Unit P at Kromdraai have uncovered additional fossil hominin material attributed to both *P. robustus* and early *Homo* and date to around 2 Ma, providing insight into a significant period in hominin evolution. Among these newly recovered fossils is a large, well-preserved patella (KW 8182). Given its specific role in increasing the lever arm for the quadriceps, the patella is an informative element for reconstructing bipedal locomotion in early hominins. However, fossil hominin patellae are exceptionally rare. The paucity of this bone in the fossil record makes KW 8182 an important addition to the narrative of hominin knee joint mechanics. The current study presents an analysis of the KW 8182 patella, which sheds light on the knee kinematics and locomotor behavior represented at Kromdraai. Although the fossil is missing a portion of the posteroinferior aspect, much of the morphology is intact and therefore capable of comparative analyses. Here, linear measurements and 3D shapes are compared between the KW 8182 patella, a sample of extant primate patellae, and other hominin patellae preserved in the Plio-Pleistocene fossil record. The relative anteroposterior thickness of KW 8182 falls within the range of modern human patellae, suggesting a similar role for the quadriceps during bipedal gait. Results from these analyses increase our understanding of the locomotor behavior of the Kromdraai hominins as well as hominin knee joint mechanics.

Modeling amelogenesis and tooth shape with continuum models of ameloblast movement using a new variable: ameloblast transition rate (ATR)

PEARSON W. MILLER[1] and MACKIE C. O'HARA[2]

[1]Center for Computational Biology, Flatiron Institute, [2]School of Anthropology and Conservation, University of Kent

Amelogenesis, perikymata distribution, and enamel thickness are inextricably linked, but anthropologists and dental researchers have yet to uncover their intricate relationships. Mathematical models provide an effective means to test dependencies of striae of Retzius and perikymata distributions on key developmental factors such as dailysecretion rate (DSR) and enamel extension rate EER. Based on a minimal set of assumptions about the behavior of individual ameloblasts, we develop a coarse-grained continuum model of enamel deposition, which we simulate using recently developed deep learning techniques. In addition to DSR and EER, we introduce an Ameloblast Transition Rate (ATR) controlling the termination of secretion as a function of ameloblast location: taken together, the various parameters of our model allow us to simulate the dependence of tooth shape on cell kinematics. We validate our simulationsby replicating several empirical features using histological sections of 6 clinically extracted upper premolars from the United Kingdom. Our model is then employed for a series of parameter space scans, allowing us to fully quantify the dependence ofmorphological characteristics on ameloblast behavior. By understanding the internal and incremental connections between ameloblast movement, perikymata distribution, enamel thickness, and overall enamel crown shape we significantly improve our ability to interpret developmental variables in fossil hominin teeth. Future models will incorporate non-human primate comparative species to evaluate variation in amelogenesis processes.

Identifying selection signatures across Mexican Indigenous populations using a new bioinformatics tool for whole-genome data

FERNANDA MIRON[1], AUSTIN W. REYNOLDS[1], D PÉREZ-CALIXTO[2], ENRIQUE MORETT[3] and ISRAEL AGUILAR-ORDÓÑEZ[2]

[1]Department of Anthropology, Baylor University, [2]Department of Supercomputing, National Institute of Genomic Medicine, Mexico, [3]Institute of Biotechnology, National Autonomous University of Mexico

Over the past few years, the exponential increase in computational power and the development of next-generation sequencing technologies have paved the way to identify genomic regions that appear to be shaped by natural selection. Although the study of selection signatures increases our understanding of evolution and genetic structure, Latin American populations remain underrepresented in genomic research. To date, the limited number of American Indigenous genomes impairs the effective implementation of selection analyses and generates an opportunity to better understand health and human diversity. Previous studies have revealed that Mexico's Indigenous population may be genetically adapted to the unique infectious disease and dietary landscape of the region. Here, we present a comparative analysis of genetic adaptation in whole genome data of 76 individuals from different Mexican Indigenous Populations, sub-divided into north-center-south groups. To do this, we developed a simple Nextflow pipeline for detecting recent evidence of selection in whole-genome data through Population Branch Statistics (PBS) and Integrated Haplotype Scores (iHS). Our results show regional variation in selection signatures and evidence of adaptation to pathogenic environments, thus supporting previous hypotheses of Mexican Indigenous adaptations to diseases introduced during the colonial period. Code and brief manual (from installation to testing run) of the developed pipeline are publicly available from the following GitHub repository: https://github.com/fernanda-miron/nf-selection

Structural Issues in the Criminal Justice System and their impact on Forensic Anthropology

JILLIAN A. MITCHELL and CONNIE D. FELLMANN

Anthropology & Geography, Colorado State University

Malpractice in crime labs is often seen as the result of behaviors stemming from individual "bad" actors. However, they may stem from larger structural issues within the system including lack of both regulation and state oversight as well as limited funding. While these issues are documented in the work of medical examiners and coroners, it remains unclear how they might impact the work of forensic anthropologists. To better understand how these issues may impact forensic anthropologists we conducted surveys and interviews with practicing ABFA certified forensic anthropologists. Our online survey consisted of 27 questions including long and short written answers, multiple choice questions, and ordinal scale responses. The survey and interview questions were designed to measure personal experience through four main categories:

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

1) access to adequate lab space, equipment, and team members, 2) adherence to best practices, regulations, and ethical guidelines, 3) funding, and 4) oversight of the profession at the state and federal levels. In total we received 31 anonymous survey responses and conducted 2 virtual face-to-face interviews. Our results suggest three major places of concern including: 1) difficulty in acquiring suitable team members, 2) expectation for respondents to take on casework pro-bono, and 3) lack of state and federal oversight regarding accreditation/licensing for forensic anthropologist. While not exhaustive, these data provide some insight to common barriers impacting the field and makes recommendations on how the barriers can be diminished.

'Genetic architecture' differences between sexes can be confounded by gendered effects

MIRIAM MIYAGI[1] and SARAH S. RICHARDSON[2]

[1]Organismic and Evolutionary Biology, Harvard University, [2]Studies of Women, Gender, and Sexuality, Harvard University

This abstract is submitted as part of the 'Born Which Way? Biological and Genetic Engagement in Sex, Gender, and Sexuality Research' symposium.

Increased availability of large human genome datasets has opened a new arena for researchers searching for essential sex differences: 'sex-specific genetic architecture'. Proponents of this framework posit that the gene-to-trait map differs between sexes in a consistent way, such that identical alleles can have unequal or even opposing effects depending on an individual's sex. Much of the evidence supporting these claims comes from comparing allele effect sizes estimated from sex-stratified genome scans and attributing any variation to fundamental biological differences between sexes. However, few of these studies consider gender as another potential causal factor for sex-correlated signals. In this talk, we will theorize how gendered experiences can create the appearance of sex-differentiated genetic architecture via gene-by-environment interactions and demonstrate how the statistical frameworks used for finding genomic sex differences, such as genetic correlation analyses, cannot differentiate between the effects of sex and gender.

Artificial neural networks to reconstruct missing perikymata in worn teeth

MARIO MODESTO-MATA[1,2], LUIS DE LA FUENTE VALENTÍN[2], LESLEA HLUSKO[1,3], MARINA MARTÍNEZ DE PINILLOS[1,4], IAN TOWLE[1], CECILIA GARCÍA-CAMPOS[1,5], MARÍA MARTINÓN-TORRES[1,6] and JOSÉ MARÍA BERMÚDEZ DE CASTRO[1,6]

[1]Departamento de Paleobiología, Centro Nacional de Investigación sobre la Evolución Humana (CENIEH), [2]Ingeniería y Tecnología, Universidad Internacional de La Rioja (UNIR), [3]Department of Integrative Biology, University of California Berkeley, [4]Laboratorio de Evolución Humana (LEH), Universidad de Burgos, [5]Facultad de Ciencias, Universidad Autónoma de Madrid, [6]Department of Anthropology, University College London

Dental studies are key to understanding the evolution of the growth and developmental processes of extinct hominins. Central to these studies is the intrinsic nature of dental tissues (enamel and dentin), as they record periodicity lines in their histological structure, enabling us to calculate very accurately their formation times. Approaches to assess periodicity often include sectioning or synchrotron scanning, both of which are destructive either at the macro or micro scale. In order to avoid damaging fossils, perikymata can also be assessed on the crown surface. However, this approach requires unworn teeth, which are scarce in the fossil record.

We address the need for a non-destructive method for assessing periodicity across a wider range of fossil specimens by overcoming the obstacle of wear. We developed a package in R, named as toothR, to reconstruct the obscured perikymata on slightly worn teeth. We then applied artificial neural network analysis (ANN) to estimate the number perikymata lost in the first deciles of the crown height. We employed 164 unworn modern human teeth where all perikymata were counted along their crown heights. The results indicate that ANN can estimate the number of perikymata in the first three deciles with less than 5% of error in all tooth types.

The user friendly software provides future studies with a higher level of accuracy, increased sample sizes, and more robust insight to the paleobiology of our ancestors.

Funding for this research is supported in part by the European Research Council Advanced Grant Project 101054659—Tied2Teeth

Seasonality in the relationships between fluctuating asymmetry in deciduous teeth and environmental temperature during gestation

EMILY MOES[1] and HEATHER EDGAR[1,2]

[1]Department of Anthropology, University of New Mexico, [2]Office of the Medical Investigator, University of New Mexico

External environmental variation during gestation impacts the physiology of human development *in utero*, affecting birth weight, disease risk, and longevity, but evidence for these impacts has not yet been explored in dentition. We examined the relationship between variation in gestational environmental temperature and fluctuating asymmetry (FA) in deciduous dentition. FA measures developmental instability by quantifying random deviation in body structures. Because deciduous teeth form during prenatal life, dental FA captures signals of stress during gestation. We measured dental casts representing 159 child participants (ages 3-6 years) with health history records from the longitudinal Burlington Growth Study. FA was calculated from crown dimensions and intercusp distances. Temperature information was sourced from historical weather statistics based on the nine months preceding each participant's birth date, binned into trimesters. Individuals were grouped based on birth season (n=24-54) to control for seasonal temperature variation. Using multiple regression for each subgroup, we tested for the following effects on FA: high and low temperature extremes within each trimester; greatest variation within one month of each trimester; sex; and year and month of birth. Backwards selection indicates that the most predictive model for each subgroup differs in its selected temperature variables ($p<0.05$; adj. $R^2=0.15$-0.35). However, extreme temperature lows during the first two trimesters have significant association with FA in Spring, Summer, and Fall subgroups. Winter births differ such that FA is not significantly impacted by any temperature stress. These results suggest the effect of temperature stress during gestation varies based on season and trimester of exposure.

Funding was provided by the Wenner-Gren Foundation: Dissertation Fieldwork Grant; and University of New Mexico: New Mexico Research Grant, Joseph Powell Anthropology Endowment Award, Anthropology Research Development Award.

Precolonial violence: Analysis of traumatic injuries from a communal burial site in South Africa

CALVIN G. MOLE[1,2], DEANO D. STYNDER[3], JUDITH C. SEALY[3] and VICTORIA E. GIBBON[1]

[1]Division of Clinical Anatomy and Biological Anthropology, Department of Human Biology, University of Cape Town, [2]Division of Forensic Medicine and Toxicology, Department of Pathology, University of Cape Town, [3]Department of Archaeology, University of Cape Town

Violent injury in children from the Holocene of southern Africa has rarely been reported. This study reports injuries observed in the skeletal remains of children recovered from a communal burial site at Ladismith, Western Cape, South Africa, with the aim of determining the circumstances surrounding their deaths. The burial site contained a minimum of ten individuals of varying ages and both sexes, dated to *c.*550 BP. The remains were exposed by animals and subsequently collected by members of the public. Most skeletons are incomplete, probably due to unsystematic recovery. Skeletal injuries were assessed macroscopically and using computed tomography for timing (antemortem, perimortem, postmortem), mechanism (blunt, sharp, perforating) and extent of injury. Trauma analyses revealed no perimortem injuries amongst adults, although adult crania were missing and could

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

not be examined. Three children (ranging from 5 – 7yrs of age at death) presented with perimortem perforating injuries to the neurocranium. The observed lesions displayed characteristics of blunt-sharp force impact. The locations and directions of impact indicate deliberate violence directed from above, most likely using a metal tipped spear with a blade at least 110 mm long, 10 to 50 mm wide, and 2 mm thick. While the motive for this attack remains unclear, this is the earliest evidence for use of an iron spear in this region. The results further extend the timeframe and location for the practice of communal burial in the Holocene of southern Africa and support the hypothesis that communal, or mass burials were often associated with violence.

This research was supported through Gibbon by the National Research Foundation, South Africa (Grant No. 115357 and 120816), and the Department of Human Biology, UCT.

Exploring astragalar morphology by means of a high density sliding semilandmark approach: insights on the evolution of primate locomotor behavior

ORIOL MONCLÚS-GONZALO[1], DAVID M. ALBA[1], ANNE-CLAIRE FABRE[2,3,4] and JUDIT MARIGÓ[1]

[1]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, [2]Vertebrates Kuratorin Säugetiere, Naturhistorisches Museum Bern, [3]Institute of Ecology and Evolution, University of Bern, [4]Life Sciences Department, Vertebrates Division, Natural History Museum

The astragalus is one of the most examined postcranial elements in functional studies, as it is the main facilitator of plantar and dorsal flexion and contributes to the inversion-eversion and abduction-adduction movements of the foot. In primates, which usually navigate through the arboreal milieu, this bone is critical to accommodate the complex positional behaviors that are required to move across the different substrates. For this reason, we quantified the morphology of the astragalus using a novel sliding semilandmark approach in a large sample of extant primates comprising the whole diversity of the group. The relationship between astragalar shape and locomotor behavior was also assessed by means of two-block partial least-squares analyses among astragalar shape and percentages of locomotor repertoire compiled from field studies. We found that "prosimians" (a paraphyletic grouping including strepsirrhines and tarsiers), platyrrhines, and catarrhines occupy different regions of the morphospace and differ in the degree of disparity and amount of phylogenetic signal displayed by this bone. Moreover, two-block partial least-squares analyses confirm the significant correlation between astragalar shape and locomotor behavior, denoting the strong functional signal embedded in the shape of the bone as well as its articular facets alone. Our results support that the astragalus is a good predictor for the locomotor repertoire of extant primates, thus indicating its utility to infer the locomotor behavior of extinct species. In addition, differences in morphospace occupation and morphological disparity between groups of primates also indicates the profound impact of locomotion on primate evolution.

Funded by: MCIEI (PID2020-116908GB-I00, PID2020-117289GB-I00), Generalitat de Catalunya (CERCA Programme, and 2017 SGR 086 and 2017 SGR 116) and AGAUR/European Social Fund (2021 FI_B 00524).

Bayesian tip-dating approaches to inferring the hominin tree

CARRIE S. MONGLE[1,2], KELSEY D. PUGH[4,5], DAVID S. STRAIT[3] and FREDERICK E. GRINE[1,6]

[1]Department of Anthropology, Stony Brook University, [2]Turkana Basin Institute, Stony Brook University, [3]Department of Anthropology, Washington University in St. Louis, [4]Division of Anthropology, American Museum of Natural History, [5]New York Consortium of Evolutionary Primatologists, [6]Department of Anatomical Sciences, Stony Brook University

Time-scaled branches on phylogenetic trees are necessary to model morphological change over evolutionary time. As such, dated phylogenies form the basis of most phylogenetic comparative analyses of fossil taxa. Despite widespread interest in using phylogenetic comparative methods to model hominin evolution, few examples of rigorously dating the hominin tree have been attempted. Here we conduct a Bayesian tip-dated ("morphological clock") analysis of early hominins using a comprehensive craniodental character matrix for 15 hominin species and two hominoid species. We pair this matrix with geochronological dates representing the full known ranges of fossils comprising each operational taxonomic unit. Analyses were conducted in MrBayes using the CIPRES Science Gateway. Topology of the resulting maximum credibility tree does not differ appreciably from that of non-dated Bayesian analyses of this character matrix, with two exceptions. First, the addition of a temporal component results in *Paranthropus aethiopicus* being reconstructed at the base of the *Paranthropus* clade, rather than nested in a sister relationship with *P. boisei*. Second, this tree differs from non-dated Bayesian analyses in the unresolved placement of more poorly sampled taxa (e.g., *Kenyanthropus platyops*, *Australopithecus garhi*). Moving forward, this time-scaled phylogeny of hominin taxa can serve as a foundation for comparative analyses of hominin evolution.

Prenatal growth rates and the evolution of encephalization in hominids

TESLA A. MONSON[1], ANDREW P. WEITZ[2], MARIANNE F. BRASIL[3,4] and LESLEA J. HLUSKO[4,5]

[1]Anthropology, Western Washington University, [2]Environmental Science, Western Washington University, [3]Berkeley Geochronology Center, [4]Human Evolution Research Center, [5]Centro Nacional de Investigación sobre la Evolución Humana (CENIEH)

Gestation is one of the earliest and most critical stages of ontogeny. The evolution of pregnancy and gestation have been obscured by the fact that these life history traits are difficult to infer from fossils. However, we recently published work demonstrating that prenatal growth rates in the hominid fossil record (neonatal mass in grams divided by gestation length in days) can be reconstructed from endocranial volume (ECV) and molar proportions using models developed from extant catarrhines. Prenatal growth rate (PGR) increased rapidly in hominids over the last six million years, leading to a human-like PGR (more similar to humans than to any other extant ape) between 0.5 to 1 million years ago. Here, we further explore the statistical relationship between ECV and PGR more broadly across primates (n=68 species). ECV and PGR are significantly correlated in extant primates (R^2=0.94, p<0.001), although some species, like humans, deviate from the regression line. Primate adult body mass is also correlated with neonatal body mass (R^2=0.92, p<0.001), and adult brain size is correlated with neonatal brain size (R^2=0.98, p<0.001). Because adult body mass and brain size are largely set by the trajectory of gestational growth, these findings support that prenatal growth rate plays a crucial role in the development of the encephalized human brain. We discuss the implications of these findings for the evolution of body and brain size in the hominid lineage.

A.P.W. was supported by the Washington Research Foundation, and M.F.B. was supported by the John Templeton Foundation for the duration of this research.

The pernicious anemia cohort study: identifying differences in a heterogenous presenting disease

BROOKE MORRIS[1], KOUROSH R. AHMADI[2] and AUSTIN W. REYNOLDS[1]

[1]Department of Anthropology, Baylor University, [2]Department of Nutrition & Metabolism, School of Biosciences and Medicine, University of Surrey

Many rare autoimmune diseases present with heterogenous symptoms, making definitive diagnosis a difficult and extended process. One such disease, Pernicious Anemia (PA), is caused by autoimmune attacks on gastric parietal cells in the small intestines, preventing absorption of the essential vitamin B12. PA patients often struggle receiving accurate and timely diagnosis (average TTD between 2 – 5 years) due to symptoms that

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

mimic other diseases and a lack of definitive diagnostics, resulting in irreversible neurological complications such as permanent damage of the myelin sheath, peripheral nerve lesions, muscle atrophy, and even death. As a result of these heterogenous symptoms and the lack of clinical consensus on diagnostics, patient phenotypes are usually described case-by-case. Here we attempt to improve PA diagnosis by conducting computational phenotyping on a cohort of 2200 self-reported PA patients. Using symptom and comorbidity data collected from a patient support group, we find unique predictive symptoms and coexisting disease patterns that are more frequently seen in PA patients. Patients who received a positive diagnosis on an antibody test are more likely to have hypothyroidism (p=0.0004) and Grierson Syndrome (p=0.0201), while those that did not test positive for PA were more likely to have random fevers (p=0.0052), suffer from clumsiness (p=0.0463), and vertigo (p=0.0128). Our results demonstrate the importance of using patient support groups to further refine disease phenotypes. This work has important implications for clinician diagnosis of PA and time to diagnosis for patients.

The Uncertain Death – Estimating Mortality Structure by Random Sampling

DARIA MOSER[1], SANDRA L. PICHLER[2] and KATHARINA FUCHS[1]

[1]Institute of Clinical Molecular Biology, Kiel University, [2]Integrative Prehistory and Archeological Science, University of Basel

Imprecise data produced by commonly applied age-at-death estimations profoundly impacts all research into age-dependent mortality in past societies. Wide and heterogenous age categories do not meet the need for unbiased data presentation. The current scientific practice does not allow for solid, large-scale cross-population studies.

With the Uncertain Death estimation (UCD), we are proposing an approach to estimate mortality structure by repeated random sampling of imprecise age-at-death estimations assuming a normal distribution of probability-of-death. An R package is available. In order to demonstrate the applicability of the UCD, we present a proof of principle study on a population with known age-at-death, the Bass-Mercyhurst collection. Milner and Boldsen (2012) applied transition analysis and consecutive maximum likelihood estimation (MLE) to the population.

A comparison of UCD and MLE and Kaplan-Meier survival analysis yielded a significant improvement of the accuracy of mortality profiles (p-value<0.05) for 4/4 and 3/4 data subsets respectively. No significant difference was found between UCD and age category assignment. UCD is incorporating the uncertainty inherent in the data. It is empirically shown to outperform the tested methods. UCD allows for comparative studies into age-dependent mortality in past societies. It does not rely on a large sample size of precise estimations to produce results. UCD provides the opportunity to run fast and simple analyses of mortality structures on a large dataset without reducing the information contained in the raw data, thereby facilitating a way to study patterns in age-dependent mortality on a large scale.

This research was funded as part of the CRC1266 "ScalesofTransformation" by the German Research Foundation

Basicranial Sexual Dimorphism Using a Landmark-Based Geometric Morphometric Approach

BENJAMIN H. MOSS

Department of Geography and Anthropology, Louisiana State University

This study explored size and shape differences of the basicranium in male and female human crania using landmark coordinate data from 100 crania of European descent housed at the Southeast Texas Applied Forensic Science Facility at Sam Houston State University in Huntsville, Texas. Twenty-three basicranial landmarks were recorded and evaluated with geometric morphometric methods to assess size and shape differences of the basicrania. A Student's t-test of centroid sizes showed significant differences between male and female means with males being larger overall. Procrustes ANOVA showed that there were statistically significant differences in shape between males and females. Principal component analysis and relative warp graphs were used to characterize and illustrate the morphology of the anterior basicranium, which exhibited relative shape homogeneity between the sexes. Though shape differences were relatively subtle, miniscule shape differences between males and females were observed in the area of the spheno-occipital synchondrosis. Males tended to exhibit a more flexed anterior basicranial region. The carotid canals were positioned more superiorly in relation to the posterior inferior potion of the sphenoid greater wing in males than in females. The results of this study found that basicranial size is a better indicator of sexual dimorphism than shape. This study also agrees with previous research, which suggests that basicranial sexual shape differences may be population specific.

This project was funded by the Nancy J. Berner Student Research Support Fund and the Torrence and Wyvonne Townsend Innovation Fund through Wichita State University.

Comparing aggression in bonobos and chimpanzees: Self-domestication or convergence with monkeys?

MAUD MOUGINOT[1], MARTIN SURBECK[2], MICHAEL L. WILSON[3] and NISARG DESAI[4]

[1]Anthropology, University of Minnesota, [2]Human Evolutionary Biology, Harvard University, [3]Ecology, Evolution and Behavior, University of Minnesota, [4]Neuroscience, University of Minnesota

Chimpanzees (*Pan troglodytes*) and bonobos (*Pan paniscus*), our two closest living relatives, differ strikingly in many aspects of their behavior. While chimpanzees act aggressively and sometimes kill their enemies, bonobos are considered more peaceful. Two hypotheses seeking to explain these contrasting patterns of aggression include the self-domestication hypothesis, which proposes that humans and bonobos have experienced selection against reactive aggression, and the monkey convergence hypothesis, which proposes that bonobos have evolved to resemble female-bonded societies of cercopithecoid monkeys. In this study, we tested those hypotheses by analyzing data from focal follows of male chimpanzees from Gombe National Park, Tanzania, and male bonobos from Kokolopori, Democratic Republic of Congo. Consistent with expectations, we found that chimpanzees exhibited higher rates of aggression by males towards females (GLMM, β[chimpanzees] = 0.794; 95% CI = [0.128, 1.46]), and higher rates of aggression by females towards males in bonobos (GLMM, β[chimpanzees] = -5.65; 95% CI = [-4.06, -1.97]). Surprisingly, however, we found higher rates of aggression among males in bonobos than in chimpanzees (GLMM, β[chimpanzees] = -1.07; 95% CI = [-1.88, -0.253]). Moreover, we found that the best predictor of male bonobo mating success was the rate of aggression towards females (GLMM, β = 0.22, 90% CI = [0.36, 1.21]), even though such aggression occurred infrequently (16 interactions out of 2,047 hours of observation). These results align better with predictions of the monkey convergence hypothesis than the self-domestication hypothesis.

Epigenetics, gene expression, and stress in mothers and offspring in the Democratic Republic of Congo: Biocultural investigation of the intergenerational effects of stress

CONNIE J. MULLIGAN[1,2], EDWARD QUINN[1,2], CHU J. HSIAO[1,2,3] and FELICIEN MASANGA MAISHA[4,5]

[1]Anthropology, University of Florida, [2]Genetics Institute, University of Florida, [3]College of Medicine, University of Florida, [4]Emerging Pathogens Institute, University of Florida, [5]Maisha Enyanya, Goma, Democratic Republic of Congo

According to the Developmental Origins of Health and Disease hypothesis, early life exposure to stress has important consequences for later life health. Epigenetically-determined changes in gene

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

expression may be one mechanism that mediates this effect. We work in eastern Democratic Republic of Congo, where 25 years of conflict and post-conflict unrest have subjected women to extreme stress and sexual violence. Maternal and newborn blood and placental samples, follow-up offspring samples, and culturally-relevant data on maternal stress have been collected from 200 mother-offspring dyads. Associations between maternal stress and newborn birthweight with genome-wide DNA methylation (Illumina EPIC array) and gene expression (Clariom D chip) in mothers, newborns, and placenta were investigated.

We report the following results: 1) Twenty-six CpG sites in mothers and newborns were associated with three measures of maternal stress and one of the 26 CpG sites was also associated with birthweight, thus linking increased maternal stress, altered newborn DNA methylation, and reduced birthweight; 2) Low birthweight was associated with epigenetic age acceleration over the first three years of life, suggesting that the impact of low birthweight on later life disease may be mediated by accelerated epigenetic aging; 3) War trauma was associated with global gene expression in the placenta and with birthweight; mediation analysis indicated that ~14% of the effect of war trauma on birthweight was mediated by a placental gene expression component. Our study provides evidence that epigenetic and gene expression changes may help explain how stress and violence impact health in an intergenerational manner.

NSF grants BCS-1231264, BCS-1540372 and BCS-1719866, NICHD grant F30HD097935, University of Florida (UF) Clinical and Translational Science Institute, UF College of Liberal Arts and Sciences, and UF Informatics Institute.

The insects in the hive and your mind's eye! Maasai Children's Empathetic Attitude towards Honeybees

ZAHEER MUNSHI[1], NICEPHOR PIUS LESIO[2], AMINA KIHWELO[3] and EVANCE LAIZER[4]

[1]NA, Hopkins School New Haven, [2]Natural Resources and Tourism, Tanzania Forestry Research Institute, [3]NA, Tanzania Wildlife Research Institute, [4]NA, Tanzania Wildlife Research Institute

The importance of bees and beekeeping can be embedded in individual minds from early childhood days. The Tanzanian Maasai, noted for their pastoral life, have seen recent initiatives like sustainable beekeeping activities in their area. The key research question is how the Maasai children are faring with the introduction of beekeeping in their society. Research involved interviews of adult Maasai followed by a survey of one hundred and ninety-six Maasai children from a school recently engaged in beekeeping activities. All adult interviewees indicated positive feelings towards beekeeping, despite how 'modern' or 'traditional' they feel. To illustrate, Maasai A, male, 45 years old, who perceives himself to be a 'modern Maasai', said that honey is a big part of Maasai traditional medicine. He also believes that his tribe should engage in beekeeping more as they can earn money by selling bee-related products. Maasai B, age 27, who believes himself to be a traditional Maasai said, he did remember childhood memories of harvesting honey from forests, which his family ate and used for chest pain, acknowledging the importance of bee-related products. Further, school children survey findings showed their enthusiasm and empathy towards bees. 91% believe bees are important for the environment, 84% believe beekeeping activities are beneficial, and 70% would like to learn more about bees in school. Showing empathy, 73% (68%) children responded negatively to destroying bees' nests close to home (park). Work in progress study of one-hundred and nineteen Maasai parents indicates their favorable attitude towards bee-related school curriculum.

Association of Māori and Pacific-specific Genetic Variants with Gout

SHUBHRA MURARKA[1], NICHOLAS SUMPTER[2], RIKU TAKEI[3], NICOLA DALBETH[4], LISA STAMP[5], JANAK DE. ZOYSA[4], RINKI MURPHY[4], ANNE-KATRIN EMDE[6], STEPHANE CASTEL[6], KAJA WASIK[6], KEOLU FOX[1], TONY MERRIMAN[3] and MEGAN LEASK[6]

[1]Anthropology, University of California- San Diego, [2]Biomedical Sciences, University of Alabama-Birmingham, [3]Division of Clinical Immunology and Rheumatology, University of Alabama-Birmingham, [4]Medicine, University of Auckland, [5]Medicine, University of Otago Christchurch, [6]Variant Bio Inc.

Gout, an arthritic disease that causes joint inflammation from immune responses to urate crystals, was long known as the "disease of kings" and thought to only affect European royalty. Often overlooked, Māori and Pacific people have a prevalence of gout of approximately 6-8%, suggesting genetic factors as a possible contributor. >90% of Genome Wide Association Studies (GWAS), the gold standard for identifying genetic-disease association factors, include only individuals of European ancestry. Marginalized communities continue to be excluded from genetic studies, and resultant medical treatments may be less effective. Consequently, little knowledge exists of the genetic diversity of Polynesian people. Here, we aim to identify high frequency genetic variants specific to Polynesian people in previously identified genes that associate with gout.

We used a dataset of 29.2 million genetic variants from a study cohort of 2,593 Polynesian people. The sample was restricted to variants that were: 1) rare (<0.1% minor allele frequency (MAF)) or not reported in 1000 Genomes or the Genome Aggregation Database (gnomAD); 2) common in Polynesia (>1% MAF), and 3) within candidate gout genes. These variants (n=24,836) were tested in association analyses for gout. We ran logistic regressions and adjusted for age, sex, and principal-component vectors.

We identified nine genetic variants within candidate gout genes that were strongly associated (p 1 x 10-4) with gout. These variants may be important for understanding the genetic factors of gout and may ultimately help develop personalized health therapeutics for historically marginalized populations of the Pacific.

This research was funded by VariantBio, EmersonCollective, Indigenous Futures Institute, and the Fox Lab at the University of California-San Diego.

How reliable are musculoskeletal models from fossil remains with badly-preserved femora?: An assessment using artificially damaged subject-specific MSk models

ALISON A. MURRAY[1], NETANYA KARMEL[1], PAVLOS SILVESTROS[2] and JOSHUA W. GILES[2]

[1]Department of Anthropology, University of Victoria, [2]Department of Mechanical Engineering, University of Victoria

Musculoskeletal (MSk) models enable the estimation of muscle and joint forces in the body throughout the gait cycle, data of utility in understanding relationships between locomotor morphology and costs among fossil hominins. However, the accuracy of MSk model outputs is affected by scaling and the definition of joint and muscle coordinate systems; both of these must often be estimated when building models based on the morphology of fragmentary fossil bone. The current research assesses the extent to which estimating hip joint center of rotation and hip muscle attachment coordinates affects the accuracy of MSk model muscle force production estimates. Ten freely-available, previously validated subject-specific MSk models were modified after artificially removing the subject's proximal femur and approximating the missing coordinates using a scaled proxy femur from another subject. Subject-specific motion, force, and muscle architecture parameters were applied to each pair of unmodified and modified models, and average percent errors were calculated between median hip muscle force estimates at every 10% of the gait cycle. The average percent error was ~15%, but varied widely by muscle and gait phase, ranging from <1% error for gluteus minimus to ~25-70% error for piriformis. That much error in some force estimates is problematic for the reconstruction of a specific muscle group's performance from fragmentary remains, especially if other parameters must also be estimated. Future work will need to assess the effect

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

of other commonly-estimated values on model outputs, and ultimately determine the uses for which MSk models can be effective in biological anthropology.

This research was funded through an NSERC Discovery Grant (RGPIN-02442-2021) and an NSERC Undergraduate Student Research Award.

The Influence of Tail Use and Vertebral Level on Prezygapophyseal Morphology in the Galagid Tail

LYDIA C. MYERS

Department of Anthropology, The University of Texas at Austin

Tail use among primates is diverse, with both behavioral and mechanical functions. Primates with tails use them during locomotion for stability on unstable substrates and body direction during leaping, resulting in anatomical changes in the caudal vertebrae based on tail use. The zygapophyses are expected to be functionally important in tail movements, as they form the synovial joints between the caudal vertebrae. The majority of tail anatomy research has focused on prehensile tail use, concealing the diversity of tail use in the non-prehensile category. Tail use during vertical clinging and leaping likely impacts caudal vertebral anatomy (*e.g.*, zygapophyses) in comparison with other forms of primate locomotion. This study evaluates variation in prezygapophyseal articular surface morphology between vertical clinging and leaping galagids and those that are primarily arboreal quadrupeds. µCT scans of eight species of galagids (n = 25) were segmented and the proximal caudal vertebrae (those bearing zygapophyses) were extracted as 3D surfaces. The prezygapophyseal articular surfaces were cropped from the 3D surfaces, and measurements of overall curvature, orientation relative to the sagittal plane, and surface area were quantified. Variation was evaluated based on degree of vertical clinging and leaping specialization and vertebral level. Results show no significant difference in prezygapophyseal articular surface morphology among locomotor specialization categories but significant differences across vertebral levels, suggesting that locomotor behavior is potentially not the main driver of variation in caudal vertebral anatomy, but there may be variation in movement patterns along the proximal tail.

A landscape archaeological approach to accumulative stone throwing (AST) in West African chimpanzees (*Pan troglodytes verus*)

ROBYN A. NAKANO and AMMIE K. KALAN

Anthropology, University of Victoria

In Boé National Park in Guinea-Bissau, wild Western chimpanzees (*Pan troglodytes verus*) have been observed engaging in a potentially cultural behaviour: accumulative stone throwing (AST). Individuals habitually throw rocks at particular trees, making AST a unique instance of non-foraging stone tool use. Although previous research suggests that AST has a communicative function and is influenced by the trees' acoustic properties, it is unclear what factors impact individual site selection. I identify patterns in the spatial proximity of certain resources, landscape features, and chimpanzee and human space-use to AST sites by mapping their distribution using QGIS. The study area encompasses approximately 100 km^2, with data drawn from spatially explicit observations collected during reconnaissance surveys by previous research teams in 2014 and 2017. These include direct and indirect chimpanzee observations, tree and rock sources, landscape features and signs of human activity. The presence or absence of AST sites is modeled in R using binomial generalized linear models to determine the influence of resources, features and space-use elements on the likelihood of AST site presence. Consistent with some predictions based on chimpanzee behavioural research, site selection is influenced by the proximity of certain elements but not others. At the time of data collection, there were a total of 56 AST sites with 14 actively used by chimpanzees. Improved understanding of primate behaviour can inform inferences relevant for hominin evolution and the development of behavioural flexibility and provide support for the maintenance of biological and cultural diversity in endangered chimpanzee populations.

This abstract draws on research supported by the Social Sciences and Humanities Research Council.

Comparative ontogenetic analysis of the occipital condyles in humans, chimpanzees, gorillas, and *Australopithecus afarensis*.

THIERRA K. NALLEY[1], FAYE MCGECHIE[2], NEYSA GRIDER-POTTER[3], JEREMIAH E. SCOTT[1], WELDEYARED H. REDA[4] and ZERESENAY ALEMSEGED[4]

[1]Medical Anatomical Sciences, Western University of Health Sciences, [2]Basic Medical Sciences, University of Arizona College of Medicine-Phoenix, [3]Cell Systems and Anatomy, University of Texas Health at San Antonio, [4]Organismal Biology and Anatomy, The University of Chicago

Variation in the position and orientation of the occipital condyles is well documented in hominids and has been linked to differences in positional behavior, especially the evolution of upright posture in bipedal hominins. Less is known about how the shape and curvature of the condylar joint surfaces vary and what the implication is for function. This study examines curvature of the occipital condyles in African apes, humans, and *Australopithecus afarensis* within a developmental framework. We estimated condylar radii of curvature (ROC) and facet areas using three-dimensional landmarks for 72 specimens of extant *Gorilla*, *Pan*, and *Homo*. Individuals were assigned to three age-groups based on dental eruption: juvenile, adolescent, and adult. We used resampling methods to evaluate ROC differences across genera and between age-groups within genera. For the extant taxa, we found that the condyles of *Pan* are more curved than those of *Homo* and *Gorilla* at the juvenile and adult stages. Juvenile gorillas have less curvature than juvenile humans, but these two genera are not distinguishable at the adolescent and adult stages. Chimpanzees show little evidence for developmental change, whereas condylar curvature increases in humans and gorillas following the juvenile stage. The pattern of condylar shape and developmental change for *A. afarensis* is ambiguous owing to small sample sizes, but the available evidence is consistent with a pattern that is similar to the one found in *Pan*. These results suggest that variation in condylar curvature in hominids is not well correlated with differences in overall body posture or locomotor patterns.

American Association of Anatomy; The University of Chicago Biological Sciences Department

Age- and Sex-based patterns of chimpanzee suspensory behavior and substrate use

SHARIFAH NAMAGANDA[1], LAUREN A. SARRINGHAUS[2] and LAURA M. MACLATCHY[1]

[1]Anthropology, University of Michigan, [2]Biology, James Madison University

The hominoid arboreal niche requires navigation on small terminal branches, even at large body sizes. Suspensory behaviors are important to this niche, and it has been reported that chimpanzees use suspension most predominantly while feeding among small strata. In this study, we examine factors, in addition to support size, that influence suspensory locomotor performance. We analyzed focal follow data (n=946 hours) from 76 individuals of different ages and sexes to investigate the association between positional behavior, support use, and behavioral context in *Pan troglodytes schweinfurthii* from the Ngogo community, Kibale Forest, Uganda. Multinomial logistic regression revealed that the type and diameter of support, as well as age, sex, rank and a combination of their effects, are significant predictors of positional behavior. Results show that suspensory positional behavior is most prevalent in terminal branch strata, but depending on the behavioral context, different ages and sexes engaged in this positional mode at variable rates. For instance, adult males, having the largest bodies, engaged in more suspensory postures than any other age-sex category during feeding,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

but engaged in the lowest frequency of suspensory locomotion during feeding. These findings are consistent with previous research indicating that chimpanzees exhibit terminal branch adaptations in which positional repertoire is influenced by support size. These adaptations serve as the foundation for a relationship that is more nuanced than has previously been shown, one in which body size, substrates, and age-sex effects all interact to determine how chimpanzees move through the arboreal environment.

Funding provided by the NSF (SBE 1850328) and the Leakey Foundation.

Integrating shape, cortical thickness and bone modeling data: A novel method applied to an ontogenetic series of chimpanzees mandibles

SELIM NATAHI[1,2], ZEWDI J. TSEGAI[3,4], ALEXANDRA SCHUH[5] and SARAH E. FREIDLINE[6]

[1]Center for Interdisciplinary Research in Biology, Collège de France, [2]Department of Comparative Cultural Psychology, Max Planck Institute for Evolutionary Anthropology, [3]Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, [4]Department of Organismal Biology and Anatomy, University of Chicago, [5]PACEA, Université de Bordeaux, [6]Department of Anthropology, University of Central Florida

Approaches to analyse the relationship between shape and cortical thickness using whole-bone methods are becoming increasingly prevalent. However, this is highly complex in bones that are irregular in shape and especially across a growth series. Here, we present a novel, integrative method that aims to comprehensively understand changes to bone structure during growth using an ontogenetic series of mandibles belonging to *Pan troglodytes verus* (N=10). This holistic method incorporates data from 3D landmark-based geometric morphometrics, parametric mapping of cortical bone thickness and bone surface modeling. Using a full width at half maximum technique, we created a surface representing the internal cortical layer of the mandible. Combining a set of slid (semi)landmarks and a semi-automated procedure allowing the computation of a series of cross-sections along the mandibular corpus, the mandibular cortical thickness was quantified for each individual via a ray casting approach. Surface bone modeling data was collected on the mandibles using a confocal microscope and digital maps were computed using a score representing the percentage of bone resorption in each area. Via covariation analyses, the three methods were combined and are highly suitable for providing novel insights into biological mechanisms underlying mandibular developmental changes throughout ontogeny. The interaction of shape changes, bone modelling activity and cortical thickness during growth contributes to interspecific differences in adult morphology of the cranial and postcranial skeleton. Therefore, applying our approach to extant and extinct taxa can improve our understanding of the processes driving skeletal phenotypic variation among fossil hominins.

We acknowledge the Fyssen foundation (AS and SN), the Marie Skłodowska-Curie Grant #101025719 (ZJT), the University of Central Florida, and the Max Planck Society for funding.

Revisiting the "challenge hypothesis": Muscle mass, not aggression, mediates an association between testosterone and dominance rank in wild male chimpanzees

JACOB D. NEGREY[1,2], TOBIAS DESCHNER[3] and KEVIN E. LANGERGRABER[4,5]

[1]Department of Pathology, Wake Forest University School of Medicine, [2]Department of Anthropology, Boston University, [3]Institute of Cognitive Science, University of Osnabrück, [4]School of Human Evolution and Social Change, Arizona State University, [5]Institute of Human Origins, Arizona State University

The "challenge hypothesis" famously posits that testosterone promotes reproductively salient aggression. A variant of this hypothesis proposes that dominant individuals have higher average testosterone levels than subordinates because dominants are more aggressive. Although research on male chimpanzees (*Pan troglodytes*) has proven influential in shaping this modified challenge hypothesis, clear associations between inter-individual variation in testosterone and aggression rates are lacking for chimpanzees. Rank-related variables other than aggression, such as lean muscle mass, may plausibly account for observed correlations between testosterone and rank. We therefore tested associations between urinary testosterone, dominance rank, total aggression rates, and urinary creatinine (a proxy for lean muscle mass) in wild male chimpanzees (n=34) at Ngogo, Kibale National Park, Uganda. Using multivariate regression, we found that rank was positively associated with aggression rates as well as testosterone and creatinine levels. Testosterone levels were positively associated with creatinine levels but negatively associated with aggression rates. Mediation analyses indicated that creatinine levels mediated the relationship between testosterone levels and dominance, but aggression rates did not. Together, these results suggest that high average testosterone levels do not translate to high average aggression rates. When compared to lean muscle mass, aggression appears inadequate to explain why dominant male chimpanzees have higher testosterone levels on average than subordinates.

Boston University Graduate School of Arts and Sciences, Nacey Maggioncalda Foundation, National Geographic Society (9824-15), National Institutes of Health (5R01AG049395), National Science Foundation (BCS-1613393), and Wenner-Gren Foundation.

Answering nature's call: Diet, agricultural practices and climate change at Altenerding (Germany) during the Early Medieval Period (400-700CE)

DEBORAH L. NEIDICH[1], MARGARET A. JUDD[2] and SANDRA LÖSCH[3]

[1]Anthropology, University of Missouri, [2]Anthropology, University of Pittsburgh, [3]Physical Anthropology, Institut of Forensic Medicine, University of Bern

This project represents ongoing research of Bajuwaren individuals in the Early Medieval Period (n=218) from the necropolis of Altenerding (400-700 CE) at Erding, Germany. Part Temporal isotopic differences in diet were tested and were further analyzed to detect if adult community members were equally affected by dietary change.

New dietary $\delta^{13}C$ and $\delta^{15}N$ values are presented for unprovisioned (n=8) and provisioned adult burials from the Younger Merovingian (n=22) periods, increasing the dietary isotope samples from the necropolis to 70 individuals. Data from Late Antique (n=20), Older Merovingian (n=20), have been previously published and were incorporated into this study.

Age and sex further contextualize dietary stable isotopes to assess behavioral differences between temporal cohorts. Previous research indicated possible differences between male and female diets, as well as dietary differences between individuals in provisioned and unprovisioned burials. Archival and archaeological research was also used to assess potential differences between cohorts.

Dietary analysis indicated that the adult Bajuwaren diet was dependent on animal proteins and C_3 foods like wheat, barley, and rye [$\delta^{13}C$=−20.3 to −16.8‰, $\delta^{15}N$ =+7.9 to +11.4‰]. A stark increase in $\delta^{15}N$ values during the Younger Merovingian suggest a shift in agricultural practices, possibly as a response to environmental disruptions caused by the Late Antique Little Ice Age (536-ca.600 CE). Ethnohistoric literature from this period supports this theory, as practices like manuring fields to curtail fallow periods in crop rotation were introduced around this period. Manure is nitrogen rich and is documented to increase $\delta^{15}N$ values in consumers.

Funding came from NSF DDIG Award #2006750, UCIS and SSDD from the University of Pittsburgh, and contributions from Museum Erding, Erding, Bavaria with consent of the descendent community of Erding.

Mycobacterium tuberculosis diversity across the pre-Hispanic Andes

ELIZABETH A. NELSON[1], ADITYA K. LANKAPALLI[2], MARIA SPYROU[3,4], AINASH CHILDEBAYEVA[4], ÚSHILD VÚGENE[5], EVELYN GUEVARA[6], J. MARLA

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

TOYNE[7], TIFFINY A. TUNG[8], ALEXANDER HERBIG[4] and KIRSTEN I. BOS[4]

[1]Genomes and Genetics, Institut Pasteur, [2]School of Life Sciences, University of Warwick, [3]Institute for Archaeological Sciences, University of Tübingen, [4]Department of Archaeogenetics, Max Planck Institute for Evoluationary Anthropology, [5]The Globe Institute, University of Copenhagen, [6]Department of Forensic Medicine, University of Helsinki, [7]Department of Anthropology, University of Central Florida, [8]Department of Anthropology, Vanderbilt University

The Late Intermediate Period of the Peruvian Andes (LIP, 1000 - 1400 CE) is characterized by socio-cultural, environmental, and demographic transitions, including the back-migration of people from the highlands to the coast. A severe drought, the decline of the Wari empire, and the movement of people to dispersed settlements occurred concurrently with an increase in archaeological evidence of skeletal tuberculosis (TB) across the Andean region. Paleogenomic analysis has revealed human infections of the MTBC member, *M. pinnipedii*, in LIP coastal and low-land populations of Peru. However, the diversity and distribution of MTBC strains contributing to the LIP rise in skeletal TB is unknown. Likewise, although archaeological evidence of cross-cultural influence demonstrates the rich interactions of dispersed LIP Peruvian populations, it remains unclear if this will be reflected in pathogen transmission and strain diversity. In this work, we examine MTBC strain diversity of Andean Peru in two distinct contemporaneous cultural groups from different ecological zones: the highlands and the subtropical forest. We report seven genomes from the central Andean highland site of Huari and one MTBC genome from the Chachapoya cliff side tomb of Diablo Huasi, located in the subtropical jungle of the eastern slopes of the Andean massif in Amazonas. Phylogenetic analysis consistently revealed a close relationship to modern *M. pinnipedii* strains, with Diablo Huasi showing greatest homology to modern forms. Our results provide insights into *M. pinnipedii* evolution and geo-cultural distribution across the three macro-ecological zones of the Andes: the coast, highlands, and subtropical forest of the eastern slopes.

Metagenomic analysis of an early Christian cemetery Godalming of the Late Anglo-Saxon to Early Norman period (Surrey, UK, 800-1125 AD)

ELIZABETH A. NELSON[1], NASREEN BROOMANDKHOSHBACHT[2], SAM LEGGETT[3], FLAVIO DE ANGELIS[4], TODD RAE[5], ROB POULTON[6], LARS FEHREN-SCHMITZ[2], LIA BETTI[7] and CARLOS EDUARDO AMORIM[4]

[1]Department of Genomes and Genetics, Institute Pasteur, [2]Department of Anthropology, University of California Santa Cruz, [3]School of History, Classics and Archaeology, University of Edinburgh, [4]Biology Department, California State University Northridge, [5]School of Life Sciences, University of Sussex, [6]Archaeological Unit, Surrey County, [7]School of Life and Health Sciences, University of Roehampton

Metagenomic analysis of shotgun sequencing reads from high throughput sequencing permits the evaluation of microbes and host DNA from ancient samples. This method possesses limited bias and permits the detection of pathogens. This is particularly useful in cases where burial structures signal the likely presence of disease but historic records and skeletal material are absent of any diagnostic indicators. Here, we apply this method to a cemetery from an early Christian site of Godalming that offers a time transect spanning the Anglo-Saxon to Early Norman periods, a time that is relatively understudied in the field of paleo-pathogenomics. We report the analysis of 78 individuals whose burials displayed a variety of interment characteristics: most possess no grave goods, except for a handful of daily objects and some were accompanied by ash-like halos around the head and pillow stones. Our preliminary analysis revealed the presence of several pathogens (*Neisseria meningitidis*, *Streptococcus pyogenes*, *Salmonella enterica subsp. enterica, Streptococcus pneumoniae*, and *Klebsiella pneumoniae*), including evidence of oral pathogens such as *Tanerella forsythia*, *Streptococcus oralis*, and *Streptcoccus mutans,* known to cause periodontal disease. The identification of these pathogens offers molecular data towards the reconstruction of their life histories and provides insight into the presence of these pathogens in this region and time period. The preliminary analyses offer data for future strategic methods to reconstruct ancient pathogen genomes and evaluate their evolution and impact within this community. We present our preliminary metagenomic findings and discuss our future directions of research.

Research reported in this publication was supported by the National Institute of General Medical Sciences of the National Institutes of Health under award number R35GM142939.

Exploring the Laws of Developmental Direction using a Documented Skeletal Collection

JENNIFER S. NELSON[1], LESLEY HARRINGTON[1], EMILY HOLLAND[2] and HUGO FV. CARDOSO[3]

[1]Anthropology, University of Alberta, [2]Anthropology, Brandon University, [3]Archaeology, Simon Fraser University

OBJECTIVE: Many human growth studies note a trend of differential variation in limb segment lengths, where more distally situated bones show greater variability relative to those nearer the axial skeleton. It has been proposed that this varying sensitivity stems from the sequence of development, where bones further from the head develop later and are more susceptible to fluctuations in growth conditions. The present study aimed to explore limb dimensions within this theoretical framework, known as the *laws of developmental direction*, using diaphyseal lengths of 45 children (0-12 years) from a documented skeletal collection of low socioeconomic status.

METHODS: Using existing growth standards, z-scores were generated for diaphyseal length measurements of all six long bones. Diminished growth was defined as a z-score of ≤-2. Differences between mean z-score values of the upper and lower limbs, as well as of the proximal and distal segments of each limb, were assessed using paired samples *t*-tests.

RESULTS: The lower limb and forearm were significantly more delayed in growth relative to their proximal counterparts (p=<0.001; p=<0.001), while the lower leg was significantly less delayed in growth relative to the proximal segment (p=<0.001).

DISCUSSION: The findings of increased sensitivity in the lower limb and forearm relative to their proximal counterparts are consistent with the *laws of developmental direction*, while the observation of comparatively greater diminished growth in the proximal leg segment does not align with the theorized developmental gradient. These results reveal the complexity of human growth and developmental plasticity in response to biocultural factors.

Funding for this project was provided by SSHRC - Social Sciences and Humanities Research Council of Canada

Considering the impact of somatic mutations on cranial structures

BRIANA T. NEW and KYRA E. STULL

Anthropology, University of Nevada, Reno

Research in biological anthropology emphasizes linkages between cranial variation and higher frequency genetic variants (e.g., single nucleotide polymorphisms [SNPs]) because they enable genotype-phenotype analyses on a population level. These studies are vital for understanding genetic contributions to cranial development and the distribution of phenotypes across populations. However, the degree of plasticity in skeletally mature cranial structures across an individual's lifetime remains unclear. This study compares rare single nucleotide variants (SNVs) with a minor allele frequency < 1% that were extracted from head and neck squamous cell carcinomas and basicranial interlandmark distances (ILDs) to investigate the relationship between somatic mutations and adult cranial structures.

Adult individual-level matched computed tomography scans and whole exome sequencing datasets were drawn from the National Cancer Institute's Clinical Proteomic Tumor Analysis Consortium. Relationships between synonymous and nonsynonymous SNVs and ILDs were

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

assessed through factor analysis for mixed data and correlations analyses. Variants associated with the genes MUC16, MUC17, MDGA2, PKD1, RYR1, SPATA31D1, LRP, LRP6, HELZ2, SHANK2, and PIK3CA demonstrate significant correlations to basicranial ILDs. Results are compared to current genotype-phenotype literature and potential effects of disease on human cranial structures are considered. SNPs are inherited and may impact cranial structures during development in traceable ways across populations, but SNVs are considered individual-specific and may impact changes in cranial structures within a lifetime. Studying the relationship between cranial variation and SNVs provides a potential pathway for incorporating individual life history into genotype-phenotype studies.

No funding to report.

Conserved and distinct signatures of transcriptional aging across tissues in rhesus macaques

LAURA E. NEWMAN[1,2], MARINA M. WATOWICH[3], MITCHELL R. SANCHEZ ROSADO[4], ALEX R. DECASIEN[1,2,5], KENNETH L. CHIOU[6,7], MELWEEN I. MARTINEZ[8], CAYO BIOBANK RESEARCH UNIT[9], MICHAEL J. MONTAGUE[9], MICHAEL L. PLATT[10,11,9], LAUREN J.N. BRENT[12], JAMES P. HIGHAM[1,2] and NOAH SNYDER-MACKLER[6,7]

[1]Department of Anthropology, New York University, [2]The New York Consortium in Evolutionary Primatology (NYCEP), [3]Department of Biology, University of Washington, [4]Department of Microbiology & Medical Zoology, University of Puerto Rico, [5]Section on Developmental Neurogenomics, National Institute of Mental Health, [6]Center for Evolution and Medicine, Arizona State University, [7]School of Life Sciences, Arizona State University, [8]Caribbean Primate Research Center, University of Puerto Rico, [9]Department of Neuroscience, University of Pennsylvania, [10]Department of Psychology, University of Pennsylvania, [11]Department of Marketing, University of Pennsylvania, [12]Centre for Research in Animal Behaviour, University of Exeter

While all animals age, aging processes vary within populations. Some of this variation is between individuals, but rates and patterns of aging can also differ across cells and tissues within individuals. Little is known about intra-individual variation in aging in primates, in part because most studies have only been able to measure one tissue: blood. To address this gap, we characterized patterns of transcriptional aging in a cross-sectional sample of free-ranging rhesus macaques from the island of Cayo Santiago. Using RNA-seq, we measured gene expression in liver, spleen, and skeletal muscle samples from 237 rhesus macaques ranging in age from infancy to late life. We identified over 2,000 age-associated genes (AAGs) in each tissue (local false sign rate; lfsr < 0.1) Interestingly, only 9% (n=594) of these genes differed by age in all three tissues (lfsr < 0.1), suggesting that aging patterns are highly tissue-specific. Additionally, AAGs showed lower levels of tissue-specific function and higher inflammatory signaling in older individuals (adjusted p < 0.1), likely driven by tissue-specific cell composition changes (e.g., reduction of hepatocytes in the liver of older animals; adjusted p < 0.05). To test the hypothesis that tissue specificity declines with age, we evaluated whether genes that were lower with age were more likely to be tissue-specific and found evidence for this in the liver and spleen. Our results provide insight into variation in aging between organs and are suggestive of age-associated patterns of higher inflammation and lower tissue-specific functioning in older individuals.

Supported by: National Science Foundation (BCS-2041654), Society for Integrative and Comparative Biology, Animal Models for Social Aging Research Network, NYU MacCracken, National Institutes of Health (R01-AG060931)

Spondylolysis in the past: a meta-analysis of bioarcheological and clinical literature

NATHAN A. NGUYEN[1], JEREMY WOOD[2] and JONATHAN D. BETHARD[3]

[1]Anthropology, Texas State University, [2]Anthropology, University of California, Davis, [3]Anthropology, University of South Florida

Spondylolysis is an orthopedic condition affecting a wide array of living people with various clinical symptoms. The condition has also been documented in the archaeological record across time. Despite the relatively high prevalence rate, definitive causes of spondylolysis are variable according to the current literature. This is due, in part, to a lack of uniformity both in classifying spondylolysis and in the methodology used to identify living individuals affected by this condition. In response to this, a comprehensive meta-analysis of published literature was conducted. Over 25 studies were compiled to document trends regarding the etiology of spondylolysis. Both bioarchaeological and clinical sources were included in order to obtain a larger and more complete understanding of the condition. Results indicate that overall trends in the literature suggest that spondylolysis, and later spondylolisthesis, is a condition that develops in individuals during late adolescence or early adulthood. Within the clinical literature, the rates of spondylolysis range from 3-11.5%. The bioarchaeological literature presents higher rates than modern clinical contributions; however, most of these studies are limited by small sample sizes. Alongside the typical age of development, the common conclusion in the literature is that onset is typically a result of repeated mechanical stress accompanied by varying intensity of symptoms. This meta-analysis demonstrates that bioarchaeological studies focused on spondylolysis can benefit from the incorporation of clinical literature to better understand the effects of the condition on past people.

Examining longitudinal patterns of facial size and shape in children with obesity

CHRISTINA L. NICHOLAS[1,2], JESSICA HEDGER[1], JENNIFER CAPLIN[3], MARIA THERESE GALANG-BOQUIREN[1], SAHAR ALRAYYES[4] and CAROLINE RATZ[1]

[1]Orthodontics, University of Illinois Chicago, [2]Anthropology, University of Illinois Chicago, [3]Preventive, Pediatric, and Community Dentistry, University of New England, [4]Pediatric Dentistry, University of Illinois Chicago

Many factors are thought to affect rate, timing, and direction of facial growth. Recent work has elucidated genes such as *EDAR*, *PAX1*, and *MYO1C* that likely influence facial shape. Across species of hominins, we know there have been differences in rate of growth, with earlier hominins such as Neandertals having accelerated growth relative to extant humans. While lesser than interspecies variability, we also see variation in rate of facial growth among living humans. Though this variation is likely multifactorial with both genetic and environmental influences, we herein focus on one environmental factor, relative body mass, as a potential contributor. Limited prior work in this area has suggested accelerated facial growth in children with obesity. We employed a true longitudinal growth series (the Iowa Facial Growth Study) to examine pattern and timing of facial growth longitudinally, collecting coordinate landmark and measurement data from lateral cephalograms taken at ages 4, 6, 8, 10, 12, and 14. Linear measurements included mandibular length (condylion-pogonion), facial height (nasion-ANS), and others. Principal components analysis, multilevel modeling, and regression were used to analyze the data. We found that high body mass at age 6 was weakly predictive of larger facial skeletons (centroid size) across growth (p<0.001). Our results support prior cross-sectional work indicating that childhood obesity may be associated with rate of facial skeletal growth.

Reclaiming Life Narratives: Reconstructing lived experiences of individuals in historical documented collections

LAUREN NICHOLS[1], MUNEEBAH UMAR[2], KERRI WIDRICK[1], CASSANDRA DEGAGLIA[3], AMANDA WISSLER[4], ALEISHA REYNOLDS[1], FABIAN CRESPO[5], SHARON DEWITTE[4] and MOLLY ZUCKERMAN[1]

[1]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Department of Biological Sciences, Mississippi State University, [3]Department of Anthropology, Tulane University, [4]Department of Anthropology, University of South Carolina, [5]Department of Anthropology, University of Louisville

Historical documented collections, like the Hamann-Todd Osteological Collection (HTOC), are fundamental to method and theory development in biological anthropology. However, these collections were created through structural violence (e.g., nonconsensual anatomization), and

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

recent scholarship on ethics surrounding these collections raises questions of how the biosocial conditions and lived experiences of individuals within them can be foregrounded, encouraging researchers to engage with them as once-living individuals and reducing their scientific objectification. We build on this, employing osteobiography as a humanizing strategy; we present an osteobiography of an individual, Cleveland Individual (CI), from the HTOC, who has an antemortem diagnosis of acquired syphilis. We applied a 10-biomarker skeletal frailty index (SFI) (PH/CO, Rickets/Osteomalacia, Osteoporosis, LEH, Periodontal Disease, Neoplasms, OA, IVD, RCD, Fracture) and assessed evidence of other select pathologies. We integrated these with CI's archival data and community-level historical information on early 20th c. Cleveland, OH. Preliminarily, CI has a relatively low age-at-death (38 years) and SFI (3) relative to a larger sample of those with syphilis (N=88; SFI=4.15) in the HTOC, indicative of physiological stress during growth, repetitive activity during adulthood, and possible TB co-infection. We interpret these as embodied stressors potentially associated with CI's reconstructed social identity (e.g., gender, migrant status, SES), and related processes of poverty, psychosocial and physical stress, and ante-, peri-, and postmortem structural violence. Such attempts to highlight the personhood and osteobiographically reconstruct the complex life narratives of individuals in historical documental collections may encourage more ethical research with them.

This research is supported by NSF Senior Research Grant: Reconstruction of host immunological status, host immune response (inflammatory phenotype (IP)), and heterogeneity in frailty to acquired syphilis. (Award number: 1946203)

Sex-based differences in mortality and metabolic disease in subadult skeletal assemblages of Tell Hisban

CEARA M. NICHOLSON[1], MEGAN A. PERRY[1] and TONYA N. ZECZYCKI[2]

[1]Anthropology, East Carolina University, [2]Biochemistry and Molecular Biology, East Carolina University

Heterogeneity in morbidity and mortality risk results from various underlying host-level and societal factors. Identifying these factors in ancient communities often is hindered by the invisibility of variables in the archaeological record and the methodological limitations of the skeletal analysis. These both have impacted fully understanding of the causes of infant mortality in the 19th century AD at the site of Hisban, Jordan, particularly the risk of dying with active metabolic disease. This project uses dental proteomics to estimate the sex of 16 infants (up to 2 years of age) dying with (n=10) and without (n=6) skeletal lesions indicative of vitamin C deficiency, in addition to 8 modern control samples of known sex. Identification of sexually dimorphic amelogenin proteins (AMELY and AMLEX) can indicate the biological sex of the infant, which in this cultural and temporal context likely aligns with their gender identity. With this information, we have identified no difference in the male: female ratio of infants dying before the age of 2 years from the expected intrinsic mortality risk by sex in infants. However, a greater proportion of females compared to males were found in the infants dying with active scurvy than those who did not. These results will inform future analysis of diet and weaning patterns of these infants using incremental δ13C and δ15N analysis of dentin. Since metabolic diseases are closely tied to diet and socio-cultural practices, this project is an excellent opportunity to understand this community's biological and social determinants of infant morbidity and mortality.

Investigating genetic factors associated with preeclampsia among pregnant families in the Peruvian Andes

MARIA A. NIEVES-COLÓN[1,2,3], KEYLA M. BADILLO RIVERA[4], KARLA SANDOVAL MENDOZA[1], VANESSA VILLANUEVA DÁVALOS[5], LUIS E. ENRIQUEZ LENCINAS[5], JAVIER MENDOZA-REVILLA[6,7], KAUSTUBH ADHIKARI[8,9], RAM GONZÁLEZ-BUENFIL[1], JESSICA W. CHEN[4], ELISA T. ZHANG[4], ALEXANDRA SOCKELL[4], PATRICIA ORTIZ-TELLO[4], GLORIA M. HURTADO[6], RAMIRO CONDORI SALAS[6], RICARDO CEBRECOS[6], JOSÉ C. MANZANEDA CHOQUE[10], FRANZ P. MANZANEDA CHOQUE[10], GERMÁN P. YÁBAR PILCO[10], ERIN RAWLS[2], CELESTE ENG[11], SCOTT HUNTSMAN[11], ESTEBAN GONZÁLEZ BURCHARD[11], ANDRÉS RUIZ-LINARES[12,13,14], ROLANDO GONZÁLEZ-JOSÉ[15], GABRIEL BEDOYA[16], FRANCISCO ROTHHAMMER[17,18], MARIA CÁTIRA BORTOLINI[19], GIOVANNI POLETTI[6], CARLA GALLO[6], CARLOS D. BUSTAMANTE[4,20], JULIE C. BAKER[4], CHRISTOPHER R. GIGNOUX[21], GENEVIEVE L. WOJCIK[22] and ANDRÉS MORENO-ESTRADA[1]

[1]Laboratorio Nacional de Genómica para la Biodiversidad (UGA-LANGEBIO), CINVESTAV, [2]School of Human Evolution and Social Change, Arizona State University, [3]Department of Anthropology, University of Minnesota Twin Cities, [4]Department of Genetics, Stanford University, [5]Departmento de Gineco-Obstetricia, Hospital Regional Manuel Nuñez Butrón, [6]Laboratorios de Investigación y Desarrollo, Facultad de Ciencias y Filosofía, Universidad Peruana Cayetano Heredia, [7]Human Evolutionary Genetics Unit, Institut Pasteur, [8]School of Mathematics and Statistics, The Open University, [9]Department of Genetics, Evolution and Environment, University College London, [10]Universidad Nacional del Altiplano, Universidad Nacional del Altiplano, [11]Department of Bioengineering and Therapeutic Sciences, University of California San Francisco, [12]Aix-Marseille Université, [13]Department of Genetics, Evolution and Environment, and UCL Genetics Institute, University College London, [14]Ministry of Education Key Laboratory of Contemporary Anthropology and Collaborative Innovation Center of Genetics and Development, Fudan University, [15]Instituto Patagónico de Ciencias Sociales y Humanas, Centro Nacional Patagónico-CONICET y Programa Nacional de Referencia y Biobanco Genómico de la Población Argentina (PoblAr), Ministerio de Ciencia, Tecnología e Innovación, [16]Genética Molecular (GENMOL), Universidad de Antioquía, [17]Instituto de Alta Investigación Universidad de Tarapacá, [18]Programa de Genética Humana, ICBM Facultad de Medicina, Universidad de Chile, [19]Departamento de Genética, Instituto de Biociências, Universidade Federal do Rio Grande do Sul, [20]Department of Biomedical Data Science, Stanford School of Medicine, [21]University of Colorado Anschutz Medical Campus, [22]Department of Epidemiology, Bloomberg School of Public Health, John Hopkins University

Preeclampsia, a multi-organ complication of pregnancy, is a leading cause of preterm delivery affecting approximately 5-7% of global pregnancies. The heterogeneity of preeclampsia poses a challenge for understanding its etiology and molecular basis. However, risk for the condition increases in high altitude regions such as the Peruvian Andes. To investigate the genetic basis of preeclampsia and its relationship to altitude, we characterized genetic diversity in a cohort of Andean families (N=883) from Puno, Peru, a high-altitude city above 3,500 meters. We generated genotype data for 439,314 genome wide positions, determined ancestry patterns, scanned for signals of selection and mapped associations between genetic variants and preeclampsia phenotype in case-control families. A transmission disequilibrium test (TDT) revealed associations with variants on chromosome 13 of the fetal genome in a region containing clotting factor genes *PROZ*, *F7* and *F10*. These genes are of biological importance in pregnancy physiology for placental and blood vessel function. Our findings suggest that coagulation plays an important role in the pathology of preeclampsia and potentially underlies susceptibility to other pregnancy disorders exacerbated with altitude. We also identified a potential adaptive signal on a locus previously implicated in pregnancy complications: the *ADAM12* gene on chromosome 10. Our work has implications for the general understanding of preeclampsia etiology and lists candidate variants for future replication and functional validation in other Latin American populations. This discovery of a novel association relevant to pregnancy biology in the Puno family cohort also underscores the importance of conducting genetic research with diverse populations.

Funded in part by National Science Foundation Awards 1711982 and DGE−1147470; Mexico CONACyT Awards PNPC 003649 and FONCICYT/50/2016; International Center for Genetic Engineering and Biotechnology Italy Award CRP/MEX15-04_EC.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Exploring complexities in human pigmentation genotype-phenotype relationships

HEATHER L. NORTON

Anthropology, University of Cincinnati

Pigmentation is one of the most highly variable and easily visible phenotypic traits in the human species. While pigmentation phenotype was once thought to be under the control of a limited number of genes, more recent estimates suggest that over 100 loci may be involved, with sometimes variable effects in different populations and in different tissues (e.g., skin vs. eyes vs. hair). A clearer picture of the relationship between genotype and pigmentation phenotype is critical for an accurate understanding of the genetic architecture of complex traits and to identify how microevolutionary forces impact phenotypic diversity across the species. To trace how our conception of pigmentary genotype and phenotype relationships have changed over time, I conducted a comprehensive review of published pigmentation genetics papers published over the last 25 years. This analysis identified several factors that have contributed to changing views about pigmentation genotype-phenotype relationships over this time period, including improved genetic methodologies (e.g., the advent of GWAS and whole genome sequencing), a shift to more quantitative phenotypic measurements, and the inclusion of larger and more diverse populations in pigmentation genetic studies. Finally, this paper concludes by asking how the lessons learned over the past 25 years may impact new applications in both biological anthropology and adjacent fields. For example, how should our growing grasp of the complexity of pigmentation genetics influence phenotypic reconstruction in paleoanthropology and forensic science?

Utility of African Herbivore Community Enamel Isotopes for Reconstructing Paleoenvironments: Challenges and Opportunities

ALEXANDRA L. NORWOOD[1], BIAN WANG[2] and JOHN D. KINGSTON[1]

[1]Department of Anthropology, University of Michigan, [2]Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences

Paleoenvironmental reconstructions based on isotopic analyses of fossil sites typically rely on data from multiple herbivore taxa, with the assumption that this dietary spectrum represents the community's range and can ultimately provide insights into local or regional vegetation patterns. However, it remains unclear how representative the sampled taxa are of the broader community and how well these data correspond to specific environmental parameters. To refine paleoenvironmental reconstructions, we must first address these underlying assumptions. This study examines links between modern faunal communities' enamel isotopic spectra, biome types, and climate in sub-Saharan Africa, which includes diverse communities and biomes. This region is one of the most comprehensively isotopically sampled globally and is of particular relevance to the study of hominin evolution. Our extensive data compilation reveals that published enamel isotopic data from sub-Saharan Africa typically sample a small percentage of the taxa at a site and that some biome types, like sub-tropical savannas, are dramatically overrepresented compared to forests in these modern data sets. Multiple attempts at statistical analysis of mammalian herbivore enamel isotopes, biome type, and climate parameters, including linear models and cluster analyses, found no significant correlation between these variables. These results confound any simple understanding of how community isotope profiles map onto specific environments, forcing us to identify and develop more precise approaches and to isotopically sample modern ecosystems more strategically. This will ultimately allow us to more accurately identify the isotopic spectra of paleo-communities and link the isotopic dietary signatures to specific biomes based on modern analogs.

A rare case of permanent teeth fusion from late medieval / early modern period Sisak, continental Croatia

MARIO NOVAK[1], IGOR ERJAVEC[2], MARIO CARIC[1], JOSIP BURMAZ[3], DZENI LOS[3], MISLAV CAVKA[4] and MARIN VODANOVIC[5]

[1]Centre for Applied Bioanthropology, Institute for Anthropological Research, [2]School of Medicine, University of Zagreb, [3]., Kaducej Ltd., [4]University Department of Diagnostic and Interventional Radiology, University Hospital Centre Zagreb, [5]School of Dental Medicine, University of Zagreb

"Dental twinning" is a developmental anomaly caused by congenital, inherited, acquired and/or idiopathic factors resulting in the union of two and, on more rare occasions, three adjacent teeth. The union itself is caused by the physical pressure between two adjacent teeth during their growth and development. Clinical literature indicates that "dental twinning" usually occurs in three different manners: germination (shizodonthia), fusion (synodonthia), and concrescence. Today, this anomaly is registered in 0.1-5% of teeth with an equal distribution between males and females with somewhat higher frequencies in individuals of Asian ancestry. However, archaeological examples of permanent "dental twinning" from Europe are still extremely rare.

Here we present a case of fusion of permanent first and second right maxillary incisors observed in a middle-aged (30-40 years) male from the late medieval / early modern period site of Sisak in continental Croatia. In order to gain a better insight into this interesting case we employed several analytical methods: (i) macroscopic analysis, (ii) X-ray and Multislice computerized tomography (MDCT), and (iii) micro-CT analysis. The fused tooth has a single crown with a slight groove running along the lingual side. Radiographic examination confirmed that the teeth are completely fused involving both the crown and the root. The anomaly is unilateral as the left maxillary incisors have a normal morphology and are completely separated.

This is the first archaeological case of permanent teeth fusion from Central/Southeastern Europe and one of the rare examples of such an anomaly in bioarchaeological record in general.

Genomic perspectives on the settlement of the Caribbean and their implications for seafaring in the Archaic Age of the Americas

KATHRIN NÖGELE

Department of Archaeogenetics, Max Planck Institute for Evolutionary Anthropology

Boats and rafts recovered from archaeological contexts provide direct evidence for seafaring in the past. However, in certain climatic conditions, such as the hot and humid climate of the tropics, wooden structures seldomly preserve. Even though it is evident that people have had to cross waters to settle the islands in the Caribbean, only a few boats have been recovered from the Ceramic Age period (2800 BP – 500 BP), and none from the preceding Archaic Age (7000 BP – 2800BP). Therefore, there is debate about the quality of seafaring practiced by the different Caribbean communities of the past. Where direct evidence is missing, other markers can provide evidence for the intensity of seafaring. Genomic analyses have shown connections between islands during the Ceramic Age, evidenced by close and deeper genetic relationships between the Bahamas and Hispaniola. Evidence from the Archaic Age is more indirect and still disputed. A discussion of the genetic affinities to groups outside the Caribbean can not only provide insights into the initial settlement of the Caribbean but speak to the seafaring capabilities of Indigenous communities in the past, cautioning to reconsider the migration routes in their dispersal across the Americas.

Evolution of *Paranthropus robustus* upper fourth premolars from Swartkrans in association with aridification and a more mechanically challenging diet across time

MACKIE C. O'HARA[1], SIMON CHAPPLE[1], MARK HUBBE[2], PATRICK MAHONEY[1], WILLIAM S. MCGRAW[2], GARY T. SCHWARTZ[3], MATTHEW M. SKINNER[1,4] and DEBBIE GUATELLI-STEINBERG[2]

[1]School of Anthropology and Conservation, University of Kent, [2]Department of Anthropology, Ohio State University, [3]School of Human Evolution and Social Change, Arizona State University,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

[4]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Paranthropus robustus is known from South Africa and is characterized by, among other features, molarized premolars. A recent examination of *P. robustus* crania revealed temporal trends such that younger specimens are characterized by larger teeth and more anteriorly positioned sagittal crests and zygomatic roots, features associated with high bite force production. A drying period and expansion of shrubland-type vegetation corresponding to the same time period suggests that *P. robustus* adapted to an increasingly mechanically-challenging diet.

Here, we test whether the external and internal architecture of upper fourth premolars (UP4s) of *P. robustus* followed an evolutionary trajectory similar to other cranio-dental features suggestive of more mechanically challenging diets. Digital 2D slices through the principal cusps (n=10) were generated, representing ~1 million years of *P. robustus* evolution across Member 1 Hanging Remnant (n=8), Member 2 (n=1), and Member 3 (n=1). Trends in metrics quantifying tooth shape, tooth size, overall enamel thickness, and regional enamel distribution were evaluated using Jonckheere-Terpstra tests. At alpha=0.05, significant increases in crown area and enamel thicknesses at the lingual cusp tip and lingual lateral wall region were identified. At alpha = 0.10, significant increases in absolute crown strength, average enamel thickness, and buccal cusp tip thickness, along with significant decrease in the proportional thickness of the buccal lateral wall were identified. We consider alpha=0.10 reasonable given the sample size and preliminary nature of this investigation. We conclude that, even within sites, *P. robustus* underwent evolution in dental form, likely in response to environmental and dietary shifts.

This study was supported by Max Planck Society, The Ohio State University, National Science Foundation, the European Union's Marie Skłodowska-Curie Individual Fellowship, and the Horizon 2020 research and innovation program.

Optimal control simulations of three-dimensional walking in humans and bipedal chimpanzees

MATTHEW C. O'NEILL[1], ARAVIND SUNDARARAJAN[1] and BRIAN R. UMBERGER[2]

[1]Department of Anatomy, Midwestern University, [2]School of Kinesiology, University of Michigan

Simulations of musculoskeletal motion based on optimal control theory permits estimation of biomechanical parameters that cannot be measured directly, either due to invasiveness (e.g., individual-muscle forces) or the absence of any experimental data (e.g., fossil hominins). However, this approach requires defining a cost function that is optimized to generate the motion. Here, we assess four functions based on minimizing muscle fatigue to generate data-tracking and predictive three-dimensional (3-D) simulations of human and bipedal chimpanzee walking.

Human and chimpanzee musculoskeletal models were used for tracking and predictive simulations of bipedal walking at matched dimensionless speeds (v'=0.56). A direct collocation framework implemented using OpenSim-Moco was used to simulate a full walking stride, while minimizing a cost function equal to the sum of muscle activations given by $J=\sum A_m^{exp}$, where exp = 1, 2, 3, or 10. The quality of the simulations were assessed based on the root mean squared difference (RMSD) between the simulated and experimental 3-D kinematics (IK) and ground forces (GRF).

Tracking simulations closely matched the experimental data, producing similar RMSD values for humans and chimpanzees (IK: 2 deg; GRF: 0.02 body weights). For predictive simulations, where the experimental data are not part of the cost function, the RMSDs were higher, as expected, with variance among the different exponents. Initial results suggest higher muscle activation exponents generally predict more realistic kinematics and ground forces. Investigation of additional performance criteria will yield further insights into the most robust cost functions for optimal control simulations of ape or fossil hominin locomotion.

Supported by NSF BCS-2018436, NSF-2018523

Out of a Beringian Incubator?

DENNIS H. O'ROURKE[1,2], JUSTIN TACKNEY[1,2], CAROLINE KISIELINSKI[1,2], LAUREN NORMAN[1,2], ROLFE MANDEL[1,3], JOHN HOFFECKER[4] and RICHARD SCOTT[5]

[1]Anthropology, University of Kansas, [2]Center for Genomics, University of Kansas, [3]Odyssey Archaeological Research Program, University of Kansas, [4]Institute of Arctic and Alpine Research, University of Colorado, [5]Anthropology, University of Nevada, Reno

Recent genomic surveys and claims of great antiquity of people in the Western Hemisphere suggest a greater complexity of early migrations and patterns of variation in the Americas than previously assumed. These new insights necessitate a more detailed understanding of the earliest population(s) to understand subsequent evolutionary and demographic dynamics of descendant groups.

Our new genomic scale data of ancient Arctic individuals provide additional insights regarding dispersals into North America and how these shaped contemporary patterns of variation. Coupled with new data generated by others on neutral genetic markers and loci that have been targets of selection, these new data narrow the possible location(s) of isolation in the far North that resulted in the emergence of the Native American genome. Additionally, we report early results of the use of *sed*aDNA analysis at open air sites in the Yukon and the Central Plains. These data demonstrate the utility of this proxy method beyond cave sites where it has been used previously and provides insights into the paleoecology in these regions. It is in these environments that the earliest people entered who ultimately possessed the nascent diversity of Native American genomes. This is especially relevant for assessing the time and ecology of early people in eastern Beringia at Bluefish Caves, the Arctic plain, and mid-continent North America.

Increasing use of the growing array of proxies made possible by the newest methods in environmental DNA and geoscience research continue to refine genomic inferences from archaeologically derived materials.

This research is supported by NSF grant BCS-1849338, the Odyssey Archaeological Research Program, and Yukon government archaeology. We are grateful for research permission from the Vuntut Gwitchin First Nation.

Assessing the Accuracy of Lower Limb Skeletal Measurements Using External Landmarks from CT Images

MIGUEL OCHOA[1], DYLAN J. SIMON[2] and PATRICIA A. KRAMER[1,3]

[1]Department of Anthropology, University of Washington, [2]Department of Biology, University of Washington, [3]Department of Orthopaedics and Sports Medicine, University of Washington

Biomechanical and energetics studies of living humans typically use the location of external landmarks as proxies of skeletal measurements, because the only method to determine the internal skeletal anatomy of living humans requires radiographic or CT imaging. Such procedures are invasive, are expensive, and expose the participants to deleterious radiation. The accuracy of external proxies, however, has not been determined.

In this study, we assess the accuracy of using external anatomical landmarks to determine internal skeletal measurements using cadaveric CT scans acquired from the New Mexico Decedent Image Database (NMDID). 28 landmarks (16 skeletal, 12 external) were identified and measured from CT scans on 82 individuals using OsiriX (Pixmeo, Geneva). 32 males and 50 females (20-40 years old) with no evidence of lower limb trauma were assessed. Skeletal lengths for femur and tibia and skeletal crural index were calculated, as well as external thigh and shank measurements and external crural index. Linear regression was conducted to determine the degree to which external crural index predicted skeletal crural index.

We found that less than 65% of the variation in skeletal crural index can be predicted by external crural index ($p < 0.01$, $r^2 = 0.62$) . Further analyses

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

demonstrate that stature, age and biological sex did not add to the ability of external to predict skeletal crural index, while mass does ($p=0.004$, $R^2=0.65$). Our results demonstrate that using external crural index as a proxy of skeletal crural index is problematic and caution should be exercised when using this method.

The origins and life histories of enslaved Africans from Lagos (Portugal) revealed by multi isotope analysis

VICKY M. OELZE[1], XUEYE WANG[1], LUIZA BAO[2], CARINA LEIRIÃO[3], JOSEPH B. OGUNSETIRE[4], ANA GONZALEZ RUIZ[5], LUIS SANCA[6], NAIMA TUCKER[7], SOFIA N. WASTERLAIN[5,8] and MARIA TERESA FERREIRA[5,8]

[1]Anthropology Department, University of California Santa Cruz, Santa Cruz, USA, [2]NA, University of Coimbra, Coimbra, Portugal, [3]Department of Life Sciences, University of Coimbra, Coimbra, Portugal, [4]Institute for Research and Advanced Training (IIFA), University of Evora, Evora, Portugal, [5]Research Centre for Anthropology and Health, Department of Life Sciences, University of Coimbra, Coimbra, Portugal, [6]Anthropology Department, University Nova de Lisboa, Lisbon, Portugal, [7]Forensic Science Program, National University, San Diego, USA, [8]Centre for Functional Ecology, Laboratory of Forensic Anthropology, Department of Life Sciences, University of Coimbra, Coimbra, Portugal

Valle da Gafaria (15th to 17th centuries) is the earliest and largest burial site of enslaved Africans ever found in Europe. While bioarchaeological evidence proves these people were of African origin, it remained unclear from which regions they were abducted and at what stages of their lives this occurred. We present multiple isotope data obtained from early and late forming teeth of 66 individuals from Valle da Gafaria, and assess these individuals' diet and mobility patterns during different life stages. The carbon and nitrogen isotope values vary considerably ($\delta^{13}C$: -22.1 to -7.3‰; $\delta^{15}N$: 6.7 to 12.9‰) indicating different dietary customs, ranging from C_4 plant (sorghum zone), and C_3 plant (rice zone) based diets, to diets based on proteins from terrestrial (pastoralists) and marine animals (coastal fishery). The $^{87}Sr/^{86}Sr$ ratios range from 0.70932, typical for many coastal regions of the world including southern Portugal, to a highly radiogenic ratio of 0.73267, so far only described for the Angolan highlands. Only 15% of all individuals show evidence of large scale migration in adolescence, with $^{87}Sr/^{86}Sr$ ratios considerably changing between early and late forming teeth. We corroborate this evidence with the highly variable human oxygen isotope data from Valle da Gafaria ($\delta^{18}O$: -6.9 to 1.4‰). The combination of these isotopic data with the first bioavailable Pan-African Sr isoscape allows us to calculate the likelihood of specific regional African origins of the individuals historically discarded at Valle da Gafaria and to return to them at least some aspects of their identity and heritage.

This project was funded by the National Geographic Society (#NGS-92850R-22) and the Webster Foundation.

First study of a mother aye-aye's (*Daubentonia madagascariensis*) anxiety behaviors peripartum

REBECCA V. OLSON, LISA M. PACIULLI and DAVID Q. WATTS

Biological Sciences, North Carolina State University

Anxiety is a negative psychological state induced by stress triggers that can be seen in animals in the form of repetitive, rhythmic movements known as stereotypies. Primate mothers face anxiety due to birthing, infant health, and social relations. In this study, a mother aye-aye (*Daubentonia madagascariensis*) was observed to assess anxiety behaviors. It was hypothesized that the behaviors would change over time. With Duke IACUC approval, Pelco IMM12027-1S cameras were placed in a Duke Lemur Center (DLC) aye-aye mother's enclosure to record her activity. Over three days peripartum, three hours of footage (12:00-15:00) were viewed, and continuous focal animal sampling was used to note the time, duration, and type of repetitive scratching, grooming, etc. Data were then analyzed using a Kruskal-Wallis Test and a sample means test. The results showed that the day before birth, the mother repeatedly constructed and deconstructed nests three times more than engaging in any other behavior (ns), while on the day of birth, the mother groomed and scratched herself a lot (n=80x, n=62x, respectively, ns). The day after birth, the mother was hyper-alert (n=12x). Thus, the hypothesis was supported as the mother exhibited signs of anxiety by engaging in different stereotypies over the three-day period. While limitations such as a small sample size (n=1) and possible abnormal parturition behavior are evident, this study is the first to examine maternal anxiety in aye-ayes. The results can help husbandry staff create more comfortable environments for the rare and difficult-to-see captive aye-ayes.

Funding generously provided by NC State's Provost's Professional Experience Program

Individual behaviours imprinted in teeth of southern African hunter-gatherers and hunter-herders during the Holocene

JUDYTA OLSZEWSKI and VICTORIA E. GIBBON

Human Biology, University of Cape Town

Non-masticatory wear defines advanced wearing that can be affiliated with parafunctional habits, including using the teeth as a third hand, and these behaviours can induce advanced or characteristic wear patterns across isolated or multiple teeth. In a holistic study on archaeological southern African hunter-gatherers and -herders (sAHGH), non-masticatory wear was found and assessed to elucidate individual behavioural habits across the Holocene (11,700 years).

A total of 22 out of 369 individuals demonstrated non-masticatory wear, the majority were female (55%, 12/22), followed by males (22.7%, 5/22) and indeterminate sex (22.7%, 5/22). The ages inconsistently spanned young to old adults (18 to 50+ years). Wear examples were often isolated abrasions or demonstrated as 'grooves' or 'notches', in anterior teeth or running transversally across the teeth. One individual demonstrated interproximal grooves at the cementoenamel junction, possibly from using a tool to clean between the teeth and alleviate inflammation. These characteristics have been widespread in global literature but have not been widely reported in previous archaeological studies on sAHGH teeth. The examples corresponded with several occupational tasks or parafunctional habits and were unique findings in our study as they elucidated individual behavioural habits.

Recording and reporting these findings were critical to contributing to an individualised perspective on past sAHGH populations. Where many bioarchaeological studies are designed to provide an overarching view of a population, individual cases of non-masticatory wear provide a glimpse into the lifelong habits that shaped the individual and the population to which they contributed their efforts.

The National Research Foundation's (NRF) financial assistance is acknowledged (Gibbon NRF Grant #467192). Opinions expressed, and conclusions arrived at, are those of the author and not necessarily attributed to NRF.

Testing for shape convergence in the primate and carnivoran forearm

CHRISTIANNE ORMSBY

Anthropology, University at Albany

The relationship between arboreal locomotion and forearm morphology is well-studied in primates, but the degree to which these form-function relationships can be generalized to other large-bodied arboreal mammals is unknown. The order Carnivora displays a wide range of locomotor behaviors, including arboreal specializations with a high degree of forearm supination and pronation for climbing, bridging, and leaping. Here, I present a geometric morphometric analysis comparing proximal radius morphology among primates and carnivorans to test for convergence in forearm morphology as it relates to locomotor behavior. Eight landmarks (type I and type II) were used to characterize the shape of the radial head, which rotates in the radial notch of the ulna, and the articular surface of the radial head, which allows for a more uniaxial movement

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

on the capitulum of the humerus. Ordination of the landmark data using principal components analysis reveals anteromedial-posterolateral compression of radial head shape in terrestrial carnivorans that trends towards a rounder shape in arboreal taxa. The complexity of radial head topography tends to increase in carnivorans that exhibit a greater breadth of locomotor behaviors. In primates, radial head topography is higher in taxa that are not strictly arboreal, such as vervets. Primates that are dedicated arborealists (e.g., specialized for brachiation or suspension) have a very rounded radial head with limited topography. Overall, there is weak evidence for convergence in radial morphology of carnivorans and primates—the radial head of primates is consistently much rounder compared to the more elliptical and varied morphology in carnivorans.

Paleogenomic insights of ancient Mexico: Genetic origin and sex determination of human remains from the archaeological zone of Cañada de la Virgen

DANIELA OROZCO-PEREZ[1], VIRIDIANA VILLA-ISLAS[2], MARIA A. NIEVES-COLÓN[3], MARIA C. ÁVILA-ARCOS[2], RAFAEL MONTIEL[1], GABRIELA ZEPEDA GARCÍA MORENO[4], ANDRÉS MORENO-ESTRADA[1] and KARLA SANDOVAL[5]

[1]Human evolutionary and population genomics, National Laboratory of Genomics for Biodiversity (UGA-LANGEBIO), CINVESTAV, Irapuato, Mexico, [2]Population and Evolutionary Genomics, International Laboratory for Human Genome Research (LIIGH), UNAM, Querétaro, Mexico, [3]Department of Anthropology, University of Minnesota Twin Cities, Minneapolis, USA, [4]-, National Institute of Anthropology and History (INAH), Guanajuato, Mexico, [5]-, Equality and Gender Office of the Centre for Research and Advanced Studies (CODIGO-C), Cinvestav).

Cañada de la Virgen is a pre-contact archaeological zone in Central Mexico in Guanajuato. The complex was occupied between 540 and 1050 A.D., when monumental Mesoamerican structures were erected, including a pyramid and ceremonial structures. The origin of the groups that inhabited the site is an open question. Osteological analyses and radiocarbon dating of human remains have classified the excavated burials according to sex and timescale. We used paleogenomics to gain additional insight into their population history, assess their potential origins within Mexico, and characterize the biological sex of the individuals buried at the site. We sampled and sequenced 19 human skeletal remains, including two individuals who pre-date the construction of the monumental pyramid complex. Shotgun sequencing demonstrated six samples had over 1% endogenous DNA and were enriched for deeper sequencing. We compared the ancient low-depth genomes to genome-wide data from present-day indigenous populations from Mexico using PCA and ADMIXTURE and found that their ancestry composition is largely heterogeneous as individuals share genetic affinities with diverse populations within Mexico. We assigned chromosomal sex and found that one of the most notable burials -"El Jerarca"-, previously assigned as male based on archeological context, was genetically inferred as female. This individual was associated with the highest status according to their offerings and location, challenging the gender narrative of leading characters in ancient Mexico. Overall, our results suggest that this complex may have multiple genetic origins and illustrate a unique perspective of sex roles and practices in prehispanic societies.

CONACYT Mexico (Grant number FONCICYT/50/2016) and The Newton Fund (Grant number MR/N028937/1)

From *Australopithecus* to *Homo*: what the outliers (*Homo floresiensis*, *Homo naledi*, and *Homo luzonensis*) tell us about "the transition that wasn't"

CALEY M. ORR[1,2] and MATTHEW W. TOCHERI[3,4,5]

[1]Department of Cell & Developmental Biology, University of Colorado School of Medicine, Aurora, Colorado, USA, [2]Department of Anthropology, University of Colorado Denver, Denver, Colorado, USA, [3]Department of Anthropology, Lakehead University, Thunder Bay, Ontario, Canada, [4]Human Origins Program, National Museum of Natural History, Smithsonian Institution, Washington, District of Columbia, USA, [5]Australian Research Council Centre of Excellence for Australian Biodiversity and Heritage, Wollongong, New South Wales, Australia

Cladistically, there is no limit to how many species may belong in a genus and generic bounds are typically defined by the perceived "adaptive coherence" of species that compose a monophyletic grouping. As noted by Kimbel and Villmoare (2016; Philos. Trans. R. Soc. Lond., B Biol. Sci. 371:20150248), *Homo* represents a diversity of lineages exhibiting varying mosaics of features such that key derived characters might not appear, even among taxa well-nested within the genus. Conversely, some features appear in australopiths, suggesting a deeper phylogenetic origin for many of these supposed adaptive signatures. Consequently, the "transition" from *Australopithecus* to *Homo* may not have been as dramatic an adaptational affair as traditionally reconstructed. Not considered were three species (*H. floresiensis*, *H. naledi*, and *H. luzonensis*) that persisted into relatively recent times yet preserve morphological characters that appear primitive in many aspects. Here we evaluate craniodental versus postcranial characters of these three species to assess the adaptive coherence of *Homo* when they are included. Our analysis suggests that although craniodental synapomorphies unite these taxa with other specimens traditionally nested within *Homo*, the mosaic nature of some features, especially in the postcrania, reflect the piecemeal evolution of supposed adaptive signatures of the genus. This phylogenetic perspective renders dubious the exercise of identifying the adaptive bounds of *Homo* and the addition of these three taxa reinforces the conclusions of Kimbel and Villmoare (2016) that the transition from australopiths to *"Homo"* did not co-occur with an adaptively coherent suite of characteristics.

Maternal-Infant Health in Roman Tragurium: Bioarchaeological Investigations of the Very Young

ANNA J. OSTERHOLTZ[1], LUJANA PARAMAN[2] and JULIANNE PAIGE[3]

[1]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Curation, City Museum of Trogir, [3]Department of Anthropology, University of Nevada-Las Vegas

Paleopathological analysis of the very young (less than 6 months of age at death) can give a window into overall social conditions and maternal health. Excavations in the modern city of Trogir (Croatia) provided an excellent case study for this type of analysis. During development projects in 2011, 2016, and 2020, individuals of all ages were recovered. From these excavations, a total of 65 individuals under the age of 6 months at death were analyzed from two different contexts: a potential villa rustica site (VR, private cemetery dating to approximately AD 0-400) and the city necropolis (TCN, municipal cemetery located at a crossroads dating to approximately AD 400-700). These individuals were scored for pathological conditions and age at death distributions between the VR and TCN. Results of this analysis show incredibly high rates of cribra orbitalia (CO), porotic hyperostosis (PH), increased porosity, and periosteal reaction for both assemblages, ranging from 50% to 100% presence for these indicators. These results and the distribution of indicators (including CO, PH, and increased porosity on the sphenoid) are consistent with identification of scurvy and rickets) but given the environment and access to coastal resources (which should have provided appropriate nutrition and synthesis of vitamin D), these results are unexpected. This presentation will detail the paleopathological analysis as well as hypothesize the presence of lead poisoning in this assemblage, consistent with recent publications on lead poisoning in the Roman world. We will also discuss next steps in analysis to confirm or refute this hypothesis.

Funding provided by the College of Arts and Sciences Strategic Research Initiative and the Cobb Institute of Archaeology, Mississippi State University

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Variation in External and Internal Morphology of the Knee among *Pan*, *Papio*, and *Pongo*

ANTONIO R. OTERO[1], AMERICA CAMPILLO[2], LILY J.D. DEMARS[2], SIMONE SUKHDEO[2], TIMOTHY M. RYAN[2] and ADAM D. GORDON[1]

[1]Anthropology, State University of New York University at Albany, [2]Anthropology, Penn State University

Primate knee anatomy reflects locomotor differences due to the different forces and loads placed upon the knee by distinct locomotor modes. These differences are reflected in both external and internal morphology. This study aims to determine whether the femur and tibia, as well as both the external and internal morphologies, differ similarly among species. This pilot study sample consists of wild caught adult males and females for *Pan troglodytes* (n=15), *Papio anubis* (n=5), *Papio cynocephalus* (n=3), *Papio ursinus* (n=1), and *Pongo pygmaeus* (n=10). Landmarks and semilandmarks were placed along articular surfaces using the extension SlicerMorph in the program 3D Slicer. The complete landmark datasets were further reduced to functionally relevant areas (patellar surface; medial/lateral condyles). Five trabecular parameters were calculated using BoneJ. Three volumes of interest (VOIs) were placed in the femur (patellar surface; medial/lateral condyles) and two VOIs were placed in the tibia (medial/lateral condyles). Principal components (PCA) and linear discriminant function (LDA) analyses were run on the various datasets. PCA and LDA results for the femur are as expected (*Pan*/*Pongo*-*Papio* separation). For the tibia, *Pan*/*Pongo* group together for trabecular parameters while *Pan*/*Papio* group together for shape with a greater discrepancy between the medial and lateral condyles compared to the femur. These results suggest that the femur and tibia, along with their functionally relevant areas, do not always differentiate in a similar manner. These differences are most likely caused by body mass, phylogenetic history, and locomotion due to distinct biomechanical stressors placed upon the femur and tibia.

The Forensic Data Bank after almost 40 years: data standards, data preservation, and lessons learned

STEPHEN D. OUSLEY and RICHARD L. JANTZ

Anthropology, University of Tennesse, Knoxville

The Forensic Data Bank (FDB) at the University of Tennessee, Knoxville, was established in 1985 through a grant from the National Institute of Justice to help identify human remains from an American forensic context. Currently the FDB has data from almost 5,400 individuals, with 1,717 from voluntary body donations. The rest come from forensic cases (some of which remain unidentified, others are identified years later), and Institutional and Museum collections. Skeletal sources other than body donation are important because the modal age for donated skeletal collections is typically over 60, but most forensic cases come from much younger persons.

Craniofacial data were first recorded as 1-D craniometrics for backward compatibility to W.W. Howells' large database. Craniometric and postcranial measurement standards were established through inexpensive laboratory guides and were the metric basis for the *Standards* by Buikstra and Ubelaker (1989).

In 1998, craniofacial data collection at UT moved from 1D to 3D using digitizers, requiring more explicit care and attention to craniofacial landmark definitions. 3D landmark coordinates allows geometric morphometric analysis, but also calculation of traditional craniometrics, and better classifications, especially of fragmentary remains. In recent years more skeletal data have been collected from Africa, China, Mexico, Guatemala, Portugal, Italy, Germany, Japan, Korea, and Thailand. This international emphasis is important because of changing needs, such as the deadly immigrant crises in the US as well as Europe, rising ethnic violence, and the increasing need to investigate human rights violations in many parts of the world, an ethical and moral obligation.

The Bioarchaeology of Experience: A Theoretical Approach to Interpretations of Skeletal Trauma

BRIAN D. PADGETT

Department of Anthropology, The Ohio State University, SNA International, Defense POW/MIA Accounting Agency

The bioarchaeology of experience is a methodical approach to the interpretation of skeletal trauma as a reflection of lived experiences contextualized against the sociocultural environment for a more nuanced understanding of past social behavior. The bioarchaeology of experience draws from several theoretical models, and was conceived within the framework of skeletal trauma, though it is applicable to the interpretation of other pathological observations.

The emphasis is on an inductive analysis of acute violent trauma as evidence in the re-construction of the lived reality of the individual. The interpretation of micro-events that result in skeletal trauma can structure support for a behavioral model for the conduct of violence. This approach is a way to inductively reason a hypothesis for the structured performance of violence; from the inflicted injury outward, to the violent incident, to the greater conflict, to the sociopolitical context that underwrote the motives of opponents. To illustrate the application of this approach, observations of the remains of an individual who lived during the Yayoi period of Japan are presented for consideration as a reflection of attitudes and roles in the performance of intergroup violence.

Although violent conflict is a vehicle for social change, this approach can be applied to other catalytic episodes in the development of social complexity. The value of the bioarchaeology of experience is a new focus on the record of skeletal trauma of the individual, as well as the perceptions of other unseen social actors, and an affirmation of the interpretive skillset of the analyst.

Funded by The Ohio State University Alumni Association.

Weathering the storm: long-term implications of red ruffed lemur (*Varecia rubra)* feeding ecology following a tropical cyclone

LESLIE A. PAIGE[1,2], LUCA SANTINI[3], DELAÏD C. RASAMISOA[4], MCANTONIN ANDRIAMAHAIHAVANA[5], DEAN GIBSON[4], JOSIA RAZAFINDRAMANANA[6], NATALIE VASEY[7], GIUSEPPE DONATI[1] and TIMOTHY M. EPPLEY[4,7]

[1]Social Sciences, Oxford Brookes University, Oxford, UK, [2]Anthropology, Washington University in St. Louis, St. Louis, MO, USA, [3]Biology and Biotechnology "Charles Darwin", Sapienza University of Rome, Rome, Italy, [4]Conservation Science and Wildlife Health, San Diego Zoo Wildlife Alliance, Escondido, CA, USA, [5]Mention Zoologie et Biodiversité Animale, Faculté des Sciences, Université d'Antananarivo, Antananarivo, Madagascar, [6]Mention Anthropobiologie et Développement Durable, Faculté des Sciences, Université d'Antananarivo, Antananarivo, Madagascar, [7]Anthropology, Portland State University, Portland, OR, USA

Tropical cyclones can have numerous detrimental effects on ecosystems, including on primate populations. A region of particular concern is northeastern Madagascar, a hotspot for frequent cyclones and home to numerous threatened lemur species. One is the Critically Endangered red ruffed lemur (*Varecia rubra*), a predominantly frugivorous species with a narrow distribution. We examined whether *V. rubra* exhibited dietary adjustments following a stochastic cyclone event. Data collection on *V. rubra* feeding ecology began in March 2018 following the impact of cyclone Eliakim. We constructed monthly dietary profiles, Simpson's diversity indices, and classified feeding heights from 2,076 focal observation hours. To control for seasonality in food availability, we compared the months directly following the cyclone in 2018 with matched time periods (March-May) from subsequent years (2019 – 2021). Ripe fruits were consistently the largest percentage of *V. rubra* diet; however, immediately following the cyclone the lemurs consumed a greater percentage of unripe fruits and young leaves compared to following years. While Simpson's indices remained constant, the dietary profile post-cyclone differed from subsequent years by consumption of fewer

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

plant species. *Varecia rubra* foraged on lower levels of tree canopies following the cyclone than observed in later years. These shifts in diet and microhabitat use are likely a response to the loss of fruiting resources, as these may be easily damaged by cyclones. Overall, our study highlights a high degree of ecological flexibility in diet and microhabitat use by *V. rubra* that allows them to cope with unpredictable periods of food scarcity following cyclones.

Ancient Metagenomics, Stable Isotope Analysis, and Archaeological Contexts Provide Interdisciplinary Insights into Classic Period Maya Inequality in Southern Belize

HORVEY M. PALACIOS[1,2], NADIA C. NEFF[3,4], ERIN E. RAY[3,4], TANVI P. HONAP[1,2], DOUGLAS J. KENNETT[5], KEITH M. PRUFER[3,4] and CECIL M. LEWIS[1,2]

[1]Anthropology, University of Oklahoma, [2]Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, [3]Anthropology, University of New Mexico, [4]Center for Stable Isotopes, University of New Mexico, [5]Anthropology, University of California Santa Barbara

Classic Period Maya centers were characterized by status differences resulting in differential access to power and resources. We hypothesize that social inequalities form a foundation for individual and community-level variations in oral health and diet, and that these variations can be identified using integrated molecular methods. As part of a consortium of community-focused studies, we investigate the biological consequences of social inequity through an analysis of ancient oral microbiomes and stable isotopes ($\delta^{13}C$, $\delta^{15}N$) of Maya individuals. We draw these samples from four sites in southern Belize that have been extensively investigated. Ancient DNA was extracted from human dental calculus and partial uracil deglycosylase-treated double-stranded libraries were prepared for shotgun metagenomic sequencing using Illumina technology. Bioinformatic pipelines were used for microbial community profiling and contamination assessment. SourceTracker analysis suggests well-preserved oral microbiome profiles were recovered from commoner (n=2), likely elite (n=3), and elite (n=4) individuals. Purified human bone collagen was analyzed via IRMS for $\delta^{13}C$ and $\delta^{15}N$. Statistical analysis of elite (n=24) versus commoner (n=7) isotopic niche areas ($‰^2$) with the SIBER package in R indicate greater variation in dietary macromolecular sources of commoners than of elites. These data suggest a relationship between social status and differential access to wild and domesticated food resources. This research introduces a pilot approach to integrating biochemical methods for the study of social inequality in the past. Such approaches strengthen reconstructions of community health and diet throughout the ancient and contemporary Maya social landscape.

Funded by National Science Foundation grants titled "Hominid Dental Metagenomes for Pathogen Evolution Research" (NSF BCS-2045308), "Long-Term Human-Environmental Interaction In a Lowland Tropic Setting" (NSF BCS-1632061), and Alphawood Foundation (2014-2022).

Paleoenvironmental Reconstruction of the Okote, KBS and Upper Burgi Members of Koobi Fora Formation Via Ecomorphology of Bovid Distal Metapodials

MAGDALENA PALISSON[1], MEGAN G. MALHERBE[2], FRANCES FORREST[3], FELIPE I. MARTÍNEZ[1], DAVID R. BRAUN[4] and EMMANUEL NDIEMA[5]

[1]Escuela de Antropología, Facultad de Ciencias Sociales, Pontificia Universidad Católica de Chile, [2]Institute of Evolutionary Medicine (IEM), University of Zurich, [3]Department of Sociology and Anthropology, Fairfield University, [4]Center for Advanced Study of Human Paleobiology, The George Washington University, [5]Department of Archaeology, National Museums of Kenya

The Omo-Turkana Basin is a crucial area for studying the environmental pressures of the Pleistocene and early hominin evolution in east Africa. Over the last 2 million years, the basin has been characterized by dramatic environmental fluctuations and great diversity of hominins coexisting in this territory.

We utilise a new method for conducting bovid ecomorphological analysis to shed light on the paleoenvironmental conditions of selected Pleistocene sites within the Koobi Fora Formation. Fossil data was obtained from the Upper Burgi (1.98–1.87 Ma), KBS (1.87–1.56 Ma), and Okote (1.56–1.38 Ma) members and compared with modern individuals with known habitat preferences. Bovid distal metapodials were analysed using 3D geometric morphometrics to quantify environmental and landscape changes during this period. The anatomy of the Bovidae family is an invaluable proxy for environmental reconstruction as they are characterized for being habitat specific, as well as having morphological adaptations for specific environments.

The majority of Upper Burgi, KBS and Okote specimens were classified into open habitat category, in line with previous studies. Moreover, our findings indicate a heterogeneous distribution through the habitat categories, suggesting that the east Turkana ecosystem was highly variable across both territory and time. The main contribution of this research is that the presence of mosaic environments among sub-regions and members of the Koobi Fora Formation is evident. The complexity of the context in which radical morphological and behavioural transitions take place in hominin evolutionary history is highlighted, providing further insight into this key period.

Joan Cogswell Donner Field School Scholarship, The Leakey Foundation.

Sex estimation of human skeletal remains: combinations of small, irregular bones produce high probabilities of accuracy

ANNIE S. PANAGEAS[1], BOBBIE J. LEEPER[2] and ANNE M. BURROWS[3]

[1]Forensic Science & Law, Duquesne University, [2]Physician Assistant, Seton Hill University, [3]Physical Therapy, Duquesne University

Accurate estimation of sex is a critical step in the process of identifying human skeletal remains. Together the pelvis and skull give near 100% accuracy, but these bones are not always present. Often, only small and irregular bones are present so the development of methods using them to identify sex of human skeletal remains is important. Previous investigators developed methodologies for small and irregular bones, but they typically used one bone and have produced varying results. To further explore the utility of small and irregular bones in sex estimation of human skeletal remains, we tested the hypotheses that there are significant size and shape difference between male and female small and irregular bones, and that combinations would produce better validity than single bones. We used a contemporary sample of cadavers from gross anatomy labs (N=30; 14 females & 16 males) to assess select linear dimensions for each bone: the 1st metatarsal, medial and intermediate cuneiforms, patella, clavicle, hyoid, and 1st metacarpal. We also calculated shape ratios for each bone. All data were subjected to Student's unpaired t-tests to assess sexual dimorphism in bones. Data were also subjected to linear discriminant analyses to ascertain the most accurate combinations of bones for predicting sex. Results reveal that these bones and ratios are sexually dimorphic and that combinations of these bones produce higher likelihood of predicting correct sex than using just one bone. These results support the hypothesis that combinations of bones result in higher accuracy of sex estimation than single bones.

Dynamic simulation of macaque jaw mechanics during a complete power stroke of mastication

OLGA PANAGIOTOPOULOU[1], DALE ROBINSON[2], JOSE IRIARTE-DIAZ[3], ANDREA B. TAYLOR[4] and CALLUM ROSS[5]

[1]Department of Anatomy and Developmental Biology, Monash University, [2]Melbourne School of Engineering, University of Melbourne, [3]Department of Biology, University of the South, [4]Department of Basic Science, Touro University, [5]Department

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

of Organismal Biology and Anatomy, University of Chicago

Finite element analysis (FEA) is a powerful tool for studying form-function relationships in the primate jaw during feeding. We have previously shown that, as in humans, during simulated chewing in adult rhesus macaques: the working (chewing) side posterior corpus is twisted about its long axis, everting the alveolar process; bent and negatively sheared in sagittal planes; and laterally bent in transverse planes. The balancing side mandibular corpus is twisted about its long axis, inverting the alveolar process, bent sheared in sagittal planes. Our study was the first to show that food effects on the strain regime are most salient in areas not traditionally investigated. However, our model is a static model of a specific time in the power stroke, whereas strain patterns vary throughout the power stroke due to variation in relative timing of jaw elevator muscle activity. To quantify the effects on the mandibular strain regime of dynamic changes in relative muscle force we conducted a dynamic FEA of strain during a complete power stroke using in vivo muscle force data. Our results show that peak von Mises stresses and principal and shear strains in the lingual symphysis and balancing-side corpus occur between 40-50% of the gape cycle, when the activation peaks of the working- and balancing-side medial pterygoids and superficial masseters have started to decline, and the balancing-side deep masseter force peaks. These results yield a more complete understanding of the biomechanical behaviour of the macaque jaw during feeding.

Funding was provided by a Monash Biomedicine Discovery Institute Career Continuity Grant and a FAPESP grant to OP.

Detecting marginalised groups and epidemic stress in the historical record through cause of death entries in the 1918-19 influenza pandemic in Cape Breton Island (Unama'ki), Nova Scotia, Canada

JOSEPH M. PARISH

L'nu, Political, and Social Studies, Cape Breton University

The stresses of an epidemic are now quite familiar to everyone as we complete our third year of the COVID-19 pandemic. Its effects range from the mundane to the catastrophic, from simple inconveniences to the disruption of whole economic sectors. In such times of broad social stress, the normal rhythms of institutions and infrastructure become compromised and the result can be loss of efficacy and efficiency in systems. Some measure of this may be recorded in our paperwork as the very cases that the medical community is required to document in death records suffer from a lessened attention to details just when the details are what we will need most to understand this pandemic in present and future studies. This study suggests that this disrupting effect is shared under all epidemic conditions and can be detected in the historical record. For the last four years, the Cape Breton Island 1918-19 Influenza Project has transcribed the death records of over 11,000 inhabitants from 1918-1924 in all four counties of the island. This study indicates that the length of description entries for primary and contributory causes of death were significantly lower for females and juveniles (<15) and that this was also lower during the pandemic (1918-1919) than after the pandemic (1920-1924). It is suggested that identifying females and juveniles (<15) as marginalised groups within the historical record is possible using this measure. The stressful environment of the pandemic period vs. the post-pandemic period can also be characterised.

Adapting laboratory techniques developed for the extraction and analyses of ancient DNA for use in the identification of burned forensic remains

CODY E. PARKER[1], ERIN RAWLS[1], KATELYN L. BOLHOFNER[2,4], LAURA FULGINITI[2], ROBERT OLDT[4], STEVIE WININGEAR[1], SREETHARAN KANTHSWAMY[4], SUHAIL GAFOOR[1], GIOVANNA VIDOLI[3], JOANNE DEVLIN[3] and ANNE C. STONE[1,5,6]

[1]School of Human Evolution and Social Change, Arizona State University, [2]Office of the Medical Examiner, Maricopa County, Arizona, [3]Forensic Anthropology Center, Department of Anthropology, University of Tennesee, [4]School of Math and Natural Sciences, Arizona State University, [5]Center for Evolution and Medicine, Arizona State University, [6]Center for Bioarchaeological Research, Arizona State University

The thermal alteration of forensic remains can make identifying decedents using DNA analysis challenging, as the preservation and biochemical characteristics of recovered DNA can be heavily degraded. While this degradation differs in the manner of accumulation from that found in archaeological remains, many of the same patterns of damage can persist. Here we present a two-phase investigation into how adapting laboratory techniques developed for the extraction of DNA from archeological remains has the potential to aid in the identification of thermally altered forensic remains using both "real-world" case samples (phase one) and samples obtained from the controlled burning of donor cadavers (phase two). We investigate potential gains in overall DNA yield and quality, STR profile recovery, and mitochondrial and SNP enrichment efficacy. Preliminary results suggest that ancient DNA extraction techniques more efficiently recover DNA from highly thermally altered bone samples in terms of raw yields per input material, as well as exhibiting and overall higher likely-hood of those yields meeting minimum criteria for downstream analyses. We also find that DNA extracted using ancient DNA techniques is more likely to result in the generation of at least partial STR profiles in our most degraded samples. Additionally, we also note an acute point of DNA degradation in thermally altered remains beginning at exposures to temperatures > 350 °C. While this research is still ongoing, we feel that the further adaptation of similar bio-archaeological techniques shows great promise in advancing the analyses and outcomes of challenging forensic cases.

This work is funded by the National Institute of Justice (NIJ), Award Number: 2019-DU-BX-0044.

Bone Strength in the Medieval and Early Modern Black Friars Cemetery, Odense, Denmark

KAELA PARKER[1,3], JAY STOCK[2] and ROB HOPPA[1]

[1]Anthropology, University of Manitoba, [2]Anthropology, Western University, [3]Anthropology, Economics, and Political Science, MacEwan University

The cross-sectional geometric shape of long bone diaphyses reflect, in part, in vivo loading throughout the lifespan. Thus, general patterns of mechanical loading applied to bone during life can be inferred from the cross-sectional geometric properties of a long bone's diaphysis. The current study examines temporal differences in lower limb loading in the Black Friars cemetery sample from Odense, Denmark (1240-1607 CE). Cross-sectional geometric properties (cortical area, bending rigidity along the maximum and minimum axes and the anteroposterior and mediolateral axes, torsional rigidity, and diaphyseal shape) at the femoral midshaft were calculated for 160 right femora; 60 from the medieval period (42 males, 18 females) and 100 from the early modern period (53 males, 47 females). The socioeconomic status of burials was lower in the later period, it was hypothesized that this would be associated with an increase in habitually strenuous physical labour as reflected by greater femoral robusticity among the urban poor buried in the early modern period. The hypothesis was rejected as femoral robusticity decreased in the early modern period, significantly so for males. Factors which may explain this trend include a reduction in mechanical loading, compromised bone formation or remodeling among the urban poor, and inclusion of the Dominican Friars in the medieval sample. The Dominican order, documented as highly mobile, actively recruited males from affluent families, possibly biasing the medieval sample.

This research was supported with funding from a SSHRC Doctoral Fellowship (#753-2018-2041 to K. Parker), SSHRC Insight Grant (#435-2017-729 to R. Hoppa), and the University of Manitoba.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Evaluating expertise and the importance of credentials within forensic anthropology

NICHOLAS V. PASSALACQUA[1], NATALIE LANGLEY[2], MARIN A. PILLOUD[3] and MARIATERESA TERSIGNI-TARRANT[4]

[1]Anthropology and Sociology, Western Carolina University, [2]NA, Mayo Clinic, [3]Anthropology, University of Nevada, Reno, [4]NA, Saint Louis University

Using Collins and Evans (2004) model of expertise, we examined interactional expertise in forensic anthropology by posing 11 questions about the discipline to 27 voluntary participants with varying degrees of experience in forensic anthropology (this was approved by the IRBs of all authors' institutions). The authors ranked the respondents' forensic anthropology expertise using a five-point scale ranging from 'expert' to 'no knowledge' based on respondent backgrounds in the discipline. All interviews were recorded and transcribed for anonymization. Next, 11 voluntary evaluators with varying backgrounds in forensic anthropology evaluated the transcripts to estimate the level of expertise of the respondents. Evaluators rated each respondent's answers individually, and provided an overall rating of perceived expertise for each respondent.

Results indicated there was little to no agreement between author-assigned expertise, and the expertise level assigned by the evaluators based on respondent answers (polychoric correlation = 0.007; weighted Cohen's kappa = 0.354); correlations did increase when rankings were dichotomized into expert and non-expert (tetrachoric correlation = 0.473; weighted Cohen's kappa = 0.501). The questions most highly correlated with expertise focused on specific methods and standards development within the discipline. Factors evaluators reported to assess expertise included use of discipline-specific terminology and the overall length of the answers. These results indicate that accurately identifying expertise in forensic anthropology may be challenging for both experts and non-experts at least based on interactional (i.e., non-practical) assessments. Our results support the necessity of disciplinary credentials for demonstrating expertise via certification, with licensure being the next logical step.

Global Variation in Fused Premolar and Molar Roots

ARIELLE J. PASTORE and GEORGE R. SCOTT

Anthropology, University of Nevada, Reno

In contrast to early hominins, modern human root numbers are polymorphic traits. UP1 and UM2 may have one to three roots, and LM2 may have one to two (excluding accessory roots). While the evolutionary significance of root fusion is unclear, understanding the contemporary global variation is imperative to studies focused on population histories, movements, and genetics. Due to the difficulties involved in observing root traits within samples, researchers are often limited in their ability to investigate such topics. This study provides the current global frequencies of root fusion of UP1, UM2, and LM2 drawn from 235 unique samples, accompanied by statistical methods analyzing the variance within and between each region. Initial one-way ANOVA analyses report significant differences in frequency means between major global regions for all three teeth. UP1 shows the highest frequencies of root fusion, LM2 shows the lowest frequencies, and UM2 frequencies are intermediate between the two. Overall, regions of Sub-Saharan Africa consistently report the lowest incidences of root fusion, while Arctic regions report the most. These patterns of variation at a global scale provide a better context for future work involving root fusion and its relation to diet, genetics, or migration histories. Further analysis of the global distribution of root fusion in concordance with population genetics research may elucidate the evolutionary mechanisms driving this trait.

Enamel thickness in the stem hylobatid *Kapi ramnagarensis*

BIREN A. PATEL[1,2], ANNA DI[2], KELSEY D. PUGH[3,4], ASHLEY S. HAMMOND[3,4], ALEJANDRA ORTIZ[5], CHRISTOPHER C. GILBERT[4,6,7,8], CHRISTOPHER J. CAMPISANO[10,9] and RAJEEV PATNAIK[11]

[1]Integrative Anatomical Sciences, Keck School of Medicine of USC, [2]Human and Evolutionary Biology, University of Southern California, [3]Anthropology, American Museum of Natural History, [4]NYCEP, [5]Anthropology, New York University, [6]Anthropology, Hunter College of CUNY, [7]PhD Program in Anthropology, Graduate Center of CUNY, [8]Paleontology, American Museum of Natural History, [9]Institute of Human Origins, Arizona State University, [10]School of Human Evolution and Social Change, Arizona State University, [11]Geology, Panjab University

Molar enamel thickness (ET) has been extensively studied in extant and fossil hominids. In contrast, existing ET data for hylobatids are limited to two species (*Symphalangus syndactylus* and *Hylobates muelleri*) with small samples sizes (n=3-9 teeth/species depending on molar position). Based on these data, ET has been described as either "intermediate thin" or "thin" in *Hylobates* and *Symphalangus*, respectively. Thinner ET in *Symphalangus* may be related to a more folivorous diet. Which of these patterns is derived in hylobatids is not known because fossil stem members of this clade have only recently been recovered. Here we quantify lower third molar (M_3) ET in the stem hylobatid *Kapi ramnagarensis* from the middle Miocene (Lower Siwaliks) locality of Ramnagar. The isolated molar was µCT scanned (11µm) and the resulting images yielded satisfactory tissue contrast between enamel and dentine pixels. 3D surface renderings of the enamel cap and underlying dentine crown (identified above the cervical plane) were created from which scale-free 3D relative ET (3DRET) was calculated. Measurements needed to calculate 2D relative ET (2DRET) were obtained from a virtual plane which was identified between the dentine horns of the two mesial cusps. Calculations of 3DRET and 2DRET in *Kapi* were then compared to a sample of extant hylobatids M_3s (n=15) from all four genera: *Symphalangus*, *Hylobates*, *Hoolock* and *Nomascus*. *Kapi* has substantially lower 2DRET and 3DRET than *Hylobates*, *Hooloch* and *Nomascus*, and is at the lower end of the *Symphalangus* sample. Thus, "thin" enamel, and possibly folivory, might be primitive for hylobatids.

Funding provided by NSF BCS Awards: 1945736, 1945618, 1945743

Development of rhesus macaque mimetic musculature and ontogenetic aspects of macaque social behavior

JORDAN T. PATER[1] and ANNE M. BURROWS[2]

[1]Biology, Duquesne University, [2]Physical Therapy, Duquesne University

Rhesus macaques (*Macaca mulatta*) have long been used as a model for the evolution of some aspects of human social behavior. These macaques have a clear-cut dominance hierarchy with a well understood facial display repertoire. However, we know little about the ontogenetic changes in gross mimetic musculature and facial display behavior. In an effort to illuminate our understanding, we dissected facial masks from 10 *M. mulatta* cadavers that died naturally, shortly after birth. We made a midline incision using a scalpel beginning at the dorsal cervical region and passing through the occipital, frontal, nasal, and upper/lower lip regions. The left side of the face was peeled off to reveal facial muscles forming a face 'mask', which was then set aside to air dry for increased color contrast before further analysis. Results reveal that, unlike adult *M. mulatta*, infant rhesus macaques have extrinsic external ear muscles and muscles associated with the lower lip that are very gracile and poorly developed. Nonetheless, musculature associated with the upper lip and nares are well developed, individually distinct, and robust. Concurrent investigations into infant facial display repertoire are ongoing. However, it is well known that neonatal rhesus macaques imitate adult facial displays as early as 10 days. Additionally, the neonate's sex and rank of the mother impact their achievements in facial imitation, with sons of high-ranking mother's scoring highest in these abilities. Our current results may reflect simple variation in mimetic musculature ontogeny or they could reflect some of these developmental aspects of facial expression.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Identifying handsaws from cut marks on bone: A microscopic trait analysis

SARAH E. PATTERSON and SHELBY S.J. PUTT

Sociology and Anthropology, Illinois State University

In New York City, it is estimated that for every 224 homicide cases, one will involve human dismemberment. These cases can be difficult to solve, as dismemberment is often used by the criminal to conceal other forms of forensic evidence. In dismemberment cases involving a handsaw, the saw leaves behind characteristic traces on the bone, such as saw marks (kerfs), bone islands, harmonics, and exit chipping, which we hypothesize can be used to identify the type of saw used by the perpetrator. The current study expands on previous research into saw blade cut mark characteristics by examining features on limbs that were fully fleshed when cut. Using microscopy, we tested whether the cut marks (N=54) on mature white-tailed deer (*Odocoileus virginianus*) long bones could be traced back to one of nine handsaws of different brands and blade set types used to make the cuts. Measurements of kerfs, including cut width, blade width, teeth per inch, tooth width, and tooth height, were obtained from photographs taken under an Olympus model BX51M metallurgical microscope. The presence and frequency of blade harmonics, bone islands, and exit chipping were also noted. ANOVA and Tukey post-hoc tests revealed a significant difference between the kerf dimensions produced by different blades. Combined with our qualitative assessment, these results demonstrate that cut mark characteristics can be used to determine the blade that created them. If applied in forensic cases, this technique may aid in identifying the dismemberment tool used in the crime and will generate more reliable convictions.

Examining the Gender Similarities Hypothesis in the Community of St. Bride's Lower (1600-1849 CE)

TAYLOR PEACOCK

Department of Archaeology, University of Cambridge

Recent feminist critiques have challenged the interpretation of sex/genders as oppositional in scientific analysis. Building on this, the *gender similarities hypothesis* argues that we should approach gendered analysis from a place of similarity and consider the overlap and nuance to gendered experiences. In bioarcheology, common practice takes a comparative, oppositional approach to understanding experiences between sex estimation categories, and no studies have considered bodies from a similarity perspective. This study explores whether approaching skeletal data and estimated sexes from a place of similarity changes our understanding of the past. Data from 391 adult (>18 years) individuals from St. Brides Lower (1600-1849 CE) cemetery on numerous skeletal indicators: degenerative joint disease, fractures, dental disease, and enthesis, were analyzed between sex estimation categories using inferential statistics alongside effect size measures. Results found that when compared, differences between estimated males and females for most skeletal indicators were not statistically significant with small effect sizes. Cranial fractures and proportion of calculus were statistically significant, but the effect sizes were small, while Schmorl's nodes were statistically significant with a large effect size. In taking a *similarities* approach, the results suggest that in most experiences skeletal bodies reflect a variation and spectrum of experiences and biologies, with differences between estimated males and females small and overlapping, rather than oppositional and different. Results from cranial fractures and calculus also suggest that when using inferential statistics, differences between estimated males and females were still small, with large overlaps, challenging how we interpret sex/gender differences in the past.

This presentation draws on research supported in part by a Social Sciences and Humanities Research Council Canada - Doctoral Fellowship Grant 752-2021- 0305.

Hard working people during the transition from the pre-Neolithic to Neolithic at Man Bac, Vietnam

OSBJORN M. PEARSON[1], HIROFUMI MATSUMURA[2], MARC F. OXENHAM[3,4], NGUYEN KIM DUNG[5], NGUYEN LAN CUONG[5] and TRINH HOANG HIEP[5]

[1]Department of Anthropology, University of New Mexico, USA, [2]Department of Anatomy, Sapporo Medical University, Japan, [3]School of Archaeology and Anthropology, Australian National University, Australia, [4]Department of Archaeology, School of Geosciences, University of Aberdeen, UK, [5]Archaeology, Institute of Archaeology, Socialist Republic of Vietnam

The Man Bac site in northern Vietnam belongs to the Phùng Nguyên Culture, dates to 3800-3600 BP, and includes 95 burials of a pottery-using population that practiced fishing, hunting, horticulture, and some rice agriculture. The people of Man Bac present a mosaic of cranial and dental morphology that suggests a new population had arrived and partially absorbed the earlier Hoabinhian hunter-gathers. The present study analyzes the cross-sectional geometry of the midshaft humeri and femora from Man Bac. Published long bone dimensions from Man Bac were used to predict J, which was transformed into Zp (polar section modulus) by dividing by half of the maximum midshaft diameter. Zp was standardized for body size by dividing by the product of maximum long bone length and body mass (predicted from femoral head diameter). These data were compared to a world-wide set of 36 comparative groups (16 female, 20 male; 15 of the groups included both sexes). The results show that both males and females from Man Bac have exceptionally robust size-adjusted humeri. The mean for Man Bac males is only exceeded by Near Eastern Neandertal males and equaled by those of Tierra del Fuego and Mesolithic European males. In comparison to other females, the Man Bac females' mean is exceeded only by that those of Buriat females and Skhul-Qafzeh females (both samples of n=1). In contrast the Man Bac femora appear unremarkable. The elevated humeral robusticity of the Man Bac people suggest both sexes engaged in strenuous work.

National Science Foundation, Wenner Gren Foundation, Boise Fund, Grant-in-Aid No. 15405018 and No. 20370096 from the Japan Society for the Promotion of Science, and Toyota Foundation (Grant No. D06-R-0035).

The evolutionary genomics of Type 2 Diabetes

LAURA PEREZ[1], LAUREL MOYSE[2] and GEORGE PERRY[1,2,3]

[1]Department of Anthropology, Pennsylvania State University, [2]Department of Biology, Pennsylvania State University, [3]Huck Institutes of the Life Sciences, Pennsylvania State University

The genetic architectures of multiple human complex diseases have been increasingly clarified with genome-wide association studies (GWAS) now involving up to millions of individuals. Combining published GWAS results with evolutionary genomics analyses allows us to explore the trajectory of disease-associated loci and cautiously make indirect inferences concerning the evolutionary histories of such traits. Here, we investigated the evolutionary histories of loci associated with Type 2 Diabetes (T2D) for two different human populations, East Asian (EAS; GWAS n=211,793 individuals) and European (EUR; n=231,436 individuals). The recently increasing prevalence of T2D in many populations has motivated the hypothesis that modern rates of T2D may reflect mismatch. Under such a scenario, previously beneficial alleles that may have undergone positive selection could now be associated with increased risk of disease. To examine the plausibility of the mismatch hypothesis for T2D in these two populations and on different evolutionary timescales, we studied the intersection and directionality of trait-associated alleles with two evolutionary genetics statistics, Singleton Density Score (SDS) and Integrated Haplotype Score (iHS). SDS can identify signatures of polygenic selection occurring within the last ~3,000 years, while iHS detects relatively older signatures of strong positive selection, back to ~25,000 years. Our preliminary results suggest that there may have been relatively recent increases in the frequencies of trait-decreasing alleles among T2D-associated SNPs in EAS (T2D-associated SNPs=1136; tSDS = -0.08; Permutation test

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

p-value=0.0033). Our ongoing work includes accounting for potential effects of linkage disequilibrium on these results and expanding our analytical framework to include iHS results.

Do white-faced capuchin monkeys have social norms?: New data from the Lomas Barbudal Monkey Project in Costa Rica

SUSAN E. PERRY

Anthropology, UCLA

Cultural evolution researchers still debate whether humans are unique among species in having social norms, i.e. moralized, group-specific, socially learned, shared understandings of the rules by which social life should be conducted, maintained via moral emotions that inspire impartial third parties to punish violators of these rules. I sought to establish what behaviors spark outrage in capuchins by recording the details of social context whenever a capuchin aggressed against or screamed at another monkey. Food theft, certain types of sexual interaction, and branch-breaking displays were situations that elicited outrage often enough to warrant documentation of which other monkeys witnessed these events, and how they responded. Three decades of long-term data on ten groups were used to measure degree of maternal kinship and relationship quality (using focal follow data and ad libitum data) between the bystander monkeys and the monkeys involved in the putative norm violation. This population fails to meet three of my operational criteria for social norms: (1) There is very little between-group variation in the patterning of social behaviors relevant to the putative social rules identified. (2) The rate at which third party bystanders aggress against putative norm violators is low (0.6-7.0%). (3) Using a logistic regression modeling framework, the most salient predictor of whether third party bystanders punish putative rule violators is the quality of bystanders' relationships with those violators, suggesting that bystander behavior is driven more by grudge-holding against particular individuals with whom they have poor-quality relationships than by altruistic enforcement of a group-wide behavioral standard.

Templeton World Charity Foundation, Inc., National Science Foundation (grants 1638428, 0613226, 848360, 1232371,1919649), National Geographic Society (5 grants), Leakey Foundation (5 grants), Wenner-Gren Foundation, Wild Capuchin Foundation, MPI-EVAN, UCLA

Postcopulatory mate choice in the female olive baboon (*Papio anubis*)

RACHEL M. PETERSEN[1,2], JACLYN ANDERSON[3], EMILY NONNAMAKER[4], CHRISTIAN ROOS[5,6], CHRISTINA M. BERGEY[7,8], AMANDA D. MELIN[10,11,9] and JAMES P. HIGHAM[1,2]

[1]Department of Anthropology, New York University, New York, NY, USA, [2]NYCEP, New York, NY, USA, [3]Cumming School of Medicine, University of Calgary, Calgary, AB, Canada, [4]Department of Biological Sciences, University of Notre Dame, Notre Dame, IN, USA, [5]Gene Bank of Primates, German Primate Center, Göttingen, Germany, [6]Primate Genetics Laboratory, German Primate Center, Göttingen, Germany, [7]Department of Genetics, Rutgers University, Piscataway, NJ, USA, [8]Human Genetics Institute of New Jersey, Rutgers University, Piscataway, NJ, USA, [9]Department of Anthropology and Archaeology, University of Calgary, Calgary, AB, Canada, [10]Department of Medical Genetics, University of Calgary, Calgary, AB, Canada, [11]Alberta Children's Hospital Research Institute, University of Calgary, Calgary, AB, Canada

In many mammals, including primates, marked sexual dimorphism and male coercion may limit the ability of females to exhibit direct mate choice, and create selection for cryptic choice mechanisms. Within primates, discrepancies between mating observations and paternity suggest that cryptic female choice may be widespread, but there is a dearth of information on how mechanisms of cryptic postcopulatory choice might operate. This study aimed to elucidate postcopulatory mechanisms capable of influencing paternity probabilities, and explore the role of genetics in postcopulatory female choice in a nonhuman primate model, the olive baboon (*Papio anubis*). We conducted genetic sequencing of 22 olive baboons, and characterized pre- and postcopulatory vaginal pH and gene expression, both of which may influence sperm survival. We examined the role of both genome-wide genetic characteristics (multi-locus heterozygosity and kinship) and as well as genotype at the major histocompatibility complex (MHC), a multi-gene family that plays an integral role in immune system function and precopulatory mate choice. We found that postcopulatory changes in the vaginal environment were associated with male and female genotype. In general, vaginal pH decreased after copulation, however the largest postcopulatory decreases in vaginal pH were observed when females mated with genetically similar males. Moreover, postcopulatory expression of one olfactory receptor gene (OR51F2) and one immune response gene (LURAP1L) increased in response to copulations with males with low MHC complementarity. Since vaginal pH and immune responses may both impact sperm survival, our results offer potential mechanisms by which females may influence paternity after copulation.

This work was funded by the Wenner Gren Foundation and the National Science Foundation's Doctoral Dissertation Research Improvement Grant

Expanding on Potential Applications of Dental Microwear Texture Analysis to Wildlife Management

ALEXANDRIA S. PETERSON

Environmental Dynamics, University of Arkansas

UN projections show that by 2030, 60% of the 8.5 billion global human population will live in urban areas. Coyotes (*Canis latrans*) are adept at exploiting anthropogenic subsidies in urban areas. As these carnivores become habituated to human provisioning, they present a human/wildlife conflict issue. It is important for wildlife management to track the use of anthropogenic subsidies through time. This study tests if the use of dental microwear texture analysis, a method used extensively by biological anthropologists and paleontologists, can track the exploitation of anthropogenic subsidies in wild canids. Using museum specimens from 1960s-1970s and a small sample donated by the Arkansas trapping community in 2021, dental microwear texture analysis was conducted on a sample of n = 129 first molars of *C. latrans*. County populations at time of collection were recorded for each specimen to compare coyotes in high and low population regions. Molars were scanned using a white-light confocal profiler and surfaces characterized with scale-sensitive fractal analysis and ISO texture parameters. Results show significant differences in dispersion, particularly for scale of maximum complexity (*Smc*) and dale volume (*Sdv*). Notably, *Smc* of the modern coyote sample shows less variance than the museum collection. This is consistent with a narrower diet for urbanized individuals. Such results suggest that dental microwear may prove useful for long term monitoring efforts of urban wildlife. Incorporating museum specimens broadens the temporal range of observations, providing more context for anthropogenic impact on animal populations.

Research was funded by the Graduate and Professional Student Council Research Grant at the University of Arkansas.

Unclaimed Identities: Bioarchaeological analyses on a commingled assemblage from a Second World War context in Berlin, Germany

EMMANUELE DR. PETITI[1], SUSAN PROF. POLLOCK[2] and JULIA DR. GRESKY[1]

[1]Natural Sciences, German Archaeological Institute, [2]Department of Near Eastern Archaeology, Freie Universität Berlin

Between 2014 and 2016 three pits containing commingled human bones were found during repair works at the Freie Universität Berlin. Originally, the site was part of the Kaiser Wilhelm Institute for Anthropology, Human Heredity and Eugenics (KWI-A). The KWI-A directly contributed to the racist and murderous politics of the Nazi regime and reportedly the institute received human samples from the infamous Nazi doctor in Auschwitz, Josef Mengele. Thus, our research aimed to test whether the assemblage resulted from the collection of human samples from modern contexts, such as concentration camps.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

As by request of the representatives of the holocaust victims, no invasive analyses were carried out. Our study assessed MNI, biological and taphonomic profiles. Specifically, the latter focused on agent-specific modifications, along with morphological patterning of the post-depositional fractures. The large size of the assemblage also offered an unprecedented opportunity to compare the methodological standards currently available for taphonomic studies.

The results indicate that the human remains belong to at least 107 individuals, of all ages and both sexes and that their original burial place was not at the KWI-A site. The differential bone representation and the pattern of taphonomic changes rule out a modern origin from concentration camps, rather suggesting that the assemblage might have originated from one or more archaeological contexts.

Not only do these results provide an innovative contribution to the methodological debate on taphonomic studies in bioarcheology, but they also address ethical issues about the unclaimed identities of the individuals represented by the assemblage.

Malar/Fe-malar: Sexual dimorphism of the zygomatic bone among apes

ALESHA PETTIT

Anthropology, University of Nevada Las Vegas

Sexual dimorphism has been observed and documented in various aspects of primate morphology. Classic examples include general differences in body size, color, pelvis shape, cranial cresting, etc. This study examines mid-face morphology among apes in the context of sexual dimorphism, with specific attention to the zygomatic bone and surrounding regions. In general, morphological differences in females and males are related to sexual selection, either for sexual attraction of the opposite sex or competition that exists among same sex conspecifics, typically males, for access to females. Exploration of sexual dimorphism of the face must also consider regional integration regarding functional components such as mastication, vision, etc. and how these influence or constrain dimorphic traits. In this study we test the hypothesis of dimorphism for the following hypothesized relationships: 1) zygomatic shape covaries with sex, 2) orbit shape covaries with sex, and 3) the zygomaticotemporal space covaries with sex. CT scans of primate skulls were analyzed using the medical software programs Analyze Pro and Checkpoint, yielding 3 dimensional coordinates. This study used skulls from 60 gorillas, 60 chimps, and 80 humans, with near equal females and males of each species. Morphometric and statistical analyses from Morphologika, MorphoJ, and Excel were used to determine the statistical significance among the different species. Results indicate that there are significant differences in zygomatic bone shape and the surrounding regions between females and males within all three species, despite substantial ranges in traditional measures of sexual dimorphism among these species.

Possible Perimortem Bite Marks On A Neanderthal Cranium

BRIAN PIERSON

Department of Anthropology, Pierce College

The La Chapelle-aux-Saints 1 specimen is a *Homo neanderthalensis* skeleton discovered in France in a rock shelter burial. The fossil skull exhibits nine circular defects in the frontal bone. These defects are examined in detail, and I propose a possible cause. The methods used in this examination are derived from modern forensic methodologies using caliper measurements of the cranium and comparison with similar finds in Europe.

The circular defects found on the cranium were measured by caliper and are consistent in size, shape, and depth with the P3 and canine teeth (both maxillary and mandibular) of the Pleistocene spotted hyena (*Crocuta crocuta spelaea*) which lived in the area and impacted other megafauna and Neandertal sites. These animals tend to use those teeth while involved in scavenging and bone crushing activities leaving behind circular or ovoid defects. Furthermore, these defects seem to exhibit the signs of perimortem trauma of bending and adhesion which are evident in many of the defects in the frontal bone of the specimen. Perimortem trauma is defined as damage to the bone made at or around the time of death while the bone tissue is still relatively fresh and malleable, the timing depends on the environmental conditions.

Perhaps the most interesting aspect of this is that the scavengers did not disarticulate the body or access the interior soft tissues. This suggests that the body may have been disturbed by scavenging hyenas, they were stopped and then the body was recovered and buried.

Traditional craniometric data for Asia and the Pacific: a resource for biological and forensic anthropology

MICHAEL PIETRUSEWSKY

Anthropology, University of Hawaii at Manoa

W.W. Howell's craniometric online data provide broad world-wide coverage of cranial variation. However, there are significant gaps in its geographic and temporal coverage. One region of the world that is particularly underrepresented is the Asia-Pacific region, an area that encompasses the islands of Oceania (Polynesia, Micronesia, and Melanesia), Australia, Island and Mainland Southeast Asia, and East Asia (China, Taiwan, Japan, Korea and Mongolia). The aim of this study is to make available traditional craniometric data that complement existing online data for a more in-depth examination of craniometric variation for this region. The dataset consists of thirty-four traditional craniometric measurements, which follow the methods of Howells and/or Martin, recorded in 3,525 male and 1,806 female adult modern, near modern, and Late Pleistocene crania from the Pacific and Asia. The crania are from 55 museum and university research collections in New Zealand, Australia, Europe, Japan, China, Vietnam, Thailand, and the United States. Unless otherwise indicated, all measurements were recorded by the author from 1975 to 1997, a time when ethical concerns in bioarchaeology were either nascent or just emerging. Due to institutional policies, repatriation, and reburial, many of the crania represented in this dataset are no longer accessible making this an important resource for forensic and biological anthropology. Results of previous biodistance studies that utilize portions of the dataset have revealed important insights into the population history of the Asian-Pacific region. Descendant native groups have a vested interest in these data and we look forward to working with them.

Ethics and the American Board of Forensic Anthropology

MARIN A. PILLOUD[1] and NICHOLAS V. PASSALACQUA[2]

[1]Anthropology, University of Nevada, Reno, [2]Anthropology and Sociology, Western Carolina

In cases of professional misconduct, the primary method of adjudication and disciplinary action, if necessary, is an ethics investigation through one's home institution and/or professional organizations to which an individual may belong. Home institutions may be limited in adjudicating such cases without clear understandings of the type of misconduct that may be discipline specific and they may be averse to taking punitive actions against faculty without outside ethical charges to guide their actions. As such, professional organizations are best equipped to handle such cases and emerge as disciplinary leaders. Because certification by the American Board of Forensic Anthropology (ABFA) is a valued credential within forensic anthropology, maintaining certification is a priority; thus, complaints to the ABFA are frequently investigated, rather than having individuals simply end their membership to avoid an investigation.

The ABFA's Code of Ethics and Conduct consists of 12 directives guiding conduct in a variety of circumstances, the Code of Ethics is a living document in the Bylaws of the organization that is frequently updated. The ABFA's Ethics Committee screens submitted complaints and acts as the investigative body if a complaint is valid. Upon the conclusion of an investigation, The Ethics Committee presents its findings and recommendations to the ABFA Board of Directors

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

for discussion and a vote for resolution. This presentation will further outline the ABFA's Code of Ethics and Conduct and its experiences with investigations of misconduct and highlight how this model of adjudication could be adopted by other organizations.

Building a Forensic Anthropology Program and Postdoctoral Fellowship at WMed: Towards Filling a Critical Gap in Training and Professional Development for the Discipline

CHRISTINE M. PINK[1], JERED B. CORNELISON[1], JESSICA K. JUAREZ[1] and SAGE PLETKA[2]

[1]Pathology, Western Michigan University Homer Stryker M.D. School of Medicine, [2]Biology, University of Indianapolis

Forensic anthropology as a discipline fails to provide uniform training on standards of practice during graduate education. We introduce the WMU Homer Stryker M.D. School of Medicine (WMed) Forensic Anthropology Postdoctoral Diversity Fellowship. This 2-year opportunity through the Department of Pathology and Office of the Medical Examiner (OME) focuses on training and research. It supports early-career professionals that identify with an underrepresented group in forensic science. The fellowship works toward filling a critical gap in advanced training as well as diversifying the profession.

The Forensic Anthropology Lab at WMed sustains a high caseload, varied in composition (urban, semi-urban, and rural), for 30+ OME and consult counties. The lab also houses the Skeletal Teaching and Research Series (STaRS), a modern documented assemblage. Program requirements are modeled on the Accreditation Council for Graduate Medical Education with a basic set of standards, explicitly defined core competencies, and evaluation criteria that prepare fellows to work unsupervised. This type of fellowship should become the standard rather than the exception for training. The eventual result being dramatic improvement in consistency and quality of forensic anthropology in the U.S.

A primary aim of the program is enhancing diversity, equity, inclusion, and belonging (DEI) in the field. For too long the burden of DEI initiatives and fighting racism has fallen on the marginalized. The onus should be on those with power, platforms, and job security. It is their responsibility to nurture students and early-career professionals. We hope other institutions will develop similar programs, thus pushing forensic anthropology forward.

Infectious Disease Distribution Across an early 20th Century Rural and Urban Divide

PAIGE PLATTNER[1], BLAIR COE SCHWEIGER[1], STACEY K. SOUTH[2], AMANDA MAGPIONG[2], ROBIN G. NELSON[3], RICK WA. SMITH[2,4,5] and AUSTIN W. REYNOLDS[1]

[1]Department of Anthropology, Baylor University, [2]Department of Sociology and Anthropology, George Mason University, [3]School of Human Evolution and Social Change, Arizona State University, [4]Women and Gender Studies, George Mason University, [5]Indigenous Science, Technology, and Society Lab, Faculty of Native Studies, University of Alberta

The practice of farm tenancy has been core to the history and economy of north central Texas over the last 150 years, having the highest concentration of this practice anywhere in the southern US. However, the impact of these exploitative labor practices on health outcomes remains largely unknown. Here we investigate the differential impact of infectious disease on tenant farmers during the early 20th century using historic census and death records. We collected residence, occupation, and cause of death information for over 2000 individuals born between 1890 and 1910 in Dallas, Texas and the surrounding rural counties of Ellis, Hill and Navarro. We hypothesized that the urban samples would have a higher rate of infectious disease due to the nature of turn-of-the century urbanization; and furthermore, that rural men will have a higher rate of infection than women due to the gendered division of labor at the time. Interestingly, we found no statistically significant difference between sex and the rate of infectious disease death, but found that 3.53% more rural people were dying of infectious diseases than their urban counterparts. This work provides an initial look into the social and biological impacts of structural violence across the southern US.

Re-evaluating the behavioral implications of sexual dimorphism in hominins using paternity and group size data in primates

J. MICHAEL PLAVCAN

Anthropology, University of Arkansas

The social behavior of early hominins has long been a topic of interest and debate, and sexual dimorphism in tooth size and body sized provide key evidence through their link to sexual selection. However, inferences of social behavior have been limited by poor correlations between measures of social behavior and sexual dimorphism. Recent work suggests that paternity skew in primates, and thereby sexual selection, is strongly contextualized by group size, with strong correlations between group-size adjusted paternity skew and both size and canine dimorphism. This suggests that a re-examination of the behavioral implications of sexual dimorphism in hominins might provide a novel perspective. Data on paternity skew, group size, and dimorphism in skull size, body mass, and canine tooth size were gathered from the literature and from personally collected data sets for 50 primates and several hominins. Multiple estimates of hominin dimorphism were used for both craniodental and postcranial remains. Estimates of dimorphism in *Australopithecus afarensis* and *Paranthropus* are consistent with very strong sexual selection and reproductive skew, while those for *A. africanus* imply strong, but less intense reproductive skew. The implications of the dimorphism estimates for group size do not provide a single estimate, but rather can contextualize implied paternity skew for different female group sizes. Thus, for example, if *A. afarensis* lived in small groups, males likely approached monopolization of paternity within groups. For larger groups males likely showed strong paternity skew within groups, consistent with male agonistic dominance hierarchies or multi-level society organization.

Herding, playing, eating, and learning: Samburu pastoralist kids daily activities

JACKSON S. PLEMMONS[1], CHARLES E. HILTON[1] and BILINDA S. STRAIGHT[2]

[1]Anthropology, University of North Carolina-Chapel Hill, [2]Gender & Women's Studies, Western Michigan University

In contemporary northern Kenyan pastoralist societies, kids make substantial economic contributions to their family's household and settlements. Qualitatively, pastoralists kids are known to perform a variety of household economic activities such as fetching firewood, getting water, caring for younger siblings, helping to prepare meals, and herding small livestock (i.e., goats and sheep). Quantitatively, little is known regarding duration, physical exertion levels, and energetic requirements of such daily tasks performed by Samburu pastoralist kids and the division of labor between genders. In order to establish a better quantitative baseline of the overall physical, energetic, and caloric demands on boys and girls, our study collected and analyzed physical activities of Samburu kids in conjunction with daily food consumption in a community where traditional diet has been replaced with low quality processed food such as maize meal. Samburu kids daily activities and behaviors were recorded using a focal-follow methodology over 24- and 48-hour periods, sampling 9 boys and 7 girls. Physical activity levels (PALs) were examined by using non-invasive accelerometers and time allocation observations. Food consumption was monitored through direct observations and measurements by volume for each food type with additional 24-hour food recalls. An association between high heart rates and activities that involve playing and herding was identified. While playing and herding were found to be the most physically demanding activities, the frequency of these activities varied

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

across the individuals observed. The implications of these observations are discussed within the context of energy balance during childhood in an energy-poor environment.

This research was funded by a UNC-Chapel Hill Summer Undergraduate Research Fellowship and National Science Foundation Award #1728743, "A Bio-Cultural Investigation of Intergenerational Epigenetic Mechanisms" (Bilinda Straight, PI).

Rendering Theory to Practice: Actionable Approaches to Ethics in Digital Human Osteology

AMBER M. PLEMONS[1] and MICAYLA C. SPIROS[2]

[1]Anthropology, University of Kentucky, [2]Anthropology, Michigan State University

While many ethical concerns are raised for displaying human remains in digital media[1-5], no discipline-wide action has addressed these concerns. Digital tools are critical for collecting, storing, and sharing information involving human skeletal remains, as well as accessible education and research. However, human remains must be obtained and presented ethically in digital space[6-8].

Text analysis of ethics statements for five organizations (AABA, AAFS, ABFA, BABAO, and SWGANTH) demonstrate how associations are discussing digital osteology, as well as BABAO's statement specifically for digital imaging. Text mining was carried out in R to identify term frequencies related to digital osteology. Four organizations do not discuss digital ethics, while BABAO directs readers to their statement on digital imaging. These data illuminate a gap in standards for digital ethics and osteology, hindering anthropological works from progressing alongside technology.

We propose pathways forward to making digital pedagogical tools, training, and collections openly accessible while ensuring these media are ethical. These pathways include ethics curriculum, ethical statements on digital tools, and professional certification. To achieve this, we are establishing a cross-cultural, disciplinary working group to develop a cohesive digital ethics statement, standard protocols, and an ethics course. The group will then develop an ethics board for reviewing digital tools for either certification as open access or password protected tools.

Attendees can express interest in the working group and participate in interactive polls via QR code. This presentation is a space for discussion on excelling technological advancement while accommodating the sensitivity of displaying the deceased.

Ontogenetic biomechanics of tufted (*Sapajus*) and untufted (*Cebus*) capuchin mandibles

TAYLOR A. POLVADORE[1], CAITLIN B. YOAKUM[2], PARKER M. TAYLOR[1], MARIANA DUTRA FOGAÇA[3], MEGAN A. HOLMES[4], MYRA F. LAIRD[5,6], JANINE CHALK-WILAYTO[7] and CLAIRE E. TERHUNE[1]

[1]Anthropology, University of Arkansas, [2]Anatomy, Arkansas College of Osteopathic Medicine, [3]Neotropical Primates Research Group, NeoPReGo, [4]Family Medicine and Community Health, Duke University School of Medicine, [5]Integrative Anatomical Sciences, University of Southern California, [6]Basic and Translational Sciences, University of Pennsylvania, [7]Biomedical Sciences, Mercer University School of Medicine

Cortical bone geometry is commonly used to investigate biomechanical properties of primate mandibles. However, the ontogeny of these properties is less understood. Here we investigate changes in cortical bone contours throughout capuchin ontogeny. *Sapajus* spp. are known to consume relatively hard/tough/large foods, while *Cebus* spp. exploit smaller, less mechanically challenging foods. Previous research indicates these dietary differences are present early in development and adult *Sapajus* mandibles can resist higher bending, shear, and torsional loads. We hypothesize that 1) mandibular robusticity increases through ontogeny in both genera, and 2) *Sapajus* exhibit greater resistance to shear, bending, and torsional loading compared to *Cebus* across ontogeny. Using microCT scans of 20 *Cebus* and 33 *Sapajus* from early infancy to adulthood, cross-sectional properties of the mandible were calculated at the symphysis, P_3, and M_1. If the tooth had not erupted, its position within the crypt was used.

In both taxa, resistance to shear, bending, and torsional loading increases across ontogeny. Significant increases during ontogeny varied by genus and tooth, suggesting taxon-specific developmental patterns. Between genera, we observed significant differences in these biomechanical properties post-M_1 eruption. For example, older juvenile and adult *Sapajus* can withstand larger wishboning loads compared to same-aged *Cebus* (p<0.017). Our results suggest that, relative to *Cebus*, *Sapajus* has greater resistance to bending and torsion due to their exploitation of more mechanically challenging foods, but this only occurs as they reach physical maturity. Eruption of M_1 and M_3 especially result in significant changes to biomechanical properties of the mandible in these taxa.

This research was supported by the National Science Foundation's Biological Anthropology directorate (BCS-1945771 [JCW], BCS-1944915 [MAH], BCS-1945283 [MFL], BCS-1945767 [CET], BCS-1944642 [CBY]).

Community-level patterns of interpersonal violence: A study of fragmented and commingled crania from Early Bronze Age Bab adh-Dhra', Jordan

KERI PORTER, JULIA JOHNSTON and SUSAN G. SHERIDAN

Department of Anthropology, University of Notre Dame

Despite methodological and analytical advances, fragmentary/commingled collections of human skeletal are under-investigated in bioarchaeology. This research addresses the problem by utilizing fragmented and commingled cranial remains to understand interpersonal violence at the Early Bronze Age (EBA) site of Bab adh-Dhra'. During the EBII-III (3,100-2,300 BCE), charnel houses were the preferred method of burial with the A22 charnel house being the largest excavated. Over time, the skeletal remains from A22 have been burnt, fragmented, and comingled, making typical research methods focused on complete individuals difficult to impossible. Previous studies on violence using the A22 remains adapted to these limitations by focusing on crania that could be reconstructed to >75% preservation. This research used a zonal approach to analyze preservation of individual frontals, parietals, and occipitals from A22 to incorporate previously unanalyzed skeletal remains and increase the number of elements that could be included in statistical analysis. Prevalence of cranial depression fractures (CDFs) was calculated for each element and zonal location. Using only elements with >50% preservation, CDFs were most prevalent on the frontal. When zonal locations of elements with >50% preservation were used, the midline frontal squama had the highest prevalence with the right frontal squama and posterior left parietal showing similar prevalence of CDFs. Although these results cannot inform on individual experiences of violence at Bab adh-Dhra', they represent the presence and pattern of interpersonal violence within the community. This approach may be applied to other fragmentary and commingled collections to improve overall understandings of violence in the past.

Genetic analyses confirm the presence of *Cebuella niveiventris* in Bolivia

LEILA M. PORTER[1], STELLA DE LA TORRE[2], PEDRO PÉREZ-PEÑA[3] and LILIANA CORTÉS-ORTIZ[4]

[1]Anthropology, Northern Illinois University, [2]School of Biological and Environmental Sciences, Universidad San Francisco de Quito, [3]Instituto de Investigaciones de la Amazonía Peruana, [4]Ecology and Evolutionary Biology, University of Michigan, Ann Arbor

Recent genetic analyses of populations of pygmy marmosets from Brazil, Ecuador and Peru have indicated that two genetically distinct species are present, *Cebuella pygmaea* in the northwest and *C. niveiventris* in the south. However, no previous

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

research has examined genetic markers of Bolivian marmosets to determine their appropriate species designation. In this research project we extracted DNA from fecal samples noninvasively collected from one group of pygmy marmosets near the Estación Biológica Tahuamanu in northwestern Bolivia. We amplified fragments of two mitochondrial markers, the cytochrome b (cyt *b*) gene and the control region from 10 fecal samples. We analyzed the phylogenetic relationships of the Bolivian marmoset samples using both maximum likelihood and Bayesian inference approaches including previously published data. Our results indicate that the pygmy marmosets in northwestern Bolivia should be classified as *Cebuella niveiventris*, allowing us to confirm the southern distribution range of this taxon. These results will help establish appropriate conservation management plans for this species in Bolivia and in the region.

We thank the Chicago Zoological Society's Chicago Board of Trade Endangered Species Fund for supporting this research.

Ancient DNA Study of an Afro-Diasporic Population in La Quebrada, Peru

LAURA POTT[1], JAIME ZOLIK[1], JOSÉ LUIS SANTA CRUZ ALCALÁ[2], CLAIRE MAASS[3] and MARIA NIEVES COLÓN[1]

[1]Anthropology, University of Minnesota, [2]Archaeology, Universidad Nacional de San Marcos, [3]Defense POW/MIA Accounting Agency

Between the 15th and 19th centuries, European colonizers forcibly transported more than 12 million Africans to the Americas through the Transatlantic Slave Trade. Around 500 were forcibly brought to Hacienda La Quebrada in San Luis district, Peru. In 2016, excavations at this old estate uncovered the burials of at least 245 individuals in a cemetery that church archives and oral histories from residents identify as a burial ground for enslaved Africans. We are collaborating with archeologists and community members in a community-engaged research project designed to learn more about these individuals. To investigate the preservation of these skeletal remains and their suitability for ancient DNA analysis, we identified a subset of individuals (n=30) with varying levels of macroscopic skeletal preservation and successfully sampled calculus, cementum, and dentin from them. We detected quantifiable DNA in 21 out of 30 dentin samples (70%), as measured by fluorometric quantification. In this small sample, we found that variables like macroscopic preservation or age-at-death do not predict whether a sample yielded quantifiable DNA. We have prepared single-stranded DNA libraries for shotgun sequencing, which will provide information about the proportions of endogenous DNA preserved in these samples and identify which libraries are the best candidates for target enrichment and deeper sequencing. Future work will include identifying the biogeographical origins and kinship relationships between these individuals, which will contribute to understanding the origins and lives of African and Afro-descendant communities during the colonial period in Peru.

This work was funded by Rust Family Foundation for Archaeological Research, American Association of Biological Anthropologists Cobb Professional Development Program, and University of Minnesota Department of Anthropology Wilford Funds Award.

Integrating Genetic and Archaeological Patterns for the Peopling of Northeast Asia, Beringia, and the Americas

BEN A. POTTER

Anthropology, University of Alaska Fairbanks

In recent years, archaeogenetic analyses have generated new complexities in the problem of the peopling of the Americas, yet they have yet to be well integrated with archaeological datasets. Here, I develop a provisional model for the initial peopling of Siberia, Russian Far East, Beringia, and the America synthesizing both records. The model includes paleoecological constraints and integrates recent work in Beringia to evaluate lifeways of early Beringians and identify the most plausible routes used to enter the Americas south of the ice sheets. In brief, multiple lines of evidence indicate isolation of First Americans (FAM) in Northeast Asia, south of Beringia, between ~20-16 kya. As climate ameliorated during deglaciation, Ancient Beringians and other FAM populations expanded north into Beringia using high residential mobility strategies. Different migration routes, separated by Cordilleran Ice Sheet, facilitated the divergence of (1) SNA, moving through the emerging ice free corridor ~15.3-14.3 kya and (2) NNA, moving through the northwest coast route. While NNA was restricted to the coast north of Puget Sound, SNA expanded in a radial pattern throughout North and South America between 14.9-13.9 kya. Beringian archaeological data indicate year-round occupations in deep interior rivers and associated bottomlands, focused on Pleistocene megafauna, but with considerable diet breadth, including upland hunting in periglacial areas. This adaptation facilitated movement along glacial edges south into continental North America. Ancient Beringians persisted until ~6 kya when they were absorbed or replaced by NNA groups from the south.

Contingency, adaptation, and the evolution of heel strike plantigrady

THOMAS C. PRANG

Department of Anthropology, Washington University in St. Louis

Keith's multi-stage model is an ultimate explanation centered on the evolutionary history of human anatomy, which includes contingency and adaptation at its core. Evolutionary contingency is the concept that chance historical events can influence evolutionary outcomes. In contrast, adaptation through natural selection refers to a deterministic aspect of evolutionary patterns and processes, which can produce convergent phenotypes. Humans and African apes share a heel strike plantigrade foot posture, whereas most other primates utilize heel-elevated foot postures, and the morphology of the talus and calcaneus may reflect this variation. This study tests the hypothesis that heel strike plantigrady is a terrestrial adaptation contingent upon an evolutionary history characterized by orthograde climbing and suspension. Specifically, I incorporate data collected on atelines, who converge with hominoids on features related to climbing and suspension. The data consist of 25 geometric mean-standardized linear distances collected on the talus and calcaneus of 49 anthropoid taxa (N = 400). Principal components analysis was used as an ordination and dimensionality reduction technique for evolutionary modeling analyses. The best-fitting evolutionary model supports the hypothesis by placing humans and African apes in a selection regime derived from an ancestral hominoid regime represented by orangutans and hylobatids. Although ateline rearfoot morphology converges with that of hominoids, they are placed in a distinct selective regime associated with evolution from a generalized platyrrhine-like ancestral morphology. Therefore, both contingency and adaptation have shaped the foot morphology of monkeys, apes, and humans, which has profound implications for ultimate explanations surrounding the origin of bipedalism.

This research was supported by a Wenner-Gren Dissertation Fieldwork Grant

Evolutionary modeling of the hominid face

KELSEY D. PUGH[1,2], SANTIAGO A. CATALANO[3,4], MIRIAM PÉREZ DE LOS RÍOS[5], JOSEP FORTUNY[6], BRIAN M. SHEARER[2,7,8], ALESSANDRA VECINO GAZABÓN[1,2,9], ASHLEY S. HAMMOND[1,2], SALVADOR MOYÀ-SOLÀ[10,11,6], DAVID M. ALBA[6] and SERGIO ALMÉCIJA[1,2,6]

[1]Anthropology, American Museum of Natural History, [2]NYCEP, New York Consortium in Evolutionary Primatology, [3]Unidad Ejecutora Lillo, Consejo Nacional de Investigaciones Científicas y Técnicas – Fundación Miguel Lillo, [4]Facultad de Ciencias Naturales e Instituto Miguel Lillo, Universidad Nacional de Tucumán, [5]Unidad de Antropología física, Departamento de Biodiversidad, Ecología y Evolución, Facultad de Ciencias Biológicas, Universidad Complutense de Madrid, [6]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, [7]Department of Cell Biology, NYU Grossman School of Medicine, [8]Department of Foundations of Medicine, NYU Long Island School of Medicine, [9]Richard Gilder Graduate School, American Museum of Natural History, [10]ICREA, Institució Catalana de Recerca i Estudis Avançats, [11]Unitat d'Antropologia Biològica, Departament de Biologia

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Animal, Biologia Vegetal i Ecologia, Universitat Autònoma de Barcelona

Living hominids (great apes and humans) and hylobatids ("lesser" apes) exhibit differences in face shape and size, which, taken together with the meager hylobatid fossil record and phylogenetic uncertainty of putative fossil hominids, makes reconstructing hominoid evolutionary history challenging. Using a sample of extant anthropoids and key fossils (e.g., *Aegyptopithecus, Victoriapithecus, Ekembo, Afropithecus, Pierolapithecus, Sivapithecus*), we produced a stepwise series of morphometric analyses to capture and model the evolution of key aspects of anthropoid face form. First, we enlisted a PCA of Procrustes coordinates (67 landmarks) and a phylomorphospace approach to examine the evolutionary relationships of 3D face shape and size. Second, we reconstructed the ancestral states of selected facial features defined by linear and angular measurements. We find that hominids are well separated from other anthropoids in shape and size space and that all inferred ancestral nodes within the hominoid clade are reconstructed closer to modern hominids than to other clades. Hylobatids are highly divergent in the direction of platyrrhines, pliopithecoids, and *Colobus*, and our evolutionary modeling infers that each of these taxa evolved from a larger faced ancestor. Modern and fossil hominids can also be distinguished from other anthropoids by several linear features, including low midfacial prognathism, a somewhat elongated clivus, and a taller face. Our results support the hypothesis that the crown hominoid and hominid last common ancestors were more similar to modern hominids than to hylobatids in face shape and size, and that some features of the hylobatid face are likely associated with secondary size reduction.

Grant support acknowledgements: This work is part of R+D+I projects PID2020-116908GB-I00, PID2020-117289GB-I00, PID2020-117118GB-I00, funded by MCIEI/10.13039/501100011033/, and it has been further supported by the Generalitat de Catalunya/CERCA Programme.

Canine Microwear in Relation to Diet in Four Sympatric Sumatran Primates

PUTU PUJIANTARI[1], LUCAS DELEZENE[1], J. MICHAEL PLAVCAN[1], MARK TEAFORD[2] and PETER UNGAR[1]

[1]Department of Anthropology, University of Arkansas, Fayetteville, [2]Department of Basic Science, Touro University, California

As most microwear studies are done on molars and incisors, canines remain understudied, in part because of their pronounced sexual dimorphism in many primates. Canine microwear of sympatric *Macaca fascicularis, Hylobates lar, Hylobates agilis, Presbytis thomasi* and *Pongo abelii* was studied to see if it reflects documented differences in diet and anterior tooth use. Maxillary canine replicas were scanned at 100x using a Sensofar PLu Neox white-light confocal optical profiler. The distolingual-incisal facet of the tooth was analyzed to reduce interference from the honing mechanism. Both microwear feature and texture analyses were employed to improve the characterization of wear patterns on canine surfaces that lack flat facets. Microware 4.02 software was used to identify tallies, average length, breadth, and orientation. Mountains Map software was used to measure feature complexity (*Asfc*), scale of maximum complexity (*Smfc*), anisotropy (*epLsar*) and heterogeneity (*HAsfc9* and *HAsfc81*). MANOVA tests had significant results for both analyses; however, ANOVAs reveal that *HAsfc* and *Smfc* provide the best separation among taxa by texture analysis. Tukey's HSD and Fisher's LSD were used to determine which species differed significantly for a given attribute. In feature analysis, both hylobatid species significantly differ from the other three species. In texture analysis, the pair of *H. lar* and *Po. abelii* significantly differ for *Smfc.* Discriminant function analysis shows that *epLsar* is the most important variable in microwear texture analysis to distinguish among species.

This research is funded by the LSD Leakey Foundation.

Climate exposures in utero associate to epigenetic age acceleration in a global climate change hot spot

XI QIAO[1], DUY NGO[2], CHARLES E. HILTON[3], C. OWUOR OLUNGAH[4], AMY NAUGLE[5], CLAUDIA LALANCETTE[6], BELINDA L. NEEDHAM[7] and BILINDA STRAIGHT[8]

[1]Statistics, Western Michigan University, [2]Statistics, Western Michigan University, [3]Anthropology, University of North Carolina - Chapel Hill, [4]Anthropology, Gender, African Studies, University of Nairobi, [5]Psychology, Western Michigan University, [6]Epigenomics Core, University of Michigan, [7]Public Health, University of Michigan, [8]GWS, Western Michigan University

Climate change will have substantial consequences for human health, with a disproportionate impact in global hot spots; in communities engaging in climate-sensitive livelihoods; and in the elderly, pregnant women, and young children. Not enough is known about the environmental factors, biological mechanisms, and potentially modifiable behaviors that may contribute to climate vulnerability or resilience. Exposure to stress in utero and early childhood has implications for lifelong health and longevity through developmental conditioning. Calculations of epigenetic age based on DNA methylation have been found to be accurate predictors of chronic disease and longevity. However, studies in infants and children are just beginning, and human epigenetic age based on in utero climate exposures has not been investigated. We assessed epigenetic age acceleration using PedBE, Horvath, Hannum, skinHorvath clocks in 213 Samburu children (pastoralists, northern Kenya). Multivariate linear mixed models were used to examine the effect of in utero exposure to drought, regional climate contrasts, and ambient temperature on age acceleration. Considering pregnancy-timed stressors and other covariates for adjustment, the optimal models were determined by DICs. Estimation and 95% credible interval of effects were obtained using MCMC approach. We found a positive association with epigenetic age acceleration based on in utero exposure to drought, negative associations based on ambient temperature, and associations based on drought-relevant maternal stress covariates. We conclude that some temperature stressors may confer an adaptive advantage for future heat shocks, but the multiple deleterious stressors of drought require targeted behavioral adaptations to achieve climate resilience.

This research was funded by National Science Foundation Award #1728743, "A Bio-Cultural Investigation of Intergenerational Epigenetic Mechanisms" (Bilinda Straight, PI).

Detecting dental cortisol through mass spectrometry: Recent methodological advances

LESLIE QUADE[1], LUKÁŠ KUČERA[2], SOŇA GROSSOVÁ[2] and MIROSLAV KRÁLÍK[1]

[1]Anthropology, Masaryk University, [2]Analytical Chemistry, Palacký University Olomouc

Cortisol is a glucocorticoid hormone secreted from the adrenal glands in a diurnal rhythm and in response to stressors. As such, studies of modern human and non-human populations regularly assess cortisol concentrations in bodily fluids and hair as a measure of stress experience. Recent research has detected cortisol from within human permanent and deciduous tooth structures from both modern and archaeological contexts. These findings have important implications for studies of chronic stress when only skeletal materials are available.

To date, dental cortisol concentrations have been assessed through salivary Enzyme-Linked Immunosorbent Assays (ELISA). However, mass spectrometry combined with separation techniques offers several advantages including increased precision in analyte detection. In this proof-of-concept study, dental enamel samples from seven teeth were assessed for cortisol concentrations via liquid chromatography combined with a triple quadrupole mass spectrometer, allowing multiple-reaction monitoring. Sampled teeth included two permanent teeth from archaeological contexts, and three permanent and two deciduous teeth donated by living individuals.

All but one enamel sample generated detectable cortisol concentrations with values ranging from 0.2-1.5 ug/dL. Although mass spectrometry is commonly utilized in assessments of

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

cortisol in other tissues, this represents the first application of these methods to modern or archaeological dental structures. These results continue the advancement of the dental cortisol methodology, providing new opportunities for analysis and comparisons of dental cortisol data. Dental cortisol concentrations have the potential to provide new opportunities for assessing stress in the past but also for connecting bioarchaeology with assessments of stress in living populations.

Postdoc2MUNI CZ.02.2.69/0.0/0.0/18_053/0016952; Wenner-Gren Post PhD Grant 1248655869

Human-specific variation in conserved embryonic enhancers may underlie differences in human skeletal muscle important for bipedal locomotion

SAMANTHA R. QUEENO[1], ALEXANDER OKAMOTO[2], DANIEL RICHARD[2], MATTHEW C. O'NEILL[3], TERENCE D. CAPELLINI[2,4] and KIRSTIN N. STERNER[1]

[1]Anthropology, University of Oregon, [2]Human Evolutionary Biology, Harvard University, [3]Anatomy, Midwestern University, [4]Broad Institute, MIT and Harvard University

Research suggests that selection for more efficient bipedal locomotion increased the expression of fatigue-resistant MyHC-I (i.e., slow myofibers) in hominin lower limb muscles over the past 7-8 million years. This trait distinguishes humans from other mammals, including African apes. To understand the evolution of species-specific differences in muscle MyHC-I content, we must first identify human-specific variation within the spatiotemporal regulators of MyHC gene expression (e.g., *cis*-regulatory elements, CREs), which often generate phenotypic novelty and lead to evolutionary divergence between species. Here, we begin by characterizing the regulatory landscape of mouse muscles with divergent MyHC-I content at two time points to define genomic regions underlying MyHC-I expression. We dissected slow- (soleus and vastus intermedius) and fast-biased (gastrocnemius and vastus lateralis) muscles from three adult and three pooled litters of *FVB/NJ* mice and isolated regions of open chromatin using ATAC-seq. We used peak calling algorithms (MACS2 p-value<0.05) to identify thousands of potential CREs that are shared across biological replicates. We identified a subset of CREs unique to each muscle, myofiber bias, anatomical region, and time point, as well as those shared across these categories, and retained only those active in human muscle. We annotated these sequences with GREAT and found that most are located distal to transcription start sites (e.g., potential enhancers). Interestingly, embryonic CREs were enriched with human accelerated regions (HARs), suggesting that these may be loci of potential importance to the evolution of MyHC-I expression in human muscle.

This research was funded by a National Science Foundation Doctoral Dissertation Research Improvement Grant (proposal 1945809) and a Leakey Foundation research grant.

Investigating the intersection between bone signaling, exercise, and biomechanics post injury

KARYNE N. RABEY[1,2], SIMON WU[3], SHIRLEY DUIA[3], EMILY MOORE[4], MATTHEW WT. CURRAN[1], K MING CHAN[5] and CHRISTINE A. WEBBER[1,3]

[1]Surgery, University of Alberta, [2]Anthropology, University of Alberta, [3]Neuroscience and Mental Health Institute, University of Alberta, [4]Biological Sciences, University of Alberta, [5]Rehabilitation Medicine, University of Alberta

Damage to peripheral nerves alter quality of life through substandard nerve regeneration, irreparable muscle atrophy, and irreversible bone demineralization. Current orthoses limit movement, which further damages balance, gait, and bone strength which leads to higher risks of fractures.

Combining ground reaction forces (GRFs), motion capture analyses, imaging, and hormonal serum levels in animal models and human patients, this work seeks to better understand how bone-activating training can result in better recovery. First, mice are divided into control (CON) and voluntary wheel-running (EX) groups and half get their sciatic nerve cut and repaired (n = 40). Each are micro-CT scanned before, midway, and at the end of the experiment. Kinetic and kinematic data are collected weekly until range of motion is regained. Concurrently, post nerve repair surgery patients are split into CON and EX-groups (n = 20). EX-group weight bear within the first week and start daily treadmill walking. DEXA scans and biomechanics data are collected for 6 months. Data are analyzed using a three-way split plot analysis of variance with time, sex, and treatment allocation as independent factors (p<0.05).

In mice, EX-group voluntarily ran 1 km/hour despite injury which resulted in improved tibial bone mineral density (EX = 0.27 g/cm^3; CON = 0.21 g/cm^3) and gait recovery within 4 weeks. So far, EX patients similarly attain significantly better ankle strength, range of motion, and bone health profiles compared to CON-group. Future steps involve introducing a wearable bionic neural modulator with physiological feedback that is personalized for faster functional recovery.

Canadian Institutes of Health Research (CIHR) Project Grant; University Hospital Foundation (UHF) Medical Research; Edmonton Civic Employees (ECE) Research Grant.

Mammalian trabecular bone patterns in relation to environmental variables

ANNA J. RAGNI

Institute of Human Origins, Arizona State University

Trabecular bone architecture has historically been associated with locomotor behavior, but we still do not know to what extent other factors, such as environmental variables, may influence trabecular structure across mammals. Here, trabecular bone architecture is measured in the radius and tibia of mammalian taxa through development and compared to environmental data for each taxon's home range. I hypothesize that trabecular measures are related to mean annual temperature, mean annual precipitation, maximum latitude, and minimum latitude. Sixty individuals across thirty species of mammals were microCT scanned at high resolution. Spherical volumes of interest were selected in homologous areas of the distal radius and distal tibia and analyzed in Volume Graphics StudioMax. Juvenile trabecular architecture, adult trabecular architecture, and ontogenetic changes in trabecular architecture were compared to environmental data using phylogenetic generalized least squares analyses. Environmental data show few significant relationships to trabecular architecture through ontogeny and in juveniles, with no significant relationships in adults. Juvenile trabecular spacing and mean annual precipitation are significantly correlated in both the radius and tibia, even after controlling for body size. Ontogenetic change in trabecular number and maximum latitude are significantly correlated in both the radius and tibia, even after controlling for body size. These correlations do not necessarily imply causation but deserve further research with more precise data points. These results show that environmental differences generally do not need to be considered when interpreting trabecular architecture across mammals, particularly when using an exclusively adult sample.

This work was funded by a Peter Buck Postdoctoral Fellowship

Craniometric variation among the Meroitic elite interred at Saï Island, Sudan: Implications for the understanding of mobility

BRENNA J. RAISOR[1], STEPHANIE M. FUEHR[1], TOSHA L. DUPRAS[2], YANN ARDAGNA[3] and VINCENT FRANCIGNY[4]

[1]Department of Anthropology, University of Central Florida, Orlando, FL, USA, [2]College of Arts and Sciences, Texas Tech University, Lubbock, TX, USA, [3]CNRS-EFS-UMR 7268 ADES, Anthropologie Bioculturelle, Droit, Ethique et Santé, Aix-Marseille Université, Marseille, France, [4]CNRS, UMR 8167, Orient & Méditerranée, Sorbonne Université, Paris, France

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

This project explores craniometric variation among adult individuals interred in two Meroitic-period (300 BCE – 350 CE) cemeteries at Saï Island, Sudan: 8-B-5.A (religious elite) and 8-B-52.B (wealthy elite). Due to the lack of historic information detailing mobility patterns of Meroitic individuals in Nubia, it is difficult to know if individuals interred at Saï Island were local or non-local. This study investigates whether individuals from these contemporaneous cemeteries exhibit differences in cranial morphology to shed light on patterns of Meroitic Period mobility. Twenty-four craniofacial measurements from 76 adult individuals were included—65 from 8-B-52.B and 11 from 8-B-5.A. Missing data were imputed using the K-nearest-neighbor imputation. To account for sexual dimorphism, all values were z-scored by sex using the geometric mean. Principal component and k-means cluster analyses were used to elucidate patterns of cranial shape variation among all individuals in the sample. These analyses identified three clear clusters, with all individuals from 8-B-5.A assigned to the same cluster. Individuals from 8-B-5.A exhibit most of their variation along the first principal component, while individuals from 8-B-52.B—many overlapping with those from 8-B-5.A—spanned the full range of variation with little clustering. These findings imply that, based on homogenous cranial morphology, the religious elite interred at 8-B-5.A were likely less mobile or originated from the same genetic population, while the wealthy elite at 8-B-52.B may have included non-locals or individuals originating from different genetic populations—results that may suggest differential patterns of mobility between the elite social strata at Saï Island, Sudan.

The Accuracy and Bias of Transition Analysis Age Estimation Priors in Historical and Modern Populations

SHEANA S. RAMCHARAN, ALLYSON M. SIMON and LUIS CABO

Applied Forensic Sciences, Mercyhurst University

Age-at-death estimates are a crucial component of the biological profile, essential for victim identification in forensic anthropology, and for demographic, taxonomic and evolutionary interpretations in biological anthropology. In this study, we examined the differences in accuracy of the alternative statistical priors (archaeological and forensic) used in *ADBOU*, an age estimation software based on Transition Analysis (TA). TA is a multifactorial method that relies on Bayesian statistics to estimate confidence intervals of age that are less dependent of sample age distribution than the age ranges of traditional methods. The study sample consisted of 75 individuals from the Hamann-Todd Osteological Collection (HTOC), as a historical sample reference, and 18 individuals from the Mercyhurst University Donated and Case Collection (MUC), as a modern forensic sample. The differences in age estimation error between the archaeological and forensic priors was found non-significant for both the HTOC (t=0.238, p=0.406) and the MUC (t=0.138, p=0.445). However, we found significant differences in the direction of age estimation bias between the archaeological and forensic priors for both the HTOC (t=1.919, p=0.028) and the MUC (t=2.625, p=0.006). The results indicate that the forensic prior is more biased toward underestimating age than the archaeological prior, both in historical and modern forensic samples. Future studies using a larger modern sample would be useful to confirm this observation.

Spatial patterns of relatedness and dispersal within a fragmented landscape in two species of mouse lemur

MALCOLM S. RAMSAY[1], BERTRAND ANDRIATSITOHAINA[2,3], FREDERIK KIENE[4], ROMULE RAKOTONDRAVONY[2], SHAWN M. LEHMAN[1] and UTE RADESPIEL[4]

[1]Department of Anthropology, University of Toronto, [2]Faculté des Sciences, de Technologies et de l'Environnement, Université de Mahajanga, [3]Planet Madagascar, Madagascar, [4]Institute for Zoology, Stiftung Tierärztliche Hochschule Hannover

Habitat loss and fragmentation are threatening animal populations worldwide. Primates living in fragmented landscapes potentially have reduced opportunity for dispersal and gene flow between isolated patches of habitat, which can lead to localized extinction. However, these processes do not affect all organisms equally and thus it is important to study the species-specific effects of habitat loss and fragmentation. In this study we examined the spatial patterns of relatedness and dispersal in two species of sympatric mouse lemurs (*Microcebus murinus* and *M. ravelobensis*) in Ambanjabe, a fragmented dry forest landscape in northwestern Madagascar. We generated genomic data for 77 *M. murinus* and 35 *M. ravelobensis* individuals using RADseq markers, calculated dyadic relatedness values and inferred dispersal within the landscape. We identified 46 and 18 related dyads in *M. murinus* and *M. ravelobensis,* respectively. When comparing the two species, related *M. ravelobensis* dyads were found significantly closer together, all within 200 m of their relative. Conversely, related *M. murinus* dyads, in particular those including males, were found farther apart, at distances of up to and above 1500 m, suggesting a greater dispersal capacity, even across the matrix. When comparing all related dyads using Mantel tests, we found negative correlations between relatedness and geographic distance in both species. Overall, these results suggest that *M. murinus* and *M. ravelobensis* are responding differently to habitat fragmentation, and that the higher dispersal ability of *M. murinus* may be facilitating population connectivity and their persistence in fragmented landscapes.

Funding was provided by the European BiodivERsA initiative (no. 2015-138), the German Federal Ministry of Education and Research (no. 01LC1617A), and NSERC (Canada).

A Web Application for Biological Identification from Radiographic Proximal Femur in A Thai Population

PATARA RATTANACHET[1], WANNAKAMON PANYARAK[2], KITTICHAI WANTANAJITTIKUL[3], PHASIT CHAROENKWAN[4], WATTANAPONG SUTTAPAK[5] and PASUK MAHAKKANUKRAUH[1,6]

[1]Anatomy, Chiang Mai University, [2]Oral Biology and Diagnostic Sciences, Chiang Mai University, [3]Radiological Technology, Chiang Mai University, [4]College of Arts Media and Technology, Chiang Mai University, [5]School of Information and Communication Technology, University of Phayao, [6]Osteology Research and Training Center, Chiang Mai University

Radiographic proximal femur aided by machine learning (ML) can provide a viable alternative to anthropological analysis for biological identification. The objective of the present study was to evaluate performances of ML algorithms for sex, age, and stature estimation from radiographic femurs, which will then be implemented on an openly accessible web application.

Radiographic images of 354 left proximal femora were obtained and stored in DICOM format, of which sex (193 males and 161 females), stature (range, 140-190 cm), and age (range, 19-94 years) were documented. We measured dimensions and quantified bone density using the image processing software. The linear measurements indicated sex and stature whereas trabecular density represented age-at-death. We recorded all parameters in Excel format, and then trained and validated the ML algorithms with the said data.

Five-fold cross-validation was used to validate the performance of our algorithms. K-nearest neighbor model achieved the highest accuracy of 92.4% in predicting sex. Age estimation models were formulated for each sex; The top-performing algorithms were linear regression (LR) with root mean square error (RMSE) of 12.81 for males and gaussian process regression with RMSE of 12.83 for females. For stature prediction, LR slightly outperformed other algorithms with RMSE of 5.91 for both sexes.

The web-based application was created with Python-based tools to automatically measure femoral dimensions and calculate trabecular bone density from radiographic DICOM files.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

These parameters were then computed based on the ML-based models to predict an individual's biological information, providing a user-friendly approach for global audience.

This research is supported by the Faculty of Medicine, Chiang Mai University (grant no. MC004-65).

Humans as reservoirs: Historical microbiomes uncover hidden zoonotic pathways

KRISTEN M. RAYFIELD[1,2,3], KARISSA S. HUGHES[1,2], SABRINA B. SHOLTS[3] and COURTNEY A. HOFMAN[1,2,3]

[1]Anthropology, University of Oklahoma, [2]Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, [3]Anthropology, National Museum of Natural History, Smithsonian Institution

A rise in emerging and re-emerging infectious diseases requires a deeper investigation into human-animal relationships and their associated interactions with their environments. Zoonotic disease transmission events are most frequently recognized within the terrestrial environment in a single direction of transmission from nonhuman animals to people. However, these human-mediated epidemiological events include marine ecologies. Historical alterations to the marine biome linked to disruptive human activities (e.g., conversion to upland habitat, pollutant runoff, and exploitation of marine species) have shaped modern marine mammal populations such as California sea lions (CSL) (*Zalophus californianus*). Using dental calculus (n=60) subsampled from CSL held at the Santa Barbara Natural History Museum and the National Marine Mammals Laboratory at the Smithsonian Institution collections we reconstruct the oral microbiomes of CSL and link microbial diversity within the oral microbiome to anthropogenic alterations to CSL. Metagenomic analysis consistently identified *Desulfomicrobium, Porphyromonas, Synergistetes,* and *Gemella asaccharolytica* which are consistent within human dental calculus. We also recovered low abundance of *Klebsiella pneumonaie*, which can be enriched for further analyses and address if any human-mediated alteration to the microbiome allowed for easier zooanthroponoses transmission of *K. pneumoniae* into the CSL population. Finally, we regularly recovered CSL host DNA and highlight the reasons we should explore animal microbiomes for human-animal interaction. Our project offers a novel approach in assessing the scale of human influence on shifting historical ecologies through the analysis of dental calculus from historic collections. Incorporating such analyses can open the door in developing datasets to identify unrecognized zoonotic pathways.

The research was supported by National Science Foundation (18-504) Biological Anthropology Doctoral Dissertation Research Improvement Grant.

The legacy of Bill Kimbel's impact on paleoanthropology: a network analysis of his work

AMY L. RECTOR[1], LUCAS K. DELEZENE[2], KRISTI L. LEWTON[3], THIERRA K. NALLEY[4], DIDIER H. VERGAMINI[5] and MARIE VERGAMINI[1,6]

[1]Anthropology, School of World Studies, Virginia Commonwealth University, [2]Department of Anthropology, University of Arkansas, [3]Department of Integrative Anatomical Sciences, University of Southern California, [4]Medical Anatomical Sciences, Western University of Health Sciences, [5]ANSYS, [6]Integrative Life Sciences, Virginia Commonwealth University

Bill Kimbel was an active scholar of paleoanthropology for over 40 years. His leadership and work with the Hadar collection, *Australopithecus afarensis*, species concepts, and Pliocene hominin diversity resulted in a publication record that was deeply impactful: there were few areas of exploration in the record of our *Australopithecus* or early *Homo* ancestors that were not shaped by the work of Bill Kimbel. Here, we use citation network analyses to both assess and visualize the widespread influence and impact of Bill's work on our field.

Citation network analyses can be used to analyze and visualize the impact of specific authors or themes on a discipline. In this study, we use both CitNetExplorer and Gephi to analyze publication lists derived from Web of Science and Google Scholar. We explore themes of research most associated with Bill's work, and illustrate the impact of his major scholarly contributions through visualizations of the citation networks created as scientists in our field cited his expertise.

Results of our analyses suggest that of the primary themes associated with *A. afarensis*, early *Homo*, and Pliocene hominins, several of Bill's major works, such as his 1994 *Nature* paper on Hadar discoveries, serve as primary anchors for observation and inquiry. Our constructed author networks illustrate this same result: Bill Kimbel's work was often one of the central pillars for areas of exploration in paleoanthropology. Our field was made richer and better by the expertise of Bill Kimbel, and network analyses illustrate how profound his legacy will remain.

Dietary estimation of Plio-Pleistocene cercopithecids using dental functional morphology

HAILAY G. REDA[1], SCOTT W. SIMPSON[2,3], YOHANNES HAILE-SELASSIE[4] and STEPHEN R. FROST[1]

[1]Anthropology, University of Oregon, [2]Anatomy, Case Western Reserve University, [3]Physical Anthropology, Cleveland Museum of Natural History, [4]Institute of Human Origins, School of Human Evolution and Social Change, Arizona State University

Cercopithecids have been important proxies for understanding the paleoenvironments of early hominins and understanding their diets can increase their value in this regard. Stable isotopic analysis is one method of dietary reconstruction that estimates the amount of C3 versus C4 foods actually consumed. These data can be complemented using dental functional morphology to estimate the degree of adaptation to eating fruits and leaves. This study combines stable isotopic data from the literature with estimates using dental functional morphology of 317 eastern African fossil cercopithecids (4.6 – 3.0 Ma). Our model is based on 224 M_3s from 29 extant species with independent dietary data. Percentage leaves was significantly correlated with relative cusp height (*r2*= 0.334) and percentage fruit with crown flare (*r2*=0.409) across the samples. Morphology shows no significant differences in folivory and frugivory among *Theropithecus* (n=139) populations across localities despite significant temporal size increase and consistently high $s^{13}C$ (n=139). The $s^{13}C$ for*Cercopithecoides meaveae* (-11.8 ‰, n=2) and *Kuseracolobus aramisi* (-12‰, n=25) indicate both consumed mostly C3 foods, but dental morphology suggests *K. aramisi* (n=28) was more folivorous than more terrestrial *C. meavae* (n=7). Dentally, *Pliopapio alemui* (n= 37) was less frugivorous than cf. *Parapapio ado* (n= 20) from Koobi Fora, and *Parapapio cf. ado* (n= 15) from Kanapoi, but comparable to papionins from Galili. In summary, while *Theropithecus* shows similarity in tooth shape, both colobines and papionins differ in adaptations to folivory and frugivory across sites. With other data, this can help to understand the ecological context of early hominins.

Leakey Foundation, Sasakawa Young Leaders Fellowship Fund (SYLFF), University of Oregon

Intraspecific variation and sexual dimorphism in the face of *Australopithecus afarensis*: an allometric perspective

WELDEYARED H. REDA[1], PHILIPP GUNZ[2] and ZERESENAY ALEMSEGED[1]

[1]Department of Organismal Biology and Anatomy, The University of Chicago, [2]Department of Human Evolution, Max-Planck-Institute for Evolutionary Anthropology

Australopithecus afarensis (~3.7-3.0 Ma), is a widespread early hominin species discovered in eastern and central Africa. We know a great deal about its paleobiology and paleoecology, yet better characterizing intraspecific variation is still essential to better understand its evolutionary history. Continued fieldwork and virtual reconstruction of fossils have expanded the sample size of the species spatiotemporally, ontogenetically and size range. Here, we revisit the facial morphology of *A. afarensis* and explore variation and sexual dimorphism using geometric morphometric analysis. Based on existing fossil data, comparative analysis of linear measurement

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

shows that variation in *A. afarensis* is lower than that seen in African apes. Most facial features of *A. afarensis* are variably documented across individuals of different size and sex. For example, the average-sized A.L. 822-1 individual shows an overall facial morphology documented in the classic female *A. afarensis* but it also has a robust masticatory apparatus similar to larger, male individuals. In this regard, geometric morphometric analysis (n = 356) reveals that facial shape in average-sized individuals is similar to what is seen in larger males when size differences are standardized. Thus, our results suggest that patterns of variation across sex and size range and how that relates to the distribution of ancestral versus derived facial traits deserve further investigation in the light of expanded sample size. In sum, our study offers a new insight into the taxonomic significance of facial features and degree of variation in early hominins which are relevant to our understanding of their phylogeny.

This project is funded by the Wenner-Gren Foundation and the Biological Sciences Division Office of Inclusion and Diversity, The University of Chicago.

An Examination of NAGPRA within the Illinois Medicolegal System

ARIELLE Y. REICH and KRYSTIANA L. KRUPA

Anthropology, University of Illinois, Urbana-Champaign

This paper presents preliminary findings related to compliance with the Native American Graves Protection and Repatriation Act (NAGPRA) [1] within Illinois medicolegal offices. Under NAGPRA, Indigenous Ancestors must be repatriated by all "museums," which has only recently been realized to include medical examiner and coroner (MEC) offices [2]. Illinois enacted the Human Skeletal Remains Protection Act (HSRPA) in 1989 [3], which states that a coroner must be contacted should *any* human skeletal remains be discovered on land within the state, including private land. The coroner must then reposit the remains to the Illinois State Museum should they be determined non-forensic. However, the present study's findings show only two inadvertent discoveries in Illinois deemed Indigenous Ancestors have a NAGPRA public notice on file. Furthermore, the National NAGPRA databases showed no evidence of plans for repatriation of Indigenous Ancestors in Illinois MEC offices. Especially in considering Illinois burial laws and the recent realization of national MEC NAGPRA noncompletion, the number of unrepatriated Indigenous Ancestors inadvertently discovered in Illinois is expected to be greatly underrepresented. These findings are discussed considering factors that may have contributed to these potential trends: 1) Ancestors in holdings/collections are not being repatriated in a timely manner [4]; 2) new inadvertent discoveries are not being reposited properly by medicolegal personnel and/or 3) Ancestors already stored in medicolegal offices not being reported and having no plans for NAGPRA compliance [3]. The paper concludes by discussing next steps in identifying paths forward for the repatriation of Ancestors by Illinois MEC offices.

Market integration alters sleep-wake patterns among Malaysian Orang Asli

KATHLEEN D. REINHARDT[1], THOMAS S. KRAFT[2], AMANDA J. LEA[3], IAN J. WALLACE[4], AUDREY ARNER[3], ROMANO NGUI[5], YVONNE AL. LIM[5], STEVEN KW. CHOW[6], IZANDIS BIN MOHD SAYED[7], COLIN NICHOLAS[8], KEE-SEONG NG[9], MICHAEL ANTLE[1] and VIVEK V. VENKATARAMAN[1]

[1]Department of Anthropology and Archaeology, University of Calgary, [2]Department of Anthropology, University of Utah, [3]Department of Biological Sciences, Vanderbilt University, [4]Department of Anthropology, University of New Mexico, [5]Department of Parasitology, Universiti Malaya, [6]Federation of Private Medical Practitioners' Associations of Malaysia, Kuala Lumpur, Malaysia, [7]Hospital Orang Asli, Gombak, Malaysia, [8]Center for Orang Asli Concerns, Subang Jaya, Malaysia, [9]Department of Medicine, Universiti Malaya

Industrialized societies are experiencing a global epidemic of sleep disorders, in which extended lack of sleep has been associated with a number of adverse health effects. Because circadian rhythms are entrained to environmental exposure, studying sleep quality and quantity in a cross-cultural framework across environmental gradients is vital for understanding the global sleep epidemic. As part of the Orang Asli Health and Lifeways Project (OAHeLP), we hypothesized that small-scale societies undergoing market integration experience disruption of circadian rhythms and extended sleep loss due to increased exposure to artificial lighting at night-time and a constructed environment. We deployed wearable accelerometers among two groups of Orang Asli (the Indigenous peoples of Peninsular Malaysia) experiencing different levels of market integration: peri-urban Temuan (N= 9), who live in government-built stone houses with electricity, and rural-living Temiar horticulturalists (N = 12), who live in traditional thatch housing without electricity. Temuan individuals displayed a shorter sleep duration (5 ± 1.7-h) compared to the Temiar (7 ± 3.2-h). Both groups displayed similar waking times, while the Temuan had more flexible sleep-wake patterns with a later sleep onset. The Temiar experienced a higher frequency of brief awakenings lasting more than 5-min during sleep. Our data suggest that market integration alters sleep-wake patterns due to artificial lighting and permanent housing. These results are consistent with the *circadian entrainment hypothesis*, which suggests that changes in the sleep ecology of industrialized societies can be attributed to circadian disruption.

National Science Foundation BCS-2142091

Ecology, Group Size, and The Evolution of Aggression in *Pan*

GRIFFIN T. RENNER[1], MAUD MOUGINOT[2] and KRISTIN CROUSE[3]

[1]Anthropology, Stony Brook University, [2]Anthropology, University of Minnesota, [3]Ecology, Evolution, and Behavior, University of Minnesota

Our two closest living relatives, chimpanzees (*Pan troglodytes*) and bonobos (*Pan paniscus*), differ in their aggressive behavior, especially in between-sex interactions with higher female-to-male but lower male-to-female rates of aggression in bonobos compared to chimpanzees. Researchers have proposed that bigger party size and different environmental conditions such as higher food quality, lower patchiness, and lower seasonality in bonobos compared to chimpanzees might have driven these differences. However, these hypotheses are difficult to test without comparable behavioral and environmental data on multiple populations. Thus, we used an agent-based model, B3GET, to simulate a "proto*Pan*" population, which shares morphological and behavioral similarities with real-world bonobos and chimpanzees. In total, we ran 18 simulations for 30 to 60 generations with different starting environmental conditions (i.e., food quality, seasonality, patchiness) and recorded group sizes and aggressive interactions from 713 individuals. We found that group size was the strongest predictor of male-male (model average parameter estimate (MAPs) = 0.33; 95% CI [0.32, 0.34]) and female-male (MAPs = 0.54; 95% CI [0.32, 0.75]) aggression, supporting that bigger party size in bonobos compared to chimpanzees might have driven differential aggression patterns. Patchiness was the strongest variable for predicting male-female aggression (MAPs = -2.16; 95% CI [-2.28, -2.04]) and the second-best variable affecting other types of aggression, supporting the idea that higher patchiness decreases the rate of aggression. These findings indicate that group size and environmental conditions, including patchiness, might be key to explaining the differences observed in *Pan*'s aggressive behavior.

Identifying growth plate specific genes using the unusual ossification of the mammalian metatarsal and pisiform

PHILIP L. RENO[1], KELSEY M. KJOSNESS[1], SUNDAE PARK[2], LAUREN WILSON[1], SARAH N. DOELP[1], SHERRIE A. WALLACE[1] and DOUGLAS B. MENKE[2]

[1]Bio-Medical Sciences, PCOM, [2]Genetics, University of Georgia

Primates vary in skeletal proportions, and humans have uniquely shorted pisiforms. Both are the result of regulation of growth plate patterning. Genes regulating differential growth are generally unknown. We utilize normal variation in mammalian skeletal ossification to identify genes specific to growth plate patterning. Third metatarsals (MT3) form only a single distally placed

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

growth plate, and the pisiform (in non-human mammals) is the only carpal to form a growth plate. We compared gene expression in distal versus proximal MT3s and pisiform versus other carpals; tissue pairs that control for the effects of age, systemic growth factors, and biomechanical environment. Using RNA-seq in 4- and 9-days old mice we identify numerous differentially expressed genes (DEGs). Gene ontology (GO) analysis revealed MT3 DEGs are disproportionately associated with limb development/growth and factors associated with the Fzd8-Ror2-Wnt5a pathway. Significant pisiform-carpal GO terms include skeletal and cartilage development and abnormalities of the wrist. We identified a limited set of DEGs shared by both the MT3 and pisiform-carpal comparisons, including *Wnt5a*. *Wnt5a* is expressed in the perichondrium and columnar/hypertrophic cell boundary in both the distal and proximal MT3. However, the related *Wnt10a* gene is strongly expressed in the distal but not proximal MT3 bone collar. This conforms with previously identified roles for Wnt genes in regulating osteogenesis and cell polarity within the growth plate and provides potential genetic targets that may harbor regulatory adaptations associated with the evolution of primate limb proportions and human pisiform reduction.

This work is supported by grants from the NSF IOS-1656315 & BCS-1638812.

Characterization of color vision variation in a group of wild *Ateles belzebuth* in Amazonian Ecuador

SAM RETTKE[1], D. MAX SNODDERLY[2,3], ANDRÉS LINK[3,4] and ANTHONY DI FIORE[1,3,5]

[1]Department of Anthropology, The University of Texas at Austin, [2]Department of Neuroscience, The University of Texas at Austin, [3]Tiputini Biodiversity Station, College of Biological and Environmental Sciences, Universidad San Francisco de Quito, Cumbayá, Ecuador, [4]Departamento de Ciencias Biológicas, Universidad de los Andes, [5]Primate Molecular Ecology Laboratory, The University of Texas at Austin

Color vision among primates is remarkably diverse. Catarrhines and howler monkeys have independently acquired routine trichromacy through duplication of the middle-to-long-wavelength-sensitive (M/LWS) opsin gene on the X-chromosome. Most platyrrhines and some strepsirrhines, however, possess polymorphic color vision due to allelic variation at a single M/LWS locus; heterozygous females are trichromats, while males and homozygous females are dichromats. This variation allows the correlates of different color vision phenotypes to be evaluated within a single population. Yet such investigations are rare, and the selective advantages of individual phenotypes remain unclear. Previous studies have found that spider monkeys- a genus of large-bodied frugivorous platyrrhines- have two possible opsin alleles determined by a SNP site in exon 5; in reconstituted pigments they have absorption spectra with peaks at 553 and 538 nm, respectively. Using fecal-extracted DNA, we sequenced exon 5 for 43 members of one social group of white-bellied spider monkeys (*Ateles belzebuth*) that has been monitored at Tiputini Biodiversity Station since 2005. We identified 13 male dichromats (six P553, seven P538), 10 female dichromats (eight P553, two P538), and 20 female trichromats (P553/P538). We then compared foraging activity for dichromat versus trichromat adult and subadult females, but found no differences in observations of feeding on major food types. Preliminary analyses likewise revealed no difference between dichromat and trichromat adult females in interbirth interval or number of offspring produced. Future work may assess other aspects of foraging behavior and fitness to better understand the maintenance of multiple color vision phenotypes in this population.

Funded, in part, by NSF BCS-1638822, the Harry Frank Guggenheim Foundation, the National Geographic Society, and The University of Texas at Austin.

Physical Effects of Castration on the Male Skeleton

KATHRYN L. REUSCH

Sociology and Anthropology, Metropolitan State University of Denver

Castration was practiced on individuals assigned male at birth by many societies over the last 10,000 years for varying cultural and religious reasons. Castration was frequently performed between the ages of 6-10, but could also be done while an individual underwent puberty or after they finished puberty. While many studies have assessed the social effects of castration, with some discussion of soft tissue changes, few have examined the skeletal effects of castration. This paper combines original research on castrate skeletons with published studies of castrates to define the effects of castration on the growth, development, and maintenance of male skeletons. The majority of these effects are caused by deficits in both androgens (more plentiful on the male end of the sex spectrum) and estrogens (more plentiful on the female end of the sex spectrum) in the bodies of castrates. Due to the lack of both sets of hormones, those castrated before puberty grow and develop skeletons that take on very intermediate characteristics. These effects occur not only along the male-female sex spectrum, but also along the child-adult developmental spectrum. Those castrated during or after puberty take on some of these characteristics, but to a lesser extent than those castrated prepubertally. Understanding the skeletal changes caused by castration is useful not only for gaining a more holistic understanding of past individuals, but for anticipating similar effects in present-day individuals whose hormones may be low or changing due to exogenous or endogenous factors, such as those who are intersex or transgender.

Sex-biased gene regulation varies across human populations as a result of adaptive evolution

ADAM Z. REYNOLDS[1] and SARA D. NIEDBALSKI[2]

[1]Anthropology, University of New Mexico, [2]Human Evolutionary Genetics, Institut Pasteur

Gender disparities in health and disease are widespread, but their molecular underpinnings remain poorly understood. One mechanism affecting gender-specific disease phenotypes is sex-biased gene expression. Prevalent throughout both the autosome and sex chromosomes, sex-biased expression is known to vary by tissue, developmental stage, and disease context. Using RNA-Seq data and whole genome sequences from hundreds of individuals, we test whether humans exhibit variation in sex-biased gene expression across eleven human populations from diverse environments and evolutionary backgrounds. We find that sex-biased gene expression in humans is highly variable, mostly population-specific, and demonstrates between-population reversals. Expression quantitative trait locus (eQTL) mapping reveals sex-specific regulatory variants that show evidence of recent positive natural selection, suggesting that human have acquired population-specific sex differences in gene regulation through adaptive evolution. Our results indicate that sex-biased gene expression is more flexible than previously thought and may be influenced by environmental variation and the unique evolutionary histories of different populations. In an era of increasingly personalized medicine, this study highlights the importance of understanding population-level adaptation in functionally-relevant molecular pathways underlying gender disparities in health and disease.

This work was supported by a New Mexico-INBRE Award from the National Institute of General Medical Sciences (5P20GM103451) and staff at the National Center for Genome Resources.

Sleep In the Time of COVID-19: College Students Internal and Social Times are Better Aligned under Stay-at-Home Mandates

ALICIA D. RICE[1], OLIVIA SATHER[1], KENNETH P. WRIGHT JR[2], CÉLINE VETTER[2], MELANIE A. MARTIN[3] and HORACIO O. DE LA IGLESIA[1]

[1]Biology, University of Washington, [2]Integrative Physiology, University of Colorado Boulder, [3]Anthropology, University of Washington

Late chronotype, or preference to wake up and sleep in late, is prevalent in university students, but it is at odds with their morning social obligations like work and school. This misalignment between

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

their circadian clock and social constraints leads to short sleep duration and social jetlag, which are associated with adverse health conditions. Because of the Covid-19 pandemic many universities implemented remote learning and meeting options, which cut down commute times and gave students more flexibility with their sleep timing. To assess the effect of the Covid restrictions on college student sleep and light exposure, we recorded actimetry and light data in different cohorts of undergraduates at the University of Washington pre-Covid (2019), during-Covid (2020), and post-Covid (2021). Our results show that during Covid restrictions the discrepancy between school day and weekend wake times, midsleep, and sleep duration were diminished. For instance, mid-sleep during school days pre-Covid occurred later on weekends (5:14pm ± .21) than school days (4:24pm ± .23), but it did not differ under Covid restrictions. Furthermore, light exposure timing during-Covid did not differ between school days and weekends, the morning exposure to light started later on weekends than school days for pre- and post-Covid students. Finally, we found that while the interindividual variance in sleep parameters increased under Covid restrictions the intraindividual variance did not change. Our results suggest that increased freedom to choose bedtimes during Covid allowed university students to default to their preferred circadian timing and better align that timing to their social times.

The fossil second metatarsal from the Middle Pleistocene site of Sedia del Diavolo (Latium, Italy)

ALESSANDRO RIGA[1], ANTONIO PROFICO[2], HANNA RICE[3], TOMMASO MORI[1], ALESSIA NAVA[4], LUCIA MANCINI[5], DIEGO TREOSSI[5], DAVORKA RADOVCIC[6], LUCA BONDIOLI[7,8] and DAMIANO MARCHI[2,9]

[1]Biology, University of Florence, [2]Biology, University of Pisa, [3]Sport and Health Sciences, University of Exeter, [4]School of Anthropology and Conservation, University of Kent, [5]Elettra, Sincrotrone Trieste S.C.p.A., [6]Department of Geology and Paleontology, Croatian Natural History Museum, [7]Department of Cultural Heritage, University of Bologna, [8]Servizio di Bioarcheologia, Museo delle Civiltà, [9]Centre for the Exploration of the Deep Human Journey, University of Witwatersrand

The Sedia del Diavolo archaeological site, located in the low valley of the Aniene river (Italy), yielded a lithic assemblage referrable to the Middle Palaeolithic as well as numerous fossil remains including two human specimens: a partial femoral diaphysis (SdD1) and a complete second metatarsal (SdD2). A recent geochronological reappraisal of the site dated Sedia del Diavolo between 295,000-290,000 ya making it one of the oldest occurrences of the Levallois technology in Europe. Here we present new advanced morphological analyses of SdD2.

We obtained micro CT-scans of SdD2 and used the cross-sectional geometric approach to investigate the robustness of the diaphysis, and the 3D geometric morphometric approach to analyse the shape of the epiphyses. Results were compared to a series of modern human second metatarsals and fossil *Homo* specimens, including *Homo neanderthalensis* and *Homo naledi*.

Results show that SdD2 is characterised by thicker cortical bone than *H. sapiens* and *H. neanderthalensis*. Moreover, the distribution of the bone around the longitudinal axis as well as the shape of the proximal epiphysis make it more similar to *H. sapiens* than to *H. neanderthalensis*. Although results may be influenced by the presence of the stress fracture, the analyses suggest that the metatarsal belonged to an individual whose morphology was less derived than the more recent *H. neanderthalensis* comparative specimens. Furthermore, the individual likely experienced high levels of physical activity and mobility providing valuable information on activity levels of Middle Pleistocene *Homo* in Europe.

Paleogenomic insights into cooperation and conflict in the ancient Andes from positive selection on oxytocin pathway genes

JAMES K. RILLING[1,5,6,7,8], SOPHIE K. JOSEPH[1], ELIZABETH WAGMAN[1], NABEEL DIAB[1], NICHOLAS RYU[1], MINWOO LEE[1], RANDALL HAAS[2,3], MARK S. ALDENDERFER[3,4] and JOHN LINDO[1]

[1]Anthropology, Emory University, [2]Anthropology, University of California Davis, [3]Collasuyo Archaeological Research Institute, Puno, Peru, [4]School of Social Sciences, Humanities, and Arts, University of California Merced, [5]Department of Psychiatry and Behavioral Sciences, Emory University, [6]Center for Behavioral Neuroscience, Emory University, [7]Emory National Primate Research Center, Emory University, [8]Center for Translational Social Neuroscience, Emory University

Human societies are characterized by norms that restrict selfish behavior and promote cooperation with other group members. The oxytocin system may be an important mechanism supporting the evolution of this cooperation. Oxytocin promotes parochial altruism, and acts in both the nucleus accumbens and the anterior cingulate cortex to promote social bonding and social cohesion. Expression of the *CD38* and *OXTR* genes are known to affect oxytocin secretion and binding, respectively, in these brain areas. It has been suggested that genes involved with parochial altruism may have been selected for during past time periods when warfare and conflict were frequent and population centers grew. The Peruvian Andes provide an excellent opportunity to evaluate this hypothesis, as the rich archaeological record from the region shows a history of warfare beginning approximately 2500 years before present, followed by a period of political consolidation and agricultural intensification. Through allele trajectory modeling using both ancient and modern whole genome datasets, we present evidence of strong positive selection on the *OXTR* and *CD38* alleles linked with increased oxytocin signaling in the nucleus accumbens and the anterior cingulate cortex. This evidence suggests that increased oxytocin secretion and receptor binding in these brain areas may have facilitated group cohesion and coordination that enabled improvements to agricultural production, political consolidation, and success in intergroup encounters in the Andes during the beginnings of the Tiwanaku and Pukara states.

This work was supported by NSF BCS-1926075, NSF BCS-1945046, the National Geographic Society (5245-94) and the H. John Heinz III Charitable Trust.

The shape of the Neanderthal pelvis: implications of a new reconstruction of Kebara 2 for childbirth

REBEKA RMOUTILOVÁ[1,2] and MARTIN HAEUSLER[3]

[1]Department of Anthropology and Human Genetics, Charles University, Prague, Czech Republic, [2]Hrdlička Museum of Man, Faculty of Science, Charles University, Prague, Czech Republic, [3]Institute of Evolutionary Medicine, University of Zürich, Switzerland

The shape of the Neanderthal pelvis is controversial, with some authors suggesting a transversely oval pelvic canal and an associated unique non-rotational birth pattern, whereas others proposed a similar pelvic shape and birth pattern as in recent humans. The only nearly complete Neanderthal pelvis is preserved in the presumed male Kebara 2 skeleton. Particularly the left hipbone, the sacrum and the right pubis are, however, severely crushed, which resulted in significant differences between previous reconstructions, although they only considered the right hipbone and half of the sacrum. We performed a new pelvic reconstruction based on micro-CT scans by segmenting all individual pieces along their fracture lines and virtually reassembling them after removing adhering matrix. We constantly double-checked our virtual reconstruction against manually reassembled real models using 3D prints of the Kebara 2 pelvic fragments and their mirror images. The remarkable symmetry of the reconstructed left and right hipbones confirmed the absence of any significant plastic deformation. The sacrum showed a lumbosacral transitional anomaly with a double promontorium, which has implications for the pelvic incidence and inferences of lumbar lordosis. Further, the ischium appeared to be more gracile and the ilium narrower than in recent humans. Conversely, we found a virtually identical pelvic canal shape compared to recent humans and no evidence for an invagination of

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

the vertebral column or for a different relationship of the pelvic inlet to the hip joint. A unique birth pattern in these hominins is, therefore, unlikely provided a similar sexual dimorphism as in recent humans.

This project was financially supported by the Swiss National Science Foundation (grant IZSEZ0_210923).

An assessment of the effectiveness of partial mandibles for identifying hominid specimens to species

CHRIS ROBINSON[1,2,3], ZERESENAY ALEMSEGED[4], CALLUM F. ROSS[4], AMANDA SMITH[5], ANDREA TAYLOR[6] and CAROL WARD[7]

[1]Doctoral Program in Anthropology, The Graduate Center, City University of New York, [2]Department of Biological Sciences, Bronx Community College, [3]New York Consortium in Evolutionary Primatology, [4]Department of Organismal Biology and Anatomy, University of Chicago, [5]Department of Anatomy, Pacific Northwest University of Health Sciences, [6]Department of Basic Science, Touro University California, [7]Department of Pathology and Anatomical Sciences, University of Missouri, Columbia

Mandibles are the most commonly recovered skeletal element in the hominin fossil record and mandibular characters are included in most hominin species diagnoses. However, nearly all fossil hominin mandibles are incomplete. While previous studies have found that using landmark data from only the symphysis, corpus, or ramus can be used to assign a mandible to an extant hominid genus, it is unknown whether partial mandibles preserving one of these three regions can be readily identified to species, or whether certain landmarks in these regions are taxonomically diagnostic. To explore this question, landmark data were collected on 153 mandibles of extant hominids. Landmarks in each region were superimposed using Generalized Procrustes analysis. Principal component analyses were run on the superimposed landmarks to visualize separation between two species each of *Gorilla*, *Pan*, and *Pongo*. PC scores were then used in discriminant function analyses to determine how accurately specimens could be allocated to species using data from each of the three regions.

Results suggest that all three regions are taxonomically informative, with species identification percentages ranging from 77-100%. Ramus landmarks were most effective for differentiating *Gorilla* and *Pongo* species from one another, while *Pan* species were most accurately identified using symphyseal landmarks. *Pongo* species were most difficult to differentiate from one another for all regions. Interestingly, restricting corpus landmarks to one side of the mandible did not affect species classification accuracy, suggesting that fossil specimens preserving only one side of the mandible can be readily identified to species.

This research was funded by NSF BSC 1515053

A context for connectivity: Stable isotope insights to late Pleistocene and early Holocene habitat heterogeneity in eastern and southern Africa

JOSHUA R. ROBINSON

Archaeology Program, Boston University

Investigating the dynamics of later Pleistocene and early Holocene Middle and Later Stone Age behaviors have increasingly turned towards attempts to understand relationships among sites as interconnected networks rather than isolated locations on the landscape. Our understanding of the connectivity of these populations requires also considering environmental data as part of these broader landscapes. To this end, carbon and oxygen stable isotope data are compiled from 18 sites – 6 in eastern Africa and 12 in southern Africa – accounting for 1334 total published samples spanning the time period of ~ 195,000 years ago to ~ 1000 years ago. Isotope datasets are standardized by calibrating radiocarbon dates and considering variation in the carbon values of atmospheric CO_2. Eastern Africa was characterized by at least three different, but contemporaneous, habitats from open grasslands in inland areas to grassy-woodland mosaics in the Ethiopian Rift, and woodland forests along the coasts. In southern Africa, a complex picture arises with winter rainfall and extensive C_3 vegetation in the west and the Lesotho highlands but expanded C_4 grasslands along the Paleo-Agulhas Plain and in the east, especially after ~ 35,000 years ago. These patterns are not consistent though, with the interior of southern Africa up to the Zambezi drainage often revealing environmental and habitat conditions out of phase with coastal sites. As researchers employ modeling approaches more regularly in attempts to reconstruct potential networks, the thorough integration and multi-site analysis of local paleoecological datasets will be critical assets in model refinement and functionality.

Funding for sites analyzed by the author was supported by the National Science Foundation (BCS-1245803) and the Rust Family Foundation (RFF-2017-31).

Just gal pals! The differential treatment of sexual behavior among nonhuman great apes

MICHELLE A. RODRIGUES[1] and KIRSTY E. GRAHAM[2]

[1]Social and Cultural Sciences, Marquette University, [2]School of Psychology and Neuroscience, University of St. Andrews

In primatology, there is a tendency to separate out sexual and socio-sexual behaviors, roughly along the lines of reproductive and non-reproductive sexual behavior. In conjunction with behavioral ecology models that predict sexually dimorphic behavioral strategies, primatology perpetuates a heteronormative distinction that penetrative copulation between males and females has primarily reproductive, but no social value. Correspondingly, sexual behaviors between same-sex pairs are assumed to be motivated by a distant social goal that is more tangibly rewarding. Reviewing the literature on bonobos as a case study, we interrogate these assumptions, as they frequently engage in same-sex sexual behavior. The majority of literature frames same-sex sexual behavior, as a means to other ends, such as food or coalitionary support. Few studies explicitly recognize and acknowledge pleasure as a proximate mechanism. Acknowledging the proximate rewards of same-sex sexual behavior, and that these behaviors are rewarding in themselves, can generate testable hypotheses. Recognizing how past literature has obscured the functions of these behaviors can lead to new insights into understanding primate behavior. We caution again using studies of nonhuman primate sexual behavior to draw simplistic conclusions about human gender and sexuality and highlight that just as increasing the number of women in primatology has led to greater research on female primates, making primatology more inclusive for LQBTQIA+ researchers and foregrounding queer perspectives can lead to new research questions and approaches. This abstract is part of the Queering research: Uses of LGBTQIA+ perspectives and queer theory in biological anthropology symposium.

Sex differences in life conditions in the population of Cercado Grande de los Santuarios (Tunja, Colombia. 2350-450 AP): physical activity and physiological stress

CLAUDIA M. ROJAS-SEPULVEDA[1] and MARLON SANCHEZ-HASTAMORIR[2]

[1]Anthropology, Universidad Nacional de Colombia, [2]Anthropology, Search Unit for Missing Persons in the context and due to the armed conflict (UBPD by its acronym in Spanish)

Human groups living in the plateau of Cundinamarca and Boyacá in the central part of the Colombian territory at the arrival of the Europeans, have been proposed as matrilineal societies regarding ethnic and political affiliation, but they have also been characterized as patrilocal. This study aims to explore if this could have had an impact on differential life conditions between men and women in the Cercado Grande de Los Santuarios-CGS. This site has been considered as paramount to the population dynamics, because it was a center for ritual, political and interchange activities. This project studies indicators of physiological stress (dental hypoplasia, porotic hyperostosis, cribra orbitalia and periostosis) and physical activity (entheseal changes and degenerative joint disease) in order to evaluate differential life conditions between men (n=66) and women (n=49) in the series from

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

CGS. Frequencies of physiological stress indicators are higher for the male group while those of physical activity are lower. Discussion will turn around the role of geographic mobility of women as a new explanatory factor of physical stress and, especially, as a protective factor to infection. This possibility has not been considered before in the area.

The Instituto Colombiano de Antropología e Historia-ICANH funded part of the research

Effects of Diet on Brain Size Across Primates

MILENA L. ROMANO, KEELY Q. MAYNARD and STEPHANIE A. POINDEXTER

Anthropology, University at Buffalo

Overall primate brain size and the relative size of specific regions were thought to be associated with sociality, but recently, researchers have reported both strong associations with ecological variables and social variables further perpetuating discourse on which selection pressures are actually influencing primate brain evolution. Here we revisited the role of diet in brain size evolution by merging multiple datasets treating diet as a continuous variable and as a discrete variable. We also consider dietary breadth, by categorizing each primate species into one of two categories based on the diversity of their diets, specialist (n=36) and flex (n=23). We ran a series of phylogenetic generalized least-squares regressions to identify any links among dependent variables: hippocampus volume, main olfactory bulb volume, accessory olfactory bulb volume and neocortex volume, against independent variables: the proportion of key diet items (percentage of fruits and seeds, leaves, and animal parts), diet type (frugivore, omnivore or folivore) and dietary diversity. The percentage of fruits and seeds was the best fit model for explaining the variation in the brain size of each region and using diet categories was the second-best predictor. The accessory olfactory bulb, main olfactory bulb and neocortex in flex species had a higher mean than specialist species, comparable to the hippocampus which had a lower mean in flex species. Based on these results, how we characterize diets does matter, and there are likely different selection pressures between the flex and specialist species.

Palaeoecological and climatic evaluations during the Middle-to-Upper Palaeolithic transition in the Italian Peninsula through stable isotopic analysis

MARCO ROMBONI[1], MARIO F. ROLFO[2], GIOVANNI BOSCHIAN[1], DAMIANO MARCHI[1] and SERGIO TOFANELLI[1]

[1]Department of Biology, University of Pisa, [2]Department of History, Culture and Society, University of Rome Tor Vergata,

During the Middle-to-Upper Paleolithic transition (45,000-35,000 years ago), Europe witnessed a crucial population turnover characterized by the replacement of Neanderthals by Anatomically Modern Humans (AMHs). In this process, Italian Peninsula played a key role in due to its geographical position (at the centre of the Mediterranean) and broad environmental diversity. Several Late Pleistocene sites from the Italian peninsula (32,000-45,000 years ago) with Neanderthals/AMHs frequentation evidence have been selected to collect representative faunal remains for isotopic investigation The analysis of carbon, nitrogen and oxygen stable isotope ratios ($\delta^{13}C$, $\delta^{15}N$ and $\delta^{18}O$) in bone collagen and teeth enamel allows us to obtain palaeoecological and environmental information such as temperature, water availability, CO2-concentration, nitrogen availability, salinity, irradiance, and geological background. These preliminary isotopic results represent the first data for the Italian Late Pleistocene and reveal a heterogeneity in $\delta^{13}C$ and $\delta^{15}N$ data from sites studied, as well as an interesting positive shift in $\delta^{15}N$ values. A comparison between obtained isotope data and values from central and south-west European herbivore revealed a similar trend across the area, with statistically significant variations over time. These analyses offer a useful environmental tracer that can be measured in the archaeological sites themselves and can be directly radiocarbon dated, resulting in complement to the paleoclimatic proxies from oceanic and ice core records. The findings also support the hypothesis that the increase in $\delta^{15}N$ values in Europe represents shifts in the ecosystem nitrogen isotope baseline, that should be considered when comparing the diets of Neanderthals and AMHs.

Age-dependent dental topography variability in Eastern Chimpanzees

ALEJANDRO ROMERO[1], STÉPHANIE TORRIJOBOIX[1], LUCA FIORENZA[2], ALEJANDRO PÉREZ-PÉREZ[3] and JORDI GALBANY[4,5]

[1]Departamento de Biotecnología, Universidad de Alicante, [2]Biomedicine Discovery Institute, Department of Anatomy and Developmental Biology, Monash University, [3]Departament de Biologia Evolutiva, Ecologia i Ciències Ambientals, Universitat de Barcelona, [4]Departament de Psicologia Clínica i Psicobiologia, Universitat de Barcelona, [5]Institut de Neurciències, Universitat de Barcelona

Geographically distinct subspecies of chimpanzees across sub-Saharan Africa are ecologically flexible, presenting broad diets. Previous studies found that mechanical food properties differently impact on occlusal morphology as crown wears down. However, little is known about whether behavioral ecology influences the dynamics of molar shape as the enamel wears. Here, we used three-dimensional (3D) topographic metrics to investigate age-dependent shape changes of lower first molars (M1s) in *Pan troglodytes schweinfurthii* from Democratic Republic of Congo of known geospatial origin. Specimens were classified according to age category 1 (M1 in occlusion and unerupted M2; *n*=23) and 2 (M1-M2 in full functional occlusion and unerupted M3; *n*=25). 3D models of M1s were generated from high-resolution polyurethane replicas using a structured-light 3D scanner. Meshes were post-processed to collect relative crown height (occlusal relief), occlusal surface changes in elevation (slope) and sharpness (angularity) using the R package doolkit. Regression analyses revealed significant different dental topographic trajectories between age-cohorts with increasing latitude. A lack of difference within younger specimens suggests similar occlusal topographic features despite geographical variation. However, older chimpanzees from northern forest-savanna habitats are characterized by a significant reduction in cusp heights and slopes when compared to specimens inhabiting southern lowland forests, that show steeper slopes and relatively taller crowned molars as wear accrues. These differences may be associated with age-related variation in food toughness and abrasiveness. Our findings denote that ecological constraints largely impact on tooth-shape changes depending on wearing, and provide new insights about dental functional demands.

This research was supported by grants from the Spanish Ministerio Ciencia Innovación (PID2020-114517GB-I00 to AR and PID2020-112963GB-I00 to APP).

Skeletally mature individuals that experienced hurricane Hugo exhibit increased craniofacial fluctuating asymmetry

ASHLY N. ROMERO and CLAIRE E. TERHUNE

Department of Anthropology, University of Arkansas

The right and left sides of bilaterally symmetric organisms should be perfect reflections of one another because both sides of an organism develop under the same genome and environment. Fluctuating asymmetry (FA) is random deviation from bilateral symmetry that are associated with changes in an organism's environment. An ontogenetic sample of 275 macaques from Cayo Santiago were used to investigate FA levels in relation to hurricanes and the effect of developmental period in which individuals experienced these events. Using geometric morphometrics, FA magnitude was measured for all crania and then individuals that experienced 0, 1, or 2 hurricanes were compared using a one-way ANOVA. Individuals that experienced hurricanes during fetal life, skeletal immaturity, or skeletal maturity were compared using a two-way ANOVA with skeletal maturity and age at the time of the hurricane as main effects. Results indicate that FA does not increase with the number of hurricanes an individual experienced. However, the development

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

period in which an individual experienced a hurricane does show a trend toward increased FA for individuals that were skeletally mature at the time of the hurricane. Individuals that were skeletally immature at the time of the hurricane had the lowest levels of FA. This was statistically significant for Hugo (p=0.01) but not Georges (p=0.6). This result could reflect increased buffering during skeletal immaturity when bone growth is most prolific, and simultaneously may indicate an inability to handle perturbations during skeletal maturity when bone resorption rates are increasing.

Intersectional Forensic Anthropology: Moving Towards an Equitable Ethical Framework

SARAH M. ROSEN

Anthropology, Durham University

Intersectionality as a theoretical paradigm emerged in Black Feminist literature to illustrate the multifaceted ways in which marginalised groups experience systemic oppression. As a theoretical lens, Intersectionality has proven to be an invaluable approach when examining systemic and institutional violence across academic subjects. Forensic anthropology has come under considerable criticism on a number of occasions, often in highly publicised ways, for its ethical standards. Subsequent changes to these ethical practices have largely been in response to such criticism. An Intersectional approach to ethical practice in forensic anthropology has significant potential for improving equitable and ethical practice within the discipline, by shifting our approach to pre-emptive rather than reactionary strategies.

This paper presents three case-studies that demonstrate the importance of an Intersectional approach—the forensic identification of the *desaparecidos* of 'post-conflict' Guatemala, the forensic identification of 9/11 victims by the Office of the Chief Medical Examiner of New York, and the forensic identification of the Grenfell Tower victims. The Intersectional analysis of ethnographic and quantitative data from these forensic efforts highlights both the successes and challenges of their approaches. This analysis revealed that despite their distinct contexts, each was subjected to similar systemic political, socioeconomic, and academic influences that both negatively and positively impacted their ability to identify human remains. In light of these similarities across contexts, this paper introduces a Intersectional heuristic model for practitioners to actively engage with these challenges in a manner which empowers and equitably serves communities after tragedy.

Climate change impact on maxillary sinusitis prevalence in medieval ireland

IRMINE ROSHEM[1], JENNA DITTMAR[1], DEIDRE DRAIN[2], REBECCA CROZIER[1], MARC OXENHAM[1,3] and EILEEN MURPHY[2]

[1]Archaeology, University of Aberdeen, [2]Archaeology, Queen's University Belfast, [3]Biological Anthropology, Australian National University

Medieval Northern Europe experienced two distinct and protracted climate oscillations: the Medieval Warm Period (MWP) – 9th to 14th centuries– and the Little Ice Age (LIA) –14th to 18th centuries. The first climate transition led to a sharp cooling of temperatures that significantly impacted people's lives. While palaeoclimate reconstructions are commonly employed, they often ignore the substantive impacts on human health. To better understand the relationship between climate variability and health, this research focuses on the interaction between climate change and respiratory health throughout the medieval period. To assess this, maxillary sinuses of individuals from two medieval Irish sites – Ballyhanna (n=162), Ranelagh (n=82) – were osteologically examined for evidence of chronic maxillary sinusitis. The study design included investigations of prevalence in cohorts that lived before (n= 91) and after (n=153) the 14th-century climate transition. The results show that at both sites the prevalence rates are high, i.e., 67% at Ballyhanna and 62.75% at Ranelagh. Further, the rate of maxillary sinusitis was higher during the MWP. Notably, the difference in odds ratio between older and younger adults decreased from 66% (p=0.261) in the MWP to 34% (p=0.4144) in the LIA. In both groups, females are more affected than males, mirroring modern population studies and suggesting a relationship between the risk of developing maxillary sinusitis and societal gender roles. However, the difference in prevalence rates between sexes decreases after the climate transition. The complex climatic and socio-economic factors explaining these results are discussed in this paper.

A case of pediatric thalassemia from Phaleron Cemetery (Athens, Greece): Implications for life and death

JESSICA E. ROTHWELL[1,2], HANNAH LIEDL[3] and JANE E. BUIKSTRA[1,2]

[1]Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona State University, [2]The Malcolm H. Wiener Laboratory for Archaeological Science, American School of Classical Studies at Athens, [3]Department of Archaeology, Durham University

Beta-thalassemia variants are inherited blood disorders that are known to have high incidence in modern populations from the Mediterranean basin and were also present in antiquity. These hemoglobin disorders disrupt the mechanism for binding of the malaria parasite to red blood cells and therefore can be advantageous in regions where malaria is endemic. Thus, evidence of thalassemias in skeletal remains can inform upon not only the disease experience of people in the past but also their environment. While macroscopic examination of over 160 non-adult burials interred in the Archaic Greek cemetery of Phaleron (700-480 BCE) revealed a large number of individuals with pathological bony changes consistent with prolonged nutritional stress, burial IV_237, an individual who died between 1 to 2 years of age, presents a unique case of bony changes consistent with thalassemia. This study identified porotic alterations of the cranial vault suggestive of an anemic condition, along with changes in the postcranial skeleton consistent with thalassemia, thus supporting the possibility of endemic malaria in the region where the people buried at Phaleron lived, or in their ancestral homelands. Furthermore, lesions in the sphenoid, maxilla, mandible, and left scapula were consistent with the "Ortner Criteria" for scurvy. Because thalassemias can result in iron overload, and thus accelerated breakdown in vitamin C, this individual may have also been at increased risk of undernutrition as a comorbidity. Unique details of IV_237's burial context provide evidence of their special status in life and well as at death.

This research was funded by National Science Foundation Grant BCS-1828645 and The Malcolm H. Wiener Laboratory for Archaeological Science Research Associate Fellowship.

Bogotá workers: observation of entheseal changes in a sample from the Central Cemetery of Bogotá associated with the Republican Period

LUISA RUGE-VELASCO and CLAUDIA ROJAS-SEPÚLVEDA

Anthropology, Universidad Nacional de Colombia

Entheseal changes (EC) have been studied in precontact and forensic contexts in Colombia, but historical osteological collections have not been evaluated. The objective of this research is to contribute to the knowledge of EC in a republican collection (1850-1950) from Bogotá. This period had dramatic political, economic, and social changes, therefore, this study approached to lifestyle changes linked with physical activities. Differences by sex and age were evaluated in a sample of 100 individuals over 20 years old from the bone collection of globe B of the Central Cemetery of Bogotá, an area where impoverished population were buried. In the observation of EC, two different methodologies recording 14 and 23 observation points for each methodology, respectively. Burial records were also studied to approach occupations there registered. EC would be associated to domestic activities as "sirvientas" and "lavanderas" in women and to day labors as "jornaleros" in men.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Based on the results, no statistically significant differences were found between male and female individuals; however, the high presence of EC in the individuals under study suggests is similar in physical activity for both sexes.

Additional ape postcranial material from Napudet (Middle Miocene, Kenya) and its bearing on hominoid locomotor evolution

GABRIELLE A. RUSSO[1], THOMAS C. PRANG[2], FAYE MCGECHIE[3], SHARON KUO[4] and CAROL V. WARD[5]

[1]Department of Anthropology, Stony Brook University, [2]Department of Anthropology, Washington University in St. Louis, [3]Department of Basic Medical Sciences, University of Arizona College of Medicine - Phoenix, [4]Department of Biomedical Sciences, University of Minnesota, Duluth, [5]Department of Pathology and Anatomical Sciences, University of Missouri

Napudet is a Middle Miocene (~13 Ma) site in the Turkana Basin (Kenya) known for yielding hominoid fossils. Fieldwork from 2015-2021 produced over 70 elements of an ape partial postcranial skeleton (KNM-NP 64631). We previously reported on the comparative and functional anatomy of the Napudet ape shoulder, elbow, and lower thoracic vertebral column. Here, we describe bony elements of the lumbar spine, hand, hip, ankle, and foot recovered during the 2019-2021 field seasons. Body mass estimates from the femoral head suggest the Napudet individual was smaller-bodied (c. 11-15 kg) than the KNM-TH 28860 individual attributed to *Equatorius* (27 kg), and intermediate between estimates for female (10-11 kg) and male (20-23 kg) *Nacholapithecus.* A lumbar vertebra broadly resembles in both size and shape a lumbar vertebra (KNM-BG 35250R) attributed to *Nacholapithecus,* in part because the transverse processes arise slightly ventral to the pedicle-body junction. Similar to other Miocene apes, the femoral head is elevated from the neck, suggesting greater emphasis on mobility than observed among most monkeys. A medial cuneiform displays a first metatarsal facet with a curvature value falling within the ranges of hominoids, *Alouatta*, and *Ekembo*. The relative length of the pollical proximal phalanx is long and this value falls near atelids and hylobatids. The Napudet ape partial skeleton provides evidence for increased joint mobility of the appendicular skeleton relative to many extant anthropoids and enables a more detailed reconstruction of hominoid locomotor evolution than was available to Keith 100 years ago.

The Leakey Foundation, NSF HRRBAA #1929450, Simons Foundation, SBU OVPR Seed Grant Program

Maxillo-dental affinities of the juvenile enigmatic Northwest African Aterian fossil from Mugharet el'Aliya

CAROLIN RÖDING[1], SIREEN EL-ZAATARI[1], CHRIS STRINGER[2], RODRIGO S. LACRUZ[3] and KATERINA HARVATI[1,4]

[1]Paleoanthropology, Institute for Archaeological Sciences and Senckenberg Centre for Human Evolution and Palaeoenvironment, Eberhard Karls University of Tübingen, Tübingen, Germany, [2]Centre for Human Evolution Research, The Natural History Museum, London, UK, [3]Department of Molecular Pathobiology, New York University College of Dentistry, New York, NY, USA, [4]DFG Centre of Advanced Studies 'Words, Bones, Genes, Tools', Eberhard Karls University of Tübingen, Tübingen, Germany

Northwest Africa remains a geographical region of great interest in modern human origins, with the Jebel Irhoud hominin fossils, Morocco, representing the earliest anatomical evidence of our lineage at ~300 ka. The majority of the more recent human fossils from late MSA in this region have been associated with the 'Aterian' lithic industry, dated to ~145-20 ka.

One of the geologically youngest fossils from the Aterian is the juvenile from the site of Mugharet el'Aliya, Morocco, dated to ~35-60 ka. The taxonomic affinities of this enigmatic specimen have remained unresolved having been assigned to the *Homo sapiens* or Neanderthal lineages. The latter based on its 'archaic' / 'Neanderthal-like' features and apparent large size.

Here, we conducted a novel 3D shape comparative analysis based on surface registration on the maxillary fragment and analyzed the enamel-dentine shape of the associated teeth of the Mugharet el'Aliya fossil to clarify its taxonomic affinities. This analysis was combined with dental metric and non-metric data to integrate this fossil into the known morphological variation of the Aterian fossil record.

Our analysis showed maxillary and dental shape affinities of the subadult Mugharet el'Aliya individual with *Homo sapiens*. No size-independent affinities with Neanderthals of comparable dental age could be identified in maxillary morphology. The dental data suggests a shared high level of megadonty, especially in the UP4, throughout the fragmentary Aterian fossil record. Our study also adds to growing evidence suggesting a connection of cranio-dental traits linking western Asia, especially Qafzeh, with the Northwest African MSA.

This research was supported by the ERC (CoG 724703 & AdG 101019659), the DFG (353106138 & FOR 2237), the Cavella Foundation, the Human Origins Research Fund, and the NYU.

Dominance style and strategic sociality among alpha males in a community of wild chimpanzees (*Pan troglodytes schweinfurthii*)

KRIS H. SABBI[1,2], ELEANOR J. MATTHEWS[1], YUKUN ZHANG[1,3], MELISSA EMERY THOMSON[2,4], MARTIN N. MULLER[2,4], EMILY OTALI[4], RICHARD W. WRANGHAM[4,5] and ZARIN P. MACHANDA[1,4]

[1]Anthropology, Tufts University, [2]Anthropology, University of New Mexico, [3]Biology, University of Pittsburg, [4]Board of Directors, Kibale Chimpanzee Project, [5]Human Evolutionary Biology, Harvard University

As with many social animals, male chimpanzees earn fitness advantages from high dominance rank, leading them to compete intensely for status. However, unlike many animals where dominance is individualistic and maintained by physical intimidation, there is some evidence that chimpanzees rely on alternative strategies like strong social connections, especially when they are smaller-bodied. Here we use 24 years (1995-2019) of observational data from the Kanyawara community of chimpanzees in Kibale National Park, Uganda, to compare the social strategies of five alpha male chimpanzees to other adult males (n=24 unique individuals). During their tenure, alphas maintained higher rates of targeted aggression (LMM, Íû¥=0.046+0.011, p<0.01) and dominance displays (LMM, Íû¥=0.142+0.118, p<0.001) compared to non-alphas after controlling for age. However, they also had more mutually preferred social partners (GLMM, Íû¥=0.727+0.290, p=0.01), as opposed to one-sided partners, indicating that alpha males' invested substantial effort into maintaining social relationships with other males. Additionally, alphas were more likely to use aggression strategically to interrupt grooming interactions between other males (LMM, Íû¥=0.002+0.0004, p<0.001). Together our results indicate that alpha male chimpanzees can maintain their status by combining typically individualistic patterns of competition with investment in their own affiliative relationships and management of other males' affiliative interactions. If such a wide range of strategies occurred in hominins it would have set the stage for human-like approaches to gaining power through political alliances.

Research supported by NIH grants AI058715 and R01-AG049395; NSF grants NCS-FO-1926737, NCS-FO-1926352, BCS-1355014 and IOS-LTREB1052693; the Wenner-Gren and Leakey Foundations; Tufts University, University of New Mexico, and Harvard University.

Human sexual variation in the classroom: A graphing activity

SANA SABOOWALA

Integrative Biology, University of Illinois Urbana-Champaign

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

ABSTRACTS

Biological anthropology as a field, often in service of colonialism, has been responsible for creating and propagating classificatory models worldwide, including binary models of sex and gender. Thus, as biological anthropologists we have an obligation to address the inaccuracy of those models and teach gender and sex inclusive biology at multiple levels. This paper reflects on a graphing activity I developed for high schoolers and early undergraduate students, with the objectives of: <ul> Encouraging students to think critically about the binary models of biological sex Allow students to work with real human data Help students understand the ways in which science and scientific knowledge is dependent on choices that researchers make (i.e. that it is a subjective process) The primary activity revolves around graphing anthropometric data from the 2012 US Army Anthropometric Survey (ANSUR II) by binary sex, and looking at how histograms overlap, leading to a discussion about who gets left out of binary models of sex. The lesson also covers the pros and cons of scientific classification, the differences between sex and gender, choosing which graphs best represent data, and intersex identity. I reflect on the efficacy of this type of learning activity using feedback from a Human Genetics undergraduate course that piloted this activity. As biological anthropologists, it is our responsibility to bring these conversations into classrooms, not only because they validate the experiences of intersex and genderqueer students, but also because they more accurately reflect the reality of human variation than the binary model.

Aggressive monkeys? Green monkey behaviors inconsistent with human perceptions in Saint Kitts.

SANA T. SAIYED[1], KERRY M. DORE[2,3] and LEE T. GETTLER[1]

[1]Anthropology, University of Notre Dame, [2]Anthropology, Baylor University, [3]Biomedical Sciences, Ross University School of Veterinary Medicine

On the West Indian island of St. Kitts, green monkeys (*Chlorocebus sabaeus*) are simultaneously culturally significant and increasingly considered a pest. In response to widespread requests for intervention due to conflict, local governmental and nongovernmental organizations aim to establish a scientifically informed and sustainable monkey management strategy. While a significant amount of data exists on the monkeys' impact to agriculture, little is known about monkey-human interactions in other contexts. Our project fills this gap through a case study in a residential community with increasing reports of monkey to human aggression. We conducted year-long green monkey behavioral observations, participant observation, and interviews with community residents and workers. While all interview respondents (N=35) cited aggression from monkeys as a primary concern and regular occurrence, we recorded only 10 aggressive encounters out of 2193 total behavioral occurrences. Rather, the monkeys spent the majority of their time foraging and resting, and most encounters were within-group affiliative behaviors such as grooming (37%) and playing (39%). The limited occurrence of monkey aggression towards humans does not align with the dominant local perception of monkeys as aggressive, and analyses indicated no relationship between human presence or proximity to houses and within-group or toward-human aggressive or affiliative behaviors (all $p>0.20$). Our results suggest that humans may not have a prominent influence on monkey behaviors in this community and that perceptions of monkeys as aggressive are the result of singular occurrences rather than extensive personal experience, or the result of other factors altogether.

Bioarchaeological approaches to physical activity and lifestyle among Pre-Hispanic populations from central Argentina (late Holocene)

SOLEDAD SALEGA

CONICET, Institute of Anthropology of Cordoba, Anthropology Museum, National University of Cordoba

The aim of this work is to analyze the frequency of entheseal changes (EC) among Pre-Hispanic populations from central Argentina during the late Holocene period (2500-500 BP), and to evaluate their relationship with physical activity and lifestyle. EC were recorded in the upper and lower limbs of 90 male and female adult individuals from archaeological sites located in the Hills (n=47) and Plains (n=43) regions in the province of Córdoba. Fourteen fibrous and nineteen fibrocartilaginous entheses were scored with two different methods. Frequencies of bone changes were analyzed in each enthesis and in six functional complexes. Results showed higher prevalences of EC among older, male individuals. But when regions are considered, individuals from the Plains showed more EC frequencies since younger ages, and female individuals showed higher prevalences for the entheses of the upper limbs. Sex, age and geographical origin accounted for low percentages of variation in EC, and the strength of association between EC and significant variables was moderate to low. These results suggest the interaction of physical activity with biological characteristics of the analyzed individuals, and can be related to differences in lifestyle of the two regions considered, with a higher mobility and dependency on hunting and gathering activities in the Plains region, within an overall mixed subsistence strategy that incorporated cultivated crops.

Adolescence is a distinct life history stage: insights from chimpanzee growth and social behavior

AARON A. SANDEL[1,2], RACHNA B. REDDY[3] and JACOB D. NEGREY[4]

[1]Department of Anthropology, University of Texas at Austin, [2]Primate Ethology and Endocrinology Lab, University of Texas at Austin, [3]Evolutionary Anthropology, Duke University, [4]School of Medicine, Wake Forest University

Life history theory describes how energy is allocated to growth and reproduction across development. In mammals, infants receive energy from their mother and devote energy to growth; juveniles are energetically independent but are pre-pubertal. Adults have completed growth and devote energy to reproduction. In humans, there is a distinct adolescence prior to adulthood characterized by reproductive maturity, a growth spurt, and learning adult skills. Whether other animals share an adolescence is unclear due to inconsistent definitions and few comparative studies. We define adolescence as the period between the onset of puberty and the cessation of growth when energy is allocated to both growth and reproduction. Building on our studies of wild chimpanzees at Ngogo, Kibale National Park, Uganda, we have found that chimpanzees exhibit a distinct adolescent period from age 9 to 15 years. In a cross-sectional study of urinary markers of bone turnover (osteocalcin and collagen) we found that skeletal growth plateaus between age 14 and 18 years. Additionally, general additive models indicate that chimpanzees, especially males, exhibit a skeletal growth spurt around age 10 to 12 years. During four years of behavioral observations, we found that adolescence is also a distinct social period. Chimpanzees gain social independence from mothers and reorient toward partners who can enhance reproduction and survival. We make a case for a "biological" definition of adolescence that can be applied across species. Future work should assess whether distinct behavioral patterns correspond with this life history stage across species, as it does for humans and chimpanzees.

Funding to A.A.S. was provided by the National Science Foundation (1540259), the Leakey Foundation, and the University of Texas at Austin.

Improving the method for non-adult sex estimation using the auricular surface of the ilium in Medieval individuals from Sardinia (Italy)

ANA LUISA SANTOS[1], CINZIA ROGGIO[2], CLAUDIA ARANDA[3], ÁLVARO M. MONGE CALLEJA[1], MARCO MILANESE[4] and LEANDRO H. LUNA[5]

[1]Department of Life Sciences, Research Centre for Anthropology and Health (CIAS), Univ. Coimbra, Portugal, [2]Department of History, Humanities and Education, University of Sassari, Sardinia, Portugal, [3]Faculty of Odontology, Endodontics

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Chair and Public Health Research Institute (IISAP), Bioarchaeology and Forensic Anthropology Research Unit (UIBAF). Buenos Aires, Argentina, [4]Department of History, Humanities and Education, Laboratory of Medieval and Post-medieval Archaeology, University of Sassari, Sardinia, Italy, [5]CONICET, Multidisciplinary Institute of History and Human Sciences (IMHICIHU). University of Buenos Aires,, Faculty of Odontology, Endodontics Chair and Public Health Research Institute (IISAP), Bioarchaeology and Forensic Anthropology Research Unit (UIBAF)

Luna and co-authors (2017) developed a new method for sex estimation of non-adult individuals using the auricular surface of the ilium. This method proposed two equations (a discriminant function and a logistic regression) and two morphological variables (named MRS and OM). The estimations based on these four parameters do not usually coincide, and recent studies point that MRS tend to offer better results.

This presentation aims to evaluate the interobserver error of MRS in a 14th century sample of 30 commingled non-adult ilia from the medieval village of Geridu (Sorso, Sardinia, Italy). Five authors recorded MRS separately, without knowledge of the results obtained by the others. All coincided in 40.0% (12/30) of the cases, four in 26.7% (8/30) and three in 33.3% (10/30). The results by laterality show that they coincided more in the right bones than in the left ones (46.8% and 33.3%, respectively), without statistically significant differences (D=0.3; p=0.9). Moreover, the statistical evaluation of the interobserver error indicates that the results of the most experienced researchers tend to agree more (k=0.8; p=0.0) than those with less experience (K=0.3; p=0.3).

In conclusion, as it seems to be easier to assess the shape of MRS when the right ilia are observed, it is suggested that when that bone is not available, the analysis should be carried out using a mirrored image of the left. On the other hand, it is highlighted that the level of experience of the researchers is a variable that strongly influences the results.

Fundação para a Ciência e a Tecnologia (FCT), CIAS, UIDB/00283/2020.

Craniodental Lesions in the Genus *Pan*

CHRISTINA M. SAPATA[1], SIOBHÁN B. COOKE[2,3], CLAIRE E. TERHUNE[4] and CLAIRE A. KIRCHHOFF[1]

[1]Biomedical Sciences, Marquette University, [2]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, [3]New York Consortium in Evolutionary Primatology Morphometrics Group, [4]Department of Anthropology, University of Arkansas

Oral health reflects sources of morbidity and mortality, and likely also socioecological variables within a population. While data on craniodental lesions in chimpanzees (*Pan troglodytes*) is extensive compared to most primates, our other closest living relatives, bonobos (*Pan paniscus*), are less well studied. Here, we compare craniodental lesions in adult *Pan troglodytes schweinfurthii* (n=68), *Pan troglodytes troglodytes* (n=45) and *Pan paniscus* (n=44) to contrast patterns at the species and subspecific levels. One of us (CAK), evaluated skulls for signs of antemortem tooth loss (AMTL), TMJ osteoarthritis (TMJ OA), alveolar recession, caries, pulp cavity exposure, abscesses, dental crowding, and craniofacial trauma using standard criteria. We conducted nonparametric and descriptive statistical tests in SPSS to evaluate lesion co-occurrence and contrast taxa. Within each taxon, there were no sex differences in lesion prevalences, but several lesion types co-occurred, including TMJ OA vs. alveolar recession, and pulp cavity exposure vs. abscesses. Abscesses and pulp cavity exposures were also associated with AMTL and alveolar recession in all taxa. Additionally, *P. paniscus* showed associations between AMTL, abscesses and TMJ OA. In *P. t. schweinfurthii*, most other lesion types were associated with pulp cavity exposure and abscesses, and alveolar recession was associated with caries. When contrasting lesion prevalence between taxa, we found no differences in lesion prevalence between the two subspecies of chimpanzees. There were significant differences between chimpanzees and bonobos, including the prevalence of anterior AMTL and pulp cavity exposure of the posterior teeth. Our findings reinforce known socioecological distinctions between chimpanzees and bonobos.

NSF BCS-1551669 (SBC), NSF BCS-1551766 (CET), NSF BCS-1551722 (CAK)

The Skeletal Frailty Index (SFI) and the Biological Index of Frailty (BIF): A Comparison in the Middle Sicán, North Coast of Peru

KATHERINE M. SARGENT

School of Human Evolution and Social Change, Arizona State University

The simultaneous analysis of multiple markers of physiological stress could contribute greatly to bioarchaeological studies of frailty in the past, revealing more nuance than the analysis of any one biomarker alone. This study compared the applicability of two indices which attempt this simultaneous analysis: the Skeletal Frailty Index (SFI) (Marklein et al., 2016) and the Biological Index of Frailty (BIF) (Zedda et al., 2021). Using a sample of 521 Middle Sicán individuals from the pre-Hispanic north coast of Peru, this project compared the variation in frailty scores between methods in order to assess the relative utility of each method.

Both methods produce comparable observations, as indicated by similar coefficients of variation (V_{SFI} = 118.104; $V_{BIF(B)}$ = 131.707; $V_{BIF(A)}$ = 106.326). However, the BIF allowed for a bigger sample size than did the SFI. As such, the BIF was more enlightening in the case of the Middle Sicán. An ANCOVA of the BIF scores generated using a larger subsample of the dataset revealed that sex and site (as a crude proxy for socioeconomic status) intersected to influence frailty ($F = 2.998$, $p = 0.0001$, $\alpha \leq 0.05$). In contrast, ANCOVA tests of both BIF and SFI scores based on the same, smaller subsample revealed no statistically significant interactions between age, sex, or site. This project concluded that, while the BIF is the more flexible option and the SFI is more conservative, both methods are useful for assessing frailty in past populations.

The ups and downs of vertical climbing in Pan troglodytes

LAUREN SARRINGHAUS[1,2], BRYCE MURRAY[3], MAHIMA SRIKANTH[3] and LAURA MACLATCHY[2]

[1]Biology Department, James Madison University, [2]Department of Anthropology, University of Michigan, [3]Department of Neuroscience, University of Michigan

Vertical climbing is the most common form of arboreal locomotion used by *Pan troglodytes*. Vertical climbing has been implicated in both hominoid and hominin adaptive origins due to patterns of muscular recruitment, kinematics, reliance on orthogrady, frequency, and the essential role it plays in obtaining arboreal foods. The effects of gravity cause ascent to be more energetically costly than descent, thus ascent may be under stronger selection pressure. We use *Pan troglodytes* as a model to explore patterns of variability of vertical climbing. We hypothesize that the locomotor modes used during vertical ascent will be less variable than those during descent, and that this will be particularly apparent during ontogeny as body size increases. In our study of 132 individuals from the Ngogo population, Kibale Forest, Uganda, we quantified the number of locomotor modes used by individuals using 4k 60fps video footage collected *ad libitum* in 2020 and 2021. In total, these data yielded 638 bouts of vertical climbing. As predicted, we found descent bouts to be more variable than ascent bouts in terms of the number of modes engaged in (Welch's $t = -6.35$, $p < 0.001$). Further, there was a difference between age categories within descent bouts (Kruskal-Wallis $p < 0.01$) but no age difference within ascent (K-W $p = 0.88$). This study supports the hypothesis that vertical ascent is under strong selection. Kinematic constraints may also be important in reducing variability in ascent and should be the focus of future investigations.

This work was supported by an NSF grant # 185038 and a Leakey Foundation grant.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

ABSTRACTS

Fisher-forager mortuary complexity during the African Humid Period: the view from Lothagam Lokam, Kenya

ELIZABETH SAWCHUK[1], STEVEN GOLDSTEIN[2], KENDRA CHRITZ[3], LESLEY HARRINGTON[4], DEVYN CALDWELL[4], EMMA BETZ[3], CHRISTINE CHEPKORIR[5], EVAN P. WILSON[6], ANNEKE JANZEN[7], EMMANUEL NDIEMA[8], KATHERINE GRILLO[9] and ELISABETH HILDEBRAND[10]

[1]Department of Human Evolution, Cleveland Museum of Natural History, [2]Department of Anthropology, University of Pittsburgh, [3]Department of Earth, Ocean and Atmospheric Sciences, University of British Columbia, [4]Department of Anthropology, University of Alberta, [5]Human Evolutionary Biology, Turkana University College, [6]Department of Anthropology, City University of New York Graduate Center, [7]Department of Anthropology, University of Tennessee, Knoxville, [8]Earth Sciences, National Museums of Kenya, [9]Department of Anthropology, University of Florida, [10]Department of Anthropology, Stony Brook University

Lothagam Lokam (formerly the Lothagam Harpoon Site) near Lake Turkana, Kenya records multiple episodes of human occupation between ~10,000-7,500 years before present (BP). First excavated in the 1960s, Lokam has also yielded one of the best-known assemblages of human remains from eastern Africa during the African Humid Period (AHP), a time of moist conditions, high lake levels, and long-distance hydrological connections. However, many questions remain about the site's context and scope, particularly because skeletons were recovered from surface erosional deposits. Excavations by the Later Prehistory of West Turkana project since 2017 have revealed a more complicated picture than previously reported: burials exist in many parts of the >100,000m^2 site, and individuals from different locations have yielded direct radiocarbon dates with calibrated ranges from 7426-7407, 7561-7540, 9535-9411, and 9537-9475 cal BP (95% CI, IntCal 20) indicating at least two periods of mortuary activity. These are among the oldest direct dates on human remains in eastern Africa. Recovery of 16 new individuals, most from primary interments, along with isolated remains brings the total number of individuals to ~45, providing insight on human morphological variation and lifeways during the AHP. Osteological analysis indicates that men and women ranging in age from young to old adulthood were interred in this beach. In 2022, we recovered the first remains of a child at the site, whose distinctive burial treatment raises new questions about mortuary practices. Alongside emerging habitation and palaeoenvironmental data, bioarchaeological findings from Lokam challenge assumptions about stability within the AHP.

Funding provided by the Social Sciences and Humanities Research Council of Canada (SSHRC IDG 430-2020-00406), the Wenner-Gren Foundation (Gr. 9410) and the National Science Foundation (Collaborative Grant 2051515/2051486/2051494).

Associations between age, physical activity, and physical and cognitive function in Hadza foragers

KATIE SAYRE[1], GENE E. ALEXANDER[2,3,4,5,6,7], HERMAN PONTZER[8,9], BRIAN M. WOOD[10,11] and DAVID A. RAICHLEN[1,12]

[1]Human and Evolutionary Biology Section, Department of Biological Sciences, University of Southern California, [2]Departments of Psychology and Psychiatry, University of Arizona, [3]Evelyn F. McKnight Brain Institute, University of Arizona, [4]Neuroscience Graduate Interdisciplinary Program, University of Arizona, [5]Physiological Sciences Graduate Interdisciplinary Program, University of Arizona, [6]BIO5 Institute, University of Arizona, [7]Arizona Alzheimer's Consortium, [8]Department of Anthropology, Duke University, [9]Duke Global Health Institute, Duke University, [10]Department of Anthropology, University of California Los Angeles, [11]Department of Human Behavior, Ecology, and Culture, Max Planck Institute for Evolutionary Anthropology, [12]Department of Anthropology, University of Southern California

Physical and cognitive function are key components to quality of life during older adulthood, and finding ways to prevent or slow age-related declines in both is an important public health concern. Engaging in a physically active lifestyle appears to improve physical and cognitive function during aging. Our understanding of the role that physical activity (PA) plays in functional aging, however, comes from work with mostly sedentary populations. In this study, we examine the relationship between age, physical activity, and physical and cognitive function in a population known for exhibiting high levels of PA throughout life: the Hadza foragers in Tanzania. We recruited 122 Hadza adults (n_{female}=66, n_{male}=56; ages 19–87 years) to participate in this study. We used wrist-worn accelerometers to evaluate levels of PA, and asked participants to complete tests of physical and cognitive function. Participants in this study displayed high levels of moderate-to-vigorous physical activity (MVPA), even at older ages. We found that age was negatively associated with grip strength (p<0.001), gait speed (p<0.001), and performance on a test of processing speed (p<0.001), but not associated with performance on a test of spatial working memory (p=0.17). We also found that time in MVPA was significantly associated with gait speed—participants with the lowest amounts of MVPA displayed slower gait speeds (p<0.01)—a relationship also seen in industrialized populations. In addition to characterizing age-related differences in physical and cognitive function, we believe this study offers insight into the relationship between PA and function in a highly physically active population.

National Science Foundation [NSF-BCS 2051519 (MKS), NSF-BCS 1440867 (DAR), NSF-BCS 1440671 (BMW)], National Institute on Aging [AG019610 (GEA), AG067200 (GEA,DAR), AG072445 (DAR,GEA)], Max Planck Institute for Evolutionary Anthropology (BMW).

Body by Colonialism: Interrogating the False Binary in Bioarchaeology

BENJAMIN J. SCHAEFER

Anthropology, Field Museum of Natural History

Feminist and Queer theorists have made a profound impact on (bio)archaeological research that reimagines 'the opposition to the normative' as not mutually exclusive to the categories of sex and gender (Blackmore 2011; Geller 2016; Voss 2000). The word 'queer' derives from the German word 'quer' and can be translated in different ways depending on the context; for example, it can translate to 'askew', 'crosswise', and 'transverse'. In this sense, queer contends against the normalized, legitimized, and legible aspects of analysis. As noted by other archaeologists that engage with feminist and queer theory (Arden 2008; Blackmore 2011; Geller 2008; Hollimon 2011), the inclusion of a queer analysis is not predicated on excavating or uncovering ancient 'homosexuality'; rather it centers those that are typically at the margin, or completely left out in academic inquiry.

Bioarchaeologists and Skeletal Biologists typically rely on the remaining bony elements to make to make scientific inferences about ancient peoples. Our analyses follow standardised practice following Buikstra and Ubelaker (1990), however, many of the methods in the bioarchaeologist's toolkit do not adhere to a strict binary. This paper critically interrogates this growing awareness by specifically focusing on how queer theory changes and transforms scientific knowledge about the human body and experience within biological anthropology. Approaching the body as a fully realised blueprint prevents a deeper investigation into human behaviour and physiology outside the binary. Challenging hegemonic categories does not erase biology, rather by critically engaging with biology it refuses the false binary that haunts bioarchaeological research.

None:

Effects of height in the canopy on gait mechanics in wild lemurs

NICOLE M. SCHAPKER[1,2], AMMON HOTTENSMITH[1], JUDITH JANISCH[1], LYDIA C. MYERS[3], TAYLOR PHELPS[1], IAN BARRY[3], LIZA J. SHAPIRO[3] and JESSE W. YOUNG[1]

[1]Department of Anatomy and Neurobiology, Northeast Ohio Medical University, [2]School of Biomedical Sciences, Kent State University,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

[3]Department of Anthropology, University of Texas at Austin

Arboreal locomotion is thought to be particularly precarious. Branch diameter and orientation can impose certain biomechanical challenges to maintaining a desired trajectory. Branch discontinuity and height above ground also mean that failure to compensate for precarious branch morphology can lead to risky falls. Using high-speed cameras, we recorded the quadrupedal locomotion of four wild lemur species – *Eulemur rubriventer*, *Eulemur rufifrons,* and *Hapalemur aureus* at Ranomafana National Park and *Lemur catta* at the Anja Community Reserve. We quantified branch diameter, orientation, and height using remote sensors and tested their effects on gait kinematics (N = 60). Preliminary data indicate lemurs primarily use diagonal sequence gaits. Only *E. rubriventer* changes gait type with branch height, increasing the use of lateral sequence gaits higher in the canopy. Lemurs tend to increase duty factors as branch height increases, though variation is inconsistent between hindlimbs and forelimbs. Furthermore, *E. rubriventer* increases the mean number of limbs used to support the body during a stride on higher substrates. In contrast, *L. catta*, unlike the other lemurs, tends to increase duty factors and the mean number of supporting limbs as substrate diameter decreases. This may be due to differing locomotor environments as *L. catta* generally walked on substrates lower to the ground. Overall, these results suggest that lemurs change their gait in response to varying substrate properties and that adjustments vary among species. The results also underscore the importance of including branch height alongside more typically measured substrate characteristics like diameter and orientation.

Supported by NSF BCS-1921135 and BCS-1921314.

Organizing anatomical 3D data for long-term storage and frequent reuse

STEFAN SCHLAGER[1,2] and FELIX ENGEL[1]

[1]Biological Anthropology, Freiburg University, [2]Dept. of Oral and Maxillofacial Surgery, Freiburg University

Sharing and reusing basic research data are currently challenges to researchers in many scientific disciplines. Their benefits, including synergy effects and transparency of research, are only realized if data are well annotated and the connection between basic data and research outcome conclusively demonstrated. RDFBones is a domain ontology within the Resource Description Framework (RDF). It has been successfully applied to document research objects, processes and outcomes as semantic data models. These can be implemented into all kinds of databases but are also a perfect medium for long-term storage of research data.

With three-dimensional craniofacial data sets, RDFBones can be used to describe the processes involved in their production. It can address specific elements within these data objects and define them as input to further data processing. Semantic data modeling provides a thorough and transparent account of how basic data are used in investigations to the effect that research results can be traced back to the originally acquired data. Moreover, RDFBones semantic data models can serve as a translation layer to bridge several independent data sources and combine information from all of them.

We present the worked example of a semantic data model representing a three-dimensional landmark configuration derived from a CT scan, including the entire process chain, and employed in a geometric morphometric analysis. We also provide examples complex queries across this model as a basis for additional research. These resources include expressive in-line documentation which makes them highly appropriate for long-term storage and reuse in later, unrelated investigations.

Funded by the German Research Foundation (Deutsche Forschungsgemeinschaft, DFG).

How has Keith's multi-stage model performed in light of experimental data on locomotor mechanics in monkeys and apes?

DANIEL SCHMITT[1], ROSHNA E. WUNDERLICH[2], KEVIN G. HATALA[3] and ANGEL ZEININGER[1]

[1]Evolutionary Anthropology, Duke University, [2]Department of Biology, James Madison University, [3]Department of Biology, Chatham University

When Sir Arthur Keith first formulated his multi-stage model of human evolution, he did so with little information on fossils or experimental comparative anatomy, an approach that Washburn would call for 30 years later. Since then, kinematic and kinetic data have been collected on Old and New World monkeys and all the apes, providing robust tests of several prescient ideas Keith presented. Keith proposed that human evolution proceeded through pronograde, orthograde "hylobatian", large-bodied ape "troglodytian", and then to a "plantigrade" phase with erect limbs. Keith described significant changes in the hindlimb and fewer in the forelimb, which retained suspensory features and he explicitly connected human hindlimb and foot development with gorillas. Experimental data on Old World monkeys, suspensory New World monkeys, and apes have supported the idea of a functional shift from pronograde to antipronograde postures with forelimbs used in tension during normal and inverted quadrupedalism and climbing. Regarding hindlimb function, we know a lot about *Pan*, including pedal mechanics and pressures, less about *Gorilla* and far less about *Pongo*. Our latest experiments show that *Gorilla* hindlimb and foot mechanics are deeply reflective of humans. Chimpanzees show some of the same patterns, while orangutans and suspensory New World monkeys form an essential mechanical bridge between "hylobatian" and "troglodytian" stages. Our collective years of data on forelimb and hindlimb mechanics, especially our latest results, provide new opportunities to interrogate these key transitions. Keith's models provided explicit hypotheses to be tested and fare fairly well in light of these novel data.

Stronger maternal social bonds and higher rank are associated with accelerated infant maturation in Kinda baboons

INDIA A. SCHNEIDER-CREASE[1,2], ANNA H. WEYHER[3], BENJAMIN MUBEMBA[4], JASON M. KAMILAR[3,5], MEGAN PETERSDORF[6,7] and KENNETH L. CHIOU[2]

[1]School of Human Evolution and Social Change, Arizona State University, [2]Center for Evolution and Medicine, Arizona State University, [3]Department of Anthropology, University of Massachusetts, [4]Department of Wildlife Sciences, School of Natural Resources, Copperbelt University, [5]Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts, [6]Department of Anthropology, New York University, [7]Evolutionary Anthropology Research Group, Department of Anthropology, Durham University

Social relationships are critical components of health and fitness for humans and other animals. For female-philopatric species, affiliative relationships among females (kin and non-kin alike) can influence components of fitness that include individual survival, interbirth interval, and offspring survival. Affiliative relationships with males have attracted somewhat less attention, with most studies focusing on female-male relationships as adaptations for infanticide avoidance. Here, we use eight years of behavioral data on Kinda baboons (*Papio kindae*) to assess whether maternal social relationships—both among females and between females and males—affect infant survival, interbirth interval, and the pace of infant development. Kinda baboons are an ideal system for these analyses because males and females form strong relationships outside of the periovulatory period and in the absence of obvious infanticide threat. We calculated social metrics that reflected dominance status, total social integration, and social bond strength and paired these metrics with data on offspring survival, interbirth interval (IBI) duration, and infant behavioral maturation. Neither dominance rank nor sociality had a significant effect on interbirth interval or survival, but higher rank and the stronger affiliative relationships between a female and her top female and top male social partners predicted more rapid infant behavioral maturation. These results suggest that maternal dominance and sociality may confer advantages related to infant development and independence that ultimately

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

may permit females to more quickly invest in subsequent offspring, and point to advantages of relationships with males outside of lowering infanticide threat.

This research was supported by The Fulbright Program, American Society of Primatologists, Lambda Alpha, PEO International, IdeaWild, and the Leakey Foundation Field Site Grant.

Mantled howler monkey (*Alouatta palliata*) howling behavior across a small forest fragment and larger continuous forest in Costa Rica

AMY L. SCHREIER[1], FRANCESCA VE. KASER[1], C. ERIC JOHNSON[2], MICHAEL ENNIS[1], MICHAEL WASSERMAN[2] and LAURA M. BOLT[3]

[1]Biology, Regis University, [2]Anthropology, Indiana University, [3]Anthropology, University of Toronto Mississauga

Howler monkey loud calls, uttered by adult males, are thought to have a variety of adaptive functions including the protection of food resources and defense of females from extra-group males. We examined the relationship between howling and both resource and mate defense in mantled howler monkeys in two Costa Rican rainforests of different sizes: La Selva and La Suerte share similar flora and fauna, but La Selva is much larger and has bigger, more abundant fruiting trees than La Suerte. We therefore predicted that group size would be larger with a higher male:female sex ratio at La Selva, and that monkeys would howl for longer durations, with more howls per bout and at higher rates at La Selva compared to La Suerte. We conducted all-occurrences sampling of howling behavior and collected demographic data at La Suerte (June-August 2017/2018/2019, December-January 2019/2020) and La Selva (November 2018-February 2019, May-June 2022). Group size and male:female sex ratio were both higher at La Selva (13.1 monkeys; 1:2.3 sex ratio) than La Suerte (9.5; 1.18). Both mean howl length and number of howls/bout were significantly higher at La Selva (144.6sec; 31.4howls/bout) than La Suerte (119.9; 5.1), but howling rate was significantly higher at La Suerte (1.1howl/hour) than La Selva (0.7). Our results suggest that howl length and number of howls/bout are related to ecological resource defense, with longer howling bouts occurring in the richer habitat. In contrast, sex ratio appears to drive howling rate with males howling more frequently when group females are more limited.

A bioarchaeological analysis of structural violence and healthcare in the Middle Archaic (6000 – 3000 BC) Midwest.

ALECIA SCHRENK[1] and LORI TREMBLAY[2]

[1]Anthropology, University of Nevada, Las Vegas, [2]Humanities and Social Sciences, SUNY Delhi

Understanding patterns of healthcare and violence in prehistoric communities provides valuable information about the lived experiences of past peoples. This study uses theoretical perspectives from the Bioarchaeology of Care and Structural Violence to contextualize the prevalence of trauma and healed injuries at the Middle Archaic (6000 – 3000 BC) Midwestern site of Carrier Mills, IL. This study found that males had a higher prevalence of cranial depression fractures (4.8%) and post-cranial fractures (51%). However, females had a higher frequency of healed injuries (32%). This study explores the nuanced relationship between violence and healthcare which placed males at higher risk of injury with a lower prevalence of healing.

The coevolution of ventral infant carrying with primate vision and vocal signaling

DAVID M. SCHRUTH

Anthropology, University of Washington

Primates are characterized by generally orthograde postures and frequently longer hind legs (or arms) for specialized inter-branch locomotion. Cranial features of primates trend towards larger brains, a reduced snout, and convergent eyes. Primate origins hypotheses suggest such crainial configurations likely improve stereoscopic vision for high-impact limb landing. A recent musicality origins hypothesis suggests that proficiency in such binocular image resolution could be signaled by vocal production of a diversity of reappearing sound contours. I hypothesized that infant fur-cling carrying contributes to the origins of both of these (vocal and morphological) traits as it intensifies the physics involved and reflexes required for associated grasp-landing tasks. Using phylogenetically controlled regressions, I reanalyzed an amalgamation of socio-ecological datasets including data on infant carrying. To cover all primate taxa, while still accounting for the presumably more hazardous (ventral) form of carrying, I combined the results of two different studies. My formulation adds these independent ordinal measures together as: park (0), both (1), or ride (2) plus dorsal (1), mixed (2), or ventral (3), totaling to integers ranging from zero to five. Ventral carriage information was not available for non-anthropoids, but was added in post-hoc for lorises and Indri. Multivariate regression results highlight ventral infant carrying, along with mass, leaping, and swinging, as significant predictors for both outcome variables. This suggest ventral infant carrying, like other impactfully hazardous locomotion, may factor as a key influence on primate evolution. Future studies should include information on duration of carriage, weaning times, and higher resolution data for tarisers.

Hominids share similar bone modelling patterns of maxillary development

ALEXANDRA SCHUH[1], YANN HEUZÉ[1] and SARAH E. FREIDLINE[2]

[1]PACEA, Université de Bordeaux, [2]Department of Anthropology, University of Central Florida

Midfacial morphology varies between hominids, and particularly differs in humans for which the face is small and retracted. The underlying developmental processes for these morphological differences are still largely unknown. Here we investigate the cellular mechanism of maxillary development (called bone modeling), represented by bone formation and resorption on the periosteal surface. An ontogenetic sample of 59 present-day humans, 105 great apes (orangutans, N=37; gorillas, N=35; chimpanzees, N=33) and 32 gibbons representing the outgroup was used. Individuals were sorted into five age groups following dental development. Using confocal microscopy, digital maps were computed for each individual and age group means. Their projection onto corresponding mean shapes obtained by geometric morphometrics allowed for the visualization of both changes in the cellular process and morphology during ontogeny. Secondly, the amount of bone resorption was quantified and compared between species. We found relatively similar bone modelling patterns in all hominids, including humans. In each species, maxillary bone resorption is found near sutures, as well as in the zygomatic process, the premaxilla and the post canine region. In gibbons, bone resorption was found in the zygomatic process; however, it was rarely present in other regions, if not completely absent. This suggests that a critical tipping point for human facial evolution can be traced back to the split between hylobatids and hominids. Although present-day humans' maxillary morphology is unique among extant great apes, the cellular process underlying its development might have emerged millions of years ago.

This study received financial support from the Fyssen foundation, the Max Planck Institute, and the French government in the framework of the University of Bordeaux's research project "Human Past".

Trabecular response to variation in loading environments in the hominoid clavicle

RENA SCHWARTZ, HANNAH N. FARRELL and ZERESENAY ALEMSEGED

Organismal Biology and Anatomy, University of Chicago

Previous studies of trabecular bone structure have indicated the presence of higher trabecular bone density in both regions of soft tissue attachment (entheses) and at joint surfaces, but no studies have ventured further to see if the increase in density is achieved through different mechanisms of bone formation in the two loading environments. Here we study the

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

clavicle, to directly compare regions dominated by a compressive loading environment (joint articular surfaces) and tensile environment (muscle and ligament attachment sites) within a single bone. Using micro-CT scans of adult hominoid clavicles of wild-origin (N = 33) and the software 'medtool 4.5', trabecular thickness, trabecular spacing, and trabecular number were measured across the entire element with a multiple volume of interest approach. Preliminary results suggest that the increased trabecular bone density found in the entheses and articular surfaces is achieved through different trabecular bone modeling. In the entheses, higher density is achieved through increasing both trabecular spacing and thickness. However, on the articular surfaces, higher density is achieved through increasing trabecular number and a decreasing trabecular thickness and spacing. These findings indicate trabecular bone modeling to be more nuanced than previously acknowledged. Further, the structural differences underlying the two loading environments may have relevance for clinical studies of microfracture and the utility in fossil taxa to explore function.

Ethics in bioarchaeology: A bibliometric review of recently published articles

GEORGIA K. SCOTT and MARIN A. PILLOUD

Department of Anthropology, University of Nevada, Reno

Despite a growing number of archaeologists reflecting on the discipline's colonial roots and the unsanctioned use of human remains, little work has been done to evaluate how bioarchaeologists address these issues in the published literature. Therefore, this research undertook a bibliometric review of *Bioarchaeology International* over the past four years (2022-2018) to understand how bioarchaeologists are currently engaging with ethical issues. This analysis identified the following variables in manuscripts: ethics statement, how permission to study remains was granted, involvement/consultation with descendant communities, inclusion of destructive analyses (e.g., DNA and isotopic data), and if remains were recovered after the Native American Graves Protection and Repatriation Act (NAGPRA) was passed in 1990. The data show an overwhelming number of articles failed to engage with these ethical issues; articles did not discuss descendant communities, nor did they have a statement on ethical treatment of remains or how permission was granted. The majority of articles included remains recovered after the passing of NAGPRA and more than half of the research analyzed involved some form of destructive analysis. These results serve as a reminder to researchers that ethical praxis should begin with research design and needs to be explicitly stated in publications. To address these issues, it may be necessary for granting agencies and journals to require such statements, and this in fact is a growing trend within biological anthropology. Future work will continue to explore additional articles and journals to further document current ethical practices in research and publishing.

The meaning of megadonty: predicting dietary mechanical properties in *Australopithecus* and *Paranthropus* using relative premolar size

JEREMIAH E. SCOTT[1], CHRIS A. ROBINSON[2,3,4], LUCAS K. DELEZENE[5] and DARRYL J. DE RUITER[6,7]

[1]Department of Medical Anatomical Sciences, Western University of Health Sciences, [2]Department of Biological Sciences, Bronx Community College, City University of New York, [3]Doctoral Program in Anthropology, The Graduate Center, City University of New York, [4]New York Consortium in Evolutionary Primatology, [5]Department of Anthropology, University of Arkansas, [6]Department of Anthropology, Texas A&M University, [7]Evolutionary Studies Institute, University of the Witwatersrand

Postcanine megadonty is a hallmark of the australopith masticatory apparatus. This feature is widely considered an adaptation for processing mechanically challenging foods, but the nature of the challenge is unclear. Previous work has shown that the relative size of the premolar row is correlated with dietary mechanical properties among extant primates. In this study, we use this comparative framework to estimate dietary elastic modulus (*E*) and toughness (*R*) in four australopiths: *Australopithecus afarensis*, *Australopithecus africanus*, *Paranthropus robustus*, and *Paranthropus boisei*. Relative to jaw length, australopiths have maxillary premolar occlusal areas that are larger than those of extant catarrhines and within the range of platyrrhines and strepsirrhines with three premolars. Phylogenetically informed predictions of dietary *E* and *R* for the australopiths are associated with wide prediction intervals, limiting meaningful inferences in some cases. Nevertheless, a few patterns are evident. First, estimated values for australopiths suggest that they did not regularly feed on foods with particularly high *E*, though occasional consumption of such items cannot be ruled out. Second, there is some evidence that foods with high *R* were an important component of australopith diets, especially in the case of *P. boisei*. Thus, the results of this study suggest that, if food mechanical properties drove the evolution of premolar megadonty in australopiths, then toughness is likely to have been the key variable. This conclusion aligns with studies of dental microwear in undermining the hypothesis that australopiths were adapted for hard-object feeding.

An Analysis of Pet Primate Ads for Five Freedoms of Animal Welfare

MELISSA SEABOCH and SYDNEY CAHOON

Anthropology, Salt Lake Community College

The Five Freedoms form the basis of animal welfare legislation and recommendations. Though it is widely concluded that primates are not appropriate pets, our previous research found online ads for 551 pet primate for sale. We used mixed methods to analyze 236 of these ads which included qualitative data for evidence of whether these primates experienced the Five Freedoms. Freedom from pain/injury/disease was most evident as 55 ads indicated the animals were "healthy"/"vet-checked". "Bottle fed"/"hand fed" were listed in 83 ads with 16 ads indicating "formula". Only two ads indicated primate-specific foods ("monkey biscuits"/"Zupreem Marmoset Diet"). While this suggests freedom from hunger, it also suggests the animals are not free to express natural behaviors. Additionally, "pizza" and "grapes" were listed. Freedom from physical discomfort was evident in only three ads which listed "heat lamp"/"sun lamp". No ads directly addressed freedom from fear/distress and most used positive descriptors, such as "friendly" or "happy". However, sellers are likely not equipped to recognize fear/distress in primates. Privately owned primates in unnatural physical and social environments do not have the freedom to express most natural behaviors. Sociality was the natural behavior most evident in the ads. Twelve ads described the animal as "troop-raised"/"mother-raised" and 10 ads indicated that bonded pairs were being sold. Ninety-three ads described the animals as socialized, 24 ads with people and 20 ads with other animals. Based on our analysis, pet primates do not experience the Five Freedoms, providing another reason that primates should not be kept as pets.

The Kyushu University Museum Skeletal Collection 3D Surface Scan Sharing Project and Related Ethical Considerations

NORIKO SEGUCHI[1,2], SHIORI YONEMOTO[3] and JAMES F. LOFTUS III[4]

[1]Faculty of Social and Cultural Studies, Kyushu University, [2]Department of Anthropology, The University of Montana, Missoula, [3]Laboratory of Information and Multimedia Sciences, Kyushu University Museum, [4]Japan Society for the Promotion of Science, Kyushu University

In recent years, the use of 3D scanning of archaeological and forensic human remains and geometric morphometric analysis have become popular in biological anthropology. 3D scanning and the generating of 3D virtual models are very useful for curation and preservation purposes, and are easily shared remotely.

Recently, the Kyushu University Museum launched a high-resolution 3D surface scanning project of the archaeological collections housed at the museum and have been generating 3D models of their human skeletal remains. This allows for obtaining complex measurements, observing surface contours and micro-details on

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

the surface, and utilizing mathematical analysis. The museum plans to create an online database of 3D-scanned data and archaeological information and to provide worldwide access to scholars who are interested in conducting the research.

The local outreach activities by the Kyushu University Museum are especially important. The museum has been creating opportunities to publicize their 3D models and bioarchaeological analysis research findings to residents and children of local communities. Creating 3D replicas and using them for educational dissemination provides an opportunity to enhance public understanding of the study of ancient human bones. In fact, these local outreach efforts have brought out community-driven research questions.

Although there are many beneficial aspects to 3D databases, consideration of research ethics regarding 3D scan data and models of human remains has come to the forefront of concerns. We review the discussions by the museum before the launch of the open online database concerning ethical considerations related to practices, intellectual property, and outreach to local communities.

This work was supported by the MEXT KAKENHI Grant No. JP19H05737, JP20H00048, and the Japan Society for Promotion of Science Research Fellowship for Young Scientists Program No.19J21494.

Dietary breadth, biogeography, and resource tracking in early hominins

YEGANEH SEKHAVATI and DAVID S. STRAIT

Anthropology, Washington University in St. Louis

The degree of ecological generalization (eurytopy) or specialization (stenotopy) of a taxon is thought to influence the likelihood of that taxon to disperse. For example, it has been predicted that species with narrow diets are more likely to track resources during periods of environmental change than those with broad diets. Early hominins exhibit variation such that species consuming a mix of C3 or C4 foods have isotopically broad diets, and those primarily consuming C3 or C4 foods have isotopically narrow diets. Here we test whether dispersals are more common among species with isotopically narrow diets using the R package *BioGeoBEARS*. We examined two phylogenetic trees that differ in the position of *Australopithecus sediba*. For each tree, we fit trait-independent and trait-dependent models in which having a narrow diet affects the probability of dispersals. Results suggest that trait-dependent models received 54.5% of the AICc weight in tree 1 and 45.8% in tree 2. Averaged across all models, macroevolutionary dispersal rates are estimated to be 52% and 43% lower for species with narrow diets in trees 1 and 2, respectively. This suggests that hominin species with isotopically narrow diets may not engage in resource tracking but rather may exhibit flexibility in dynamic environments.

Factors Underlying Bony Lesions in a Central California Prehistoric Population: Causative or Reactive Responses to Inflammation and Immune System Activation

GRACE A. SELECKY[1], JESSICA M. CRONIN[2], SAMANTHA E. YAWITZ[1], ABIGAIL H. SORENSON[3], REBECCA S. JABBOUR[4] and GARY D. RICHARDS[5]

[1]Department of Molecular and Cell Biology, University of California, Berkeley, [2]Department of Integrative Biology, University of California, Berkeley, [3]Department of Computing, Data Science, and Society, University of California, Berkeley, [4]Department of Biology, Saint Mary's College of California, [5]Department of Biomedical Sciences, A.A. Dugoni School of Dentistry

Native North Americans show high frequencies of rheumatoid arthritis (RA) but lack HLA alleles classically associated with a genetic predisposition. Whether this susceptibility to RA was present in prehistoric populations is unknown, as it may have arisen in the 1800s as a protective mechanism against *Mycobacterium tuberculosis* infection. Here we evaluate immune system pathways that link an expression of a rheumatoid-like arthritis with an *M. tuberculosis* infection in prehistoric California.

In a sample of 8564 prehistoric California individuals, 2570 showed bone pathology. Of the latter, six showed evidence of *M. tuberculosis* infection. These individuals derive from the Hotchkiss Mound (CCo-138), a prehistoric Central California shellmound. In this population, 318 individuals have bone pathology, with 68.24% possessing joint lesions. We also compiled comparative paleoepidemiological profiles for two other shellmound populations, Ala-328 and Ala-307.

The incidence of joint lesions at CCo-138 is like other shellmound populations. However, the CCo-138 population expresses a highly destructive, symmetrical polyarticular arthritis, unique to this locality. The pattern of joint destruction resembles RA. However, extensive destruction of vertebral/rib synovial joints, related processes, and associated periosteal bone deposits appears like the spondyloarthropathies or osteoarthritis. Individuals with *M. tuberculosis* express extensive erosive lesions of the midthoracic/upper lumbar vertebrae but lack a periosteal response or synovial joint involvement.

This co-occurrence of *M. tuberculosis* and a uniquely patterned joint disease is unique in prehistoric California. The population likely expressed an autoimmune-induced arthritis that was significantly upregulated in the presence of the tuberculosis bacterium, resulting in joint destruction spanning a rheumatoid-osteoarthritis pattern.

Tooth crown biomechanics in the molars of *Australopithecus africanus* and *Paranthropus robustus*

RACHEL S. SENDER and DAVID S. STRAIT

Biological Anthropology, Washington University in St. Louis

Teeth must perform two functions simultaneously – they must fracture foods without being fractured themselves. Tooth strength is therefore an important measure of feeding performance. This study uses finite element analyses (FEA) to compare crown strength in the teeth of apes and fossil hominins. CT scans were obtained from one relatively unworn upper second molar from each of *Pan troglodytes, Gorilla gorilla,* and *Pongo pygmaues,* as well as two such teeth from each of *Australopithecus africanus* and *Paranthropus robustus*. Scans were converted into finite element models (FEMs) that were assigned the material properties of enamel and dentin. The FEMs were loaded in three ways to simulate: 1) contact between a hard object and a single cusp tip, 2) contact between a hard object and all major cusp tips, and 3) contact between a soft object and the surface of the entire occlusal basin. The bite force was oriented perpendicular to the occlusal plane and had a magnitude calculated as the maximum bite force previously estimated in chimpanzees isometrically scaled to two thirds the volume of each of the FEMs. Maximum principal (tensile) stress was recorded in the tooth crowns and stress levels were used as an inverse proxy for strength. Our results show that the *Australopithecus* and *Paranthropus* teeth are stronger than ape teeth during loading regimes that simulate hard object feeding, but that fossil hominin teeth can be unexpectedly weak during bites simulating soft object feeding. This may have implications for understanding the evolution of hominin diets.

Cooperative genetic interaction and dental developmental timing

VALERIE SGHEIZA[1] and HELEN LIVERSIDGE[2]

[1]Anthropology, University of Illinois Urbana-Champaign, [2]Institute of Dentistry, Barts and the London School of Medicine and Dentistry, Queen Mary University of London

The Cooperative Genetic Interaction (CGI) theory proposes that dental development is the product of neural crest cell migration, local molecular signaling gradients in the oral epithelium, and homeobox gene activation. CGI incorporates both Field and Clone theory. We examine CGI through dental developmental staging by testing two hypotheses. First, variation in development will increase distally within tooth classes. Second, distal developmental variation within tooth classes will correlate with age-at-transition between stages. The sample consisted of Moorrees et al. (1963) scores of left mandibular permanent

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

teeth from panoramic radiographs of 880 London children 3-22.99 years of age stratified by year of age, sex, and Bangladeshi or European ancestry. Hypothesis 1 was tested on restricted multivariate cumulative probit models using plotting of variance coefficients. Hypothesis 2 was tested on unrestricted univariate cumulative probit using Bayes Factors on linear regression coefficients calculated for each individual stage transition across trials. Aside from large variance in M3, variance did not consistently increase or decrease within classes. Standard error of the variance increased distally within classes, but error bars were overlapping. When mean age-at-transition was regressed on standard deviation, the mean regression coefficients across stages were positive for all teeth, indicating increasing variation with increasing age. The largest Bayes factors were PM1=554 and M2=122. Developmental variation within tooth classes was neither inconsistent with CGI nor strongly supportive. Later age-at-transition was associated with larger standard deviations, but this association did not increase distally within classes. Evidence for CGI was therefore mixed.

Gait kinematics in response to substrate diameter and orientation in wild cercopithecoids

LIZA J. SHAPIRO[1], LYDIA C. MYERS[1], JUDITH JANISCH[2], NICOLE M. SCHAPKER[2,3], IAN BARRY[1], TAYLOR PHELPS[2], TOBIN HIERONYMUS[2] and JESSE W. YOUNG[2]

[1]Department of Anthropology, University of Texas at Austin, [2]Department of Anatomy and Neurobiology, Northeast Ohio Medical University, [3]School of Biomedical Sciences, Kent State University

Technological advances have made it possible to directly "field-test" functional associations between locomotor kinematics and natural substrate variation that are difficult to simulate in the lab, providing a deeper understanding of primate locomotor adaptation. Our recent work has addressed ecological and phylogenetic influences on quadrupedal kinematics in eleven platyrrhine species. We are expanding this research to include eight cercopithecoid and eight lemuriform species – an unprecedented field-based kinematic dataset. Here, we present preliminary data collected at Kibale National Park, Uganda, on *Cercopithecus mitis* and *Cercopithecus ascanius* (n=42 strides). We quantified quadrupedal gait kinematics from high-speed video and used remote sensing to measure substrate diameter and orientation. Both species used predominantly diagonal sequence gaits across all substrates, with *C. mitis* showing a higher frequency of lateral sequence gaits (*C. mitis*: 37% of strides; *C. ascanius*: 4% of strides). As with wild platyrrhines, *C. mitis* and *C. ascanius* did not adjust limb phase or gait type and showed variable speed adjustments in response to changing substrate diameter. Neither species significantly adjusted limb phase in response to changing substrate orientation - a relationship that was variable among platyrrhines. Overall, these two cercopithecoid species exhibited relatively invariable kinematics in response to substrate conditions. Future analysis of additional cercopithecoids and a phylogenetic analysis of quadrupedal kinematics across broader primate clades are needed to confirm these results. This study confirms the consistent use of diagonal sequence gaits in quadrupedal primates and the robusticity of primate gait kinematics in response to the rigors of the arboreal habitat.

Supported by NSF BCS-1921135 and BCS-1921314.

Exploring sleep, health, and social threat among Indigenous Wixárika living in Guadalajara, Mexico

ERIC C. SHATTUCK[1,2,3], LEELA MCKINNON[1,4], RENÉ CROCKER SAGASTUME[5], IGOR RAMOS HERRERA[5], PARI TEMAI GONZÁLEZ[5], ADDY VILLASEÑOR[5], YARA MARTIN[5], PAOLA PÉREZ[5], SOFIA MUÑOZ[5], THANKAM S. SUNIL[6] and DAVID R. SAMSON[1,4]

[1]Department of Anthropology, University of Toronto, Mississauga, [2]Institute for Health Disparities Research, University of Texas, San Antonio, [3]Department of Public Health, University of Texas, San Antonio, [4]Centre for Urban Environments, University of Toronto, Mississauga, [5]Departamento de Salud Pública, Centro Universitario de Ciencias de la Salud, Universidad de Guadalajara, [6]Department of Public Health, University of Tennessee, Knoxville

Threats to "social safety" include loneliness, social conflict, devaluation, and exclusion and are known to contribute to multiple negative health outcomes, including increased inflammation, increased mortality, and worse health behaviors. Social threats have also been associated with poor measures of sleep health. Intriguingly, poor sleep itself can contribute to emotional dysregulation and social conflict, suggesting a feedback loop wherein social threat is worsened through its effect on sleep. However, data supporting these conclusions generally come from Western/Global North samples. Here, we test the relationship(s) between sleep, social threat, and emotional dysregulation in a small pilot sample (n = 20, 65% women, mean age = 33) of indigenous Wixárika from Guadalajara, Mexico. Objective sleep measures (total sleep time, sleep efficiency, and wake after sleep onset) were collected with CamNtech MotionWatch 8 devices, which participants wore for up to 30 consecutive nights. Subjective sleep quality, loneliness, social support, and emotional dysregulation were assessed by surveys. Subjective sleep quality, but not objective measures, correlated with higher loneliness ($r=0.51$, $p<0.05$) and emotional dysregulation ($r=0.49$, $p<0.05$) as well as worse physical ($r=0.49$, $p<0.05$) and mental ($r=0.60$, $p<0.01$) health. No relationship was found between emotional dysregulation and social threat measures. The correlations remained when accounting for age and sex, but not physical or mental health. While additional data are needed to fully test our hypothesized model, results suggest a complex interplay between social threat and subjective – but not objective – measures of sleep and health.

The embodiment of farmwork in disease risk and immune function

JOANNA GRACE SHAW[1], DIANA MENDOZA[2,3], SOPHIA BOLAÑOS-ROBINETTE[2,4], DIANA ROMAN[5], JOSIE ROMERO[6], GILBERTO ROSAS[1,2,7], KORA MALDONADO[1,8], ELLEN MOODIE[1,10,2,7,9], CHAREE THOMPSON[11,12] and JESSICA BRINKWORTH[1,2]

[1]Department of Anthropology, University of Illinois at Urbana-Champaign, [2]Carl Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, [3]Community Health Partnerships of Illinois, Champaign, Illinois, [4]Illinois Migrant Education Program, Chicago, Illinois, [5]Department of Inclusion and Intercultural Relations, University of Illinois at Urbana-Champaign, [6]Department of Food Science and Human Nutrition, University of Illinois at Urbana-Champaign, [7]Department of Latina/Latino Studies, University of Illinois at Urbana-Champaign, [8]Department of American Indian Studies, University of Illinois at Urbana-Champaign, [9]Center for Global Studies, University of Illinois at Urbana-Champaign, [10]Unit for Criticism and Interpretive Theory, University of Illinois at Urbana-Champaign, [11]Biomedical and Translational Sciences, University of Illinois at Urbana-Champaign, [12]Department of Communications, University of Illinois at Urbana-Champaign

Food production is a dangerous 1.1 trillion-dollar industry in the United States that employs a largely marginalized workforce and reports the highest rates of injury and illness of any industry in the nation. Under the U.S. policy of "agricultural exceptionalism" (AE), farmwork occurs under limited labor regulations. As such, farmworkers experience social and physiological stressors known to impact health and immune function in combination, an amount not replicated by many industries. These stressors include social disruption, exposures to dangerous organic dusts, long work hours, and low wages. Here, we examine how farmwork is biologically embodied in workers by quantifying stressors and immune activity experienced by an Illinois farmwork force. With research associates and translators from aligned communities, we met with 59 farmworkers and surveyed them for stress type and load, collected blood, and retrieved agricultural dust samples from clothing. We also collected blood from 30 non-farmworkers. Farmworkers tended to be young, male, parents and without health coverage. Few H2A workers traveled with family. Approximately 50% of farmworkers were cost-burdened/severely cost burdened by housing, a signal financial stress. Nearly 70% of workers reported moderate/severe acute fatigue. LPS assays demonstrate that all had substantial

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

exposure to agricultural dust, which can trigger a proinflammatory response. Complete blood cell counts revealed farmworkers maintained significantly higher levels of normal neutrophils compared to non-farmworkers, suggesting a noninfection-based shift in bone marrow regulation ($p<0.0001$). In combination, these findings suggest that farmworkers experience high stress through working conditions that is concurrent with major shifts in immunomodulation.

On the origin of species complexes

MYRON SHEKELLE[1], ALAN TEMPLETON[2] and CHUCK CANNON[3]

[1]Biology, Western Washington University, [2]Biology, Washington University in St. Louis, [3]Center for Tree Science, Morton Arboretum

Many species exist within a species complex of closely related taxa, where sympatry is absent and hybridization at parapatric boundaries is common. This is particularly common within Primates where, for example, on the island of Sulawesi all 7 tarsier species and all 7 macaque species fit this pattern. Likewise, this pattern is the rule, rather than the exception for lorises, gibbons, macaques, baboons, and many other primates. A term common among botanists for this pattern is syngameon. We propose a mechanism, whereby natural selection favors substructured populations wherein the interaction of evolutionary mechanisms promotes greater evolvability. Our model recalls an old debate within evolutionary biology concerning the nature of variation in natural populations. We observe that empirical evidence reveals that many organisms live within hierarchically substructured populations, demes, species, syngameons, and such, that share limited but nonzero gene flow, and which are ideally suited for shifting balance to operate. In such populations, the interaction of gene flow/admixture, mutation, drift, and selection promote greater evolvability, while the mechanisms promoting cohesion within subpopulations may be sexual selection, partial reproductive isolation, and/or ecological differentiation. Recent case studies where this perspective seems relevant include the adaptive value of gene flow between polar bears and brown bears, while lack of gene flow has recently been proposed for the extinction of dire wolves where other canids persisted. This framework might also be particularly useful for understanding the evolution of Middle Pleistocene hominins, *Homo sapiens*, *H. neanderthalensis*, and Denisovans.

Current funding for MS is from the Margot Marsh Biodiversity Foundation, Primate Conservation, Inc.

Dry matter digestibility and stable carbon and nitrogen isotope analysis of captive northern galagos (*Otolemur garnettii)* fed experimental "frugivorous" and "invertebrate" diets

ZACKARY R. SHEPARD[1], JAMES E. LOUDON[1], KATHERINE B. SMITH[2], MICHAELA E. HOWELLS[3], ANDRES M. GOMEZ[4], OLIVER C.C. PAINE[5,6] and MATT SPONHEIMER[6]

[1]Anthropology, East Carolina University, [2]Anthropology, The University of Southern Mississippi, [3]Anthropology, University of North Carolina, Wilmington, [4]Animal Science, University of Minnesota, [5]Anthropology, San Diego State University, [6]Anthropology, University of Colorado, Boulder

Northern galagos (*Otolemur garnettii*) are small, nocturnal, acrobatic primates that are difficult to observe in free-ranging settings. To better understand the feeding ecology of *O. garnettii*, we provided a captive colony of eleven galagos (five females and six males) experimental "frugivorous" and "invertebrate" diets that simulated the seasonal dietary shifts that this species faces in the wild. We analyzed the stable carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) values of the foods in the "frugivorous" and "invertebrate" diets and note both diets included primate biscuits to ensure the nutritional stability of each galago. The "frugivorous" diet also included blackberries, raspberries, and tamarind, while the "invertebrate" diet included crickets, mealworms, night crawlers, and red worms. The stable isotope values of these foods were compared to the fecal $\delta^{13}C$ and $\delta^{15}N$ values collected from each galago. We accounted for the contribution of each food in the diets to interpret the $\delta^{13}C$ and $\delta^{15}N$ fecal values of the galagos. When averaged, across all foods within the diet, the galago's "invertebrate" diet was significantly lower in ^{13}C ($P<0.05$) and higher in ^{15}N ($P<.001$) and their $\delta^{15}N$ fecal values were significantly higher ($P<0.01$) when they were consuming this diet. Digestibility trials revealed the galagos were more efficient at digesting the "invertebrate" diet (DMD = 76.6±7.0%) compared to the "frugivorous" diet (DMD = 72.0±5.1%) which may mean "invertebrate" foods are more readily incorporated into their tissues. Therefore, structural differences in these substrates may be why the dietary offsets between foods and feces better aligned with the "frugivorous" diet.

This project was supported by a grant from the National Science Foundation (RAPID Award #1840977).

Frequent caretaking not associated with health risks in non-custodial grandmothers

SOFIYA SHREYER and ACHSAH F. DORSEY

Anthropology, University of Massachusetts Amherst

As the world population ages, grandmothers are increasingly stepping into demanding caregiving roles—in the U.S, more than 13 million children are living with their grandparents. Many studies examining health of caretaking grandmothers focus on custodial grandmothers, and find caregiving is linked with heightened depression and stress, exacerbation of existing conditions, fatigue, decreased attention to their own medical needs, and worse perceived health. Research on grandmothers who do part-time care is lacking. We compared the health of 10 grandmothers who do infrequent care (<10 days per month) and 10 grandmothers who do frequent care but are not primary caregivers (>15 days per month) in Western Massachusetts to explore how caregiving intensity impacts non-custodial grandmothers. Women were asked about their demographics and caregiving, and self-administered stress (PSS, Perceived Stress Scale), depression (PHQ-9, Patient Health Questionnaire), and physical activity (CHAMPS Physical Activity Questionnaire for Older Adults) questionnaires. Height and weight were measured along with grip strength with a dynamometer and bone density with an ultra-sonometer. Linear regressions were performed in SPSS with stress, depressed mood, BMI, physical activity, grip strength, and bone density as independent factors and caretaking intensity (low vs high) as dependent, and controlled for age, marital status, employment, and financial comfort. Grandmothers who do more care reported significantly less depressed mood ($p=0.002$). Models including other health factors were not significant. Our findings suggest that higher levels of non-custodial care are not associated with health risks for women, and may carry benefits for mental health.

The impact of a non-binary sex estimation on accuracy of males and females

ELENA SIERRA-SERRANO[1], SYDNEY REID[2] and JOHN ALBANESE[2]

[1]Archaeology, Simon Fraser University, [2]Integrative Biology, University of Windsor

Accurate sex estimation has an enormous weight in an unknown individual's biological profile, and the methods used should produce useful information in a forensic context. The goal of this research is to investigate the impact that incorporating a non-binary category has on male and female individuals. To this end, accuracies of two existing sex estimation methods (Albanese 2003 and Albanese 2013), were compared with and without an "intermediate" category. This included individuals from the Terry, Grant, Coimbra, and Lisbon Collections.

Results indicate that when intermediate individuals are recognized as their own category, those allocated as male or female increase their accuracy from 1 – 3% to 7% depending on the method and collection tested. Both methods showed

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

higher accuracy, with Albanese 2003 having the best certainty overall and Albanese 2013 showing the greatest improvement in accuracy under a non-binary approach.

Currently, there is no guidance in the forensic literature on how to approach sex estimation from a non-binary perspective. Our results suggest that incorporating a non-binary category into existing sex estimation methods does not hinder accuracy of those allocated as male or female, plus it can prove advantageous. However, more research on other methods and collections is needed. There is also potential for "intermediate" individuals to be more fully represented as such, in their biological sex and ultimately their identity. Yet, this is an umbrella category including many different manifestations. Its boundaries and purpose should be investigated as community-based research in consultation with the communities in question and their advocates.

Relatedness of Cause of Death and Skeletal Markers of Physiological Stress in the Hamann-Todd Collection

ALLYSON M. SIMON[1], TEMPEST D. MELLENDORF[1], COLLEEN M. CHEVERKO[2], MELISSA A. CLARK[3] and MARK HUBBE[4]

[1]Department of Applied Forensic Sciences, Mercyhurst University, [2]Division of Biomedical Affairs, Edward Via College of Osteopathic Medicine-Louisiana, [3]Department of Criminology, Anthropology, and Sociology, Cleveland State University, [4]Department of Anthropology, The Ohio State University

The cumulative burden of physiological stress during an individual's life is reflected in a complex interaction of frailty, mortality, and disease susceptibility. Such accumulated responses are often related to causes of death (COD), which can be used as an indicator of a population's living conditions. Given the importance that cumulative stress has on the discussion of past human societies in bioarchaeology, this study explores the relatedness of COD and markers of physiological stress in the Hamann-Todd Osteological Collection (HTOC), a predominantly low socioeconomic status population from the early 20th century. We analyzed the incidence of linear enamel hypoplasia (LEH), stature, and antemortem tooth loss (AMTL) for 298 individuals. Given that HTOC individuals have been historically neglected in research, this investigation contributes to studies characterizing the lived experiences of the population. COD varied by socially ascribed race and sex within the sample. Black Americans were twice as likely to die from tuberculosis than white Americans ($x2$=4.793, p=0.029). Individuals that died from long-term disease or illness had a significantly greater prevalence of AMTL (F=4.443, p=0.001) and shorter statures for males (F=2.672, p=0.024) and females (F=2.450, p=0.037) relative to other CODs. LEH were also more common, although not significant ($x2$=1.794, p=0.180). This supports the role that physiological stress endured during development has on long-term physiological disease or illnesses that may contribute to mortality in this sample. Stressors endured during adulthood, specifically those related to conditions in long-term care institutions, are related to higher proportions of AMTL (t=3.662, p<0.001) for females in this sample.

Paleodemography of the Neolithic Age in Northern China with Special Reference to the Hamin Disaster Site

MARK SIMON[1], QUANCHAO ZHANG[2], MARTIN SIKORA[3], HUGH WILLMOTT[4], SHARON DEWITTE[5] and QIAN WANG[1]

[1]Department of Biomedical Sciences, Texas A&M University School of Dentistry, [2]School of Archaeology, Jilin University, [3]Globe Institute, University of Copenhagen, [4]Department of Archaeology, University of Sheffield, [5]Department of Anthropology, University of South Carolina

Paleodemographic studies reconstruct population dynamics and the demographic impacts of disturbances and disasters in the past. The Hamin Neolithic settlement in northeastern China (5,000 years BCE) was abandoned following rapid mass death of the majority of inhabitants from unknown causes. The biological sex and age-at-death distributions of 68 individuals at the Hamin disaster site were compared to those from 47 Neolithic cemeteries in Northern China totaling 8,211 individuals (8,000-1,800 BCE). Results demonstrated that the mortality pattern at the Hamin site differs from that of the broader Neolithic Age mortuary populations in Northern China. At Hamin, biological sex could be estimated for 29 individuals with a female to male ratio that was evenly distributed (1.07:1) as compared to the broader Neolithic period that was biased towards males (0.61:1). Moreover, age-at-death could be estimated for 44 individuals at Hamin, indicating a mortality pattern that is biased towards non-adults (0-14 years) and old adults (36-55 years), whereas the broader Neolithic Age distribution is biased towards middle adults aged 24-35 years (i.e., Hamin vs. North China: 0-14: 22.7% vs. 13.8%; 24-35: 22.7% vs. 40.3%; 36-55: 38.6% vs. 27.3%). This finding would suggest an abnormal death event, hypothetically caused by a plague-like infectious pathogen. Further empirical bioarchaeological investigation of the Hamin site and comparison with other disaster sites in conjunction with aDNA investigations will not only reveal the cause of the abandonment of the Hamin settlement, but also enrich our knowledge of the history and the evolution of pathogens and diseases.

This project is supported by NSF grant to Q.W. and S.D. (NSF # 2040388).

Investigating a novel location for assessing dental function and dietary signals at the dental root

ZANA R. SIMS

Center for Functional Anatomy & Evolution, Johns Hopkins University School of Medicine

Dentition provides a wealth of information about an animal and forms a keystone of primate evolution research. Much of the literature has focused on the easily accessible dental crown, and, as a result, dental roots remain understudied. This study seeks to introduce investigation of the cervical root cross-section (CRCS) to obtain functional signals related to diet.

A sample of catarrhine lower molars (n= 83) was selected to cover a wide range of dietary categories and preservation conditions. Resampled micro-CT slices were taken from the dental cervix and exported for analysis. The cross-sectional variables dentine area, Imax, and Imin were regressed on jaw length. Tests for normality and equality of variance were performed on residuals before ANOVAs with pairwise post-hoc tests run to examine differences due to sex, tooth position, and diet. Statistical significance for all analyses was set at (P= <0.05).

Results of regression analysis found high (range: 0.84-0.86) coefficients of determination for each variable and all models were significant. Primates with mechanically challenging diets, like folivores and tough-object frugivores, tended to fall above the regression line, whereas primates with less challenging diets fell below. ANOVA results found no differences due to sex; however, M_1 was significantly different from M_2. Differences were also identified between soft-object and tough-object frugivores, tough-object frugivores and omnivores, and omnivores and mixed folivores.

These results indicate that the CRCS effectively identifies nuanced differences in dietary categories that are not often discerned by other methods providing valuable insight into the mechanical function of teeth.

Domesticated Rats: A Look at Craniofacial Neoteny

NANDINI SINGH and MEGAN SMITH

Anthropology, California State University, Sacramento

Belyaev's domestication experiments with silver foxes and rats were the first to test the causal relationship between tameness and the domestication syndrome (DS). He proposed that selection for tameness modified the regulation of interconnected developmental systems that resulted in phenotypic-genotypic and behavioral traits found across all domesticated animals, i.e the DS. In late *Homo* evolution, self-domestication is suggested to have caused major shifts in the craniofacial form, acting through developmental changes

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

brought on by prosocial behaviors. However, recent studies have contested the unbiquity of the DS in domesticated populations. Here we examine the consistency of the DS as it relates to craniofacial neoteny – a long-considered characteristic of domesticated animals. We compare the cranial form of Belyaev's domesticated adult rats to juvenile wild rats to determine whether the domesticated rats exhibit neoteny. Our data comprise 3D landmarks taken on high-resolution micro-computed tomography images of adult and juvenile rat crania. Geometric morphometrics and statistical techniques such as principal component analysis and multivariate regressions were used to analyze the data. Results show the tame rats to share similarities with the "young adult" wild rats more so than the fully adult specimens, however, the selected rats are largely distinct in their craniofacial form from the wild animals. Our findings cannot discount neoteny as a pervasive phenotypic outcome of intentional- or self-domestication. Key molecular pathways that regulate organismal development are conserved across mammalian phylogenies. Using experimental animals in biological anthropology can open doors to new questions not possible to address with traditional datasets.

Cobb Professional Development Grant (2020-2022)

Reconstructing the history of archaic introgression in modern humans: Insights from whole genome sequences of worldwide populations

LAURITS SKOV, ELISE MARIE PAULETTE KERDONCUFF and PRIYA MOORJANI

Department of Molecular and Cell Biology, UC Berkeley

Analysis of archaic and modern human genomes has revealed evidence of gene flow from archaic hominins (Neanderthal and Denisovans) into modern humans and highlighted its critical role in shaping the genetic/phenotypic variation in modern humans. However, most studies have focused on Europeans and East Asians, with very few genomes from other parts of the world, leaving our understanding of human evolutionary history incomplete. In this study, we integrate data from four different studies including ~31,000 previously published genomes and ~2700 newly sequenced genomes from South Asia.

Using these genomes, we recover 1602 Gb of Neanderthal genome and 0.660 Gb of Denisovan genome hidden in modern human genomes. This is the largest fraction of archaic ancestry recovered. The distribution of these segments across worldwide populations provides insights about how recent founder and admixture events have shaped the remnants of archaic ancestry in our genomes. Further, we find that while most Neanderthal introgressed sequence is shared across the world, there is ~300 Mb of the introgressed Denisovan sequence that is only present in South Asians and not seen elsewhere in the world. We develop a new framework for inferring the timing of archaic admixture using the mutation clock that leverages the new mutations that have arisen on the introgressed segments since the admixture. This new approach allows us to date Neanderthal admixture to around 50,000 years ago, consistent with the dates from ancient DNA studies. Together, these analyses provide new insights about the legacy of archaic admixture in modern humans.

The Effects of Socioeconomic Status on Female Health at St. Benet Sherehog

ANASTASIA S. SLACK and CHERYL P. ANDERSON

Anthropology, Boise State University

This research investigates the impacts of socioeconomic status on female health at three pre-industrial burial sites in London, England. The analysis compares the female skeletal sample from the St. Benet Sherehog Parish (SB), a middle-status site, to the cemeteries at Broadgate (BG) and St. Thomas Hospital (ST), both representing low-socioeconomic status sites during the 17th century CE. Data for Broadgate and St. Thomas Hospital were made available by the Museum of London's Wellcome Osteological Research Database and were compared with published data for St. Benet Sherehog to test the hypothesis that women at St. Benet Sherehog exhibited better health outcomes during this period.

Results vary for the pathologies included in this study, but three differ significantly ($p < 0.05$) for St. Benet Sherehog (n=57) when compared to one or more of the other sites, St. Thomas Hospital (n=29) and Broadgate (n=30). The pathologies that are significantly different are the following: linear enamel hypoplasia (SB=33%, ST= 62%, BG=0; $p < 0.05$) dental caries (SB=40%, ST=66%, BG=67%; $p < 0.05$), and periosteal reactions (SB=49%, ST=55%, BG=7%; $p < 0.05$). Overall, the results show that the females buried at the parish at St. Benet Sherehog were less likely to exhibit these conditions. These disparities may reflect the social and economic conditions of the Stuart period, which heavily divided society by social class and gender; the middle-class females from St. Benet Sherehog were afforded better access to resources and living conditions.

Patterns of dental macrowear in living and fossil cercopithecid primates

IRENE E. SMAIL

Biomedical Sciences, West Virginia School of Osteopathic Medicine

Within extant primates, rates of dental macrowear along the toothrow have been shown to vary between species based on differences in diet, tooth morphology, and local environmental conditions. This project aims to quantify molar wear rates in a sample of fossil cercopithecid primates to assess whether patterns of relative molar wear in extinct taxa are consistent with extant species commonly used to model their paleoecologies.

Two-dimensional dental wear was measured as percent dentin exposure seen in occlusal photographs of maxillary first, second, and third molars from over 150 individuals of extant and extinct cercopithecid primates. Slope estimates from general least squares regressions performed on M1/M2 and M2/M3 tooth pairs were used to compare rates of wear along the molar row. Overall, species of *Cercocebus*, *Lophocebus, Semnopithecus,* and *Pp. broomi* had comparatively lower slopes for both tooth pairs (from 0.46 - 0.65), while folivorous *Colobus* and *Pygathrix* exhibited higher slopes (0.66 - 0.77 and 1.05 - 1.30, respectively). The papionins *G. major, Pp. jonesi* and *T. gelada* were characterized by more inconsistent wear, with a trend towards higher slopes on M1/M2 than M2/M3. Extant *Presbytis* and *Trachypithecus* displayed the opposite pattern, which may reflect the accelerated eruption of the M2 and M3 in colobines. Slope estimates for fossil *T. oswaldi* (M1/M2) and *T. brumpti* (M2/M3) fell intermediate within the sample. Regressions of *Cercopithecoides*, *T. darti*, and *Pp. whitei* were not significant for any molar pair.

This research was funded by the National Science Foundation (NSF BCS 1926163), The Leakey Foundation, and ASU's School of Human Evolution and Social Change.

Mandibular biomechanics of extant and fossil hominids: a collaboration with W. Kimbel

AMANDA L. SMITH[1], ZERESENAY ALEMSEGED[2], CHRIS A. ROBINSON[3,4,5], CALLUM F. ROSS[2], ANDREA TAYLOR[6] and CAROL WARD[7]

[1]Anatomy, Pacific Northwest University of Health Sciences, [2]Organismal Biology and Anatomy, University of Chicago, [3]Biological Sciences, Bronx Community College, City University of New York, [4]Anthropology, The Graduate Center, City University of New York, [5]NYCEP, New York Consortium in Evolutionary Primatology, [6]Basic Science, Touro University California, [7]Department of Pathology and Anatomical Sciences, University of Missouri, Columbia

Over the last ten years Bill Kimbel used his wide-ranging expertise and intellectual curiosity to catalyze and lead a collaboration on the biomechanics of extant and fossil hominid mandibles using geometric morphometrics and finite element modelling (FEM) to test hypotheses about the functional significance of variation in hominid mandible form. Mandibles are one of the most commonly preserved and morphologically variable skeletal elements in the fossil hominin record. Characteristics such as corpus robusticity, toothrow divergence and the height

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

and orientation of the rami and symphysis have been used to make inferences about the dietary ecology of extinct hominins. Some of these features may function to reduce bone strain magnitude, increase the efficiency of biting, or both, but previous work suggests that they function together to produce species-specific loading, deformation, and strain regimes. Here we present the results of our broad comparative study of mandibular biomechanics across extant hominid species. We used GM techniques to determine patterns of shape variation for four species: *Pan troglodytes*, *Pongo pygmaeus*, *Gorilla gorilla*, and *Homo sapiens* and to determine representative individuals for FEM. We constructed three-dimensional FEMs using CT scans of the female and male specimens closest to the mean for each species and assigned experimentally derived material properties and boundary conditions to simulate biting conditions. Although results confirm similar loading, deformation and strain regimes across models, regions of interest emerge where variation in strain magnitude and shape metrics overlap (the ramus and symphysis).

This research was funded by NSF BSC 1515053

Assessing the foetal position: Teaching and learning osteology using three-dimensional digital approaches.

BENJAMIN J. SMITH, STEPHANIE J. WOODLEY and SIÍN E. HALCROW

Department of Anatomy, University of Otago

Three-dimensional (3D) prints and images of human bone for teaching and learning have become more common in biological anthropology. However, there is a lack of empirical testing of the utility, effectiveness, and perceptions of the use of human remains compared with 3D learning resources. This project assessed these questions in the context of biological anthropology using foetal osteological remains and 3D representations (prints and images) of these remains. The objectives were: 1) to assess the utility of replications of foetal remains as a learning resource through bone identification and siding tasks; and 2) to collect biological anthropology students' perceptions on foetal remains as a learning resource compared with 3D replications. A series of 3D long bone (femur, humerus, and radius) prints with matching interactive 3D digital images were created from the anatomical collection in the W.D. Trotter Anatomy Museum, University of Otago, New Zealand. Participants (n=30) achieved a similar rate of correct responses for the bone identification for the resource types (40% for bone, 37% for print, 47% for image) and most reported they felt comfortable working with the bones. An overarching theme of student perception that emerged was that of 'contextual and responsive learning'. 3D resources were seen as useful supplementary resources to foetal bone. Students valued hands-on interactivity with resources and engagement with technology (including the usefulness of images in a case of visual impairment), and the authenticity of resources. Students also reflected on respecting the fragile foetal remains and ethical considerations of their use.

Inner ear otolith organ morphology predicts head and neck orientation: Uncovering the link between balance and posture in primates

CHRISTOPHER M. SMITH[1,2,6], ASHLEY S. HAMMOND[3,6], SERGIO ALMÉCIJA[3,4,6], IAN S. CURTHOYS[5] and JEFFREY T. LAITMAN[1,2,6,7]

[1]Department of Anthropology, The Graduate Center, City University of New York, [2]Center for Anatomy and Functional Morphology, Icahn School of Medicine at Mount Sinai, [3]Division of Anthropology, American Museum of Natural History, [4]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, [5]Vestibular Research Laboratory, School of Psychology, University of Sydney, NSW Australia, [6]New York Consortium in Evolutionary Primatology, [7]Department of Otolaryngology, Icahn School of Medicine at Mount Sinai

The inner ear otolith organs (utricle and saccule) establish our sense of balance along with the semicircular canals (SCCs). While the SCCs detect angular acceleration, the otolith organs detect linear acceleration, vibration, and head tilt. These sensory capabilities rely on otolith organ maculae (regions containing hair cells) and their orientation relative to gravity. As a result, these maculae provide a structural reference for the head in 3D space. Understanding the relationship between maculae and head orientation relative to the neck and gravity (head and neck posture) may therefore provide a novel way to reconstruct such posture in fossil primates.

We tested the hypothesis that maculae orientation is related to head and neck posture using virtual 3D models of 76 left inner ears derived from micro-CT scans of 13 extant anthropoid species. Bony landmarks were chosen to approximate otolith organ maculae. Planes were derived from landmarks to determine maculae orientation. Phylogenetic generalized least squares models determined correlations between maculae angulation (MA; angle between maculae planes) and three postural measures (from Strait and Ross, 1999). After controlling for phylogeny and body mass, MA significantly correlates with orbit inclination ($p<0.0001$, $R^2=0.82$) and inclination of the Frankfurt plane ($p=0.007$, $R^2=0.45$). MA significantly correlates with neck inclination ($p=0.035$, $R^2=0.28$) when controlling for phylogeny only.

These findings indicate a tight correlation between the most ancient part of the balance system and how the head is positioned within space. Understanding this link now allows us to approach aspects of posture in fossil primates using inner ear morphology.

This research was supported by an NSF Doctoral Dissertation Research Improvement Grant (award #: 2051335), the MCIEI (PID2020-116908GB-I00), and the Generalitat de Catalunya (CERCA Programme).

Sex estimation from dental crown and cervical metrics in modern global sample

EMILY SMITH, DORI KENESSEY, TATIANA VLEMINCQ-MENDIETA and MARIN PILLOUD

Department of Anthropology, University Nevada Reno

Despite forming during early childhood prior to the development of secondary sex characteristics, the human dentition exhibits sexual dimorphism. There are a handful of population-specific methods that explore sexual dimorphism of crown measurements; however, there are few explorations of global dental variation that also incorporate measurements of the cervix of the tooth. This study incorporates crown and cervical measurements to explore sexual dimorphism on a large global sample to identify the utility of the dentition in estimates of biological sex (assigned at birth).

Data were collected on donated skeletal collections of known sex in the United States and South Africa (n=579; female=191 and male=388). Maximum crown and cervical dimensions (mesiodistal and buccolingual) were collected on the left side of the dental arcade. The right antimere was substituted if observations could not be made on the left side. Univariate t-tests indicate sexual dimorphism of every single measurement. Sexual dimorphism was more pronounced in cervical measurements compared to the crown. Cervical measurements of the upper and lower canine show the highest levels of dimorphism (between 9.14% and 11.78%); however, the mesiodistal crown measurement of the lower canine is also in this range with 9.52% dimorphism. In a simple discriminant function analysis to estimate sex using only these five variables, the cross-validated model was able to correctly estimate sex in 81.0% of cases. This study highlights the utility of the dentition, particularly the cervical measurements, in sex estimation. Future work will incorporate non-binary sex designations.

Companion dogs as a model for the impact of social relationships on stress and fitness

KYLE C. M. SMITH

Anthropology, Pennsylvania State University

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Social stress causes negative health outcomes on wide-ranging metrics, and having strong social connections is associated with better health and a longer lifespan. While the mechanisms linking social factors to health outcomes have often been studied in humans and other primates, dogs offer many advantages as a model for such research. Companion dogs live in the same environment as humans and form close interspecific relationships with them. Compared to primates, dogs' accelerated life histories allow long-term health consequences to be seen over shorter timescales. I conducted a pilot study with pet dogs (n=24) in State College, Pennsylvania, to see how dogs' biological stress is affected by their social relationships and whether social cognition mediates this. Cortisol levels were used to measure dogs' stress response in the short-term (in saliva) and long-term (in hair). The diversity and composition of the oral and gut microbiomes were also characterized and discussed in relation to stress. Dog social behavior was observed during focal follows at an off-leash dog park. I discuss communicative ability as a possible factor mediating the relationship between social interactions and stress, but dogs' performance on a communicative task was not correlated with owner ratings of dogs as communicative (p = 0.135) or extraverted (p = 0.626). Overall, companion dogs are a promising model for understanding how social factors come to be embodied biologically and how social cognition alters the stress response to social interactions.

Did I Shave My Legs for This? Ecologies of Settler Sex and Kinship on the Texas Blackland Prairies

RICK W. A. SMITH[1,2,3], ROBIN G. NELSON[4] and AUSTIN W. REYNOLDS[5]

[1]Sociology and Anthropology, George Mason University, [2]Women and Gender Studies, George Mason University, [3]Indigenous Science, Technology, and Society Lab, Faculty of Native Studies, University of Alberta, [4]School of Human Evolution and Social Change, Arizona State University, [5]Department of Anthropology, Baylor University

The Blackland Prairies ecoregion of Texas has been home to the densest agricultural population in the state for nearly two centuries and remains the westernmost expanse of the large-scale cotton plantation system in the US South. The plantation system is a foundational, pervasive, and enduring form of racial violence in the United States which lay at the crossroads of Indigenous dispossessions, African slavery, and settler heteropatriarchy linked to land tenure. Following the end of the Civil War, the legal practice of slavery ended, but the plantation economy persisted in different forms, including tenant farming, sharecropping, convict leasing, and migrant labor. This project addresses this history with a theoretical grounding in Imperial Terroir, and identifies the nexus of settler sex, gender, and race as a colonial politics of nature that became the stuff of lethal ecological change. Upending questions of sexual essentialism, we ask what the plantation made natural out of its sex. We track the enduring impacts of the plantation on morbidities and mortalities in late 19th and early 20th century Texas. We collected public vital records data (N=1830) across four Blackland counties to evaluate enduring losses of life across farm labor status (p= 2.39e-06), race (1.25e-25), and marital status (p= 2.47e-85), showing that the social orders imposed on the plantation continue to shape life and death in the Blackland Prairies. In doing so we move beyond the inadequate explanatory power of a rural/urban divide and its failures to account for enduring colonial power relations in driving health outcomes.

Wild Baboon Early Life Diets: Insights from Trace Elements in Teeth

TANYA M. SMITH[1], MANISH ARORA[2], MAYA BHARATIYA[1], WENDY DIRKS[3], SCOTT MCGRAW[4] and CHRISTINE AUSTIN[2]

[1]Griffith Centre for Social and Cultural Research & Australian Research Centre for Human Evolution, Griffith University, [2]Department of Environmental Medicine and Public Health, Icahn School of Medicine at Mount Sinai, [3]Department of Anthropology, Durham University, [4]Department of Anthropology, Ohio State University

Intra-tooth patterns of trace metals barium (Ba) and strontium (Sr) have been used to infer primate nursing histories, including those of australopithecines and Neanderthals. Two elemental models have been proposed to determine the initiation of suckling, consumption of supplemental solid foods, and cessation of suckling. Here we employ laser ablation-inductively coupled plasma-mass spectrometry (LA-ICP-MS) to create comprehensive calcium-normalized barium and strontium (Ba/Ca, Sr/Ca) concentration maps of five wild baboon M1s in order to explore assumptions underlying each model. Enamel Ba/Ca increased at birth in only 1 of 5 teeth as predicted with the initiation of suckling, while Sr/Ca decreased in 3 of 5 teeth. Postnatal Ba/Ca values were high, peaking at ~0.5 years of age and then decreasing throughout M1 crown formation; all five individuals showed minimal Ba/Ca values between ~1.2-1.8 years, consistent with field reports of the cessation of suckling. Enamel Sr/Ca did not support published LA-ICP-MS spot sampling inferences as these individuals' enamel rarely showed discrete Sr/Ca secretory zonation. Increases in Sr/Ca appeared in coronal dentine beginning ~0.3-0.5 years, with varied peak value ages (~0.7-2.7 years) and no evidence of a predicted postweaning decline. Estimates of baboon weaning ages from initial Ba/Ca minima are more congruent with behavioral observations than Sr/Ca maxima, a finding consistent with studies of captive macaques of known weaning ages. Inferences of nursing histories from enamel Sr/Ca patterns alone should be reconsidered, and elevated values of Ba/Ca and Sr/Ca in teeth formed after weaning require further study as neither model fully accounts for them.

Funders: Australian Research Council; Eunice Kennedy Shriver National Institute of Child Health & Human Development, National Institutes of Health; Griffith University; and the Icahn School of Medicine at Mount Sinai.

Growth and microanatomy of the paranasal sinuses of the owl monkey (Aotus nancymaae)

TIM D. SMITH[1], S. JAMES. ZINREICH[2], SAMUEL MARQUEZ[3], SCOT E.E. KING[1], SIAN EVANS[4] and VALERIE B. DELEON[5]

[1]School of Physical Therapy, Slippery Rock University, [2]The Russel H. Morgan Departments of Radiology, The Johns Hopkins Medical Institutions, [3]Department of Cell Biology, SUNY Downstate Health Sciences University, [4]Department of Biological Sciences, Florida International University, [5]Department of Anthropology, University of Florida

The paranasal sinuses of living apes and humans grow with positive allometry, suggesting they provide a novel mechanism for bone enlargement. Here, we examine the paranasal sinuses of the owl monkey (*Aotus* spp.) across age in order to understand the timing of growth and microanatomical features of the mucosa in adults. The prediction that paranasal sinuses grow disproportionately faster than the main nasal chamber is tested. We used diffusible iodine-based contrast-enhanced computed tomography (diceCT) and histology to study sinuses in eight specimens (three newborns, three infants, two adults). Volumes of sinuses were measured using Amira software. In the adults and newborns, all sinuses were lined by a ciliated respiratory epithelium, except for the ethmoid air cells, which are lined in part by olfactory epithelium. An age comparison indicates that only the maxillary sinus and ethmoid air cells are present in newborns, and two additional sinuses (invading the orbitosphenoid and the frontal bone), do not appear until during or after late infancy. Comparing air space volumes across age between birth and adults, the main nasal airway is ten times larger in the adult *Aotus* compared to the newborn. In contrast, the maxillary sinus is nearly 24 times larger in the adult than the newborn, whereas the ethmoid air cells are less than eight times larger in the adult. These results support the hypothesis that most paranasal sinuses grow distinctly from the main nasal chamber, but ethmoid cells of *Aotus* are unique in microanatomy and growth trajectory, possibly related to orbital convergence.

Funded by National Science Foundation grants BCS-1830919 and BCS-1830894.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Endocranial Shape Change in Culturally Deformed Children's Crania: Impacts on Brain Structures and Vascular Competence

ABIGAIL H. SORENSON[1], YAEL S. SHEKEL[2], MIKAELA G. HARNOY[3], JASMINE K. SANCHEZ[3], VERONICA HONG[2], JEANNINE PILI[2], MIRIAM K. KLACZYNSKA[2], ELLORA KLEIN[4], REBECCA S. JABBOUR[5] and GARY D. RICHARDS[6]

[1]Division of Computing, Data Science, and Society, University of California, Berkeley, [2]Department of Integrative Biology, University of California, Berkeley, [3]Department of Psychology, University of California, Berkeley, [4]Department of English, University of California, Berkeley, [5]Department of Biology, Saint Mary's College of California, [6]Department of Biomedical Sciences, A.A. Dugoni School of Dentistry, University of the Pacific

The normal range of cranial shape change along the dolichocephaly-brachycephaly axis results in reorientation of neural components. This normal range of change is significantly altered in culturally deformed crania. Here we assess the degree of endocranial shape change in cradle-boarded crania relative to a non-deformed sample, the impact of these changes on neural structures and vascular drainage, and implications for functional deficits.

We CT-scanned 70 normal (5.0-7.9-year-old) and four culturally deformed crania (helical mode, standard kernel, 0.3 mm isotropic voxels). Developmental age is based on crown/root calcification and represents an average for all teeth. Endocranial shape change and movement of neural structures was assessed via principal components analysis, employing Procrustes-aligned shape variables, in Morphologika2. We employed 62 landmarks to assess global shape change and a variable number to assess individual structures/regions. Endocranial reconstructions were created from crania that were size-adjusted based on the geometric mean.

PC1-2 describe 33.1% of the sample variance. Shape change along PC1 (18.6%) comprises compression of the prefrontal to postcentral cortex into the frontal bone, with elevation/posterior movement of Broca's caps, posterior temporal lobe-cerebellum translation, cerebellar compression, anteroposterior extension of the parietal lobes, and an anteroposterior compression and inferior movement of the occipital lobe. PC2 (14.5%) mainly captures normal shape change from dolichocephaly-brachycephaly. PC3 only explains 0.7% of the variance.

Intentional/unintentional culturally-induced cranial deformation has been considered as having little impact on neural function. We show a range of structural changes that impact normal brain development in moderate-to-extreme cases of deformation that suggest altered function(s).

Student Opportunity Fund, University of California, Berkeley

WEaning Age FiNder (WEAN): a mathematical method to estimate weaning duration from stable isotope ratios of dentinal collagen

ANGELOS SOULELES, ELISSAVET GANIATSOU and CHRISTINA PAPAGEORGOPOULOU

Laboratory of Physical Anthropology, Department of History and Ethnology, Democritus University of Thrace

Nitrogen stable isotope ratios (δ15N) of incremental dentine collagen have been extensively used for the study of breastfeeding and weaning practices in ancient populations. The shifts in δ15N values reveal the duration of exclusive breastfeeding, the onset and completion of weaning. Despite the significant progress in measurement precision, the estimation of weaning is still performed by visual observation of δ15N individual profiles, a time-consuming, labor-intensive, and error-prone task. To fill this gap, we generated WEAN, a tool that enables automated estimation of weaning age based on δ15N measurements from incremental dentine collagen.

WEAN generates a refined age assignment based on regression analysis and calculates the knee/elbow point of the δ15N curvature as the individual's weaning age. We tested the accuracy of the tool by re-estimating the weaning ages of 87 individuals from published datasets.

The results show a strong agreement between the visual observation and the knee method underlining that an automatic mathematical framework can be used for the accurate estimation of weaning age. The tool can estimate the weaning age of a single or many individuals and produces visually appealing graphics (scatter and line plots) and output files.

WEAN introduces a novel and robust method for weaning age estimation that streamlines the assessment of δ15N values for the exploration of breastfeeding and weaning patterns in antiquity.

This research has been co-financed by the European Regional Development Fund of the European Union and Greek national funds under the call RESEARCH – CREATE – INNOVATE (project: ECHOES, T2EDK-00152).

The impacts of state-sanctioned marriage on morbidities and mortalities in the blackland prairies of post-emancipation Texas

STACEY K. SOUTH[1], AMANDA MAGPIONG[1], PAIGE PLATTNER[2], BLAIR M. COE SCHWEIGER[2], ROBIN NELSON[3], AUSTIN REYNOLDS[2] and RICK WA. SMITH[1,4,5]

[1]Department of Sociology and Anthropology, George Mason University, [2]Department of Anthropology, Baylor University, [3]School of Human Evolution and Social Change, Arizona State University, [4]Women and Gender Studies, George Mason University, [5]Indigenous Science, Technology, and Society Lab, Faculty of Native Studies, University of Alberta

Human biologists and public health researchers have linked marital status with a wide variety of health outcomes in contemporary living peoples. However, less attention has been given to the health impacts of marital status in the 19th and early 20th centuries, when states took a larger role in sanctioning marriage. In the United States, state and federal governments increasingly tied marriage to land tenure during the westward colonial land grabs of the 19th century, and marital norms linked to heteropatriarchal monogamy and nuclear family were canalized under the law. This study examines the impacts of state-sanctioned marriage on morbidities and mortalities in Post-Emancipation Texas. We compiled publicly available vital records data including death certificates and census records for 1,830 people born between 1880-1900 in four Texas counties (Dallas, Ellis, Hill, Navarro) located in the Blackland Prairies ecoregion. The effects of marital status on lifespan were evaluated using Kruskal-Wallis tests (p=2.46e-85) and ANOVA (p=3.16e-94). Results indicate that unmarried women (single, divorced, and widowed) lived longer than their married counterparts, while married and widowed men lived longer than their single and divorced counterparts. Disparities in health outcomes across marital statuses were evaluated using odds ratios and revealed differential morbidities in pregnancy and childbirth, infectious diseases, cancer, cardiovascular diseases, and diseases of weathering. These findings extend our understanding of the connections between marriage and health to the 19th and early 20th centuries, and shed light on some of the embodied consequences of settler sex and family.

Integration in the limbs of suspensory primates

JEFFREY K. SPEAR

Department of Anthropology and Center for the Study of Human Origins, New York University, New York Consortium in Evolutionary Primatology, NYCEP

Studies have shown that cercopithecoids have more highly integrated limbs than hominoids. This has been attributed to adaptation to derived locomotor patterns among extant apes. Whether this pattern holds across primates more broadly has not been previously tested. I examine the integration in the length of the femur, tibia, humerus, and radius in approximately 900 individuals representing sixteen taxa, including five cercopithecoids, five hominoids, four platyrrhines, and two strepsirrhines. To allow for adequate sample sizes, several species were pooled at genus level, as were indriids and quadrupedal arboreal lemurids. Variation in size among sexes and different species was standardized by centering, first within species based on sex means and then within each higher taxon based on species means. Integration was assessed by resampling each taxon and

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

measuring variance of eigenvalues of the correlation matrix. Consistent with previous work, I find that apes generally have lower levels of integration compared with cercopithecoids although, notably, I observed high integration in *Pan paniscus*. Contrary to predictions, the relationship between reduced limb integration and derived locomotor behaviors does not hold across all included taxa. The two most highly integrated taxa are Indriidae, which are specialized for vertical clinging and leaping, and *Pygathrix*, which utilize both quadrupedal and arm-swinging behaviors. Further, all four Platyrrhine taxa, including the highly quadrupedal *Sapajus*, the generalized *Alouatta* and *Lagothrix*, and the specialized *Ateles* exhibit similar, fairly low, levels of integration. These results suggest broader taxonomic sampling is necessary to assess the relationship between integration and primate locomotor evolution.

This research was funded by a Leakey Foundation Research Grant, a National Science Foundation DDRIG (award number 2041700) and Sigma Xi Grant in Aid of Research.

Facial asymmetry, inbreeding, and stress in Cross River gorillas (*Gorilla gorilla diehli*).

AMY J. SPIES[1], HALSZKA GLOWACKA[1], AMANDINE ERIKSEN[2], JASON S. MASSEY[3], MIKEL ARLEGI[4,5], YANN HEUZÉ[6], MATTHEW W. TOCHERI[7,8,9] and KATE MCGRATH[10,11]

[1]Department of Basic Medical Sciences, University of Arizona College of Medicine-Phoenix, [2]Department of Biology, University of Indianapolis, [3]Department of Anatomy and Developmental Biology, Centre for Human Anatomy Education, Biomedicine Discovery Institute, Monash University, [4]NA, Institut Català de Paleoecologia Humana i Evolució Social (IPHES-CERCA), Tarragona, Spain, [5]Departament d'Història i Història de l'Art, Universitat Rovira i Virgili, Tarragona, Spain, [6]NA, Université de Bordeaux, CNRS, Ministère de la Culture, PACEA, UMR 5199, Pessac, France, [7]Department of Anthropology, Lakehead University, Thunder Bay, Ontario, Canada, [8]Human Origins Program, National Museum of Natural History, Smithsonian Institution, Washington, District of Columbia, USA, [9]Australian Research Council Centre of Excellence for Australian Biodiversity and Heritage, University of Wollongong, Wollongong, New South Wales, Australia, [10]Department of Anthropology, SUNY Oneonta, [11]Center for the Advanced Study of Human Paleobiology, The George Washington University

Facial fluctuating asymmetry (FA) has been linked to both environmental and genetic stress in *Gorilla*. Higher facial FA is observed in eastern gorillas (mountain and grauer subspecies) compared to western lowland gorillas, with mountain gorillas exhibiting the highest FA. Eastern gorillas experienced a prolonged population decline, reducing genetic diversity. Recently, mountain gorillas underwent a further recent decline, increasing deleterious mutations and making individuals more susceptible to environmental stress and pronounced facial FA due to developmental instability. Here, we report on facial FA in Cross River gorillas, which have the smallest population size of all *Gorilla* subspecies with less than 300 individuals alive today and have also experienced a recent genetic bottleneck. Thirty fixed landmarks were placed on 20 adult crania (10 male, 10 female) and 3D geometric morphometrics was used to quantify facial asymmetry. Procrustes ANOVA revealed that FA accounted for 11% of shape variation, significantly more than population-specific patterns of directional asymmetry (DA) (0.6%), with measurement error only accounting for 1% of shape variation. Comparisons with published data for other *Gorilla* subspecies show Cross River gorillas to have higher facial FA compared to western lowland (6%) and grauer gorillas (9%), but a lower degree compared to mountain gorillas (17%). Interestingly, within the Cross River gorilla sample, males tend to be more asymmetric than females. High levels of facial FA suggest that recent reductions in Cross River gorilla genetic diversity have resulted in their susceptibility to environmental stress, which they face largely due to human encroachment and habitat destruction.

Smithsonian's National Museum of Natural History Collections Care and Preservation Fund

Problems with Paranthropus

MATTHEW SPONHEIMER

anthropology, CU Boulder

Carbon isotopic analysis has been challenging our ideas about hominin diet for nearly 30 years. The first study in 1994 revealed that Paranthropus robustus from South Africa consumed principally C3 foods (e.g., tree fruits and leaves) but also about 25% C4/CAM resources (e.g., tropical grasses and sedges). This result was largely consistent with morphological and dental microwear evidence suggesting P. robustus had a diet which included hard objects like nuts and seeds. Decades later, however, P. boisei from eastern Africa was shown to have eaten nearly 80% C4/CAM plants like the contemporaneous grass-eating primate Theropithecus. Moreover, dental microwear revealed no evidence of hard object consumption in P. boisei, suggesting a diet of tough foods such as grass or sedge leaf and stem. So Paranthropus presents us with two central problems: 1) Why do dietary proxies suggest different diets for the two robust australopiths despite their morphological congruity; and 2) How could P. boisei have consumed tough foods with teeth that seem unsuited to the task. Here we review these questions and more with a particular focus insights that can be gleaned from mammals outside the haplorrhine primates. We argue that extant Primates do not capture the ecomorphological diversity of P. boisei and other extinct primates and should not narrowly circumscribe the behaviors we ascribe to extinct taxa. We also discuss possible digestive strategies for P. boisei in light of its morphology, dietary proxy data, food mechanical properties, and comparative data on mammalian digestive kinetics.

none

Phylogenetic analysis of mitochondrial DNA haplogroup X2a, and its implications for the peopling of North America

NINA J. ST. HILLAIRE[1,2], SOL LEE[1], NICK COSTELLO[2] and MIGUEL G. VILAR[1,3]

[1]Department of Anthropology, University of Maryland, [2]Department of Biology, University of Maryland, [3]Research and Development, Family Tree DNA

North America's earliest settlers arrived through Beringia–the prehistoric continent once connecting Siberia and Alaska–and subsequently migrated southeast. Although that entryway is accepted across most sciences, researchers still debate the timing and migratory routes forward. Today, most indigenous American populations, descendants from these early settlers, belong to mitochondrial DNA haplogroups A, B, C, D, or X2a, the last found almost exclusively in Canada and the USA. Our data-based study estimates the earliest occurrence of X2a in the Americas, evaluates haplogroup distribution patterns, and assesses whether a coastal or an inland route served as the likeliest path.

Our data included the mtDNA genomes of 157 X2a individuals from commercial and scientific DNA databases, many reporting birthplaces in the USA or Canada. We also included two Ancient X2a individuals from published sources as geochronological anchors. We analyzed the frequency and variation of X2a mutations and used phylogenies to visualize lineage distribution and estimate time of coalescence.

Results suggest that X2a is approximately 12,000 years old, a date consistent with geological estimates of when an ice-free corridor formed from Alaska through Canada to central USA. Researchers postulate that earlier migrations would necessitate a coastal route and corresponding genomes would yield an earlier date. Coastal migration is consistent with many archaeological sites and date estimates for haplogroups A-D, but not inland sites nor haplogroup X2a. Spatial and temporal evidence support an inland migration pattern for X2a. These findings are important for understanding the routes and patterns of settlement of the Americas.

Oral Disease at Al-Qinifab, Sudan: Reassessing the Saso and Kondo (2019) Method

JULIANNE R. STAMER and BRENDA J. BAKER

School of Human Evolution and Social Change, Arizona State University

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Patterns of oral disease are a fundamental part of bioarchaeological investigation and have been used to understand dietary patterns, childhood health, and daily activities. Often, however, these conditions are examined separately although they interact in the oral environment in complex ways. We modify a recent multidimensional method (Saso and Kondo, 2019) to better understand how oral diseases interact in a skeletal sample (n=50) from the Qinifab School site (200-1400 CE) in northern Sudan. We hypothesized that a significant relationship exists between periodontal disease—as measured by interdental septum morphology—and average dental wear. Caries rate, rate of antemortem tooth loss (AMTL), average dental wear (ADW), cemento-enamel junction to alveolar crest distance (CEJ-AC distance), and interdental septum morphology were assessed. We modeled oral disease relationships using multiple linear regression and Principal Component Analysis. ADW explains 24.3% of the variation in severity of periodontal disease as measured by interdental septum morphology. This result suggests that habitual dental loading contributes significantly to the inflammation of the alveolar bone, supporting our hypothesis. CEJ-AC distance was not well predicted from any of the other oral conditions individually or combined, suggesting that alveolar resorption is not significantly affected by inflammation of the alveolar bone or other oral health conditions. Anterior tooth chipping and AMTL explain 15.7% of the variation between the Late Meroitic/Post Meroitic and the Christian Periods, coinciding with evidence for a dietary shift. Caries rate and AMTL are the largest predictors of estimated sex (r^2=0.2013), with females having more carious lesions and AMTL.

Dental remains of Pliocene-Pleistocene Cercopithecidae from Romania

CRISTINA STAN[1,2], VIRGIL DRĂGU»òIN[1,3], »òTEFAN VASILE[1,4] and MÁRTON VENCZEL[5]

[1]Emil Racoviță Institute of Speleology, Romanian Academy, [2]Department of Anthropology, University of Arkansas, [3]Earth, Environmental and Life Sciences Division, Research Institute of the University of Bucharest, [4]Department of Geology, Mineralogy, and Palaeontology, Faculty of Geology and Geophysics, University of Bucharest, [5]Department of Natural Sciences, »öării Cri»ôurilor Museum

Cercopithecids were common members of the Plio-Pleistocene fauna of Europe, being represented by two colobine (*Mesopithecus* and *Dolichopithecus*), and two cercopithecine (*Macaca* and *Paradolichopithecus*) genera. Following the Early Pleistocene regional extinction, primate diversity declined, with *Macaca* and *Homo* being the only primate genera to inhabit the European continent during the Middle and Late Pleistocene. The cercopithecid fossils from Romania, including published and unpublished dentognathic specimens and isolated teeth, were poorly examined in an ecological context. Here, we discuss primate fossils from the Plio-Pleistocene fossil sites of Mălu»ôteni (MN15a), Ciuperceni-2 (MN15b), and Betfia (MN17-MN18), and assign them to taxon based on both morphological and metric analyses. We also provide a summary of the paleoenvironmental conditions and an updated biochronological age for each locality.

From Mălu»ôteni, a new lower molar of *Mesopithecus monspessulanus* and the previously described *Dolichopithecus ruscinensis* are reported. Their presence is documented here in a continental, more arid Pliocene setting. At Ciuperceni, a lower incisor and a molar fragment are assigned to *Dolichopithecus ruscinensis*, while a third molar is fully comparable to *Macaca sylvanus* cf. *florentina*. The Pleistocene assemblages from Betfia yielded a molar crown from a young individual at Betfia-XIII and a juvenile premolar at Betfia-IX, both assigned to *M. s.* cf. *florentina*. We remark on the presence of macaques in an open forest landscape, under a warm Mediterranean climate during the Pliocene at Ciuperceni, and in an open, arid landscape with increased seasonality during the Pleistocene at Betfia.

Research was founded by two grants of the Romanian Ministry of Research and Innovation, CNCS – UEFISCDI, project numbers PN-III-P4-ID-PCE-2020-2282 (V.D., »ò.V.) and PN-III-P1-1.1-TE-2021-0664 (»ò.V.), both grants within PNCDI III.

Dis/Ability and Deviant Burials: Entheseal Changes Among the La Plata Population

KATHLEEN D. STANSBURY

Anthropology, University of Nevada, Las Vegas

The La Plata Population represents a series of Ancestral Puebloan sites along the La Plata River outside Farmington, New Mexico dating from 600-1200 CE. Past research has argued that several captive females in this population experienced impairment due to illness or trauma. Most of the captive females also experienced repeated head trauma, resulting in issues with mobility, neuropathological symptoms, and difficulty managing behavior. Experience of impairment in captivity is likely a combination of violence due to status and violence due to impairment or perceived inability to work. This relationship and its impacts on lived experience can be considered through the dis/ability continuum. Consideration of dis/ability will speak to the unique experience of impairment and captive status. Entheseal changes can reflect experiences of hard labor, and so provide insight into adaptations to mobility impairments as well as the physical impacts of captivity on the body (Henderson et al 2013). Preliminary research suggests that captive females were performing some level of intense physical activity, with 100% of captive females scored displaying major changes on the right arm and 50% on the left. Consideration of entheseal changes, mortuary context, trauma, and pathology through a dis/ability lens will provide more nuanced understanding of the experiences of captivity as well as how captivity itself could be disabling.

Funded by the Angela Peterson Memorial Scholarship from the UNLV Department of Anthropology.

Standardizing Sample Preparation for Tooth Enamel Carbonate Isotope Analysis

CHRIS STANTIS[1], KIRSTEN VEROSTICK[1], FRANCESCA SPENCER[1], LESLEY CHESSON[2], GREGORY BERG[2] and GABRIEL J. BOWEN[1]

[1]Department of Geology and Geophysics, University of Utah, [2]DPAA Laboratory, Joint Base Pearl Harbor-Hickam

Isotopic analysis illuminates the life history of individuals in forensic human identification. However, applications are limited by the quality and comparability of reference data. Numerous studies have investigated how laboratory methods affect the comparability of measurements made on fossil or archeological samples, but less work has focused on modern forensic materials. Here we conducted experiments targeting two variables in the preparation of tooth enamel for carbonate isotope analysis: particle size and chemical pre-treatment with oxidants and acids.

Our results show that isotopic analysis of samples as coarse particles (>250 μm) reduced CO_2 yield by 1.02%, increased the variability of yield and $\delta^{13}C$ values (1σ increase of 0.38% and 0.13‰, respectively), and produced slightly higher $\delta^{18}O$ values (by 0.18‰) relative to analysis of fine particles (<125 μm). Using different particle sizes during sample pre-treatment affected CO_2 yield significantly, with a mean difference of -0.35% for fine particles. Samples treated with buffered acetic acid and different oxidant solutions showed a systematic positive $\delta^{18}O$ shift of ~0.3‰ regardless of the oxidant, concentration, and treatment time. Acetic acid treatment, rather than treatment with oxidants, appears to cause this shift.

This work suggests that comparability and consistency of isotopic results are improved if enamel samples are ground to a fine particle size prior to analysis and the use of acid pre-treatment is standardized. More generally, documentation of pre-treatment methods is critical to ensure the comparability of enamel carbonate data within and among laboratories and its fitness for use in forensic human identification.

This research is funded through the Henry Jackson Foundation in partnership with the Defense POW/MIA Accounting Agency (DPAA).

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Shaping Childhood: morphological and developmental patterns of juvenile long bones

SARAH Y. STARK

Investigative Science Team, Historic England, Archaeology, University of Southampton

Growth and developmental plasticity have been long standing topics of interest in juvenile bioarchaeological studies. Questions surrounding morphological and developmental trajectories have been limited due to the smooth and cylindrical nature of juvenile long bones. Geometric morphometric methods (GMM) offer a potential solution to the lacune of this work and allows for developmental trajectories of whole bone morphology to be analysed and visualised in three-dimensional space.

To determine patterns of long bone morphology during growth, 178 juveniles from early Medieval to Post-medieval foetal to 12-year-olds were used in this study. Femora, tibiae, and humeri were digitised through structured-light-scanning and examined through auto3dgm with 250 pseudolandmarks. This study aims to identify how biological processes impact bone morphology during growth and if the degree of shape variation between long bone elements is associated with stronger functional signals.

The key findings were that long bone shape is statistically significant by site and period from foetal to 5 years old. The midshaft of the femora and humeri remain the most consistent throughout development in comparison to the highly variable proximal and distal regions of the femora and humeri diaphysis and metaphyses. The tibia displayed a different pattern, with more variation found in the proximal diaphysis and metaphyses and less change distally. The midshaft is likely to require a 'higher threshold' to trigger a modelling response which is low in the current sample. Thus, allowing the hip, knee, shoulder, and elbow joint morphologies to accelerate during early growth and development.

Understanding the differences in functional capacity of intrinsic hand muscles in *Homo sapiens* and *Pan troglodytes*

NADINE G. STEER[1], MARA G. FIELDS[1], EDEN MACKERETH[1], KEVIN M. MIDDLETON[2], CASEY M. HOLLIDAY[1], SAMUEL P. SULLIVAN[1], FAYE R. MCGECHIE[3], AUSTIN B. LAWRENCE[1] and CAROL V. WARD[1]

[1]Department of Pathology and Anatomical Sciences, University of Missouri, [2]Division of Biological Sciences, University of Missouri, [3]Department of Basic Medical Sciences, University of Arizona College of Medicine- Phoenix

Interpreting functional differences between the hands of humans and chimpanzees and interpreting the significance of fossil hominin hand bones requires a more complete understanding of the muscular system, which to date has been difficult to quantify.

In this study, we make a significant step in understanding hand function by comparing the biomechanical capacity of intrinsic hand muscles in *Homo sapiens* and *Pan troglodytes* using a workflow designed to study 3D lever systems and muscle architecture of musculoskeletal systems. Specimens were fixed, stained with Lugol's iodine, and µCT scanned at <61 µm voxel size. Muscles, tendons, bones and other relevant soft tissues were segmented to document the entire musculoskeletal system in 3D simultaneously for the first time. These data permit description and quantification of muscle volumes and attachments. Machine-learning algorithms using Avizo Xfiber software were used to visualize individual muscle fascicles, from which 3D force-generating capacity were calculated. We combined these data to calculate moments of individual muscles as well as muscles in aggregate acting about the joints of the hand.

Results show chimpanzee interosseous muscles are larger in size than those of humans, and lumbricals more similar. These differences contrast with the thenar and hypothenar muscles, for which humans have greater force-generating capacity for flexion, adduction and opposition than do chimpanzees. Future analyses of extrinsic hand musculature are needed for a complete understanding of the biomechanical capacity of the hands of chimpanzees and humans that ultimately will inform understanding of the function and evolution of the human hand.

University of Missouri Research Council, National Science Foundation (IOS 1457319)

Living in the same space: how two similar congeneric lemurs occupy the same landscape

TRAVIS S. STEFFENS[1,2], MALCOLM S. RAMSAY[3], BERTRAND ANDRIATSITOHAINA[2,4], ALEXANDRIA E. COSBY[1], SHAWN M. LEHMAN[3], ROMULE RAKOTONDRAVONY[4], MAMY RAZAFITSALAMA[2], HELENA TEIXEIRA[5] and UTE RADESPIEL[5]

[1]Sociology and Anthropology, University of Guelph, [2]Planet Madagascar, [3]Department of Anthropology, University of Toronto, [4]Faculté des Sciences, de Technologies et de l'Environnement, Université de Mahajunga, [5]Institute of Zoology, University of Veterinary Medicine Hannover

Studies of animal sympatry have contributed to theories in ecology and evolutionary biology. Most studies of animal sympatry have been conducted at small spatial scales characterized by little habitat variation. However, there are few data on how sympatry varies across areas subject to anthropogenic disturbance. We compared long-term data on encounter rates of *Microcebus murinus* and *M. ravelobensis* in continuous and fragmented forests to determine how these species can co-occur. Our data was collected between 2000 and 2018 from 58 sites consisting of 115 samples in Ankarafantsika National Park. A sample reflects multiple surveys (N = 2–21) along a line-transect and/or trapline within 1 year. We used standard methods, i.e., trapping (N = 16 sites; 42 samples) and line-transect visual surveys (N = 42 sites; 73 samples). Rainfall data were provided by Durrell Wildlife Trust for the same years for which survey data were collected. We found that yearly encounter rates for *M. ravelobensis* and *M. murinus* were negatively and positively associated with rainfall, respectively. We found a negative correlation between *M. ravelobensis* and *M. murinus* encounter rates in continuous forest but a positive relationship in fragmented forests. Our study demonstrates that these species can co-occur because of differential preference for continuous (i.e., *M. ravelobensis*) versus fragmented forest habitat (i.e., *M. murinus*) and different microhabitat preference (i.e., wetter, taller, denser forests for M. ravelobensis and drier habitat for *M. murinus*). Studies such as ours are important for evaluating how established theories operate in dynamic landscapes subject to anthropogenic disturbance.

German Bundesministerium fuÃàr Bildung und Forschung; Deutsche Forschungsgemeinschaft; Sigma Xi; American Society of Primatologists; Edmonton Valley Zoo; Explorers Club; University of Toronto; Natural Sciences and Engineering Research Council of Canada

Data Sharing and Repositories in the Craniofacial Identification Domain: The Collaborative Facial Soft Tissue Depth Data Store (C-Table)

CARL STEPHAN[1], PIERRE GUYOMARC'H[2] and TE WAI POUNAMU HONA[1]

[1]HuCS-ID Lab, School of Biomedical Sciences, The University of Queensland, Australia, [2]Unite Mixte de Recherche (UMR) 5199 De la Prehistoire a l'Actuel Culture, Environnement et Anthropologie (PACEA), Ministere de la Culture et de la Communication (MCC), CNRS, Universite de Bordeaux, Pessac, France

Facial soft tissue thicknesses (FSTT) have long formed the underlying quantitative basis of craniofacial identification methods. Since their first collection in 1883, there have been over 220,000 measurements of >20,500 individuals. This is a substantial volume of data, but much of it has been lost due to the absence of sharing raw values. This hinders collaborations and research developments pursuing new ideas but also repeating findings of prior studies (another integral component of science). To avoid these issues in the future the Collaborative Facial Soft Tissue Depth Data Store (C-Table @ CRANIOFACIALidentification.com) was established on Jan-2012 as an open, public and free

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

data repository. The C-Table provides raw FSTTs for 27 commonly measured and standardized landmarks. As of Oct-2022 the C-Table comprises entries from 20 investigator teams, corresponding to data for 1,971 individuals. This opens opportunities for new analysis of FSTTs in the 'big data' space (the largest single FSTT ever conducted is 1,000 individuals), but nevertheless there are challenges such as missing values and first author tendencies to hoard data. Far from removing ability of first authors to conduct more studies, the C-Table supports expanded study activity via the maximisation of data utility. Individual investigators receive benefit via increased citations paid back to their original works as part of mandatory terms of use. Moreover, contributors may benefit from additional research collaborations that the C-Table data repository seeds. These are all positive attributes that should encourage greater participation in the C-Table in the future.

This research was supported by an Australian Government Research Training Program (RTP) Scholarship awarded to Te Wai Pounamu T. Hona.

Using FORDISC 3.1 to Estimate Ancestry in a Modern Greek Sample

KAITLYN STILES

Forensic Anthropology, SNA International

FORDISC 3.1 (FD3) is currently the most practical and efficient tool for estimating ancestry through statistical analysis of craniometric variation. While generally effective in estimating ancestry in American populations (Black, White, Asian), recent studies have highlighted FD3's limitations in estimating ancestry in individuals from Latin America and Italy. One of the major reasons for this is the lack of appropriate reference samples to use for analysis.

Greece represents a unique European population due to its location on the southern and eastern borders of the geographic region of Europe. Given its position, its population is technically "European," which is nearly synonymous with "White" in forensic contexts. However, the genetic history of Greek individuals includes contributions from the Middle East and central Europe. In this study, I investigate how accurately FD3 estimates ancestry in a 20th century skeletal sample from the village of Karya in central Greece.

Results indicate that while the Karya individuals are most frequently classified as "White" or "European," that frequency is low (ca. 24-33%) and nearly equal to chance when compared to the classification frequencies of the individuals as Black, Asian, and Hispanic using reference samples from both the Forensic Data Bank and Howells' Database in FD3. These results further confirm the need for population specific reference samples in FD3 and the broader need for Mediterranean and Middle Eastern data with respect to ancestry estimation methods.

Research supported by the Defense POW/MIA Accounting Agency.

Old Data and New Problems: Mining Journals and Archives prior to 1950

CHRISTOPHER M. STOJANOWSKI[1] and WILLIAM N. DUNCAN[2]

[1]School of Human Evolution and Social Change, Arizona State University, [2]Department of Sociology and Anthropology, East Tennessee State University

Biological distance analyses compare groups or individuals to inform on the relative similarity or dissimilarity, often for the purposes of allocation. As the field has moved to an increasingly critical stance of past practices regarding the use of human remains and race as a unit of analysis for comparative frameworks, researchers are left asking how to proceed on a host of issues, including where to find comparative data. Here we present a case study in which we construct a problem-based sample for a biodistance analysis from coastal Georgia. We were tasked with assessing whether or not the Fort King George skull was a martyred priest from the 16th century. Rather than using standard databases such as Fordisc or the Howell's data set, we constructed a data set that defines regional populations of the appropriate age. Over 5000 individuals were data-mined from published and archival sources, which permitted us to calculate likelihood ratios that were more meaningful than what we would have been able to generate from standard computer programs and more widely known data sets. Ultimately, we found an Iberian identity to be the most likely, which fits with historical accounts of the skull's identity. This case study highlights the potential that legacy data have for focused problem solving as the field embraces new, community-driven questions, particularly in areas such as forensic biohistory and osteobiography.

None

Interannual assessment of fruit availability in gibbon habitat in Northwestern Thailand

DIEGO I. STOKES-MALAVE[1], MARGARET SOBASZEK[3], STEPHANIE POINDEXTER[2] and LYDIA E. O. LIGHT[3]

[1]Environment & Sustainability, University at Buffalo, [2]Anthropology, University at Buffalo, [3]Anthropology, University of North Carolina at Charlotte

Huai Kha Khaeng Wildlife Sanctuary (HKK) in Northwestern Thailand contains dry dipterocarp forest that is home to several primate species, including the white-handed gibbon (*Hylobates lar*). This forest is characterized by low fruit productivity and is considered poor habitat for frugivores, yet several established groups of gibbons exist and persist here. We can use phenological surveys to give us a more complete picture of gibbon food availability. We analyzed two phenological datasets of HKK collected in 2012 and 2018. We calculated and compared the resource availability index for total fruit production (ripe and unripe) across the months of July, August, and September. During these months, total fruit production was significantly greater in 2012 than in 2018 (p-value = <0.0001). There was very low productivity in July 2012 followed by higher productivity in August and September , while July 2018 was the most productive compared to August and September 2018. Widespread flooding occurred prior to the 2012 data collection, which may have impacted fruit production. The 2018 data, however, may be more representative of an average year of fruit availability for this forest where rainfall is typically low. Gibbons in this habitat must be adapted to minimal fruit availability and perhaps consume an increased amount of less desirable fruits, leaves, and insects to sustain themselves. This population is distinct from gibbons in other locations because of their unique choice of habitat, warranting further investigation into the role forest productivity plays in sustaining them.

New and most complete fossil assemblage of early primate *Omomys* from early Bridgerian

JULIA E. STONE and DOUG M. BOYER

Evolutionary Anthropology, Duke University

The earliest members of the primate clade are known primarily from fragmentary dental and cranial material. Two major groups from the Eocene, adapiforms, and omomyiforms, strongly influence hypotheses on the form, locomotion, and diet of the last common ancestor of primates. However, much of the fossil record, particularly regarding postcranial evidence, is still sparse and difficult to attribute to particular species. Even when taxonomic attribution of isolated cranio-dental and postcranial material is certain, such collections have limited utility for making inferences about body proportions due to within-species size variation. Therefore, it is noteworthy and of potential scientific importance when fossil cranio-dental material is found in close proximity to or (better yet) articulation with postcranial fossils, especially when those fossils represent early primate species. Here we describe a partial skeleton, of the omomyiform genus *Omomys*, from the lowest stratigraphic unit of the Bridger formation (Bridger A) in the Southern Green River Basin of Wyoming. As far as we know, this is the first specimen that appears to represent a single individual with an extensive representation of the postcranial skeleton preserved in close association with craniodental remains. The specimen includes postcrania from both the fore- and hind limbs, as well as many vertebrae. It provides

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

an important new addition to the Eocene primate fossil record unparalleled for this genus. The complete description of these fossils provides a better understanding of the overall morphology for further use in functional analyses, phylogenetic studies, and understanding of the Eocene paleoenvironment.

Funding support from NSF BCS 1440742; BCS 1552848

Serving the Dead is Serving the Living: Practices of Community Care for the 1921 Tulsa Race Massacre Victims

PHOEBE R. STUBBLEFIELD, ISIS DWYER and SAMANTHA MCCRANE

CA Pound Human Identification Laboratory, University of Florida

On June 1 1921, White residents of the City of Tulsa (City), Oklahoma systematically looted and burned nearly 40 blocks of the neighboring African American inhabited unincorporated area of Greenwood. Newspaper accounts and death certificate data record 25 adult African American deaths, 17 of whom are buried in unmarked graves in the city cemetery Oaklawn. In 2018 City Mayor G.T. Bynum called for an investigation of the 1921 Tulsa Race Massacre (TRM), to among other goals, locate the hidden burial locations of riot victims. The mayor established three committees to pursue the investigation. The History Committee was charged with securing further historical references to the event. The Physical Investigation Committee (PIC) performed site surveys and excavations for human remains, and the Public Oversight Committee, composed of Tulsa community members, became the interface between the community, the mayor's office, and the PIC's investigatory products. The TRM investigation, while progressive, exists as an ongoing racial conflict.

Here we present the strengths and weaknesses of our committee-focused organizational model, and describe the fit of our roles as aids to the Greenwood community. The TRM Investigation benefits from the forensic anthropologist being a member of the traumatized community. The authors, performing at different professional levels, observed the following best practices for community care: inclusion of community members; recognition that race has an impact on most if not all aspects of the investigation, and planning accordingly; focusing on the human rights mission; playing the long game; creating the ensemble cast; and practicing compassion.

No external funding was received to produce this presentation.

Democratizing Science is Essential for Countering Emerging Diseases

REBECCA STUMPF

Anthropology, University of Illinois, Notre Dame Institute for Advanced Study, University of Notre Dame

Systemic inequity persists in science, particularly with regard to Africa where local voices are often underrepresented in the global scientific community. The consequences of science inequity are significant and particularly detrimental in light of the urgent challenges the globe faces with regard to emerging diseases. Emerging diseases are expected to continue to increase, particularly in tropical, biodiverse areas found in many parts of Africa with increasing impact on low-resourced communities. Most scientific resources including technology, equipment and funds are concentrated outside of Africa, and many Africans have limited access to research opportunities, dissemination of findings, and funding. The power dynamics between non-African and African researchers are unbalanced, and African research contributions are often hindered and devalued. The concentration of decision-making and resources outside of Africa ultimately impacts which research agendas are set, with global consequences including the loss of information and innovation, ongoing economic disparity, and missed opportunities with regard to advancing science. Making science more equitable is paramount and requires a multifaceted approach with input, action and advocacy from diverse voices. Discussed in this paper are several inter-related considerations for increasing representation in science, including: i) acknowledging and supporting African scientific agency ii) integrating best practices for equitable collaboration, iii) proper recognition of contributions and iv) increasing representation of human diversity in scientific data and knowledge. Democratizing science leads to new perspectives, novel insights, greater innovation, and improved health equity, ultimately leading to better science. Humanity's ability to prepare for and respond to emerging diseases may depend on it.

Funding: The Notre Dame Institute for Advanced Study

Diet shift and plant toxins in hominid evolution: evidence from cytochrome P450 and Tas2r genes

ROGER SULLIVAN[1] and ED HAGEN[2]

[1]Anthropology, Sacramento State University, [2]Anthropology, Washington State University Vancouver

An increase in body mass in Pleistocene *Homo* may be explained by a diet shift from raw wild plant foods to an increase in meat eating and/or cooked plant foods. We hypothesize that a shift away from the consumption of toxin-rich wild plant foods in *Homo* will be reflected in a divergence in toxin-metabolizing and bitter-taste receptor genes in *Homo sapiens* and *Pan troglodytes*. The cytochrome P450 (CYP) 1, 2 and 3 families are relatively specialized for metabolizing xenobiotics, including plant toxins. The Tas2r bitter-taste receptor genes have evolved in vertebrates with the primary function of sensing the chemical environment. We collected data on the structure and function of all known CYP 1, 2, and 3, and Tas2r genes in *Pan* and *Homo*. *Pan* have more toxin-metabolizing CYP genes (>=26 genes) and faster metabolism of substrates than *Homo* (23 genes). These data are consistent with a hypothesis of diet shift and reduced exposure to wild plant toxins in the course of human, but not chimpanzee evolution. On the other hand the number of functional and pseudo genes of the bitter taste receptors in *Pan* (37) and *Homo* (36) is similar and more numerous, and with possibly elevated sensitivity, than in most other primate species. This contradictory finding suggests that bitter taste has been retained in humans despite a reduction in exposure to toxic plants in the course of human evolution. We discuss whether conserved Tas2r function is an adaptation for broad diet breadth in *Pan* and *Homo*.

Postmarital residence in medieval Stręgoborzyce, Poland

VICTORIA SWENSON[1,2], MARIN PILLOUD[2], ANIA SPINEK[3] and KRZYSZTOF TUNIA[4]

[1](Bio)Archaeology, Cultural Resource Analysts, Inc., [2]Anthropology, University of Nevada, Reno, [3]Anthropology, Hirszfeld Institute of Immunology and Experimental Therapy, [4]Archaeology, Institute of Archaeology & Ethnology of the Polish Academy of Sciences

Analyzing postmarital residence practices of past populations provides insight into social and economic relationships and mobility. Historical evidence suggests that Poland was a patrimonial state throughout the medieval and the early feudal period (10th-15th c. A.D.) and that the patriarchal society predates the establishment of the state. Generally, medieval village rosters only included the name of the male residents, suggesting that males were more permanent (and perhaps prioritized more) than female residents. Previous scholars have used cranial and dental data to examine postmarital residence patterns, and these analyses can be used to understand differences in migration patterns between males and females. Therefore, this study investigates postmarital residence patterns at the *Stręgoborzyce 38* site, a medieval village in Małopolska, Poland to explore postmarital residence practices.

Data were collected on cranial and dental metric and non-metric traits to test the hypothesis that the Stręgoborzyce residents practiced virilocality. The cranial and dental non-metric analyses do not show any significant variation between females and males. The dental metrics were found to be

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

more variable among males than females. The cranial metric analysis did not yield any significant results. While the skeletal data provide slightly differing results, this finding is likely due to similarities in mobility between males and females of Stręgoborzyce. The results of this analysis provide an alternate view of postmarital residence than is portrayed in the historical documents and may speak to the role of women in this medieval village. Future work will continue to explore mobility patterns across the region.

This project was made possible through the support provided by the Kosciuszko Foundation and the University of Nevada, Reno.

Cortical bone structure of the proximal phalanges varies in relation to hand use and posture in hominoids

SAMAR M. SYEDA[1], ZEWDI J. TSEGAI[1], MARINE CAZENAVE[1,2,3], MATTHEW M. SKINNER[1,4] and TRACY L. KIVELL[1,4]

[1]Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, [2]Division of Anthropology, American Museum of Natural History, [3]Department of Anatomy, Faculty of Health Sciences, University of Pretoria, [4]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand

Fingers are typically the first point of contact with the substrate during locomotion or manipulation in extant hominoids and therefore intertaxic differences in their internal bone structure should reflect differences in hand use behaviors. We used R package Morphomap on high-resolution microCT scans of hominoid non-pollical proximal phalanges to determine whether cortical structural patterns reflect variation in manual behaviors between suspensory (*Pongo*), knuckle-walking (*Gorilla*, *Pan*), and manipulative (*Homo*) taxa. Results reveal that cortical bone distribution patterns and properties reflect the varied hand postures employed by each taxon. *Pongo* cortical bone is thickest in the distopalmar region of the phalangeal shaft, consistent with frequent use of a flexed interphalangeal joint. However, overall *Pongo* has significantly thinner cortices and weaker cross-sectional properties compared with African apes, which may be explained by greater phalangeal curvature. *Gorilla* and *Pan* exhibit a general pattern of maximum thickness on the flexor sheath ridges, possibly reflecting the joint reaction forces of knuckle-walking, arboreal behaviors with relatively straighter phalanges, or a mixture of both forms of locomotion. Slight differences between the species, such as an intermediately thick dorsal shaft in *Gorilla*, may reflect locomotor variation between African apes. Humans display a unique pattern of distodorsal thickening and greater differences between the rays, relative to *Gorilla* and *Pongo*. As humans use their hands primarily for manipulation, they have relatively thin cortices and weak cross-sectional properties. These patterns of cortical bone structure reflecting differences in manual behaviors can be a relevant comparative framework for reconstructing behaviors in fossil hominins.

This project has received funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation program (grant agreement No. 819960 and No. 101025719).

Achieving kinematic identity across morphological diversity in musculoskeletal modeling

ADAM D. SYLVESTER[1] and PATRICIA A. KRAMER[2]

[1]Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine, [2]Department of Anthropology, University of Washington

Musculoskeletal modeling is emerging as a powerful approach in vertebrate paleontology. While forward and inverse dynamic approaches require different assumptions about forces and/or motions, both rely on well-defined bony morphology to parameterize joint locations and muscle geometry. Using different motion profiles complicates comparisons between modern and ancient morphologies because results reflect both morphological and kinematic differences. Here we report on an approach which permits changes in morphology while maintaining kinematic and kinetic identity.

Using a musculoskeletal model, we carried out inverse dynamic analyses of human walking trials (five participants). Next, we exported the generic human pelvis from the model and warped it to match a reconstructed A.L. 288-1 pelvis. A parallel process was used to warp the proximal half of the femur. Australopithecine pelves were size-scaled to have the same distance between hip centers as the human pelves. Generating surface meshes that are topologically equivalent allows for direct estimation of muscle geometry and accurate identification of joint centers within the modeling software. Using results from the simulations of human walking, we wrote new motion files (C3D format) to drive kinematics based on the locations of joint centers.

We compared human and australopithecine morphs for the three-dimensional locations of the joint centers as well as joint moments induced by the ground reaction force. We found that joint locations in the australopithecine morph were within 1μm of their location in human trials and moments were within 1Nm. This process allows the ramifications of morphology to be isolated from potential kinematic differences.

Using external auditory exostoses to track temporal changes in human aquatic activities in pre-Columbian Panama

VANESSA V. SÁNCHEZ AGUILARTE[1,2], JAVIER RIVERA SANDOVAL[3] and NICOLE E. SMITH-GUZMÁN[2,4]

[1]Facultad de Humanidades, Escuela de Antropología, Universidad de Panama, [2]Center for Tropical Paleoecology and Archaeology, Smithsonian Tropical Research Institute, [3]Departamento de Historia y Ciencias Sociales, Universidad del Norte (Colombia), [4]Sistema Nacional de Investigación, Secretaría Nacional de Ciencia, Tecnología e Innovación

External ear exostosis, an abnormal growth of the tympanic bone caused by exposure to cold water and wind, has been reported in pre-Columbian individuals buried near the Gulf of Panama, where seasonal coastal upwelling creates ideal conditions for their development, even in tropical climes. In this study, temporal bones from 135 human skeletons excavated from the archaeological site of Cerro Juan Díaz, Panama (50–1500 AD) were analyzed macroscopically to quantify the prevalence of the lesion and identify possible changes in its frequency during specific cultural periods in this village. A high prevalence of external auditory exostoses was found in mostly male individuals from the Early period (before 800 AD) and a complete absence of the lesion in individuals from the Late period (after 800 AD). This sharp decline coincides chronologically with the reduction in carved seashell ornaments found in coastal archaeological contexts around the Gulf of Panama, suggesting that the practice of diving declined considerably over time, possibly due to a reduced demand for seashells at the local and regional level.

This research was funded by the Smithsonian Tropical Research Institute through a short-term fellowship awarded to the first author.

Effects of long-term storage conditions on microbial composition in dental calculus

CHRISTINE TA[1], EMILY SKELLY[2], MATILDA HANDSLEY-DAVIS[2], RAPHAEL EISENHOFER[2], JOHN KAIDONIS[3] and LAURA S. WEYRICH[1,2,4]

[1]Department of Anthropology, The Pennsylvania State University, [2]Australian Centre for Ancient DNA, School of Biological Sciences, The University of Adelaide, [3]School of Dentistry, The University of Adelaide, [4]Huck Institutes of the Life Sciences, The Pennsylvania State University

Calcified dental plaque (calculus) contains a myriad of microbes that can inform researchers about past lifestyles, diets, and health but is subject to taphonomy. While a limited number of studies have examined these taphonomic processes, we know very little about how long-term storage conditions may influence the reconstruction of calculus microbial communities. Here, this study tests how different, long-term

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

storage conditions can impact the recovery and diversity of the oral microbiome in calculus. We used shotgun metagenomic and amplicon 16S ribosomal RNA metabarcoding approaches to recover oral microbiomes from calculus that was either freshly collected (FR) or left to decay for two years in frozen (FO) or room temperature (RT) conditions. All datasets were filtered using decontam, and diversity (alpha-diversity) and composition (beta-diversity) were assessed using QIIME2. Storage temperatures impacted diversity in both 16S and shotgun data sets. Specifically, shotgun sequencing unexpectedly revealed higher diversity in RT samples compared to FR samples, which was driven largely by *Corynebacterium* and *Fusobacterium* taxa. Mild impacts on composition were also observed, although these findings were impacted by the compositionality of the data sets. Other conditions, i.e., storage materials, had minimal impacts on diversity and composition, compared to the temperature. These results suggest that long-term RT storage of archaeological calculus may influence the diversity and composition of calculus samples and that storage in frozen conditions may help preserve perimortem signatures. These findings also imply that certain microbial species may "bloom" postmortem and need to be reexamined in the current calculus literature.

The Process of 3D Digitization and Data Sharing in Archaeology: A Case Study of Ongagawa-Style Pottery and Skeletal Remains in Japan

KOHEI TAMURA[1], TOMOMI NAKAGAWA[2], KOJI NOSHITA[3], AKIHIRO KANEDA[4] and HISASHI NAKAO[2,5]

[1]Frontier Research Institute for Interdisciplinary Sciences, Tohoku University, [2]Philosophy and Anthropological Institute, Nanzan University, [3]Department of Biology, Kyushu University, [4]Centre of Archaeological Operation, Nara National Research Institute for Cultural Properties, [5]Department of Anthropology, Nanzan University

Recent developments in three-dimensional measurement technologies have improved the availability of precise three-dimensional data. Sharing such data is a key issue in archaeology and biological anthropology to open up new opportunities in education, outreach activities, and disaster risk mitigation, as well as the improvements of transparency, reproducibility, and replicability in research.

In this talk, we will introduce our data set composed of over 1,000 three-dimensional models of human skulls and 700 models of pottery in Japanese prehistory. The former includes skulls ranging from the Jomon to Kofun periods, i.e., mesolithic or neolithic to the period of early state formation. The latter has been regarded as an indicator of the spread of rice farming. We will demonstrate two examples using geometric morphometrics. One is a landmark-based approach to skulls in the Kofun period, restricted to a region in western Japan. Our results suggest that regional morphological variation decayed in the later phase, presumably due to migration. The other is an outline-based approach to pottery, indicating that the pattern of morphological variation is consistent with putative routes of the spread of rice farming. By combining three-dimensional models of skeletal remains and pottery, further analyses could provide insights into the interaction between human migration and cultural transmission.

Despite intensive debates on the ethical concerns about tangible cultural heritage, consensuses about sharing digitized cultural heritage and skeletal remains have not yet been sufficiently established in Japan. We will briefly discuss ethical and legal issues in sharing such data in Japanese archaeology.

This work received financial support by JSPS (No. 19H05738, No. 21K12590, 19H04520, No. 20K22029, and No. 20K00019), and JST (No.JPMJMI20G6)

Exploring science with the preschool crowd: A mixed-media approach

ANDREA B. TAYLOR[1] and MEGAN A. HOLMES[2]

[1]Department of Basic Science, Touro University California, [2]Department of Family Medicine and Community Health, Duke University School of Medicine

Skeletal muscle fiber types are important determinants of the contractile properties of muscle fibers. The composition of muscle fiber types tells us important information about a fiber's physiologic characteristics, such as endurance, velocity of contraction, power output, and tension cost. Our recent work studying the myosin heavy chain composition of skeletal muscle fibers has revealed a remarkable degree of diversity of fiber types in the chewing muscles of primates. Some of this variation can be linked to differences in feeding behavior and diet, particularly in species that specialize on mechanically challenging foods, such as hard-object feeding tufted capuchins (*Sapajus apella*) and sooty mangabeys (*Cercocebus atys*), and species that spend a large percentage of their time feeding and thus generate many chewing cycles per day such as Western lowland gorillas (*Gorilla gorilla*). Here we use a mixed-media approach to showcase the functional diversity of fiber types in the chewing muscles of primates from four clades: strepsirrhines, platyrrhines, cercopithecoids, and hominoids. We combine a visual and tactile experience to provoke a sense of wonder at the complexity of primate chewing muscle diversity. This conceptual approach provides opportunities to explore science in a fun and engaging way while at the same time cultivating an early interest in primates.

Funded in part by the Yerkes National Primate Research Center Grants No. ORIP/OD P51OD011132 and No. U42PDP11023, and a grant from the National Science Foundation (BCS-1719743).

Investigating covariation between hyoid shape and wishboning resistance in an ontogenetic sample of tufted and untufted capuchins

PARKER M. TAYLOR[1], TAYLOR A. POLVADORE[1], CAITLIN B. YOAKUM[2], JANINE CHALK-WILAYTO[3], MARIANA D. FOGAÇA[4], MEGAN A. HOLMES[5], MYRA F. LAIRD[6,7] and CLAIRE E. TERHUNE[1]

[1]Department of Anthropology, University of Arkansas, [2]Department of Anatomy, Arkansas College of Osteopathic Medicine, [3]Department of Biomedical Sciences, Mercer University School of Medicine, [4]Neotropical Primates Research Group, NeoPReGo, [5]Department of Family Medicine and Community Health, Duke University School of Medicine, [6]Department of Integrative Anatomical Sciences, University of Southern California, [7]Department of Basic and Translational Sciences, University of Pennsylvania

Recent research on the primate hyoid apparatus suggests that feeding behaviors, such as mastication and swallowing, play important roles in shaping hyoid morphology. However, the relationship between mastication and hyoid shape is largely unexplored. Previous work has noted significantly different hyoid shapes between tufted (*Sapajus* spp.) and untufted (*Cebus* spp.) capuchins, and tufted capuchins are known to possess more robust mandibular symphyses than untufted capuchins, which aids in resisting increased wishboning stress due to their overall more mechanically challenging diet. Because the hyoid is biomechanically linked to the mandible at the symphysis via the suprahyoid muscles, increased wishboning resistance should affect lingual mandibular morphology, and thus potentially also affect the suprahyoid muscles. Therefore, we predict that hyoid shape and symphyseal cross-sectional morphology, a marker of wishboning resistance, covary.

Here, we explore the relationship between hyoid shape and wishboning resistance at the mandibular symphysis for an ontogenetic sample of 51 capuchins (31 *Sapajus*, 20 *Cebus*). While we find that symphyseal robusticity is significantly greater in adulted tufted capuchins compared to their untufted counterparts, which suggests greater wishboning resistance under asymmetric bending, results show no significant correlations between hyoid shape and the cross-sectional morphology of the mandibular symphysis at any developmental stage. Such findings suggest hyoid shape differences between tufted and untufted capuchins may not be driven by differences

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

in feeding behavior. However, the relationship between hyoid shape and mandibular robusticity should be examined at a broader phylogenetic scale to determine if wishboning affects hyoid morphology across primates.

Funding statement: This research was supported by the National Science Foundation's Biological Anthropology directorate (BCS-1945771 [JCW], BCS-1944915 [MAH], BCS-1945283 [MFL], BCS-1945767 [CET], BCS-1944642 [CBY]).

To See, or Not to See: Photo-Haiga and Early Hominin Diets

MARK F. TEAFORD

Basic Science, Touro University

"Haiga" traditionally bring together haiku poems and images with the goal of combining the two art forms to open the door for viewers' interpretations rather than dictating what should be experienced. Until recently, studies of prehistoric diets were bracketed by, and even dependent on, evidence of capabilities, in essence channeling interpretations along certain paths. A classic case in point involves traditional interpretations of the diet of the robust australopithecines, where hard-object feeding was often presented as a crucial element of their behavioral repertoire. This viewpoint has now been challenged on multiple fronts by evidence of actual performance, such as dental microwear, stable isotopes, and tooth-chipping. This has, in turn, raised questions about fundamental assumptions underlying broader concepts such as the way in which teeth process foods and the range of variation in the mechanical and nutritive properties of foods across paleolandscapes. In light of these changes, perhaps the time is right to explore alternative ways of presenting and perceiving evidence so that readers might be encouraged to stop and think more about possibilities rather than merely reaffirming what we've always thought. This "unpaper" will present examples of poems and images that will provide viewers with some food for thought on these topics.

The Early Medieval Transition: Diet Reconstruction, Mobility, and Culture Contact in the Ravenna Countryside, Northern Italy

ANASTASIA TEMKINA

Anthropology, University of Kentucky

The Early Medieval period (476–774 CE) in northern Italy was a time of political instability, migration, and invasion by Germanic groups such as the Langobards. This period of upheaval and transition resulted in substantial regional changes in diet, including a significant increase in meat consumption and the introduction of the new staple crop millet, the predominance of which is tied to Langobard control of the region. Carbon, nitrogen, and oxygen isotopes of 49 human bone samples from the sites of Chiunsano di Ficarolo and Chiesazza di Ficarolo, both located near the ancient Roman capital of Ravenna, were analyzed to better understand diet and mobility patterns during this pivotal time. Results of the analyses suggest most individuals had diets based on a mix of C_3 (e.g., barley, wheat, and rice) and C_4 plants (e.g., millet and sorghum), as well as terrestrial and aquatic proteins. Furthermore, a number of emigrants originating from North Africa and the east and south coastal regions of Italy were identified allowing for the comparison of diets between locals and non-locals. In general, local individuals tended to consume less millet and more C_3 plants and freshwater fish than non-locals. Thus, contrary to results from similar sites under the influence of Langobard migration, locals of the Ravenna countryside not only increased variability of their traditional Roman diet but also averted millet dependence. The effects of offsetting nutritional stress by increasing dietary diversity in the local populations are examined.

Tales from the Oltet Valley of Romania: Implications for hominin dispersals into Eurasia during the early Pleistocene

CLAIRE E. TERHUNE[1], ROMAN CROITOR[2], SABRINA C. CURRAN[3], VIRGIL DRAGUSIN[4], ALEXANDRU PETCULESCU[4,5], BRIANA POBINER[6], CHRIS ROBINSON[7,8], MARIUS ROBU[4] and LARS WERDELIN[9]

[1]Department of Anthropology, University of Arkansas, [2]The Mediterranean Laboratory of European and African Prehistory, Aix-Marseille University, [3]Department of Sociology and Anthropology, Ohio University, [4]"Emil Racovita" Institute of Speleology, Romanian Academy, [5]Romanian Institute of Science and Technology, [6]Human Origins Program, Smithsonian Institution, [7]Bronx Community College and the Graduate Center, City University of New York, [8]New York Consortium in Evolutionary Primatology, [9]Department of Palaeobiology, Swedish Museum of Natural History

The hominin fossil record from the early Pleistocene of Africa is relatively well-documented, in large part because of contributions from researchers like the late Bill Kimbel. However, the exact timing and sequence of the dispersal of hominins out of Africa and into Eurasia is unclear, and the fossil record for this time period remains sparse. The earliest and most secure evidence of hominins out of Africa comes from the site of Dmanisi, Georgia at 1.85 Ma, but other, earlier fossil sites have been suggested to be scattered across Europe and Asia. Here we present ongoing work from fossil sites of the Oltet Valley of Romania, including one of the most fossiliferous sites from Eastern Europe, Graunceanu. Biochronological estimates place Graunceanu in the Late Villafranchian (~2.2-1.9 Ma), and our paleoecological reconstructions identify this site as being primarily open in character, though with some nearby woodlands and water resources. Furthermore, fauna from this site represent a mixture of species typical of both Europe and Western Asia, suggesting this region served as a biogeographic crossroads. Taphonomic analyses indicate the fossils were accumulated rapidly with little weathering or transport, but we do find evidence of carnivore activity and some taphonomic signals require further investigation. Our continued work at this site has already substantively changed our understanding of European mammal biogeography by bringing to light unique fauna, both in time and space, and our ongoing analyses will contribute to our increasing understanding of the earliest hominin dispersals into Eurasia during the early Pleistocene.

This research was supported by National Science Foundation (BCS-1636686), The Leakey Foundation, "Emil Racovita" Institute of Speleology, Josiah Charles Trent Foundation and Duke University, University of Arkansas, and Ohio University.

Variations in mandibular cortical bone thickness and density with aging and tooth loss, using micro-focus X-ray computed tomography (micro-XCT)

CHARLOTTE EG. THEYE[1], MARYNA STEYN[2] and ANNA C. OETTLÉ[1,3]

[1]Forensic Anthropology Research Centre, Department of Anatomy, Faculty of Health Sciences, University of Pretoria, [2]Human Variation and Identification Research Unit, School of Anatomical Sciences, Faculty of Health Sciences, University of the Witwatersrand, [3]Anatomy and Histology Department, School of Medicine, Sefako Makgatho Health Sciences University

The mandible plays a crucial role in many biological functions, such as mastication and speech. However, aging and tooth loss may compromise its normal functioning by changing its morphology. While many studies address the macroscopic mandibular variations, there is a paucity regarding its microstructural changes with advancing age and tooth loss. Using micro-XCT scans of 330 extant human mandibles from South African skeletal collections, inner parameters, namely cortical thickness (CtTh) and cortical density (BV/TV), were measured and investigated with advancing age and across various tooth loss patterns. In fully dentate individuals, it was noticed that as the alveolar height decreases, the cortical bone thickness and density increase. An inner cortical asymmetry between basal, buccal, and lingual areas was described for CtTh, but was absent for BV/TV. With tooth loss, a general decrease in CtTh and BV/TV was observed, except at the midline where the lingual CtTh increased with edentulism. With aging, BV/TV decreased, corroborating the general decline in bone mass of the skeleton. By contrasting the effects of tooth loss and aging, it was concluded that CtTh was mainly influenced by tooth loss and not age, whereas BV/TV displayed an age-related decrease independent

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

of tooth loss. Knowledge and understanding of the precise roles of aging and tooth loss on the mandibular microstructure have implications in dentistry, as cortical thickness and density are essential for many dental procedures; but also in biological anthropology, in which the microstructure of extant human mandibles gives valuable insights into intra- and interspecific variations.

Funding by the University of Pretoria Postgraduate bursaries (General Doctoral Studentship and Research Support bursary).

Strepsirrhine Ontogeny: Evidence for an Ancestral Male Body Mass Growth Spurt in Lemuriformes

JULIE M. THOMAS, MICHELLE L. SAUTHER and STEVEN R. LEIGH

Anthropology, University of Colorado – Boulder

The recent discovery of a male juvenile growth spurt in ring-tailed lemurs (*Lemur catta*) calls into question previous conceptions regarding the evolution of lemur growth and development in Madagascar. Assessment of the ancestral or derived nature of this growth trajectory via comparisons with the ontogenies of other lemur taxa has been complicated by the methodologies implemented in these studies, particularly pooling male- and female- measurements and cross-sectional treatment of datasets, which may obscure biologically meaningful growth events. To address this issue, this investigation focused on publicly accessible databases containing repeated measures of growing individuals to generate sex- and age- specific body mass trajectories for multiple strepsirrhine species (n=28) housed at Duke Lemur Center. We applied the SuperImpositon by Translation and Rotation (SITAR) model, a shape invariant model, to mixed longitudinal data to summarize species growth curves. This methodology allowed longitudinal, rather than cross-sectional, data to determine the shape and growth features present within the growth models. We generated growth curves for fifteen of the twenty-eight species included in the dataset. These were then plotted on a strepsirrhine phylogeny. Of the fifteen models, six out of seven Lemuridae and all of the Cheirogaleidae samples exhibited evidence of a male growth spurt. Although based on small sample sizes from captive populations, parsimonious interpretation of these preliminary findings suggests that male body mass growth spurts may have been present in lemur populations 40 million years ago. Lack of model convergence in Lorisidae and Galagidae study samples prevents the estimation of an earlier date.

Graduate Student Funding Scholarship, University of Colorado – Boulder Graduate School's Summer Fellowship, University of Colorado – Boulder

Forensic Anthropology within the Federal Bureau of Investigation

RICHARD THOMAS

Trace Evidence Unit, FBI Laboratory

This presentation will address the qualifications, accreditation, and adherence to ethical standards required for the practice of forensic anthropology casework within the Laboratory Division of the Federal Bureau of Investigation (FBI). Necessary individual qualifications include Diplomate status with the American Board of Forensic Anthropology (ABFA), as well as successful completion of a training program within the Laboratory Division. This training program includes anthropological exercises including mock cases, oral examinations, and moot court presentations, as well as more general training specific to the FBI Laboratory such as evidence workflow and administrative procedures.

Additionally, the Forensic Anthropology discipline of the FBI Laboratory is accredited by the ANSI (American National Standards Institute) National Accreditation Board (ANAB) based on the ISO/IEC 17025 standards and associated ANAB AR3125 accreditation requirements. This discipline-specific accreditation is in concert with accreditation by ANAB in other areas directly contributing to anthropology casework such as a Laboratory-wide evidence management unit.

Finally, several ethical guideline documents are adhered to by forensic anthropologists at the FBI Laboratory, including annual attestation to the ANAB ethical guidelines required for accreditation, annual attestation to the ABFA ethical guidelines required for continued Diplomate status, and adherence to the American Academy of Forensic Sciences ethical guidelines as required by the Fellow level status of both anthropologists that currently staff the discipline.

An SPHARM Approach to Identifying Locomotor Signals in Middle Miocene Catarrhines from Maboko Island, Kenya

INDYA THOMPSON[1], IRISA ARNEY[2], BERNADETTE PERCHALSKI[1], JAKUB RATKOWSKI[3], BRENDA BENEFIT[4], MONTE MCCROSSIN[4] and LAUREN GONZALES[1]

[1]Physiology and Anatomy, UNTHSC, [2]Medical Anatomical Sciences, Western University of Health Sciences, [3]School of Medicine, University of South Carolina, [4]Anthropology, New Mexico State University

Maboko Island, western Kenya preserves a diverse collection of seven catarrhine proximal humeri from the middle Miocene (~15 Ma). Proximal humeri are extremely rare in the Miocene (25-5 mya), limited to only four specimens outside of Maboko. Identified taxa include cercopithecoids (*Victoriapithecus*), nyanzapithecines (*Mabokopithecus*), small-bodied "apes" ("*Micropithecus*"), and large-bodied hominoids (*Kenyapithecus*), all of which provide important insight into diversity of locomotor patterns among middle Miocene catarrhines.

This project uses weighted spherical harmonics analysis (SPHARM), a landmark-free automated method to explore locomotor signals in the Maboko sample. Meshes of five intact humeri were compared to a sample of 94 extant catarrhines and platyrrhines, spanning a range of locomotor modes (suspensory arborealism, terrestrial quadrupedalism, arboreal quadrupedalism, and knuckle walking). Principal components analyses (PCA) were run on the associated SPHARM coefficients to explore differences among these locomotor groups.

Preliminary assessment shows extant suspensory arboreal primates clustering away from both knuckle-walking and quadrupedal group along PC1 and PC2. Along PC2, further separation was observed between arboreal and terrestrial quadrupeds. The Maboko specimens show distinctions between all five of the fossil primates, particularly between two taxa previously suggested to be arboreal (*Mabokopithecus* and "*Micropithecus*") and two taxa documented as terrestrial quadrupeds (*Victoriapithecus* and *Kenyapithecus*).

Though preliminary, this analysis provides insight into the diversity of catarrhine locomotor behavior during the middle Miocene, reinforcing previous descriptions of locomotor partitioning among the Maboko specimens. Future research that includes early and late Miocene taxa may shed light into diversity of catarrhine locomotor behaviors that spanned the Miocene epoch.

Chimpanzee climbing: testing classic hypotheses of forelimb and body position

NATHAN E. THOMPSON[1], MICHAEL LOUKERIS[1] and MATTHEW C. O'NEILL[2]

[1]Anatomy, NYIT College of Osteopathic Medicine, [2]Anatomy, Midwestern University

Large-bodied arboreal mammals are characterized by many anatomical specializations, including relatively long forelimbs and short hind limbs. Classical static climbing models have linked long forelimbs to reducing forelimb force via large forelimb protraction. Or alternatively, as part of a strategy to position the body's center of mass close to the foot contact point and substrate via highly flexed hind limbs. Long extended forelimbs then allow the animal to lean away from the substrate, creating sufficiently high contact forces for propulsion. Yet, few empirical data on climbing in apes exist to test these hypotheses. Here, we used three-dimensional (3-D) marker data from two male chimpanzees during vertical climbing and quadrupedal walking to test these model predictions.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

During climbing, body-to-substrate distance was 25% lower compared with quadrupedalism (45±2 v 61±1 cm). Climbing entailed maximum forelimb protraction at touch down that was slightly higher than quadrupedalism (27–41° v 26–31°). Over a stride, elbow and knee joints were 35–40° more flexed during climbing than quadrupedalism. During quadrupedalism, the knee and elbow maintained relatively constant joint angles (elbow: ~150°; knee: ~160°) during their respective stance phases. During climbing the elbow flexed dramatically over stance phase (by 30–70°). Peak flexion coincided with minimum body-to-substrate distance. The knee slightly extended (by ~20°) during stance phase. Our results show that chimpanzees do use more protracted forelimbs during climbing, but this effect was smaller than anticipated. Chimpanzees also reduce body-to-substrate distance during climbing, but contrary to some model predictions, this is accomplished via elbow flexion.

This study was funded by NSF BCS-0935321.

Structural Variability in Long Bones as a Marker for Sex Specific Daily Activities

URSULINA P. TOMCZAK[1] and TYLER E. DUNN[2]

[1]School of Medicine, Creighton University, [2]Department of Medical Education, Creighton University School of Medicine

Differences in cross-sectional long bones can be used to understand the habitual activities of human groups. Understanding the structural variability of long bones between the sexes can lead to a useful interpretation of activity. This study examines the variability in femoral and humeral structure to extrapolate daily activities of 112 individuals from 4 Chinese sites dated from 3000-1650 BP. This sample consists of populations with differing subsistence strategies. Body mass is estimated using a sex specific femoral head body estimation equation presented by Ruff et. al. Total cross-sectional area (TA), cortical area (CA), I_{max}, I_{min}, and polar moment of area (J) are calculated for humerus and femur samples. TA, CA, I_{max}, and I_{min} are standardized via length of the respective long bone. Differences between the sexes in TA, CA, I_{max}, and I_{min} of both the humerus and the femur are assessed between 4 sites. Across sites, males are found to have higher I_{max}, I_{min}, and TA when standardized for femur length compared to females. Humeral TA, I_{max}, and I_{min} are found to be higher in females across sites when standardized for length of the humerus. This points towards a significant difference in daily activities between males and females in this sample, with males conducting much more lower limb dominant activities while females partook in activities that were demanding on the upper limb. The use of structural variability in long bones as a method of assessing daily habits can shed light on the cultural norms of past human groups.

How enamel thickness, mineral concentration and mechanical properties influence tooth wear and fractures in catarrhine molar crowns

IAN TOWLE[1,2], LESLEA J. HLUSKO[1,3], MARINA MARTÍNEZ DE PINILLOS[1,4], MARIO MODESTO[1,5], JOEL D. IRISH[6,7] and CAROLINA LOCH[2]

[1]CENIEH, Centro Nacional de Investigación sobre la Evolución Humana (CENIEH), Paseo de la Sierra de Atapuerca 3, 09002 Burgos, Spain, [2]Sir John Walsh Research Institute, Faculty of Dentistry, University of Otago, Dunedin 9054, New Zealand, [3]Department of Integrative Biology, University of California Berkeley, Valley Life Sciences Building, Berkeley, California, 94720 USA, [4]Laboratorio de Evolución Humana (LEH), Universidad de Burgos, Plaza Misael Bañuelos s/n, 09001 Burgos, Spain, [5]UNIR, Universidad Internacional de La Rioja (UNIR), Av. de la Paz 13, 26006 Logroño (La Rioja, Spain), [6]Research Centre in Evolutionary Anthropology and Palaeoecology, School of Biological and Environmental Sciences, Liverpool John Moores University, United Kingdom, L3 3AF, [7]The Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand, Johannesburg, South Africa

Variation in the structure, mineral concentration and mechanical properties of enamel across tooth crowns has been studied in both clinical and evolutionary contexts. How this variation is associated with dental tissue loss remains relatively unexplored. In this study, tooth wear and fracture patterns were compared with mechanical properties (nanoindentation of buccal-lingual sections; 13 catarrhine, one platyrrhine), mineral concentration (MC; Micro-CT scans of whole crowns; 16 catarrhines) and enamel thickness (Micro-CT scans; same 16 catarrhines). All specimens are from museum collections, with a mix of first (n=9), second (n=20) and third (n=1) molars. Mean values for different crown locations were calculated. Thickly enamelled buccal cusps (i.e., 'functional' cusps) have significantly lower hardness ($p < 0.001$) and elastic modulus ($p = 0.031$) than their non-functional counterparts (e.g., lingual hardness mean: 4.79 GPa; buccal hardness: 4.55 GPa). Cusps consistently have higher MC and mechanical properties values than lateral positions (e.g., cuspal MC mean: 2.31 g/cm^3; lateral MC mean: 2.25 g/cm^3). Lateral mesial enamel has significantly lower MC and thickness values than other locations. Non-functional cusps have higher prevalence of fracture and hardness than functional cusps, potentially as an evolutionary response. Cusps are subjected to longer and/or more extreme forces during mastication than lateral enamel, meaning that stronger enamel may help protect cusps against failure. Lateral mesial enamel is 'weaker' potentially due to increasing forces moving distally, and typically shows more substantial wear than distal positions. In sum, enamel structural/compositional data may allow additional insights into primate molar wear/fracture patterns and evolution.

Funding for this research is supported by: European Research Council Advanced Grant Project 101054659—Tied2Teeth; Sir Thomas Kay Sidey Postdoctoral fellowship from the Faculty of Dentistry, University of Otago.

Effects of daily step counts and rest bouts on bone material and structural properties in the femur of three West African primates

JORDAN N. TRAFF[1], DAVID J. DAEGLING[1] and W. SCOTT MCGRAW[2]

[1]Department of Anthropology, University of Florida, [2]Department of Anthropology, The Ohio State University

Bone is responsive to both load frequency and duration of rest periods in daily activity. This study examines femoral bone density of three sympatric primates (*Piliocolobus badius*, *Cercopithecus diana*, *Cercocebus atys*) in light of locomotor effort in the Ivory Coast's Taï Forest. *Pi. badius* takes fewer steps per day than *C. diana*, and both take significantly fewer than *C. atys*. *Pi. badius* rests the most during the day, and for long periods, while *C. diana* rests the least. Since the combination of walk cycles and rest periods differs among species, these data may offer insight into which variables most strongly influence bone quality.

For three individuals of each species, we examined bone density and structural rigidity at four slices from femoral micro-CT scans (25%, 45%, 55%, 75% proximodistal). An ANOVA indicates that the overall density differed significantly among species *(P<0.01)*, with *C. atys* having lowest density and *Pi. badius* the greatest. The cortical to total subperiosteal area ratio was also different among species *(P<0.001)*, with *Pi. badius* having a much higher ratio than *C. atys* or *C. diana*.

The differences in daily step counts among species align well with both the overall density and the higher cortical area ratio, paradoxically suggesting that fewer steps lead to denser, thicker bone. However, the closer association between *C. diana-C. atys* for both variables suggests that bone morphology is not a simple function of step counts. The longer and more frequent rest periods for *Pi. badius* may explain why they diverge so significantly.

Supported by NSF BCS -1440278 and -1440532

Modeling airflow during the nasal cycle in 3D: Implications for variation in human nasal form and function

BAONHU TRAN[1], LYNDEE A. WARD[1], HASINTHA HAK. PATABENDIGE[2], VIVEK C. NAIR[2], ELIZABETH

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

O. CHO[1], TODD R. YOKLEY[3], BRIAN H. DENNIS[2] and SCOTT D. MADDUX[1]

[1]Center for Anatomical Sciences, University of North Texas Health Science Center, [2]Department of Mechanical and Aerospace Engineering, University of Texas at Arlington, [3]Department of Sociology and Anthropology, Metropolitan State University of Denver

Inability to control for varying levels of nasal mucosal congestion due to the nasal cycle has limited evaluation of how variation in human nasal morphology influences intranasal airflow dynamics. Here, we employed Computational Fluid Dynamics (CFD) analysis, in conjunction with a newly developed *in silico* method for controlling mucosal congestion levels, to assess the nasal cycle's functional impacts on intranasal heat and moisture exchange. Three nasal models with varying levels of congestion were generated from a computed tomography (CT) scan of one male human head: asymmetrical (left/right = 90/10%), mid-cycle (left/right = 50/50%), and fully decongested (left/right = 0/0%). CFD analyses were then performed on each model to evaluate the amount of heat and moisture transferred to cold-dry (-5°C, RH=0%) inspired air. Morphological assessments of mucosal surface area-to-airway volume (SA/V) ratios indicate the decongested model exhibited a substantially lower SA/V ratio (0.57) than the mid-cycle (0.72) and asymmetrical (0.74) models. Consistent with functional expectations based on these SA/V ratios, the fully decongested model exhibited the lowest levels of inspiratory heat and moisture transfer during CFD modeling, while the overall transfer rates were similar for both mid-cycle and asymmetrical models. These results suggest that the nose's overall air-conditioning capacity likely remains relatively stable throughout the nasal cycle despite varying levels of mucosal congestion. Thus, rather than morphological variability within the nasal cycle, it may actually be the distinction between the semi-congested nasal cycle versus complete mucosal decongestion (as seen during strenuous exercise) that confounds functional interpretations of variation in nasal morphology.

Funding was provided by the National Science Foundation (#2203808), Texas Center for Health Disparities (RF00241 & RI40241), and the Association for Anatomy Innovations Program.

Minimizing contamination while collecting sediment samples from human burials for DNA analysis

CATHY N.H. TRAN[1,2], CRISTINA T. GARCIA[3], MARIA JOÃO VALENTE[4], FRANCESCO BERNA[1], HUGO F.V. CARDOSO[1,2] and DONGYA YANG[1,2]

[1]Department of Archaeology, Simon Fraser University, [2]Centre for Forensic Research, Simon Fraser University, [3]Direção Regional de Cultura do Algarve, Direção Regional de Cultura do Algarve, [4]Faculdade de Ciências Humanas e Sociais, Universidade do Algarve

Degraded human DNA is inherently vulnerable to contamination, particularly due to its lesser quantity and the variety of circumstances in which contaminant human DNA can be introduced into the environment. In the field, samples can be contaminated by individuals who have interacted with the site, including field personnel, or cross-contaminated by DNA from other organisms in the area. With risks of contamination commencing in the field, measures to minimize contamination must also commence in the field. In this study, contamination procedures were applied during the collection of sediment samples from four single graves in the 13th century Christian cemetery at the archaeological site of Poço Antigo in Cacela-a-Velha, Portugal. To minimize contamination from field personnel, sampling areas were cleared of other individuals and personal protective equipment was worn by the researcher. Each sediment sample was also collected using a disposable soil sampler (EasyDraw Syringe®) and individually stored in a plastic bag. Fourier-transform infrared spectroscopy (FTIR) was applied to obtain qualitative mineralogical information about the burial sediments, providing context for sediment composition and informing the observed preservation of DNA. To assess the effectiveness of these contamination measures, sedimentary DNA extraction methods will be tested for the recovery of authentic human DNA. This study draws upon existing recommendations while also exploring new techniques to minimize and evaluate DNA contamination during the collection of sediment samples. This study also reinforces the importance of having DNA researchers present during fieldwork to ensure that the preservation and decontamination of DNA are prioritized throughout sample collection.

This work was supported by the Social Sciences and Humanities Research Council (Joseph Armand Bombardier Canada Graduate Scholarship - Master's) and Simon Fraser University.

The lived experiences of juveniles at Early Bronze Age Karataş-Semayük as identified through dental stress markers

CHRISTINA M. TRENT[1], DONOVAN M. ADAMS[1] and ALI METIN BÜYÜKKARAKAYA[2,3]

[1]Department of Anthropology, University of Central Florida, [2]Department of Anthropology, Hacettepe University, Ankara, Türkiye, [3]Human Behavioral Ecology and Archaeometry Laboratory (IDEA Lab), Ankara, Türkiye

Early Bronze Age Karataş-Semayük, located in Anatolia on the Elmalı plain, was occupied c. 2700-2300 BCE. Occupation has been divided into six periods, with varying demographic and archaeological changes occurring between the periods. As time progressed, the community's social structure exhibited emerging social stratification and increased population size which may have, in turn, led to changes in stress and lived experience. To interpret stress throughout Karataş's occupation, 85 juveniles were analyzed for linear enamel hypoplasia (LEH) and dental fluctuating asymmetry (DFA). Individuals ranging from birth to 19 years of age were included in this study, as the assumed age of social adulthood at Karataş was about 15 years old.

Linear enamel hypoplasia was identified on 10 individuals (11.7%) aged between three and 15 years, with 50% of the individuals with stress indicators between the ages of five and eight years (n=5). Fisher's exact tests indicated nonsignificant relationships between burial period and LEH (p = 0.1396, Cramer's V = 0.2614) and burial location and LEH (p = 0.7525, Cramer's V = 0.1228). Preliminary dental fluctuating asymmetry analyses indicates higher rates of DFA in Period IV and in locations Trench 37 and Trench 98, implying higher rates of developmental instability in these groups. However, DFA analysis could not be conducted on Periods I/II due to lack of data. These results suggest that despite changing demographic and social structures at Karataş, these changes were not manifested in changing frequencies of indicators of stress and developmental instability.

Deciphering diagenesis: The utility of histotaphonomy in bioarchaeological contexts using a case study from medieval Portugal

TRENT M. TROMBLEY[1], ASHLEY E. BLAKE[1], ANTÓNIO MATIAS[2] and SABRINA C. AGARWAL[1]

[1]Department of Anthropology, University of California, Berkeley, [2]Diretor de Arqueologia, Câmara Municipal de Santarém

Social aspects of identity and demography have a long history in bioarchaeological research for their covariance with indicators of stress and skeletal health. Axes such as age, biological sex, gender, or religious identity are typically analyzed in their patterning of stress indicators to elucidate how certain communities in the past may have been susceptible to perturbations throughout the life course. Such axes inform our understanding of how past communities may have lived and died, but are seldom analyzed regarding what happens *after* death. Examining social aspects of identity in relation to taphonomic outcomes provides an exciting opportunity to examine variation in bone preservation more thoroughly. The burgeoning field of "histotaphonomy" illustrates the potential for microscopic diagenetic and bioerosive indicators to reflect levels of putrefaction and microburial environments, which can be instrumental for elucidating funerary practices or other taphonomic filters. We present here a histotaphonomic analysis of thin sections prepared from ribs from *n* = 147 individuals from a medieval Portuguese multi-faith cemetery, which allows us to compare how funerary treatments correspond with microscopic indicators of preservation. Results showcase that nearly all samples

26927691, 2023, S7S, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

(99.32%) experience bioerosion, with the majority (58.87%) experiencing heavy bacterial attack with virtually no remaining microstructure. Patterning differed slightly by funerary group, but the differences were not statistically significant. Age and sex similarly showed minor differences in bioerosive indicators. Patterning in bacterial/fungal attack, as well as cracking and collagen integrity are discussed in light of local site dynamics and funerary textiles which may have altered putrefactive intervals.

This research was funded by a 2019-2020 U.S. Fulbright Student Research Award with additional support from the UC Berkeley Summer Undergraduate Research Fellowships - Summer Mentor and Research Teams (SURF-SMART) fellowship.

Trabecular signals of ankle posture in two distal tibiae from Sterkfontein Member 4

ZEWDI J. TSEGAI[1,2], ANNALISA PIETROBELLI[3], BERNHARD ZIPFEL[4], TRACY L. KIVELL[1,5] and MATTHEW M. SKINNER[1,5]

[1]School of Anthropology and Conservation, University of Kent, [2]Department of Organismal Biology and Anatomy, University of Chicago, [3]Department of Biological, Geological and Environmental Sciences, University of Bologna, [4]Evolutionary Studies Institute, University of the Witwatersrand, [5]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand

The mosaic morphology of early hominins has led to differing interpretations of their locomotor repertoire. Whether arboreal locomotion was an important component of their behaviour, and whether they used a form of bipedalism similar to, or kinematically distinct from, recent humans remains unknown. As the internal trabecular structure of the skeleton models during life in response to behaviour, it has the potential to reveal a signal of how an individual actually behaved during life.

We analysed the internal trabecular structure of the distal tibia of two individuals from Sterkfontein Member 4 assigned to *Australopithecus africanus* (StW 358 and StW 389) and a comparative sample of *Homo sapiens* (N = 6), *Pan troglodytes* (N = 22), *Gorilla gorilla* (N = 11) and *Pongo* sp. (N = 6). We used a whole bone method of trabecular bone analysis to map the distribution of bone volume fraction (BV/TV) throughout the distal tibia.

African apes, humans and orangutans differ in the distribution of BV/TV, with chimpanzees and gorillas showing signals of dorsiflexion and plantarflexion of the ankle joint, humans showing evidence of an ankle loaded in a neutral position, whereas orangutans differ from the other taxa. Both distal tibiae from Sterkfontein show an intermediate signal, with a central concentration of trabecular bone similar to humans, however, they also have an anterior concentration of trabecular bone. This suggests that the ankle of *Australopithecus africanus* was loaded in both neutral, human-like postures, and in African ape-like dorsiflexion, indicating a locomotor/postural repertoire that differs from recent humans.

This research was supported by the Max Planck Society (ZJT, TLK, MMS), European Research Council Consolidator Grant #819960 (MMS and TLK) and Marie Skłodowska-Curie Grant #101025719 (ZJT).

Chronic disease and allostatic load among the Comcáac: An indigenous Mexican population in transition

ALEXANDRA C. TUGGLE[1] and DOUGLAS E. CREWS[1,2]

[1]Department of Anthropology, The Ohio State University, [2]College of Public Health, The Ohio State University

The Comcáac, a traditionally non-agricultural, semi-nomadic indigenous group native to the Sonoran coastal desert, have experienced significant cultural, health, and dietary transitions since being forced to settle into permanent communities and integrate into Mexico's modern market economy. Although the Comcáac have shown resilience and adaptability in stressful living conditions, overall community health has worsened with increasing prevalence of degenerative conditions: e.g., hypertension, diabetes, obesity, and dyslipidemia. Here, we address chronic disease prevalence in a sample of residents from Punta Chueca, Sonora (n = 95). To do so, we assessed physiological dysregulation using a 13-biomarker allostatic load index (ALI) derived from cardiovascular, metabolic, and neuroendocrine biomarkers. Of 95 participants, 33.7% are hypertensive (blood pressure ≥ 130/80 mmHg), 15.8% are prediabetic (HbA1C 5.7% ≥ 6.4%), 26.3% are diabetic (HbA1C ≥ 6.5%), and 33.7% are obese (BMI ≥ 30 kg/m^2). Lipid panels reveal 31% have high total cholesterol (> 200 mg/dL), 32.6% have low HDL cholesterol (< 40 mg/dL), 58.9% have high LDL cholesterol (> 100 mg/dL), and 29.5% have high triglycerides (>150 mg/dL). To construct an ALI , we used sample-specific quartile cut points for each biomarker. Estimated allostatic load averaged 3.27, (sd = 2.25, range 0-9) and associated significantly with age ($p < 0.001$), civil status ($p = 0.05$), and number of children ($p = 0.05$), but did not vary significantly by sex ($p = 0.64$). This research is the first to detail chronic disease prevalence and allostatic load for this population in transition, with implications for future morbidity and mortality.

This research was funded by the Tinker Foundation, Consejo Nacional de Ciencia y Tecnología (CONACYT), the Alumni Grant for Graduate Research and Scholarship, and the Larsen Research and Travel Award.

Impacts of adverse early life environments on bone length in wild Amboseli baboons

KRISTEN A. TUOSTO[1], OGETO MWEBI[2], DAVID PATTERSON[3], SUSAN C. ALBERTS[4] and SHANNON C. MCFARLIN[1]

[1]Center for Advanced Study of Human Paleobiology, George Washington University, [2]Osteology Section, National Museums of Kenya, [3]Department of Biology, University of North Georgia, [4]Departments of Biology and Evolutionary Anthropology, Duke University

Developmental plasticity, the variation of phenotypes produced from a single genotype in response to environmental conditions, may have evolutionary significance. However, the degree to which it has contributed to skeletal variation in the hominin fossil record remains poorly understood. In this study, we investigate how skeletal development may respond to environmental variability by examining the effects of early life adversity during gestation and the first postnatal year on long bone lengths in a well-documented wild savanna baboon population (*Papio cynocephalus*; n=30; aged 0-25 years) from the Amboseli Basin, Kenya. We hypothesize that baboons that experienced adverse early life physical and social environments will display shorter skeletal limb lengths compared to baboons from high-quality environments. We used linear mixed-effect regression models and likelihood ratio tests to examine the effects of the following predictors on limb bone diaphyseal lengths: age and sex, cumulative rainfall during gestation and the first postnatal year, respectively, and proportional maternal dominance rank treated categorically; we included social group as a random effect. Our results indicate that age and sex are significant ($p<0.05$) predictors for long bone diaphyseal lengths. Although rainfall and maternal rank improved model fit in the likelihood ratio test for diaphyseal lengths for the femur, tibia, humerus, and radius, during both gestation and the first postnatal year, only rainfall was significant or approaching significance. Specifically, lower cumulative rainfall was associated with shorter bone lengths, indicating that the developing skeleton is sensitive to the maternal environment *in utero* and early infancy.

National Science Foundation (NSF BCS 2120962, 1640477), The Leakey Foundation, and GW's Lewis N. Cotlow Award

Differences in cortical and trabecular bone morphology in the rhesus macaque hip and knee by age

CASSANDRA M. TURCOTTE[1,2,3], SHARON KUO[4,5], ADITI RAGHUNATH[2], LAUREN J. N. BRENT[6], NOAH SNYDER-MACKLER[7], SCOTT A. WILLIAMS[2,3], JAMES P. HIGHAM[2,3], TIM M. RYAN[5], CAYO BIOBANK RESEARCH UNIT[8] and SUSAN C. ANTÓN[2,3]

[1]Department of Anatomy, New York Institute of Technology, [2]Department of Anthropology, New York University, [3]New York Consortium

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

in Evolutionary Primatology, [4]Department of Anatomy, University of Minnesota, [5]Department of Anthropology, Pennsylvania State University, [6]Department of Psychology, University of Exeter, [7]School of Life Sciences, Arizona State University, [8]Department of Neuroscience, University of Pennsylvania

In humans, an aging population is associated with an increase in age-related diseases that progressively degrade the structure of bone tissue. Diseases associated with deleterious changes in bone quality contribute to loss of mobility as well as increased fracture risk and may further limit sociality and quality of life. Here, we examine elements of skeletal variation from individuals of different ages in loadbearing hindlimb joints, to understand the influence of aging on skeletal structure in male and female rhesus macaques, a common model organism for human disease development. High resolution microCT scans were collected of the hip (proximal femur) and knee (distal femur and proximal tibia) from individuals in the CPRC-NYU Rhesus Macaque Skeletal Collection.

We extracted maximum and mean bone volume to total volume (BV/TV) from whole bone 3-dimensional meshes. To explore the relationships between BV/TV, age, and body mass, we performed an analysis of covariance (ANCOVA) for each sex. Individual mass was the primary factor driving variation in bone volume in both sexes [Proximal femur: female mean p=0.005; male mean p<0.001]. However, in males, mean [p=0.006] and maximum [p=0.013] BV/TV significantly decreased with age. No such relationship was observed in females [mean BV/TV p=0.388; maximum BV/TV p=0.863]. These results highlight the impact of body mass on skeletal structure. Further work will include analyses of additional factors, such as social rank and connectivity.

National Institutes of Aging R01-AG060931, AABA Cobb Grant (to CMT). National Science Foundation BCS-1754024, NSF RAPID 1648676 NCE, Leakey Foundation grant (to JPH, SCA, SAW). NIH #P40-OD012217 (supports CPRC).

Residential Origin and Status at the Inka Site of Saqsaywaman

BETHANY L. TURNER

Department of Anthropology, Georgia State University

The Inka Empire rose to power in the 14th-16th centuries CE, expanding out of the southeastern Peruvian highlands to dominate much of the Central Andes. Inka statecraft was partly based on relocating imperial subjects, both locally and across far-flung regions, to perform varying functions. By reconstructing the residential origins of human remains from different Inka sites, especially those in the imperial heartland, one can better frame Inka statecraft from the ground up, using individuals' residential histories to interpret their lived experiences and roles within the empire.

This study presents $^{87}Sr/^{86}Sr$ data from individuals (N=74) interred at the Inka site of Saqsaywaman (N=74), which overlooks the imperial capital of Cuzco. Saqsaywaman functioned as a ritual and ceremonial complex, and the sex distribution of interments varies between the site's four sectors, suggesting variation in backgrounds and/or status among the site's residents. Enamel $^{87}Sr/^{86}Sr$ ratios, which represent those incorporated early in life during crown formation, exhibit wide ranges, especially among those from the ceremonial Suchuna (N= 41, 0.70422-0.71599) and Muyukmarqa (N=19, 0.70570-0.71999) sectors. Corresponding rib bone $^{87}Sr/^{86}Sr$ ratios, which represent those averaged over 5-10 years antemortem, exhibit much smaller ranges in the Suchuna sector (N=35, 0.70706-0.70800) but maintain a wide range in the Muyukmarqa sector (N=13, 0.70700-0.71258). These results suggest divergent residential origins among the majority of the Saqsaywaman residents, and that those buried at Muyukmarqa relocated to the site much later in life. Interpreted within Saqsaywaman's archaeological context, these results provide further insights into the respective statuses of its permanent residents.

This study was funded by the National Science Foundation (BCS #1359595)

Adaptations spread faster and are more sustainable when they arise in minority subpopulations in heterogeneous societies

MATTHEW A. TURNER[1,2], IAN HARRYMAN[2], ALYSON L. SINGLETON[3], CAROLINE MURAIDA[3], MALLORY HARRIS[4], JORDAN W. STRASSER[6], ARUSHA PATIL[5], RONAN F. ARTHUR[4], CESAR A. LOPEZ[3] and JAMES HOLLAND JONES[1,2]

[1]Division of Social Sciences, Stanford Doerr School of Sustainability, Stanford, [2]Department of Earth System Science, Stanford, [3]Emmett Interdisciplinary Program in the Environment and Resources, Stanford, [4]Department of Biological Sciences, Stanford, [5]Program in Human Biology, Stanford, [6]Department of Bioengineering, Stanford

Community-based adaptations to climate change are essential because (1) they tend to be more effective than imposed adaptation, and (2) local communities cannot depend on unlimited support from outside organizations. There is good qualitative evidence that the most successful and sustainable community-based adaptations are those where local populations lead, but this success requires these communities to solve substantial collective-action problems. Adaptation is driven by diversity, but this fact is at odds with the fact that homophily, the preferential interaction with one's own group, aids in the solution to collective action problems. In this paper, we explore the tension between diversity-driven adaptive potential and homophily-driven in-group social solidarity. We combine theory and formalisms of cultural evolution and group psychology and develop a computational agent-based model of sustainable adaptation that develops a new mechanistic understanding of community-based adaptations. We find that innovations are better sustained when they are first incubated within a small minority group, with moderate levels of homophily. This finding supports suggestions that subsistence communities can be important sources of innovation and climate-change adaptation despite—or maybe because of—their often peripheral status within states. This work can help to amplify the effect of future community-based adaptations by providing a framework for designing community social structures that optimize the use of scarce time and resources for climate-change adaptation.

This work funded by awards from the Center for Innovation in Global Health and the Center for Existential Risk, Stanford University.

Is DEI Doing Enough for Forensic Anthropology?

EVONNE TURNER-BYFIELD

Anthropology, The Ohio State University

The last two decades have seen an increase in university programs designed to combat institutional inequality and racism as institutions have taken steps to recognize the inherent value of increased minority participation. Diverse research teams promote scientific creativity, are better equipped to address complex research questions, and have lower levels of confirmation bias, among other values. In this context, Anthropologists must continue to anticipate and navigate complex sociopolitical issues by encouraging diversity initiatives. Diversity, equity, and inclusion (DEI) initiatives are in place to support the success of Historically Underrepresented Minorities (URM), with special focus on recruitment and retention of faculty and students from diverse backgrounds. However, several of the most effective strategies adopted (e.g., deemphasizing standardized test scores in admissions; collaborations with Historically Black Colleges and Universities and Hispanic Serving Institutions) have more impact on recruitment than on retention of URM students and faculty. Here, I explore the short comings of DEI initiatives at American universities through enrollment and retention data collected by NSF. The data show that, between 2009 and 2019, the total number of completed graduate degrees in Anthropology for URM students increased by only 6%, and there was a marked decrease in the number of degrees completed by URM male students, apart from Hispanic males which increased by 7%. These numbers demonstrate that DEI initiatives still fail to establish structures and resources to facilitate

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

URM students and faculty long-term success, and demonstrate the continued need to interrogate DEI initiatives, their efficacy, and ways to improve them.

Skeletal effects of cold exposure in a model of dysfunctional brown adipose tissue

REBECCA TUTINO, MIRANDA N. COSMAN, RACHEL HURWITZ, MAISEY SCHULER, ALEXIS STOKEL, ISABEL HERMSMEYER and MAUREEN J. DEVLIN

Anthropology, University of Michigan

Brown adipose tissue (BAT) may contribute to thermogenesis in humans but potential skeletal effects are less clear. Nonshivering thermogenesis (NST) in BAT, in which uncoupling protein-1 (UCP1) generates heat, might also indirectly reduce bone loss caused by cold-induced sympathetic activation. To test this hypothesis, male and female UCP1-knockout (UCP1KO) and C57BL/6J (B6) mice were housed from 3-12 weeks old at 26°C (warm), 22°C (cool), or 22°C with propranolol (PRO, sympathetic blocker) (5 mg/mL in water). We predicted that UCP1KO at 22°C would have lower bone mass compared to B6, but PRO-treated mice would not. At 12 weeks of age, we measured trabecular bone volume fraction (BV/TV), trabecular number (Tb.N), trabecular thickness (Tb.Th), trabecular spacing (Tb.Sp), and connectivity density (Conn.D) of the distal femur by µCT. In B6 females, BV/TV (-25.9%), Tb.N (-7.6%), and Conn.D (-70.6%) were lower and Tb.Sp (+8.1%) was higher at 22°C vs. 26°C (all $p<0.05$). BV/TV did not differ at 22°C vs. 26°C in B6 males ($p<0.05$). In female UCP1KO, BV/TV did not differ at 22°C vs. 26°C, or versus B6. In UCP1KO males at 22°C, BV/TV (-25.5%), Tb.N (-15.1%), and Conn.D (-31.8%) were lower and Tb.Sp was higher (+17.0%) vs. B6 (all $p<0.05$); with PRO, BV/TV (+22.5%), Tb.N (+8.5%), and Conn.D (+15.6%) were higher, and Tb.Sp (-9.3%) was lower. PRO had no effect in B6 males nor in females of either genotype. These results show that environmental temperature and NST via UCP1 have sex-specific effects on bone architecture that should be investigated in future studies.

Funding for this project was provided by NSF BCS-1638553 to MD.

Status of African authorship among conservation research output from sub-Saharan Africa: an African perspective

MARIE FIDELE TUYISENGE[1], MAIRE K. O\'MALLEY[1,2], TARA S. STOINSKI[1] and YNTZE VAN DER HOEK[1]

[1]Conservation and Research, The Dian Fossey Gorilla Fund, [2]Anthropology, Northern Illinois University

The multifaceted field of conservation, which intersects with biological anthropology, has previously been criticized as a neo-colonial science. Despite increasing acknowledgement that researchers from the Global South are critical for many reasons, the field suffers from an ongoing absence of African representation. To confront this inequity, we analyzed the status of sub-Saharan African authorship in conservation science through 2015-2021. We assessed articles where research was completed in Africa within ten conservation journals with varying impact factors to understand the rate of African senior authorship. We provide a female, African perspective to identify limitations and solutions to elevate African participation in research. Out of 1632 articles, half had senior authorship with sub-Saharan African affiliations, one-fourth had no African representation, and one-third were solely authored by Africans; however, South African representation highly skewed these percentages and numbers dropped when South African papers were excluded. African authorship varied considerably between the journals, with nominal representation (<15%) in high impact journals. We identified that despite signs of improvement, especially after the onset of the COVID-pandemic, African authors remain underrepresented in literature pertaining to their home countries. From an African perspective, in addition to high-level factors, this underrepresentation may result from accumulation of 'smaller' challenges including the disconnect between early education and scientific writing skills and the rarity of mentorship available to young African scientists. We propose these observed patterns in conservation literature reflect those within biological anthropology and discuss solutions to decolonize anthropology and conservation science, promote equity, and elevate marginalized communities in science.

The Dian Fossey Gorilla Fund

Reliability of three-dimensional computed tomography (3DCT) in sex estimation by obtaining population-specific data from the skull of an African population

ORIASOTIE O. UJADDUGHE[1,2], OLADIRAN I. OLATEJU[1] and MUBARAK A. BIDMOS[3]

[1]Anatomical Sciences, University of the Witwatersrand, Johannesburg, South Africa, [2]Anatomy, Ambrose Alli University, Ekpoma, Nigeria, [3]College of Medicine, QU Health, Qatar University, Doha, Qatar.

With rising human activities, natural disasters, criminal activities and automobile accidents, it is a necessity to identify human remains whose identity, time and circumstances of death are questionable. Sex estimation of the victim is the first approach in the identification process as it narrows the identification probability by 50%. South Africa's crime rate is high, involving mostly South African Blacks (SABs) being the largest population group. Measurements of the human skull are valuable in forensics as they provide vital information such as the sex, age and ethnicity of a subject. However, there are no data from the skull of contemporary SABs.

This study explored the reliability of skull measurements collected from 3DCT scans of contemporary SABs in sex estimation.

Skull CT records of 160 SABs (50% sex ratio; age range: 18–60; period: 2016–2022) housed in the CMJA Hospital, Gauteng, South Africa were assessed (Human Ethics number: M220108). Eight variables were measured on each reconstructed 3D-image. The reliability of the measuring technique and the validity of selected equations of Steyn and Iscan (1998), Franklin et al. (2005) and Dayal et al., 2008 were assessed.

All measurements showed sexual dimorphism except nasal breadth. The average sex-estimation-accuracy obtained for the selected equations ranged from 50-70% compared to 77.5–85.7% obtained by the previous authors.

Measurements of the skull of contemporary SABs are easily reproducible and showed sexual dimorphism. The low degree of average accuracy of tested equations, therefore, highlights the need to formulate new equations for the contemporary population.

This project was funded by the Tertiary Education Trust Fund of the Federal Government of Nigeria and the Postgraduate Merit Award of the University of the Witwatersrand, Johannesburg, South Africa.

Daily Activity Patterns among People Interred in Umm an-Nar Communal Tombs from Southeastern Arabia

JAIME ULLINGER[1], LESLEY A. GREGORICKA[2], LAURA ALLEN[3], JANETH CABAÑAS[4], SARAH CAMINITO[5], MADDY HULL[6], ANGELIQUE LINDBERG[7], CADEN RIJAL[8], ABBY SARGENT[2] and SARAJANE SMITH-ESCUDERO[9]

[1]Sociology and Anthropology, Quinnipiac University, [2]Sociology, Anthropology, and Social Work, University of South Alabama, [3]Anthropology, University of New Hampshire, [4]Anthropology, University of California Berkeley, [5]Anthropology, University of Pennsylvania, [6]Anthropology, Dickinson College, [7]Anthropology, Boston University, [8]Anthropology, Wellesley College, [9]Anthropology, University of Notre Dame

Two tombs (Unar 1 and 2), located in the United Arab Emirates, were used during the Umm an-Nar period (ca. 2700-2000 BCE) as sedentism and oasis agriculture became widespread regionally. Community members interred in these tombs across multiple generations became commingled with hundreds of others. This research examined daily activity patterns, looking for evidence of horizontal or vertical stratification that may have emerged with new subsistence and settlement patterns.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

No tomb differences were found for squatting facets on the tibia [Fisher's Exact (FE) p>0.05)] or talus (FE p>0.05), the majority of humeral entheseal sites (Mann-Whitney U, p>0.05), nor for entheseal changes or vastus notch presence on patellae (X^2, p>0.05). However, more degenerative joint disease was present in patellae from Unar 2 (p=0.003). There was no difference between right and left sides (tombs combined) for tibial squatting facets (FE p>0.05), nor for entheseal changes in patellae (p=0.08), although there was a side difference in lateral talar squatting facets (p=0.006). No sex difference was found in humeral entheseal sites (Mann-Whitney p>0.05). Finally, only seven of 191 individuals (3.7%) had evidence of external auditory exostoses, four of which were estimated to be male, suggesting that some may have been involved in pearl-diving (evidenced in material culture).

Overall, few differences were found for activity differences in arms, knees, and ankles between tombs or sexes. This is consistent with the general lack of stratification associated with the Umm an-Nar period, despite lifestyle changes and interaction with larger state systems from Mesopotamia and the Indus Valley.

This research was funded by a National Science Foundation Research Experiences for Undergraduates Award (#1852426).

An examination of the European ancestry component of self-identified Afro-Puerto Ricans

EMMA C. ULRICH[1], MARIA A. NIEVES-COLÓN[1] and JADA BENN TORRES[2]

[1]Anthropology, University of Minnesota Twin Cities, [2]Anthropology, Vanderbilt University

Contemporary Puerto Rican populations are often products of genetic admixture between Indigenous American, African, and European populations. Puerto Ricans of African descent are an understudied sub-population within Puerto Rico, and little is known about how their genetic ancestry compares to non-Afro-descendant Puerto Ricans. Here we investigate the autosomal ancestry of 30 individuals that self-identify as Afro-Puerto Rican genotyped at 750,000 loci on National Geographic's Next Generation Genochip. Admixture analyses of these individuals indicate an average genetic ancestry distribution of 54% West and Central African, 22% Southern European, 5% Western and Central European, and 5% Indigenous American. Ancestry-specific PCA (ASPCA) identified sub-continental European regions with the most contribution to Afro-Puerto Ricans compared to non-Afro-descendant Puerto Ricans and Afro-Barbadians. A preliminary ASPCA including SNP data from 25 European and North African reference populations, examining 104,955 biallelic SNPs, indicates that available reference populations may be a poor proxy for the European component of modern Caribbean admixed populations, potentially due to significant drift from European founder populations. This result also highlights the non-homogeneity of contemporary European populations and their divergence from ancestral populations. Ongoing analyses seek to increase the SNP resolution by removing particularly distant European reference populations (increasing the SNP count to 588,372) and include Afro-Puerto Ricans with a European ancestry proportion as low as 5% (previously 25%). This study considers the nature of self-identification with specific Puerto Rican sub-populations, examining the relationship between genetic ancestry and social identity. Our study also aims to examine differential ancestry contributions within Caribbean admixed populations.

Are early hominins in the Turkana Basin consistent with Hutchinson's Rule?

ALEXIS S. ULUUTKU and BERNARD A. WOOD

Center for the Advanced Study of Human Paleobiology, The George Washington University

Hutchinson's rule states that sympatric species differ in the length of their heads, mouths, and/or beaks (i.e., trophic structures) by a factor of approximately 1.3-1.4 when averaging linear measurements. In this study, we use the length ratios of measurements of hard tissue structures in and around the mouth of early hominins in the Turkana Basin to extrapolate which, if any, masticatory components were functionally separating these species. If any measurements between these species gave average ratios between 1.3-1.4, dietary functions related to those measurements may have been driving niche separation between those species, allowing for sympatry. We find that *P. boisei/H. erectus* and *P. boisei/H. habilis* fall into the 1.3-1.4 Hutchinson's rule average range for all combined measures and all post-canine measurements. *Paranthropus boisei/H. habilis* fall into the 1.3-1.4 average range in the subset of cranial measurements related to mastication. Our results suggest that because their average mastication-related linear measurements are consistent with Hutchinson's predictions, then *P. boisei* and early *Homo* were likely functionally sympatric in the Turkana Basin during the Pleistocene, as well as in the same trophic level. These data provide a foundation for future analyses investigating the nature and extent of competition between these two lineages, and may provide a quantitative test for whether extinct species in an area were sympatric.

Examining frailty relative to persistent late-stage acquired syphilis infection in individuals within historical documented collections

MUNEEBAH UMAR[1], LAUREN NICHOLS[2], KERRI WIDRICK[2], CASSANDRA DEGAGLIA[3], AMANDA WISSLER[4], ALEISHA REYNOLDS[2], FABIAN CRESPO[5], SHARON DEWITTE[4] and MOLLY ZUCKERMAN[2]

[1]Department of Biological Sciences, Mississippi State University, [2]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [3]Department of Anthropology, Tulane University, [4]Department of Anthropology, University of South Carolina, [5]Department of Anthropology, University of Louisville

The many complexities of clinical and microbiological research on acquired syphilis (*Treponema pallidum pallidum)* (e.g., limited animal models) mean that scientific understandings of its pathogenesis, especially progression to tertiary (late) stage infection relative to human host characteristics and heterogeneity in frailty, has lagged behind that of other common bacterial infections. With rising incidence, syphilis is also a reemergent public health problem. To circumvent some of the complexities, we assessed frailty relative to late-stage infection in a preliminary sample (N=25; combining individuals from the Robert J. Terry Anatomical Collection and the Hamann-Todd Osteological Collection (HTOC) to increase sub-sample size) of skeletal individuals with antemortem diagnoses of syphilis, with sub-samples of individuals with late (n=15) and early stage (primary, secondary) (n=5) infection. We applied a 5-biomarker Skeletal Frailty Index (SFI) (Periodontal disease, PH, CO, LEH, Osteoporosis). We predicted lower frailty–and inferred higher immunological competence–in those who did not progress past early-stage, but higher frailty–and lower immunological competence–in those who progressed to late-stage. Preliminary results are consistent with this hypothesis, with a lower SFI (1.6) amongst early-stage individuals compared to late-stage (1.92), though this is insignificant, likely due to small sample size (Mann-Whitney U test (p = 0.416)). These results may indicate that elevated stress facilitated persistent infection. Deeper understanding of frailty relative to destructive and debilitating late-stage syphilis may improve reconstructions of syphilis' past disease burden but also, via translational science, contribute to refined prognostic, diagnostic, and screening criteria in public health and clinical settings.

This research is supported by NSF Senior Research Grant (Award number: 1946203), and NSF EAGER: Identification of specific pathogens in human dental calculus (Award Number: 1643318)

Birnirk Inuit Genetic Relatedness and Burial Organization on the Alaskan North Slope

SARAH L. UNKEL[1], JUSTIN TACKNEY[1], LAUREN E.Y. NORMAN[1], ANTHONY M. KRUS[2,3], ANNE M. JENSEN[4,5], CLAIRE ALIX[6,7], OWEN MASON[8] and DENNIS H. O'ROURKE[1]

[1]Department of Anthropology, University of Kansas, [2]Scottish Universities Environmental Research Centre, University of Glasgow, [3]Department of

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Anthropology and Sociology, University of South Dakota, [4]Department of Anthropology, Museum of the North, University of Alaska Fairbanks, [5]Department of Anthropology, Bryn Mawr College, [6]Histoire de l'Art et Archéologie, Université Paris 1 Panthéon-Sorbonne, [7]Alaska Quaternary Center, University of Alaska Fairbanks, [8]INSTAAR, University of Colorado

Little is understood about past Inuit genomic relatedness as a factor of burial organization. As an intermediary population, Birnirk Inuit (1300-700BP) of Northwest Alaska connect descendant Thule Inuit (1000-550BP) to their ancestors across the Bering Strait. Given their temporal and geographic position, Birnirk Inuit are an important population to understand the influence of genomic relatedness on burial organization within the Inuit Tradition.

Here we report preliminary genome-wide genotypes from 14 Birnirk Inuit individuals from the Kugusugaruk site on the Alaskan North Slope. Genetic variants were targeted with the Arbor myBaits Expert Human Affinities kit, and analyses presented here were limited to an established '1240K' set. We demonstrate the use of READ to infer genomic relatedness among individuals buried across this archaeological site. We also hybridization captured ancient whole mitochondrial genomes from 4 additional individuals that, when combined with the above data, provides a set of 18 complete Birnirk Inuit mitogenomes. By comparing genome-wide (1240K) and maternal (mitochondrial) relatedness to patterns of age, sex, and spatial distribution of buried individuals within and between Kugusugaruk mounds 1 and 2, we expect that genetic relatedness will not be a primary contributor to burial organization. Through incorporation of genomic evidence and mortuary contexts, we reveal the role relatedness has on burial organization in Birnirk Inuit populations.

Research supported by NSF grants 1523059 and 1523160, a Wenner-Gren Dissertation Fieldwork Grant, KU Center for Genomics Seed Grant, the KU Research Excellence Initiative, and KU Ancient DNA Research Facility

Linking vertebral trabecular microstructure variation to hominoid locomotion, Part 1: *Homo sapiens*

MASSIEL VALCARCEL[1], STEPHANIE MUSGRAVE[1], SADEGH TALE[2], ALI GHAHREMANINEZHAD[2] and WILLIAM J. PESTLE[1]

[1]Department of Anthropology, University of Miami, [2]Department of Civil, Architectural, and Environmental Engineering, University of Miami

Locomotory differences among hominoid taxa have myriad structural and biomechanical correlates. Interestingly, the trabecular structure of lumbar vertebral centra has not been studied previously using micro-computed tomography (microCT), or at least not from a comparative, inter-specific perspective. This research uses microCT to investigate the trabecular microstructure of the lumbar vertebral bodies of *Homo sapiens* in order to quantitatively assess the relationship between that taxon's obligate bipedalism and vertebral trabecular microstructure of the lumbar region. Besides providing proof-of-concept for the approach, microCT analysis of n=15 *Homo sapiens'* third lumbar vertebrae found that, controlling for individual age, there were systematic differences in trabecular number, trabecular thickness, trabecular connectivity density, and degree of anisotropy between anterior and posterior volumes-of-interest (VOI) of lumbar vertebral centra. On an individual-by-individual basis, posterior regions of the lumbar body had uniformly fewer trabecula (averaging 0.1±0.1 fewer trabecula/mm, or a 9.8% reduction), thicker trabecula (24.4±24.4 μm thicker, a 16.6% increase), higher connectivity density (0.86±0.65 more connections/ mm^3, or 41.5% more), and were more isotropic (by 35.6±9.7%) than anterior VOIs. Thus, different loading factors and biomechanical responses appear a consequence of human lumbar lordosis. The next step in this study is to include additional taxa (e.g., *Pan troglodytes, Australopithecus).* Expanding our study sample will illuminate the relationship between locomotion and vertebral microstructure across these evolutionarily related taxa and expand our knowledge of the micro-anatomical correlates of locomotion, in particular those associated with the transition to bipedalism in hominin evolution.

This study was supported by the NSF, MRI Award 1920127. Any opinions, findings, conclusions or recommendations are the author(s) and do not necessarily reflect the views of the NSF.

Residents of the Blood Hotel can Affect Primates' Sensitivity to their Environment

NEGIN VALIZADEGAN[1,2], DANIEL CERMAK[3], MICHELLE BEZANSON[4], CLAUDIA LUTZ[2], JULIA POLLOCK[2], ELIZABETH K. MALLOTT[5] and JESSICA F. BRINKWORTH[1,2,6]

[1]Department of Anthropology, University of Illinois at Urbana-Champaign, [2]Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, [3]School of Information Science, University of Illinois at Urbana-Champaign, [4]Department of Anthropology, Santa Clara University, [5]Department of Biology, Washington University in St. Louis, [6]Department of Evolution, Ecology and Behavior, University of Illinois Urbana-Champaign

Past exposure to microorganisms has contributed to the evolution of the primate immune system, including the microbiome in the immune compartment. These microbes and their components might be affecting disease susceptibility variations across primates. As part of the un-symposium presentation, we designed a card game based on the link between the blood microbiomes and disease susceptibility. This game takes place in the blood, a harsh but nutritious environment for the microbial populations and an important immune compartment containing a high density of professional immune cells. The presence of the microbial communities in the blood hotel seems to be transient and sourced from other body organs such as the gut. The game involves combative-defensive mechanics consisting of two player sides, namely the innate immune system and the microbes, to show the relationship between the microbes and their hosts in the blood compartment. The goal is survival for the host or the microbes. Winner is determined by the capability to defend or attack successfully for longer durations. During gameplay, the players can acquire skills or change in conditions that allow them to perform a specific task and achieve points. The players will learn about the evolutionary arms-race in the primate body between the immune system and the invaders/resident microbes in this harsh blood environment.

This work was supported by the University of Illinois Urbana-Champaign, the Leakey Foundation, the SCC Joint Pollinator Garden and Composting Systems, and the National Science Foundation BCS-1750675.

Stable isotopes in fossil hominine dental enamel from Ravin de la Pluie and çorakyerler suggest differences in diet and habitat

LAUREN M. VAMOS[1], ULRICH G. WORTMANN[2], HONG LI[2], AYLA SEVIM EROL[3], GEORGE KOUFOS[4] and DAVID R. BEGUN[1]

[1]Anthropology, The University of Toronto, [2]Earth Sciences, The University of Toronto, [3]Anthropology, Ankara University, [4]Geology, Aristotle University of Thessaloniki

Thickly enameled late Miocene apes from northern Greece and central Anatolia are currently placed in *Ouranopithecus*, though debate persists on their congeneric status. Understanding the comparative ecology of the two species may help to elucidate differences in adaptation between the two. Baseline carbon isotope data on tooth enamel apatite of two equids at çorakyerler demonstrate $\delta^{13}C$ values of -10.72‰ and -8.9‰, with an average value of -9.81‰ (all values relative to VPDB, plus/minus 0.03‰). Previously published data on equids at Ravin de la Pluie show an average $\delta^{13}C$ value of -12.22‰ over six individuals, with a minimum value of -12.7‰ and a maximum of -11.8‰. Results from equids suggest that the two environments were similar, with a potential for slightly more humid, forested conditions at Ravin de la Pluie. The stable isotope compositions of *Ouranopithecus* tooth enamel apatite at both sites follow an opposite pattern to the equid samples. *O. macedoniensis* at Ravin de la Pluie has an average $\delta^{13}C$ value of -11.09‰, while in *O. turkae* at çorakyerler the average value is -11.51‰. These results are confined within the total range of variation in mammalian tooth

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

enamel apatite carbon isotope ratios, but their opposing trends compared to other local fauna indicate potential differences in the resource partitioning habits of these species. More quantitative dietary reconstruction is necessary to understand the comparative ecology and the potential differences in resource acquisition strategies between the hominines at each locality.

This presentation draws on research supported by the Social Sciences and Humanities Research Council.

Sexual Configurations Theory and Biology Beyond Biologisms

SARI M. VAN ANDERS

Psychology, Gender Studies, Neuroscience, Queen's University

As part of the "Born Which Way? Biological and Genetic Engagement in Sex, Gender, and Sexuality Research" Symposium, I discuss new theoretical models for thinking about sexual orientation and biology beyond biologisms. I describe "sexual configurations theory" (SCT), a theory, model, and measure that provides a more expansive way to conceptualize and address not just sexual orientation, but sexual status and sexual identity, including as branched (divergent) or coincident (overlapping). And, though sexual orientation is typically equated with sexed attractions, I articulate how the actual diversity in people's sexuality is better reflected in the separability of gender, sex, and "gender/sex" sexuality. Yet gender/sex sexuality is not the whole of people's sexual orientations, and I also discuss "partner number sexuality" (whether people are/want to be sexual with 0, 1, or 2+ people), and nurturance/eroticism, which can cut across other sexual domains. I describe findings from our own published empirical research with SCT, providing qualitative and quantitative data with gender/sex/ual minorities and majorities, and showing "heatmaps" of aggregated sexual configurations. Finally, I discuss what SCT means for research about "sexual orientation" and biology in ways that are more empirical, accurate, and just, articulating three biological ways forward for a biology beyond biologisms that meaningfully attends to gender/sex/ual diversity.

This work has been supported by the Canada 150 Research Chair in Social Neuroendocrinology, Sexuality, & Gender/Sex to SMvA.

First insights into human mobility in Neolithic Belgium using strontium isotopic analysis and proteomics: a case study of Grotte de La Faucille (Sclayn, Province of Namur).

IJK VAN HATTUM[1], MARTA COSTAS-RODRÍGUEZ[3], PHILIPPE CROMBÉ[2], FRANK VANHAECKE[3], KASPER HOBIN[3], SIMON DALED[4], JESSICA L.A. PALMER[1], HANS VANDENDRIESSCHE[2], MAARTEN DHAENENS[4], QUENTIN GOFFETTE[5], HÉLÈNE COLLET[6], PIERRE CATTELAIN[10,8,9], MICHEL TOUSSAINT[7] and ISABELLE DE GROOTE[1]

[1]ArcheOs - Research Laboratory for Biological Anthropology, department of archaeology, Ghent University, Belgium, [2]Department of Archaeology, Ghent University, Belgium, [3]Atomic and Mass Spectrometry - A&MS Research Unit, Department of Chemistry, Ghent University, Belgium, [4]ProGenTomics, Laboratory of Pharmaceutical Biotechnology, Ghent University, Belgium, [5]Operational Direction Earth and History of Life, Royal Belgian Institute of Natural Sciences, Brussels, Belgium, [6]Service public de Wallonie, service de l'Archéologie en Hainaut, Mons, Belgium, AWaP, l'agence Wallone du patrimoine, [7]AWEM, Association Wallonne d'Études Mégalithiques, [8]The Centre of Study and Archaeological Documentation, Museum Malgré-Tout, [9]The Centre of Archaeological Research and Heritage, University of Bruxelles, [10]The Prehistoric Service, University of Liège

So far, no strontium (Sr) isotopic mobility studies have been done on Neolithic human remains from Belgium, and information on the Sr isotopic variability in the region is scarce. This Sr isotopic study aims to explore mobility in a Final Neolithic population from the funerary cave 'Grotte de La Faucille', contribute to the understanding of bioavailable strontium in Belgium, assess evidence for male mobility using proteomic analysis, and explore possible places of origin for nonlocal individuals. The $^{87}Sr/^{86}Sr$ values of human dental enamel (n = 12) were determined. Liquid chromatography mass spectrometry-based protein analysis was employed to identify individuals of male biological sex. $^{87}Sr/^{86}Sr$ values of micro-mammal teeth, snail-shells, and modern plants from three geological areas in Belgium were measured to establish local isotopic signatures for bioavailable strontium. Nonlocality was assessed by comparing human $^{87}Sr/^{86}Sr$ isotope ratios to those for bioavailable Sr. Four out of 12 individuals, yielded $^{87}Sr/^{86}Sr$ values consistent with a nonlocal origin. Three males were detected in the sample set, of which two show nonlocal $^{87}Sr/^{86}Sr$ values. This study provides evidence for (male) mobility in Final Neolithic Belgium. The four nonlocal signatures correspond with the $^{87}Sr/^{86}Sr$ of bioavailable Sr in Dutch South Limburg, the Black Forest in Southwest Germany, and large regions of France, such as the river valleys of the Paris Basin and the Vosges. The results from this study support the ruling hypothesis - brought to light by archaeological research - of connections with Northern France, especially the Paris Basin.

The research was supported by Ghent University's special research fund (BOF) and the Jean-Jaques Comhaire fund managed by the Koning Boudewijn Stichting, Brussels.

The primate forelimb: vascularization and innervation branching patterns

MARIE JM. VANHOOF, COLETTE WAGEMANS, TIMO VAN LEEUWEN and EVIE E. VEREECKE

Development and Regeneration, KU Leuven

The branching patterns of the vascularization and innervation of the forelimb have been studied in great detail in humans, while the number of studies on nonhuman primates remains strongly limited and a full documentation is only present for a few species. In our study, we investigate these branching patterns in five catarrhine primate species: *Macaca mulatta, Hylobates lar, Gorilla gorilla, Pan troglodytes, Pan paniscus*. We dissected one forelimb specimen for each species and documented the course of the nerves, arteries, and superficial and deep veins and their relation to the forelimb musculature. We observed that the overall configuration of the blood vessels and nerves is similar in different primate species, although some apparent differences are found. In all nonhuman primates, the superficial *vena basilica* is absent. Moreover, in *Gorilla* and *Pan*, the superficial *v. cephalica* is confined to the forearm. In all nonhuman primates, we observed an *arteria interossea anterior*, which migrates to the posterior side at the level of the *musculus pronator quadratus*, but an *a. interossea posterior* is absent. For the innervation, the *nervus medianus* and *n. ulnaris* interconnect in the forearm of *Gorilla* and *Macaca*. Our study indicates that the branching patterns of the innervation show some minor differences between the nonhuman primate species, compared to the branching patterns of the vascularization. Future research should include a broader range of primate species and larger sample size for each taxon to advance our insight in inter- and intraspecific variation in innervation and vascularization of the primate forelimb.

NA

Variation in intra and inter-specific cortical thickness in extant primate femoral diaphyses: a comparative framework for inferences of behavioral diversity in early hominins

ALESSANDRA VECINO GAZABÓN[1,2,3], ASHLEY S. HAMMOND[1,2], CARRIE S. MONGLE[4,5], CHRISTOPHER RUFF[10], MARTA PINA[6,7] and MARINE CAZENAVE[3,8,9]

[1]Division of Anthropology, American Museum of Natural History, [2]New York Consortium in Evolutionary Primatology, (NYCEP), [3]Richard Gilder Graduate School, American Museum of Natural History, [4]Department of Anthropology, Stony Brook University, [5]Turkana Basin Institute, (TBI), [6]South Bank Applied BioEngineering Research, London South Bank University, [7]Institut Català de Paleontologia Miquel Crusafont, Cerdanyola del Vallès, [8]Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, [9]Department of Anatomy, University of Pretoria, [10]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

Inferences regarding postural and locomotor behaviors in fossil hominins have been drawn from the distribution of femoral diaphyseal cortical thickness relative to patterns in extant

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

primates, including recently for the Late Miocene Sahelanthropus. However, intra- and inter-specific variation in femoral cortical thickness distributions among extant primates still remain poorly known, making it difficult to identify reliable indicators of locomotor-related site-specific differences.

We used the R package Morphomap to investigate cortical bone thickness variation from computed tomographic scans of a large sample of extant primate femoral shafts including hominoids (Homo sapiens, Pan troglodytes, P. paniscus, Gorilla gorilla, G. beringei, Pongo pygmaeus, Hylobates sp.) and monkeys (Papio, Cercopithecus, Colobus, Alouatta, Ateles). Cortical thickness distribution between 20% and 80% of the femoral biomechanical length was measured, subsequently visualized as a "heat map" on the femoral shaft, and inter-taxic variations were visualized and statistically compared using principal component analyses.

Our results show that modern humans have a unique and distinctive cortical structure. Among other primates, inter-taxic variations are observed, notably with a general trend from more terrestrial to more arboreal taxa. However, intra-taxic variations are also apparent, for example, sex differences in mountain gorillas, likely related to hormonal, body size and/or behavioral differences. With a better understanding of the structural variation of the femoral diaphyseal cortex in primates, this work provides a stronger comparative framework for interpreting fossil femora and notably subtle structural variations between fossil hominins to reconstruct hominin postural and locomotor behavioral diversity.

Social norms promote adaptive collective decision-making in hunter-gatherers

VIVEK V. VENKATARAMAN[1], JORDAN HOFFMAN[1], KYLE FARQUHARSON[1], ZACHARY H. GARFIELD[2] and THOMAS S. KRAFT[3]

[1]Department of Anthropology and Archaeology, University of Calgary, [2]Institute for Advanced Study in Toulouse, Toulouse School of Economics, [3]Department of Anthropology, University of Utah

Accurate collective decision-making in the context of foraging, social life, and warfare was likely crucial to the demographic success of hunter-gatherers throughout human evolutionary history. Theoretical and empirical work in organizational science and psychology has shown that the decision accuracy of small-to-medium sized groups is a function of: i) independence, ii) diversity, iii) decentralization, and iv) the extent to which individuals share a common goal. Here we apply this framework to test whether hunter-gatherer societies adopt social norms during collective decision-making that reflect the above principles to promote decision accuracy. We conducted a paragraph-level analysis of the Probability Sample Files of the Human Relations Area Files across hunting and gathering societies. We found widespread support for the idea that social norms promote adaptive outcomes at the group level. Egalitarianism is a key underlying factor that enables hunter-gatherers to capitalize on the 'wisdom of crowds': all adults are encouraged to participate in collective-decisions, which promotes diverse viewpoints. Single individuals are unable to dominate decision-making, reducing the likelihood of conformity effects that lower decision accuracy. Goals are conceived of and acted upon in a collectivist fashion. Mutual interdependence and high levels of information-sharing in hunter-gatherer camps serve to reduce consensus costs and increase the costs of noncooperation, aligning individual-level and group-level fitness. Taken together, these results are consistent with deliberative processes functioning as problem-solving devices to maximize group-level outcomes. This is achieved by a process that is best described as dialogue, rather than debate.

Investigating Muscle Attachments and Shape Variation of the Scapulae in Extant Non-human Primates

MARIE VERGAMINI[1,3], LISA M. DAY[1,2], JESSIE TIGNOR[3], ERNESTO GAGARIN[4] and AMY L. RECTOR[1]

[1]Anthropology, School of World Studies, Virginia Commonwealth University, [2]Biology Department, Virginia Commonwealth University, [3]Integrative Life Sciences, Virginia Commonwealth University, [4]Columbia Stem Cell Initiative, Columbia University

Joint structure variation in extant Cercopithecidae correlates with substrate patterns and locomotive type. Previous joint studies suggest that locomotor repertoires of Cercopithecidae can be differentiated through shape analysis of the elbow and shoulder joints (Rector et al., 2018; Walters et al, 2020). Methods for predicting locomotor repertoires in extant and extinct Cercopithecidae can be strengthened with a better understanding of the morphological variation in the shoulder girdle. This study aims to advance 3D shoulder joint and articulation research across the primate order.

Scapular outlines were collected from a sample of 300+ extant specimens using a MicroScribe point digitizer. Points were designated based on locations of muscle attachments, like the Supraspinatus. Species were assigned substrate patterns, including ground and/or branch quadrupeds, brachiators, leapers, and knuckle-walkers. Variation in scapular shape was analyzed using Python, MorphoJ, PCAs, CVAs, PGLs, and phylogenetic ANOVAs. The analyses tested whether locomotive pattern can be established from the shape variation and muscle attachment locations on scapulae of extant non-human primates. According to our findings, locomotor repertoires can be identified by how muscle attachments influence the shape of the bone, like the Supraspinatus on the supraspinous fossa superior. We especially see this reflected in Colobinae, as they have specialized arboreal adaptations. This methodology could prove useful for fragments of fossil scapulae to pinpoint arboreal and terrestrial adaptations in extinct Cercopithecid primates.

The basket carriers from Kheny: activity related spinal deformations in two adult skeletons from the New Kingdom site of Gebel el-Silsila, Egypt

BARBARA VESELKA[1], JOHN WARD[2] and MARIA NILSSON[2]

[1]Department of Art Sciences and Archaeology, Vrije Universiteit Brussel, [2]Department of Archaeology and Ancient History, Lund University

During the 18th dynasty (1550 – 1291 BC), Gebel el-Silsila, a major quarry site, became the source of sandstone, whereby the Temple of Kheny (ancient name for Gebel el-Silsila) is postulated to have been the 'mother temple' to all future temples built with sandstone. Close to the temple, a necropolis was discovered with numerous carved-out tombs containing multiple individuals, of which some were buried in stone sarcophagi. Not all individuals were buried in tombs. Forty-seven individuals were buried on the quarry surface. Two of these individuals were male adults aged 22-25 years and 55 ± 10 years. Both individuals showed a relatively high number of fractures in the ribs and long bones in different stages of healing. Furthermore, both men showed a distinct deformation of the cervical part of the spine suggestive of considerable pressure on the head. Considering their deviant burial treatment (not inside the tombs), is it postulated that the men were not part of the elite. Yet, they were buried wrapped in reed mats near the tombs, suggesting them to be valued members of society. The numerous factures may indicate a hazardous work environment and the spinal deformation could have been the result of working as basket carriers, whereby the weight of transporting heavy rubble in a would have caused enormous pressure on the head and neck. This paper provides insight in the social differentiation at Kheny and improves our understanding of daily life in the New Kingdom quarry of Gebel el-Silsila.

Paleopathology in an extinct giant platyrrhine primate from the Late Pleistocene of Brazil

ANDRÉ VIEIRA ARAUJO[1,2,3], MÁRIO ANDRÉ TRINDADE DANTAS[3], MARIO ALBERTO COZZUOL[4], HERMÍNIO ISMAEL ARAÚJO-JÚNIOR[1], ALEXANDRE LIPARINI[4], RODRIGO MARTINS RIBEIRO[5],

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

FERNANDO HENRIQUE DE SOUZA BARBOSA[1] and LAUREN B. HALENAR-PRICE[6]

[1]PPG em Geociências, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brazil, [2]Instituto Federal do Sertão Pernambucano, Petrolina, PE, Brazil, [3]Laboratório de Ecologia e Geociências, Universidade Federal da Bahia (IMS/CAT), Vitória da Conquista, BA, Brazil, [4]Departamento de Geologia, Instituto de Geociências, Universidade Federal de Minas Gerais, MG, Brazil, [5]Instituto Federal Goiano, Rio Verde, GO, Brazil, [6]Department of Biology, Farmingdale State College (SUNY)

Cartelles coimbrafilhoi is an extinct platyrrhine primate from the Late Pleistocene of Bahia, Brazil that is currently represented by a single, very well-preserved and nearly complete skeleton. At approximately 25 kg, *Cartelles* is the largest known living or extinct New World primate. It exhibits an intriguing mosaic of craniodental and postcranial traits not found together in any other platyrrhine. Added to this list of intriguing features is now the first evidence in an extinct nonhuman primate of a potential metabolic bone disease, similar to Paget's disease. Macroscopic and radiological evidence were used to describe and diagnose this pathological condition. Radiological imaging (X-ray and CT) of the humerus, femur, pelvis, and cranium revealed abnormal growth in these bones. Diagnostic features such as thickening of the compact bone, sclerosis, and coarsened trabeculae in these bones are similar to what is commonly found in humans diagnosed with Paget's disease. The right humerus, which has a greatly expanded and flattened "brachioradialis flange" that is not present on the left humerus, shows cortical thickening with osseous expansion and loss of corticomedullary differentiation consistent with this diagnosis. Previous work has interpreted the unique morphology of the *Cartelles* skeleton in functional terms and has used the shape of the right distal humerus in particular to define the taxon as separate from the other large-bodied platyrrhines, *Protopithecus* and *Caipora*. A pathological explanation for these morphologies necessitates a reinterpretation of this skeleton and its relationship to its contemporaries.

Genetic variation affecting immune responses to *Y. pestis* during the Black Death

TAURAS P. VILGALYS[1], JENNIFER KLUNK[2], CHRISTIAN E. DEMEURE[3], JAVIER PIZARRO-CERDÁ[3], HENDRIK N. POINAR[2] and LUIS B. BARREIRO[1]

[1]Genetic Medicine, University of Chicago, [2]Anthropology, McMaster University, [3]Yersinia Research Unit, Institut Pasteur

Infectious diseases have been one of the strongest selective pressures in human evolution. However, it is difficult to link positively selected regions of the genome with specific diseases. The Black Death, caused by the bacteria *Yersinia pestis*, offers a unique opportunity to connect natural selection with the underlying pathogen as plague killed 30-50% of European individuals within a single generation. Using ancient genomic data from 206 individuals who died before, during, or after the Black Death, we identify evidence of natural selection at immune genes. 245 loci are highly differentiated within London, including four which were replicated in an independent cohort from Denmark. Genes near three of these loci are differentially regulated in response to plague and two are genetic variants which affect gene expression level (eQTL). One of these eQTL is a variant affecting *ERAP2* expression, which has evolved under balancing selection. We functionally confirm our ancient DNA results for this loci by showing that individuals with the protective allele have increased clearance of intracellular *Y. pestis*. We are expanding this work to further characterize functional variation in the immune response to plague across cell types, using single-cell RNA sequencing of immune cells infected with plague. Together, our results show that natural selection shaped the evolution of immune genes during the Black Death. Importantly, several of these loci affect modern susceptibility to inflammatory and autoimmune diseases, showing the genetic adaptation during Black Death has had lasting consequences for human health.

This work is supported by NIH R01-GM134376 to Luis Barreiro. Tauras Vilgalys is supported by NIH F32 GM140568-01.

Genetic basis of evolutionary constraints: heritability and genotypic covariation in the macaque vertebral column

CATALINA I. VILLAMIL[1] and EMILY R. MIDDLETON[2]

[1]School of Health Sciences and Technologies, Universidad Central del Caribe, [2]Department of Anthropology, University of Wisconsin-Milwaukee

Evo-devo posits that changes to developmental processes are responsible for evolutionary changes, partly by creating or removing constraints on the emergence of variation. Phenotypic integration (covariation among traits that results from genetics and development) presents a way to assess these processes in organisms that cannot be studied in the lab. Ongoing work has shown that the strength and pattern of phenotypic integration differs among primates, potentially as a result of adaptation to new behaviors. However, it is unclear to what extent we are observing the genetic component of development (e.g. protein-coding or regulatory gene sequences) versus the environmental component (e.g. muscle action, nutrition, health). Here, we provide preliminary estimates of heritability and genotypic covariation of cervical (C3,C5), thoracic (T4,T8), and lumbar (L2,L4) vertebral elements using linear measurements collected from pedigreed Rhesus macaque skeletons (N=96) housed at the Caribbean Primate Research Center. Our results show that cervical vertebrae generally display higher heritability than lumbar vertebrae, and that joints tend to be more highly heritable than other areas. Additionally, although phenotypic and genotypic covariation are generally in accord (R=0.8428-0.9408, P<0.001), estimates of integration and evolvability based on these two differ, with higher integration and lower evolvability for most but not all elements under genotypic covariation. These results suggest that much of the measured ability to respond to selection can be attributed to non-genetic processes (e.g. phenotypic plasticity). These results have implications for understanding evo-devo in primates, as well as for understanding evolutionary processes more generally and interpreting anatomy in an evolutionary context.

CIV received funding for this project from the Puerto Rico Science, Technology, and Research Trust. The CPRC is funded by NIH ORIP #2-P40-OD012217.

The *MUC19* gene in Denisovans, Neanderthals, and Modern Humans: an evolutionary history of recurrent introgression and natural selection

FERNANDO A. VILLANEA[1], DAVID PEEDE[2,4,5], KELSEY E. WITT[2,4], ALYSSA FUNK[3,4], JILL E. SCOTT[6], VIRIDIANA VILLA-ISLAS[7], MARIA C. AVILA-ARCOS[7] and EMILIA HUERTA-SÁNCHEZ[2,4]

[1]Anthropology, University of Colorado Boulder, [2]Ecology, Evolution, and Organismal Biology, Brown University, [3]Molecular and Cellular Biology, Brown University, [4]Center for Computational Molecular Biology, Brown University, [5]Institute at Brown for Environment and Society, Brown University, [6]Department of Sociology and Anthropology, Metropolitan State University of Denver, [7]International Laboratory for Human Genome Research, Universidad Nacional Autónoma de México

The gene *MUC19* encodes a member of the gel-forming mucin protein family, which is related to lacrimal and salivary gland function in humans. The *MUC19* gene is also found in Neanderthals and Denisovan, who carried their unique variants. *MUC19* is also archaically introgressed, where most modern human populations carry the Denisovan variant at low-to-intermediate frequencies. Here, we study in detail the Denisovan variant of *MUC19*, and we find that it was also introgressed into some, but not all, Neanderthal lineages. In addition, we find that global Denisovan *MUC19* frequencies in modern humans are highest in Indigenous American ancestry tracts, and confirm that positive selection is driving these high frequencies relative to other global populations. The high frequency of the Denisovan *MUC19* in Indigenous Americans is surprising, as genes are often depleted for archaic ancestry due to past strong purifying selection. Taken together, our results suggest that the Denisovan *MUC19* contributed to Indigenous American adaptation, although the functional benefits in Indigenous individuals are as-of-yet unclear. It is likely that the Denisovan variant served as the raw material

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

for positive selection as American populations adapted to novel environments. It is unknown if the Denisovan *MUC19* conferred an adaptive advantage in Neanderthals, who retained this variant in polymorphism along the Neanderthal *MUC19* variant.

This project was supported by a Leakey Foundation research grant to FAV. KEW, DEP, AF and EHS are supported by NIH grant 1R35GM128946-01. DP is a trainee under NIH-T32-GM128596.

Zambian large mammal stable isotopes show dietary flexibility at high trophic levels: implications for the Pleistocene hominin niche

AMELIA VILLASEÑOR[1], LUCAS K. DELEZENE[1], THIERRA K. NALLEY[2], JOSEPH M. MUSEBA[3] and AMY L. RECTOR[4]

[1]Anthropology, The University of Arkansas, [2]Medical Anatomical Sciences, College of Osteopathic Medicine of the Pacific, Western University of Health Sciences, [3]National Heritage and Conservation Commission, Republic of Zambia, [4]Anthropology, School of World Studies, Virginia Commonwealth University

Hominin biogeography is stymied by preservation. Most evidence for hominin evolution and its ecological drivers derives from favorable depositional environments in South Africa and the Eastern African Rift System. Yet, hominins, their prey, predators, and commensals are often large-bodied, with temporally and spatially large ranges. Large ranges can correlate with large fundamental niches, especially in the rift valley that comprises diverse ecoregions across space and time. Such may be the case with hominins and other large mammal species whose ranges span the entirety of the rift valley and its diverse environments. For example, early Pleistocene hominins from the Zambezi ecozone show a noticeable C3 shift compared to their eastern African rift congeners, while large mammalian herbivores show little variation between eastern and southern Africa.

Here, we present new stable isotope data from extant Zambian large mammal communities (31 taxa; 80 specimens) and compare our results with published values from eastern and southern Africa. While herbivores show dietary specialization that is relatively invariant across geographic regions, carnivores and omnivores are dietarily flexible across body sizes. Lions, for example, are C_3 shifted (average $\delta^{13}C$= -7.7) compared to those in eastern Africa. This is unexpected because studies from southern Africa suggest a close relationship between vegetation, herbivore body size, and predator body size; specifically, large-bodied predators often focus on large-bodied C_4 herbivores. These data contextualize why the niches of Pleistocene hominins may be more ecologically flexible than considered previously, particularly as body size and meat consumption increase.

The University of Arkansas Pandemic Relief Grant, The American Philosophical Society, VCU CHS Seed Grant

Effects of transect selection and seasonality on lemur density estimates in Betampona Strict Natural Reserve, Madagascar

EDGAR J. VILLEDA[1], BRIAN D. GERBER[2] and ZACH J. FARRIS[3]

[1]Anthropology, Northern Illinois University, [2]Natural Resources Science, University of Rhode Island, [3]Public Health and Exercise Science, Appalachian State University

Madagascar is a global conservation priority due to intense anthropogenic pressures threatening its diverse, endemic wildlife. Betampona Strict Natural Reserve (2,228 ha) protects diverse eastern rainforest wildlife, including multiple critically endangered lemur species, which are missing population estimates throughout the landscape. To provide accurate density estimates for diurnal, cathemeral, and nocturnal lemurs across both cool-dry (June-July) and hot-wet (October-December) seasons in both high and low degradation areas, we conducted repeat, standardized line transect sampling 267 km across the entire reserve. We observed a total of 10 lemur species and estimated density (D ± SE), while accounting for imperfect detection, for six lemur species including two Critically Endangered species: Indri (*Indri*, D=0.38 ind/km^2 ± 0.12) and ruffed lemurs (*Varecia variegata*, D=2.31 ind/km^2 ± 0.59). We also provide only the second known density estimates for the understudied Masoala fork-marked lemur (*Phaner furcifer*, D=1.52 ind/km^2 ± 0.52). Lastly, we compared our estimates at Betampona with other protected areas across Madagascar. We found detections and density estimates to be highest during the hot-wet season, with no strong preference for high vs. low degradation areas. These findings provide the first seasonal estimates for lemur populations across Betampona Reserve and the first cool-dry season estimates for several species for any location in Madagascar. Madagascar's forests are expected to be gone in the next 80 years, and these types of studies are critical to developing effective management and conservation objectives that will contribute to the long-term protection of these imperiled, charismatic primates.

Jaw size and cranial shape: how developmental constraints impact skull evolution

BRIAN A. VILLMOARE[1], BRI HEISLER[1] and JENNIFER FISH[2]

[1]Anthropology, University of Nevada Las Vegas, [2]Biological Sciences, University of Massachusetts Lowell

Integration of the mammalian face has been well-studied. However, the relationship between the mandible and cranium has received less attention. The mandible and upper jaw derive from the pharyngeal arches, with developmental programs independent of the rest of the bony cranium.

To evaluate the evolutionary independence of the upper and lower jaw in relation to the cranium, we followed on work by Makedonska et al (2012), who identified shifts in integration due to adaptive divergences in the cranium of 'robust' (hard object feeding) and 'non-robust' (non-hard object feeding) capuchin species. We collected and analyzed 134 landmarks and sliding semi-landmarks on the crania and mandibles of wild-shot museum specimens of *Sapujus (Cebus) apella (sensu strictu), Sapujus cay (S. apella paraguayanus), Cebus albifrons,* and *Cebus olivaceus*.

Results from geometric morphometric analysis confirm that the adaptive differences between 'robust' and 'non-robust' capuchins are visible in the overall integration of the cranium and upper face. However, when we examined the covariation of the mandible to the cranium, we saw no significantly different signals among the species, despite disparities in their dietary adaptations and their internally divergent patterns of cranial integration. This suggests that evolutionary constraints limit the relative independence of the mandible and cranium, which may derive from integration of the upper jaw in the cranial base.

The missing data problem: Imputation methods for dental nonmetric traits

TATIANA VLEMINCQ-MENDIETA, ELAINE Y. CHU, LARESA L. DERN and GEORGE R. SCOTT

Anthropology, University of Nevada, Reno

Dental anthropology has a missing data problem. For biodistance analyses that require complete datasets, dental nonmetric traits are dichotomized and calculated into frequencies. This traditional approach allows for group-level comparisons but makes individual-level analyses difficult. Imputation methods could mitigate the missing data problem and permit investigations using raw dental nonmetric scores. A subset of 704 individuals from seven of the 110 samples in a worldwide dataset collected by C.G. Turner in the 1970-80s were selected for dataset completeness. To increase sample size, seven traits for the upper (UM2 hypocone, UM1 metaconule, UM1 Carabelli's trait, UM1 enamel extensions, UP3 and UM2 root number, and reduced-pegged-missing UM3) and seven traits for the lower (LM2 groove

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

pattern, LM1 distal trigonid crest, LM1 protostylid, LM1 cusp 7, and LC, LM1 and LM2 root number) dentitions were retained and assessed separately. Five hundred datasets were simulated for 10%, 25%, 50%, 75%, and 90% of missingness. Five imputation methods – hot-deck (HD), k-NN, iterative robust model-based imputation (IRMI), median/mode (MM), and multivariate imputation by chained equations (MICE) – were assessed using pairwise Cohen's kappa for each trait. Median kappa values for each method/trait/percent missingness combination ranged from 0.84-0.95 for 10%, 0.61-0.86 for 25%, 0.31-0.79 for 50%, 0.10-0.39 for 75%, and -1.00-0.18 for 90%. The methods that performed best were MM, IRMI, and k-NN, with MM having the most consistent performance. Results indicate that imputation methods should not be used when more than 25% of the data are missing, and that imputation method performance vary by trait.

Bilateral Hip Dysplasia: A Case Study from 17th – 19th Century South Africa

CHELSEY M. VOEGT[1], GENEY GUNSTON[1], MARC NORTJE[2], JUDITH SEALY[3], LETIAN HE[4] and VICTORIA GIBBON[1]

[1]Department of Human Biology, University of Cape Town, [2]Department of Orthopaedic Surgery, University of Cape Town, [3]Department of Archaeology, University of Cape Town, [4]Department of Archaeology and Museology, Lanzhou University

The bioarchaeology of care framework (BoC) is used to study pathological conditions in people who lived in the past. It allows for an understanding of their disease experience within their context. Therefore, the aim was to critically analyse, describe and diagnose the pathological condition present on the remains of an individual and what this condition may have meant for the person. A biological profile was constructed for a single individual, comprising sex, age-at-death and ancestry. For differential diagnosis, radiographic analyses and computer tomography scans were conducted. Lastly, steps 1 and 2 of the BoC were applied. This person was a non-European middle-aged adult male found in Bloubergstrand, Western Cape. He died between 1640-1810 AD according to a radiocarbon date using bone collagen, thus, lived in the 17-19th centuries. A detailed description of morphological changes showed dysplastic hips with collapsed femoral heads. Applying differential diagnosis resulted in a most likely diagnosis of developmental dysplasia of the hips (DDH). Restricted movement and inability to heavy-lift are consequences of DDH. However, entheseal markers on the upper limbs (muscle origin/attachment sites) and his strong, healthy bones suggest resilience, some mobility and contribution to society through less physically demanding tasks. It was not possible to assess the severity of DDH experienced, nevertheless, he lived through adulthood, suggesting he was cared for and valued by his community. This study is one of the first to apply BoC framework in a South African context, illustrating the value of its application to archaeological time frames in South Africa.

Research was supported by South African National Research Foundation(NRF) [MND200507520417, 2021] and to Gibbon [Grant No.115357 and 120806], South African Women in Science and Engineering, and POSCO Asian Fellowship.

Sharing and repurposing 3D craniomandibular landmark datasets: Landmark definitions, observer error, and ethical concerns

NOREEN VON CRAMON-TAUBADEL

Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo

A large globally-distributed human craniomandibular landmark dataset was collected using a 3D digitizer in two phases (2006 and 2014) with the aim of comparing patterns of population history with matched genetic data. However, publicly sharing these data are hindered by three issues: ambiguous landmark definitions, observer error, and ethical concerns. The ambiguity of some landmarks affect geometric morphometric (GM) analyses in ways that traditional metric analyses are relatively immune to. Thus, amalgamating landmark datasets from different observers could lead to high inter-observer error, particularly if observers have not been trained to identify landmarks in the same way. Moreover, GM analyses of the dataset described here found unacceptably high levels of intra-observer error for some ambiguous landmarks given the eight year time gap between the two phases of data collection. Due to the "Pinocchio effect" non-biological variation caused by temporal observer error in some landmarks was transferred to the entire configuration due to the least-squares algorithm used in Generalized Procrustes Analysis (GPA). Identifying which landmarks were affected was extremely difficult once the datasets had been subjected to GPA. In contrast, interlandmark distances that correspond to traditional caliper measurements such as maximum cranial width, length, or height were immune to these landmarking biases, with no systematic variation introduced. Finally, and most importantly, while this dataset represents "legacy data" in the academic literature, the appropriateness of making *any* human morphological data publicly available must be considered in light of ongoing discussions regarding the ethics of studying and portraying human remains.

Funding was gratefully received from the EU-funded SYNTHESYS initiative grant, the Leakey Trust, the Cambridge Gates Foundation, St. John's College, Cambridge, the British Academy and the Leverhulme Trust (award #SG122595).

Of monsters and monkeys: Queering the study of genetic chimerism in primates

RACHEL VOYT

Anthropology, University of Texas at Austin

Evolutionary frameworks depend on concepts of sex and reproduction, yet also tend to obfuscate the diversity present in these categories. Feminist and queer science studies show that this incongruity forms part of a feedback loop in which prevailing cultural biases dictate boundaries of biological categories while simultaneously pointing toward those boundaries as scientific justification. As a result, humans existing in the margins of normative sex and reproduction are often relegated to the realm of the unnatural, the queer, and in some cases – the monstrous. This entanglement between non-normative "others" and monstrosity forms the foundation of queer monster theory, which I use here to examine conceptualizations of sex and reproduction within primatology, and more specifically, the study of chimerism. Popularly known as the literal monster of Greek myth, the chimera in biology describes organisms containing cell lines derived from at least two distinct zygotic origins. Chimerism occurs to some extent across all primates via bidirectional transplacental cell transfer during fetal development, but the highest degree of chimerism occurs in callitrichines, a small-bodied primate taxon from Central and South America. Among callitrichines, twinning is the norm, and nearly every individual exists as a chimera of their twin through early chorionic fusion between the developing embryos. I demonstrate how the genetic consequences of this phenomenon complicate current biocultural confines of sex and reproduction, and in doing so, explore the role of the "monster" in human and non-human primate biology as well as in the evolutionary paradigms used within biological anthropology more broadly.

Laws of the Land: How cultural and environmental prohibitions affect wild animal harvests in Western Madagascar

MADELYN M. WACHNUIK[1], KATHARINE E. THOMPSON[2], CORTNI BORGERSON[3], PATRICIA C. WRIGHT[1,2], JEANNE M. RANDRIAMANETSY[4], YVES M. ANDRIANANTENAINA[4], MAHEFA N. ANDRIAMAVOSOLOARISOA[5], THEOFRICO A. RAZAFINDRAHASY[4], RYAN S. ROTHMAN[2], CLAIRE SURKIS[1], RICHARD J. BANKOFF[6] and KATHERYN C. TWISS[1,2]

[1]Anthropology, Stony Brook University, [2]Interdepartmental Doctoral Program in Anthropological Sciences (IDPAS), Stony Brook University, [3]Department of Anthropology, Montclair State University, [4]NA, Madagascar Health and Environmental Research (MAHERY), [5]Zoology and Animal Biodiversity, University of Antananarivo, [6]NA, ComplexityNexus LLC

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Kirindy Mitea is one of the most heavily hunted national parks in Madagascar. A fragile, arid ecosystem, Kirindy Mitea is home to seven threatened lemurs species and numerous other species of protected wildlife. Food insecurity and poverty are well-known drivers of wildlife harvests, both in western Madagascar and globally. However, less is known about the cultural beliefs shaping lemur hunting and consumption. Cultural prohibitions surrounding wildlife exploitation vary widely across Madagascar's eighteen ethnic groups; likewise, adherence to these taboos and conservation legislation more broadly likely varies across the island. To explore the influence of cultural and conservation prohibitions on primate consumption, we interviewed 369 individuals (N = 89 households) about 1) animal capture and consumption, 2) cultural prohibitions around wildlife consumption, and 3) conservation law awareness over six months (September 2018 - March 2019) in one village outside Kiridiny Mitea National Park. We also conducted eight focus group discussions with community members to explore how taste preferences and profitability affect wildlife harvests. We found the most commonly reported taboo animals to be rodents, reptiles, and bats; lemurs were rarely reported as taboo, and these taboos did not prevent primate consumption at the village level. Participants accurately identified conservation regulations at the species level, especially for primates. However, neither cultural nor conservation prohibitions effectively depressed wildlife utilization. Taste and profitability were related to consumption for both domestic and wild species. Such information is vital to inform community-coproduced alternative meat solutions and to clarify how culture shapes wildlife conservation.

This research was funded by grants from the Safina Center, the National Science Foundation (2015213765), Global Wildlife Conservation (5095.005-0175), Primate Conservation Inc (46), and Stony Brook University.

Examining Paleopathological Preservation in Cremated Human Skeletal Remains from the Archaic Period Phaleron Site Athens, Greece

MEGAN WALSH[1], JESSICA CEREZO-ROMÁN[2] and JANE BUIKSTRA[3]

[1]Department of Anthropology, University of Oklahoma, [2]Department of Anthropology, University of Oklahoma, [3]Department of Anthropology, School of Human Evolution and Social Change, Arizona State University

We present the preliminary results from the paleopathological analysis of primary cremation pyres from the archaeological site of Phaleron dating to the Archaic Period (ca. 750-460 BCE) Athens, Greece. The main research questions are: 1) How can a comprehensive paleopathological analysis be conducted effectively in human cremated remains that are highly warped and fragmented? 2) What areas of the body better preserved? 3) Which pathologies are observable after thermal alteration? We conducted standard data collection on a subset sample of the cremations at Phaleron, creating the biological profile including inventory and estimation of sex/age at death modified for cremated human skeletal remains. Additionally, pathological data were recorded both through macro and microscopically analysis. The preservation of the bones allowed for the observation of pathologies consistent with infectious disease, non-specific stress, metabolic disease, and occupational stress in areas of the body spared by the fire. Preliminary results suggest that nearly fifty percent of the sample presented with one or more skeletal lesion(s). This suggests that pathologies, especially those frequently studied in bioarchaeology as markers of stress and illness are apparent in cremated human skeletal remains and are observable with relative clarity amongst the sample population. This project emphasizes the importance of including cremated human skeletal remains, especially those that are well-preserved, in broader pathological studies as they may add critical evidence to our understanding of health and disease in past populations.

Funding was provided by the Wiener Laboratory of the American School of Classical Studies at Athens, the National Science Foundation (NSF BCS-1828645), & the University of Oklahoma.

Coming to the Caribbean - Eighty-five years of Rhesus macaques (*Macaca mulatta*) at Cayo Santiago: A long-term model for the studies of adaptation, diseases, natural disasters and resilience

QIAN WANG

Biomedical Sciences, Texas A&M University School of Dentistry

In 1938, a group of Rhesus macaques from Lucknow, India (N26.8470° N, E80.9470°) were introduced to Cayo Santiago (CS), Puerto Rico (N18.1564° N, W65.7342°) to ensure a steady supply for biomedical research in U.S. In addition to a daily census starting in 1956, a skeletal collection has been accumulated from monkeys who lived and died on CS since 1971, in which the identity, date of birth, date of death, sex, and matriline are known for most of the specimens. A longitudinal study demonstrated that there was a trend of decrease in body mass and long bone circumferences, suggesting an acclimation in body size and proportions of Rhesus macaques. Osteological screening also demonstrates that Rhesus skeletons show oral and skeletal pathology similar to those in humans, including some of the most devastating conditions such as osteoporosis and osteoarthritis, and that diseases patterns are affected by nutrition and genetics. Moreover, CS is in the Caribbean area under constant threat of hurricanes. In the history of the rhesus monkey colony of the past 85 years, four major hurricanes (Category 3 or higher) hit CS directly, leading to loss of vegetation and shortages of food and water. However, the hurricane experience did not show perceivable negative impacts on monkey's skeletal development, suggesting resilience of this species. The CS Rhesus colony and skeletal collection have been very useful in the study of environmental and familial effects in diseases and adaption and will continue to be a powerful non-human model to the study of human conditions.

Funding Sources: The Cayo Santiago colony is supported by NIH 5P40OD012217 to Caribbean Primate Research Center. This project is supported by NSF grant #1926601 to Q.W.

Bioavailable strontium isoscapes for sub-Saharan Africa and their use in provenance studies

XUEYE WANG, GAËLLE BOCKSBERGER and VICKY M. OELZE

Anthropology Department, University of California Santa Cruz

Africa is an extraordinary continent highly relevant for research in paleoanthropology, archaeology, paleontology and extant animal ecology. Strontium isotope ($^{87}Sr/^{86}Sr$) analysis has proven to be an invaluable tool in all of these fields to reconstruct human and animal movements across African landscapes in the past and present, such as to assess habitat use of elephants, origins of ivory, landscape use of early hominin, and the origins of first-generation enslaved Africans. However, the lack of large-scale strontium isotope baseline maps (isoscapes) impeded the effective use of $^{87}Sr/^{86}Sr$ analysis in large parts of Africa. In this study, we present preliminary strontium isoscapes resulting from several collaborations with more than 100 colleagues from the fields of archaeology, paleontology, botany, conservation and primatology. Collectively, over the duration of more than 10 years, we obtained and analyzed more than 700 environmental samples (plants, soils, invertebrates and vertebrate remains) from 18 African countries and combined them with published data (n=1700), to then use a machine learning regression framework to draft the first bioavailable strontium isoscape for sub-Saharan Africa. Our results show that $^{87}Sr/^{86}Sr$ ratios span an exceptionally large range and show distinct regional patterns across Africa relating to multi-environmental factors (e.g. geology and dust inputs). In the nation of Angola alone, the $^{87}Sr/^{86}Sr$ ratios range from 0.70679 to 0.76815, making this region particularly interesting for reconstructions of individual life histories within the transatlantic slave trade. Our map lays a solid foundation for future $^{87}Sr/^{86}Sr$-based provenance studies on critical questions related to archaeology, ecology and forensic studies.

This study was funded by the Webster Foundation.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

ABSTRACTS

A new early Pliocene hominin mandible from Ileret, Kenya, with implications for the origins of *Australopithecus*

CAROL V. WARD[1], WILLIAM H. KIMBEL[2], JASON E. LEWIS[3], CASEY L. KIDNEY[4], FRANCIS H. BROWN[5], RHONDA L. QUINN[6], WILLIAM J. SANDERS[7], MEAVE G. LEAKEY[8] and LOUISE N. LEAKEY[8]

[1]Pathology & Anatomical Sciences, University of Missouri, [2]Institute of Human Origins, Arizona State University, [3]Department of Anthropology, Stony Brook University, [4]Geologic Specialist, EOG Resources, [5]College of Mines and Earth Sciences, University of Utah, [6]School of Earth, Environment and Society, Bowling Green State University, [7]Museum of Paleontology, University of Michigan, [8]Turkana Basin Institute, Stony Brook University

Australopithecus anamensis is known from deposits dated to as early as 4.2 Ma at Kanapoi and Asa Issie, which until now marked the first appearance of *Australopithecus*. In 2011, the Koobi Fora Research Project team recovered a broken and weathered hominin mandible with partial M_2 (KNM-ER 63000) along with associated vertebrate remains from Area 40 at Koobi Fora. Tephro- and magnetostratigraphic analysis indicate that these fossils date to ~4.3 Ma. Despite extensive damage, KNM-ER 63000 preserves diagnostic anatomy that warrants its assignment to *Australopithecus anamensis*. This mandible can be distinguished from *Ardipithecus ramidus* by its thick mandibular corpus and large M_2 crown. It differs from *Australopithecus afarensis* in having an inclined symphyseal axis with basally convex, cut-away external surface, lateral corpus that sweeps inferomedially beneath the canine-premolar row, and canine alveolus aligned with the postcanine axis. Faunal composition and enamel isotopes suggest that Area 40 paleoenvironments were comparable to those at Kanapoi and Mursi, with mixed habitats within a limited spatial scale. At 4.3 Ma, KNM-ER 63000 is the oldest known representative of *A. anamensis* by ~100 Ka, extending its known temporal range to be penecontemporaneous with *Ar. ramidus* from Gona and close to that at Aramis. Its morphology indicates that the reconfigured masticatory system differentiating basal hominins from earliest australopiths existed in the narrow temporal window separating the two. While not definitive, the close temporal juxtaposition of these grade-level differences we think suggests that *Ar. ramidus* was a closely related sister-taxon of *Australopithecus* rather than its phyletic ancestor.

Anthroengineering and the human nose: Investigating climatic adaptation using 3D morphometrics and computational fluid dynamics

LYNDEE A. WARD[1], HASINTHA A K. PATABENDIGE[2], VIVEK C. NAIR[2], REX MITCHELL[3], ELIZABETH O. CHO[1], TODD R. YOKLEY[4], BRIAN H. DENNIS[2] and SCOTT D. MADDUX[1]

[1]Center for Anatomical Sciences, University of North Texas Health Science Center, [2]Department of Mechanical and Aerospace Engineering, University of Texas at Arlington, [3]College of Science and Engineering, Flinders University, [4]Department of Sociology and Anthropology, Metropolitan State University of Denver

Ecogeographic variation in human nasal morphology has long been hypothesized to reflect climate-mediated pressures for heating and humidifying inspired air, with taller/narrower/longer nasal passages posited to enhance heat and moisture transfers in colder environments. However, to date, challenges in quantifying nasal soft-tissue morphology and comprehensively modeling intranasal airflow have limited empirical testing of these long-standing hypotheses. To address this issue, this study employed three dimensional (3D) models of decongested nasal airways derived from cranial CT scans from a mixed-sex sample of 21 living individuals of West African and/or European ancestry. A total of 260 semi-landmarks were collected on each nasal model to assess nasal morphology, followed by Computational Fluid Dynamics (CFD) analyses to assess intranasal temperature and humidity transfers during inspiration of cold-dry air (-5°C, RH=0%). Multivariate regression was then employed to test for statistical associations between nasal morphology and intranasal heat and moisture transfers. Results reveal a significant association between nasal shape and the temperature and humidity of inspired air entering the nasopharynx after passing through the nasal cavity (R^2=0.582, p<0.0001). Consistent with theoretical expectations, the resulting 3D shape vector indicates that taller/narrower/longer nasal passages are associated with greater transfers of heat and moisture to inspired air. This study thus provides strong empirical support for hypotheses regarding ecogeographic variation in nasal form and function. Future studies investigating how nasal morphology influences specific aspects of intranasal airflow (e.g., directionality, velocity) which ultimately mediate heat and moisture transfers are needed to develop a more comprehensive understanding of nasal airflow biomechanics.

National Science Foundation (SBE-SPRF #2203808); Texas Center for Health Disparities (RF00241 & RI40241); Leakey Foundation

Y-chromosome DNA extraction from post-cranial skeletal elements

MYKALA D. WARD

Anthropology, University of Montana

With a reported number of over 8,000 individual sets of human remains unidentified in the United States, improved methods are necessary to collect and accurately extract DNA from human bone while being minimally destructive. Methods are not standardized for where on the skeletal remains to collect bone samples and often result in sampling far more material than is needed.

The molecular yields observed in trabecular and cortical bone samples taken from human remains could help determine what sample types are needed for successful DNA analysis. With a hypothesis stating that due to the structure of trabecular bone, samples that contain only the trabecular bone yield higher amounts of DNA molecules than samples taken from cortical bone, this project took the preliminary steps in improving DNA sampling and extraction methods by analyzing the yield of Y-chromosome DNA from the two bone types.

This project sampled 40 locations throughout the skeleton from each bone type and subjected them to quantitative polymerase chain reaction (qPCR) analysis. The results contradict the hypothesis and indicate that cortical bone samples yield higher amounts of DNA than trabecular.

The data collected from this project has provided a steppingstone to improve methods of DNA sampling of human skeletal remains. The data could be used not only to improve methods in forensic contexts but could be used for military identifications, ancestry estimations for potentially Indigenous remains, etc. Further research is needed to increase the validity of the results and affect the current methods used in the field.

Allometric scaling in human lower-limb muscle cross-sectional area: implications for locomotion and sexual dimorphism

ANNA WARRENER

Anthropology, University of Colorado Denver

Muscle cross-sectional area is an important variable for understanding force generating potential and locomotor adaptation. Geometric scaling predicts area scales proportionally to (body mass)$^{2/3}$. Previous research has quantified scaling relationships between hindlimb musculature and mass in apes, but these relationships have not been clearly established in humans. Scaling in the human lower-limb is likely influenced by bipedalism and dimorphism in lean and total body mass between the sexes. To investigate these relationships, cross-sectional area in 18 muscles of the lower-limb were obtained through MRI in twenty-eight (14 female, 14 male) participants and measured in Analyze 14.0. Research was approved by Washington University in St. Louis IRB (#09-0216). Log-muscle cross-sectional areas were grouped by function (hip abductors, knee extensors and flexors, biarticulate knee/hip flexors, plantarflexors), and least-squares regressions were calculated for each group against log-body mass. All muscle groups were significantly ($p < 0.01$) correlated with mass (0.29

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

< r^2 < 0.70) and, except for the hip abductors, all groups scaled with positive allometry unlike other apes where hindlimb cross-sectional area scales isometrically in comparable muscle groups. Correlations and slopes were lower for females (0.2 < r^2 < 0.63; 0.39 < *b* < 1.02), then males (0.53 < r^2 < 0.79: 0. 7< *b* < 2.0) in all muscle groups, but still significant except for the hip abductors. These results suggest human lower-limb muscle scaling has responded to force production requirements of bipedalism, and differences in lean and total mass impact allometric equations in males and females.

The Leakey Foundation, Wenner-Gren Foundation, National Science Foundation, University of Colorado Denver

Functions of food-associated calling in the Rekambo chimpanzee (*Pan troglodytes troglodytes*) community in Loango National Park, Gabon

LINDSEY WARSHAWSKI and AMMIE KALAN

Anthropology, University of Victoria

Chimpanzees produce acoustically distinct vocalizations termed "food-associated calls" (FACs) while foraging. FACs are not emitted for all feeding events, suggesting they are not solely physiological responses to the presence of food. To better understand the function(s) of chimpanzee FACs in a natural foraging environment, this study investigates how the social and ecological contexts of wild chimpanzees (*Pan troglodytes troglodytes*) in Loango National Park, Gabon influence the probability of producing FACs. I test three hypotheses to illuminate the social correlates of chimpanzee FACs: the Recruitment Hypothesis; the Audience Effects Hypothesis; and the Feeding Coordination Hypothesis. All-day focal follows were conducted to collect continuous non-invasive behavioural data on six adult males. Behavioural data were analysed using R. Preliminary analyses show that adult males of the Rekambo community produced FACs for 31% of all feeding events. Certain individuals called more than others, with two males producing 53% of all FACs noted. Larger party sizes and changes in party composition were associated with FAC production. The majority of FACs were produced for fruit and aril (seed coverings), but calls were emitted for all food types with the exception of meat (i.e., monkey and tortoise). This study adds to the growing body of research on the function(s) of chimpanzee FACs and chimpanzee communication more broadly, as well as contributes to current cross-population research on behavioural flexibility of chimpanzees across Africa.

This study recieved funding from the American Society of Primatologists' Small Research Grant Program.

Sacrifice and Human Remains as Diety Effigies in Classic and Early Postclassic Cholula, Mexico

JAMES T. WATSON[1,2], MARTHA ADRIANA SÁENZ SERDIO[3], CARLOS CEDILLO ORTEGA[3], CAIT MCPHERSON[4] and BRIANNA HERNDON[5]

[1]Arizona State Museum, University of Arizona, [2]School of Anthropology, University of Arizona, [3]Sección de Arqueología, Centro INAH Puebla, [4]Department of Anthropology, University of New Mexico, [5]Department of Anthropology, University of California Riverside

In prehispanic Mesoamerica, the head held a symbolic importance as a source of power and the location of the soul representing vitality, the *tonalli*. Sacrifice was a common practice among many Mesoamerican societies as a way to celebrate and appease the gods and skulls were preserved for their symbolic power and reused for a number of ritual purposes as a symbol of death. Salvage archaeology work in 2009 in San Pedro Cholula, Mexico resulted in the recovery of human remains representing a at least 76 individuals (^{Total}MNI) from 33 mortuary features likely dating to the Classic and Early Postclassic periods. Most of the features represent the interment of a single individual (^{Sample}MNI = 38) but often contained fragmentary remains from other individuals. However, three mortuary features stood out as special ritual deposits that contained an interred child and crania or mandibles from probable sacrificial victims. The additional interred remains match the demographic diversity represented among sacrificial victims in other Mesoamerican sites. We argue that sacrificial remains functioned as ritual objects whereby the heads of sacrificial victims were transformed into effigies for the gods in place of ceramic effigies or other funerary objects.

Partial funding was provided by the Arizona State Museum and School of Anthropology at the University of Arizona.

A stable isotope approach to dietary composition and sex-based dietary differences in late medieval-early modern Romania

JENNA M.S. WATSON, BRIGID M. OGDEN and ANNEKE JANZEN

Anthropology, University of Tennessee Knoxville

The interaction between medieval Romanians and their environment, specifically the foods they consumed, and how biological and environmental factors influenced access to those resources is not fully understood. Stable isotope analysis was conducted on skeletal remains from three late medieval-early modern (14th–18th C.) cemetery sites in northeast Romania to reconstruct diet and explore how plant and animal protein sources varied between males and females. This research informs our understanding of what resources people were consuming, how sex may have influenced access to those resources, and provides insight into resource allocation in medieval Romanian society.

Stable carbon (δ^{13}C) and nitrogen (δ^{15}N) isotope analysis of bone collagen was conducted for 45 individuals from Suceava Fortress and Cnejilor Palace, both home to Romanian rulers, and Schiti»ôor, a nearby hermitage. The δ^{13}C and δ^{15}N values indicate that while both C_3 (wheat) and C_4 (millet) protein resources and terrestrial animal protein were being consumed at all sites, some sex-based differences in diet are evident, with females consuming a mixed C_3/C_4 diet and most males consuming a primarily C_4 diet. Both males and females were consuming similar amounts of terrestrial animal protein. These data suggest differential access to C_3 resources based on sex. Whether this is due to other factors like social status, age, or migrant status is not yet known. Future analyses will include age, social status, skeletal pathology, and migration to further disentangle whether these factors influenced access to dietary resources and contributed to patterns of stress and frailty in this population.

This research was support by a Fulbright U.S. Student Program Open Research Award, and the University of Tennessee College of Arts and Sciences and Center for Global Engagement.

The effects of substrate on human walking footprint trails

DAVID WEBB, LAURA ZACHARIAS and KAHLAN TRIPP

Anthropology, Kutztown University

A number of ancient footprint trails have been studied (Laetoli, Happisburgh, Ciur-Izbuk Cave, Willandra Lakes, etc.). To understand ancient hominins' locomotion, our best comparison is with modern humans, and it is easiest to study human walking in a laboratory setting. However, footprint trails made on tile or concrete might not be representative of those made in softer substrates like dirt or sand, suggesting that laboratory studies might not be applicable to ancient hominins. To test the validity of conclusions based on laboratory research, a group of 20 subjects walked on hard, medium and soft substrates, and three footprint trail parameters were measured: foot angle, step length and step width. Linear, mixed-effects regression was used to evaluate the effects of substrate on these parameters. Step width was significantly affected by speed and body weight, but not substrate type (p=0.74). Step length was also not significantly affected by substrate (p=0.19). However, foot angle was (p = 0.002). Even so, the effect was very small, being 0.77 deg between the hard surface and the soft one, and substrate accounted for only 1% of variation in foot angle, whereas individual variation accounted for 50%. These results are encouraging for those

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

interested in laboratory research to compare modern human footprint trails with those of ancient hominins. It is likely that trails produced on concrete, tile or wooden floors are indeed useful in understanding our ancient relatives' locomotor patterns.

This research was funded by the Kutztown University Research Committe.

A possible connection between Gravettian populations north and south of the Alps: the Venus from Willendorf

GERHARD W. WEBER[1,2,3], ALEXANDER LUKENEDER[2,4], MATHIAS HARZHAUSER[2,4], PHILIPP MITTEROECKER[2,5], LISA WURM[6], LISA-MARIA HOLLAUS[1], SARAH KAINZ[1], FABIAN HAACK[7], WALPURGA ANTL-WEISER[2,8] and ANTON KERN[2,8]

[1]Department of Evolutionary Anthropology, University of Vienna, [2]Human Evolution and Archaeological Sciences – HEAS, University of Vienna, [3]Core Facility for Micro-Computed Tomography, University of Vienna, [4]Department of Geology and Paleontology, Natural History Museum Vienna, [5]Department of Evolutionary Biology, University of Vienna, [6]Clinic of Small Animal Surgery and Reproduction, Ludwig-Maximilians University, [7]Württemberg State Museum, Stuttgart, [8]Department of Prehistory, Natural History Museum Vienna

The Venus I figurine, which was found on the left bank of the Danube in Willendorf II/Lower Austria in 1908 and dated to 30,800-29,200 years ago, is made of material that is not locally available. It is one of a few artefacts made of oolite, a particular kind of limestone. We investigated the famous Gravettian statuette using non-invasive micro-computed tomography scans with a spatial resolution of 53µm, respectively 11.5µm. We also sampled 33 oolite localities from France to the Ukraine and from Germany to Sicily to obtain thin sections for micro-morphological comparative analysis.

Based on age, texture, and fossil content, several localities could already be excluded as possible origins of the Venus raw material. For the remaining samples, we analyzed grain size distributions using Hellinger distances. One Italian locality, Sega di Ala (near Lake Garda) turned out to be indistinguishable from the six samples of the Venus, while all localities within a radius of 200km from Willendorf and those from Swabia near the Danube were significantly different. This suggests a dispersal of Gravettian groups bypassing the Alps before the Last Glacial Maximum. A pathway through the Alps may have been possible following the major river valleys of the Etsch, Inn, and Danube. Long distance travel of artefacts during the Gravettian has already been demonstrated in other cases, e.g., Mediterranean shells found in Romania. Taken together, these results sheds new light on the considerable mobility of Gravettian people at the time around 30,000 years ago.

Supported by the Amt der Niederösterreichischen Landesregierung, Abt. Wissenschaft, St. Pölten, Austria, project number K3-F-488/001-2014 and project number K3-F-488/002-2017, and the University of Vienna.

Assessment of Local Variation in Age-Related Cortical Expansion of Human Long Bones

GREGORY J. WEHRMAN[1], ALICE GOODING[2], ADAM SYLVESTER[3], DAWNIE STEADMAN[1] and BENJAMIN AUERBACH[1]

[1]Department of Anthropology, The University of Tennessee - Knoxville, [2]Department of Geography and Anthropology, Kennesaw State University, [3]Center for Functional Anatomy and Evolution, Johns Hopkins University

Limb bone cross-sectional geometry reflects effects of activity as well as local and systemic effects of aging. Age-related cortical expansion, where cross-sectional diameter increases as cortical thickness decreases, is well-documented in humans. However, it is unclear whether this process occurs uniformly throughout a limb bone cross-section or if variation in cortical expansion occurs across the cortical bone, perhaps due to variation in local loading or metabolism. If local variation of cortical expansion within a cross-section occurs, similar variation may be observed between cross-sectional slices along the length of a long bone. To address these questions, pQCT (peripheral quantitative computed tomography) scans of the forearm and leg were performed on over 100 living participants between 40 and 80 years of age to generate cross-sections of the radius/ulna and tibia/fibula. Scans were taken at five locations across each limb segment. Cross-sectional properties were calculated, and semi-landmarks were established around the endosteal and periosteal borders of each cross-section to assess age-related shape changes within and between cross-sections. Preliminary results indicate that differences in cortical thickness between the youngest and oldest age groups are found unevenly throughout the tibial and ulnar midshaft cross-sections. Specifically, cortical thickness along the posterolateral aspect of the ulna and anterolateral aspect of the tibia are not significantly different across age groups, while the medial aspects of both bones show evidence of cortical expansion. Local variation in cortical expansion suggests that global age-related shape changes of long bones may be mediated by local factors, like habitual loading patterns.

This project is supported by funding from a National Science Foundation Doctoral Dissertation Research Improvement Grant, BCS #2141878.

3D visualization of human cortical bone remodeling spaces using micro-CT data

XUAN WEI and DAVID ML. COOPER

Anatomy, Physiology and Pharmacology, University of Saskatchewan

Bone turnover is achieved by the constant process of remodeling. Microscopic investigation of remodeling utilizing histomorphometric methods is an important tool for biological anthropologists to understand human health, disease and adaptation across space and time. However, remodeling is a 3-dimensional process with the 4th dimension of time. While conventional studies offer valuable information such as osteon morphology, they are limited by the labour-intensive procedures and the spatially and temporally fragmented nature of thin sections. We investigated the morphology of human cortical bone remodeling spaces in 3D using micro-CT. Scans of adult anterior femoral midshaft sections from 9 males and 13 females aged 20-86 were visualized in 3D. Intracortical canal networks were segmented and 125 active remodeling spaces were manually identified and isolated. Our preliminary observation found that 64 of these remodeling spaces had one or more connecting canals within the network, 62 had the conventionally described morphology of clearly distinct cutting- and closing-cones, while 54 presented varied morphology, indicating that remodeling events exhibit great variation and complexity in size, shape and inter-connectivity. Research on microscopic human bone remodeling is currently only possible *ex vivo*. With the novel analytical tools developed by our lab based on an *in vivo* rabbit model, we anticipate conducting further quantitative and comparative morphological analyses with an expanded sample. Micro-CT analysis is relatively less destructive, enables 3D assessment of morphology and thus has the potential to complement conventional histomorphometric methods, thereby helping advance towards a more holistic understanding of human bone remodeling dynamics in biocultural contexts.

Bonobo party composition and proximity social networks

FRANCES J. WHITE[1] and ALEXANA J. HICKMOTT[1,2,3]

[1]Department of Anthropology, University of Oregon, [2]Texas Biomedical Research Institute, [3]Southwest National Primate Research Center

Bonobo (*Pan paniscus*) sociality and social strategies are complex with constant fission and fusion of the members of a community into temporary parties. Party membership therefore is one level of social decision whereas neighbor proximity within parties reflects another. We performed network analysis of party member and nearest neighbor data for wild bonobo adults and sub-adults from the Lomako Forest, DRC to test sex and age class differences in these strategic

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

behavioral decisions. Adult males, old males, nulliparous females and parous females differ in centrality measures based on party membership with parous females and adult makes having higher centrality than nulliparous females and old males (F=7.38, df 3,13 p <0.01). There is no difference, however, among these categories in centrality based on proximity (F=0.66, df 3,12 ns). Networks based on party composition show that party membership is based on highly connected parous females and high-ranking males with less connected nulliparous females and lower ranking males. Proximity networks show high connectivity and centrality amongst parous females with more peripheral and less connected nulliparous females and adult males, but also show strong proximity ties between each nulliparous female and the adult males. Observations of parties during feeding show that cycling nulliparous females often remain towards the periphery of a center formed by a core of closely associating parous females. These nulliparous females are the focus of attention of competing adult males.

Supported by NSF grants BNS8311252, SBR9600547, and BCS0610233 to FJW

Sex, stress, and syphilis: Assessing heterogeneity in frailty to acquired syphilis using skeletal stress markers and nutritional status

KERRI J. WIDRICK[1], ALEISHA REYNOLDS[1], MUNEEBAH UMAR[2], LAUREN NICHOLS[1], CASSANDRA DEGAGLIA[3], AMANDA WISSLER[4], FABIAN CRESPO[5], SHARON DEWITTE[4] and MOLLY ZUCKERMAN[1]

[1]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Department of Biological Sciences, Mississippi State University, [3]Department of Anthropology, Tulane University, [4]Department of Anthropology, University of South Carolina, [5]Department of Anthropology, University of Louisville

The overwhelming research foci on the origin and antiquity of *Treponema pallidum pallidum* has left other historically, anthropologically, epidemiologically, and clinically germane research on acquired syphilis relatively understudied, especially in regards to pathophysiology and associations between human host characteristics and persistent debilitating, destructive, and sometimes fatal tertiary stage infection. Here, we address potential associations between host characteristics, specifically sex and whether chronic and/or episodic experiences of physiological stress (stress) are associated with late stage syphilis through integration of skeletal data and data from morgue and death certificate records (MDCR) from a preliminary sample of individuals with antemortem clinical diagnoses of syphilis (N=85) from the Hamann-Todd Osteological Collection (HTOC). We assessed stress via a 7-biomarker (LEH, periodontal disease, neoplasms, osteoarthritis, intervertebral disc disease, rotator cuff disorder, and fracture) and 3-biomarker (porotic hyperostosis/cribra orbitalia, rickets/osteomalacia, osteoporosis) skeletal frailty index (SFI) relative to sex using a Mann-Whitney U test. For the 7-biomarker SFI, which represents stress, significant differences ($p = 0.022$; $p < 0.05$) were observed between males (n = 65; SFI: 4.17 +/- 0.187) and females (n = 20; SFI: 3.35 +/- 0.233). These preliminary results indicate that sex and stress may be largely overlooked, important host characteristics relative to heterogeneity in frailty to persistent syphilis, at least within some sub-populations, as some pre-antibiotic era clinical literature on untreated syphilis indicates. Future research will assess the relationship between stress, sex, and persistent infection with inclusion of individuals whose infection resolved at early stages (primary, secondary).

This research is supported by NSF Senior Research Grant: Reconstruction of host immunological status, hostimmune response (inflammatory phenotype (IP)), and heterogeneity in frailty to acquired syphilis. (Awardnumber: 1946203)

Exploring the Accessibility and Usability of 3D Reconstruction in Anthropological Contexts

EMILIE L. WIEDENMEYER and PETRA BANKS

Anthropology, Texas State University

Three-dimensional reconstruction of digital imaging and spatial data has wide applications in biological anthropology, helping visualize small skeletal anatomy or position larger scenes in geometric space. Reconstructed data can be exported to programs for further geoprocessing, measurement, and statistical analysis in archaeological research and forensic casework. However, most equipment and software necessary for reconstruction is expensive and unattainable for those with limited budgets (e.g., students or unaffiliated researchers), reducing overall accessibility and inclusivity in anthropological studies and applied work.

This study examined four methods of 3D reconstruction to evaluate usability, performance, accuracy, and quality of results as compared to each methods' average market price to explore overall value and realistic applicability in anthropological projects. Methods included Polycam, an iOS/Android application, software package Agisoft Metashape®, and two different portable light scanners. All methods were used to scan proximal and distal humeral epiphyses to compare small-scale execution, and Polycam and Agisoft were used to reconstruct a simulated outdoor forensic recovery to compare large-scale images.

The results indicated that while the cheaper mobile method provided a convenient and accessible option, the remaining three methods provided more accurate results with clearer images and less user error. However, standalone software and portable scanners required additional equipment for photo capture and processing, resulting in increased costs, user difficulty, and time spent processing. For researchers interested in quick captures or small-scale visualization, Polycam is a viable option given the price, but for those valuing accuracy or requiring large-scale scene reconstruction, Agisoft provided the best results.

Quality Assurance Practices as a Baseline for Forensic Anthropological Casework

JASON M. WIERSEMA, JULIE M. FLEISCHMAN and MIRIAM E. SOTO MARTINEZ

Forensic Anthropology, Harris County Institute of Forensic Sciences

The need for standard practice in forensic anthropology is well established. Thus far, most of the focus has been leveed on the development of, and adherence to method-specific standards. We argue that this focus is premature. Anthropologists and/or anthropology laboratories cannot effectively adopt OSAC or ASB standards and/or best practices without first establishing an overall, agency-specific quality assurance (QA) strategy. Adoption of standards and/or best practices without an underlying QA program cannot ensure quality practice. The parameters of the program should start with the ISO 17020 standard. A laboratory should ensure that it can satisfy the basic requirements outlined in the 17020 as a prerequisite to the adoption of standards. This process requires that a laboratory or agency invest in the development of a QA system to adequately satisfy 17020 requirements. It is insufficient to adopt Anthropology-specific standards without first satisfying the requirements of the 17020 standard. Additionally, adherence to standards can only be assured with external evaluation. Part of the investment a laboratory makes should accommodate regular auditing of the standards and their application. The Harris County Institute of Forensic Sciences' Forensic Anthropology Division (HCIFS FAD) operates from a nearly unique perspective regarding standards and QA. The HCIFS FAD is among the few that are accredited, and its members are heavily involved in the standards development process with the OSAC and ASB. This presentation will outline the lessons learned by the HCIFS FAD during the course of the development of its QA program and involvement in standards development.

Mandible size and anterior tooth reduction in extant primates

RUDOLPH J. WILKINS

Department of Anthropology, University of Arkansas

It is generally appreciated that there is a relationship between the relative size of the incisors, mandibular length, and diet in primates.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Specifically, folivores have narrower incisors relative to both mandibular length and body mass when compared to frugivores. However, it remains unknown what biological mechanism causes this disparity. This study uses ordinary least-squares (OLS) regression to evaluate the level of spatial constraint placed on the anterior dentition (i1, i2, c) by virtue of post-canine enlargement within 30 extant species. Altogether, four OLS regression models were run, varying by sex (male and female), mandibular dental measurements (anterior and posterior), and mandibular length. All measurements were log transformed to improve linearity. The residuals for each plot were compared to determine if anterior dental reduction is present within a species. Results demonstrate that this method can effectively group primates based on natural dietary preference. This is most evident in *catarrhines*. Species such as *G. gorilla gorilla* (n=39) and *T. gelada* (n=29) rely less on incisal preparation and accordingly have a smaller anterior sum relative to mandibular length. Conversely, species who primarily subsist on large, fleshy fruits, such as *P. troglodytes* (n=33) and *P. paniscus* (n=30), have the inverse relation. These results demonstrate an association between mandibular length and mesiodistal sums which may reflect crowding in the dental arcade. Future research in this topic may elucidate what factors contributed to the reduction in anterior tooth size within the hominin clade.

Comparing the degree and timing of neurocranial and viscerocranial fluctuating asymmetry and dental enamel defects

CATHY WILLERMET[1], EMILY MOES[2], HEATHER J.H. EDGAR[2] and COREY S. RAGSDALE[3]

[1]Philosophy, Anthropology, and Religion, Central Michigan University, [2]Anthropology, University of New Mexico, [3]Anthropology, Southern Illinois University Edwardsville

Fluctuating asymmetry (FA) refers to random developmental divergences from bilateral symmetry. The timing of FA should reflect developmental stress. We explore timing of FA in two areas of the cranium, the neurocranium (adult development around age six) and viscerocranium, (adult development around puberty), and compare them to the timing of observable dental enamel defects in the canine, which also develops by age six. Using a Mexican Colonial-era sample, we placed paired and unpaired cranial landmarks (18 neurocranial, 17 viscerocranial) on three-dimensional photogrammetric models. We calculated correlations between each cranial FA region and enamel defect frequency ratios (total tooth, and by crown third). T-tests separately compared the neurocranial and viscerocranial FA to the frequency of dental defects by crown third, to investigate whether defect frequency in the incisal, middle, or cervical third was associated with higher FA from either region. Ordinary least squares regression resulted in no correlation among the cranial FA scores (r=0.0187). Two enamel defect frequencies show a weak but insignificant correlation with the neurocranium defect frequency in the middle third (r=0.2527) and defect frequency in the cervical third (r=0.2834). Higher neurocranial FA scores were moderately correlated with the presence of at least one enamel defect (r=0.3574). None of the analyses involving viscerocranial FA were significant. The relationship between neurocranial FA and enamel defects in the canine correspond to the ages at which these structures form. This study adds to our knowledge about how nonspecific stress markers can help us understand how and when stress affects the body.

CMU FRCE Grant #48945; UNM Latin American and Iberian Institute Field Research Grant; AAPA Professional Development Grant; SIUE STEP Grant; UNM Research Allocations Committee.

Testing Keith's stages of hominoid locomotor evolution using Miocene ape postcrania

SCOTT A. WILLIAMS[1,2], XUE WANG[1,2], MONICA V. AVILEZ[1,2], MARIA V. GIRALDO[3], JEFFREY K. SPEAR[1,2], JENNIFER EYRE[4] and THOMAS C. PRANG[5]

[1]Department of Anthropology, New York University, [2]NYCEP, New York Consortium in Evolutionary Primatology, [3]Department of Biology, The City College of New York, [4]Department of Anthropology, Dartmouth College, [5]Department of Anthropology, Washington University in St. Louis

Arthur Keith proposed four "stages" of hominoid locomotor evolution: pronograde, orthograde small-bodied "hylobatian," orthograde large-bodied "troglodytian," and plantigrade hominin. Fossil apes discovered since Keith's time can be studied to test this hypothesis. Here, we include lumbar vertebrae and pelvic remains of *Ekembo* (*Proconsul*) *nyanzae*, *Morotopithecus bishopi*, *Pierolapithecus catalaunicus*, and *Sivapithecus indicus* in a large sample of extant anthropoids. We quantify morphology using 3D landmarks, applying 38 landmarks to penultimate lumbar vertebrae and 29 landmarks to ossa coxae (including ten semilandmarks along the iliac blade). Procrustes-adjusted data analyzed using principal components analysis (PCA) and canonical variate analysis (CVA) demonstrate that *Ekembo*'s lumbar vertebra is most similar to *Papio*, *Macaca, and Lagothrix* in the PCA and *Ateles* in the CVA. *Pierolapithecus* and *Morotopithecus* are positioned with hylobatids and *Ateles*, which overlap significantly. Both fossils classify as *Hylobates*. The *Ekembo* os coxa is most similar to *Hylobates*, and that of *Sivapithecus* falls between *Hylobates* and *Ateles*. Both classify as *Ateles*. These results suggest that phylogenetically early fossil apes like *Ekembo* were more derived in torso morphology than previously recognized, while *Morotopithecus* and *Pierolapithecus* may have engaged in brachiation and other forelimb-dominated suspensory behaviors. While the *Sivapithecus* os coxa appears to be more derived than a previous analysis indicated, it is nonetheless more primitive in morphology than expected for a potential pongine. Body size plays a significant role in the morphology of the pelvis in particular and may drive some shape similarities. Overall, we interpret our results as supporting Keith's model generally.

SAW was funded by a Leakey Foundation grant.

Genetic complexities of sex chromosome evolution

MELISSA A. WILSON

School of Life Sciences, Arizona State University, Center for Evolution and Medicine

The pathways to differentiate gonads into ovaries or testes are highly conserved across life, but the mechanisms to initiate these pathways exhibit tremendous diversity. Mechanisms to determine sex (defined here as the types of gonads and associated gametes), range from environmental, to behavioral, to genetic. Mammals, and in particular non-human and human primates have a primarily genetic initiation of gonad differentiation, resulting from genes found on a pair of differentiated chromosomes (often called sex chromosomes) where one chromosome is sex-limited (passed on only via sperm). Individuals who develop ovaries typically have two X chromosomes, while individuals who develop testes typically have one X chromosome and one Y chromosome. Because of the function in gonad development and sex determination, this pair of chromosomes – after some debate in the field – were called sex chromosomes. However, this definition both diminishes the function of the X and Y chromosomes to a single function (sex determination), and devalues the contribution of genes not on the X and Y in gonad development and differentiation. In this talk, I will present the evolutionary history of the sex chromosomes, discuss what is (and is not) known about the functional genes therein, and how these impact human health and development broadly.

Heteronormativity and reproduction in biological anthropology

MEREDITH A. WILSON

Anthropology, University of Illinois, Urbana-Champaign

This abstract is part of the symposium *Queering research: uses of LGBTQIA+ perspectives and queer theory in biological anthropology*. A common fallacy in the sciences is that being heterosexual is the dominant experience for sexually reproducing organisms. From this, comes an emphasis on the importance of reproduction, especially in studies concerned with evolutionary change. For example,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

in studies of human biology and evolution, reproduction is commonly used as the explanation for any identified or constructed sex difference. Using biological anthropology studies as a case study, I identify where and how heteronormative assumptions are reproduced in our discipline. Issues of AJBA and AJHB from January 2020 to May 2022 were analyzed and I identified original research articles that re/produce heteronormativity in their research. I selected articles based on titles that might be engaging with heteronormativity, namely ones which attempted to identify sex and/or gender differences or which were discussing reproduction of modern humans. I next read abstracts to better identify whether and how the article was re/producing heteronormativity. For this presentation I choose articles that most obviously emphasized reproduction and heteronormative coupling. I identified 24 articles that engage with reproduction and heteronormativity. I utilize feminist and queer frameworks to critically engage with these studies and to identify ways in which we as biological anthropologists can more carefully consider questions, variables, and interpretations beyond the assumption of heterosexual coupling and reproductive predominance.

Economics of territorial behavior of chimpanzees (Pan troglodytes) at Gombe National Park, Tanzania

MICHAEL L. WILSON[1], ANTHONY P. MASSARO[1] and ANNE E. PUSEY[2]

[1]Ecology, Evolution and Behavior, University of Minnesota, [2]Evolutionary Anthropology, Duke University

Mitani and Rodman (1979) proposed that primates defend territories when it is economical to do so, as measured by an index of defensibility (D), defined as the ratio of daily path length (d) to home range diameter (d'). They found that all territorial, but few nonterritorial, primate groups had D > 1. As a step towards conducting further comparisons across species, we tested the extent to which this index varies over time within a species, examining data from the Kasekela (1973-2015) and Mitumba (2000-2015) chimpanzee communities. We calculated daily path length from male focal follows and calculated home range area using minimum convex polygons enclosing 99% of observations. We found that D varied considerably for both Kasekela (median D = 0.80 (range = 0.54 – 1.5, n = 43 years) and Mitumba (median D = 0.92, range = 0.54 – 1.6, n = 14 years). This variation resulted from changes in both daily path length and home range size. During the study period, daily path length decreased and home range size increased for both communities. Given the decline and eventual extinction of Gombe's one other chimpanzee community, Kalande, during the later years of the study period, these changes all likely result from reduced competition for space. In particular, for Kasekela, D declined below 1.0 in 1990, towards the start of the Kalande community's decline, and remained below 1.0 for the duration of the study. Geographic constraints may free Gombe chimpanzees to expand their territories beyond what would be economically defensible.

Jane Goodall Institute, Leakey Foundation, NIH (R00 HD057992, R01 AI050529, R01 AI120810), NSF (BCS-0452315, BCS-0648481, BCS-1743506, BCS-1753437, DBS-9021946, IOS-1052693, IOS-1457260, SBR-9319909), University of Minnesota

Biocultural forensic anthropology: A bioarchaeological approach to understanding inequality and vulnerability in long-term unidentified persons

TERESA V. WILSON

Geography and Anthropology, Louisiana State University

Forensic anthropologists can incorporate more biocultural methods into their casework to identify the social forces that contribute to negative health outcomes, vulnerability, and marginalization in unidentified persons cases. The Louisiana Repository for Unidentified and Missing Persons, which contains anthropological, biometric, social, and spatial information about long-term unidentified persons, provides an opportunity to explore structural vulnerability. An examination of traditional paleopathological indicators of health including carious lesions, antemortem tooth loss, linear enamel hypoplasias, cranial porosities, and periostitis were used to assess 88 cold cases found in Louisiana. This health information was supplemented with other biological and cultural factors (i.e., estimated age, sex, population affinity, location of recovery, postmortem interval, material culture, and scene context) to better understand the lived experiences of long-term unidentified persons.

The majority of unidentified persons were young/middle adult (70%), male (65%), and from a BIPOC community (57%). Specific structural vulnerabilities found in Louisiana are often concurrent and can include catastrophic natural disasters, houselessness, involuntary displacement, generational trauma, systemic racism, unprecedented income inequality, substance abuse, high rates of chronic disease, and differential access to medical care. Although indicators of childhood stress were uncommon, there was a significant association between poor overall health and those who were estimated to belong to marginalized groups and those found in areas with high poverty rates and/or effected by major natural disasters. Louisiana's unidentified people may have experienced one or more structural vulnerability which highlights the need for a regional and holistic approach that can help to identify new pathways to identification.

Theory-laden forensic science: Forensic anthropology's objectivity problem (and what we can do about it)

ALLYSHA P. WINBURN[1], CHAUNESEY MJ. CLEMMONS[2] and STEPHANIE HARTLEY[3]

[1]Anthropology, University of West Florida, [2]Biology, University of North Carolina-Greensboro, [3]SNA International, Defense POW/MIA Accounting Agency

Forensic anthropologists and other forensic scientists have long touted objectivity as a core tenet of casework, research, and testimony. Yet, decades of research indicate that scientific knowledge is inherently theory-laden, and pure scientific objectivity is impossible to achieve. This presentation advocates instead for *mitigated objectivity*, calling for scientists to acknowledge and examine the subjectivities inherent in their practice and apply effective quality-control measures to constrain these implicit biases. Forensic anthropologists have increasingly engaged with issues of cognitive bias in the past decade. However, a systematic literature review reveals that only 18 peer-reviewed forensic anthropology contributions focused explicitly on cognitive bias have been published in the last 50 years (1972-2022), eight of which were journal articles. This presentation builds upon this small but essential body of research by providing concrete recommendations for the implementation of a mitigated objectivity approach to forensic anthropology. It details quality-control procedures and aims to foster discussion of their integration, including: applying linear sequential unmasking, establishing optimal orders of operations for casework, conducting blind analyses, crafting and refining replicable methods, and using comprehensive statistical frameworks to synthesize data into robust biological profile estimates. Importantly, by shifting focus from the outdated vision of neutral, detached practitioners striving to achieve unimpeachable conclusions, a mitigated objectivity approach can include space for community organization, advocacy, activism, and diverse practitioner positionalities. Mitigated objectivity emphasizes disciplinary standards that structure our practice, allowing forensic anthropologists to be whole and socio-culturally engaged persons. It is thus a more honest and ethical approach to forensic science.

Could 'Lucy' stand on an erect limb? Estimations of muscular parameters of the *Australopithecus afarensis* pelvis and lower limb with implications for functional inferences

ASHLEIGH L. WISEMAN[1], JAMES CHARLES[2] and JOHN R. HUTCHINSON[3]

[1]McDonald Institute for Archaeological Research, University of Cambridge, UK, [2]Evolutionary Morphology and Biomechanics Lab, University of

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Liverpool, UK, [3]Structure and Motion Laboratory, The Royal Veterinary College, UK

The force a muscle generates is dependent on muscle structure, in which fibre length, pennation angle and tendon slack length influence force production. Here, we test the capability of digitally reconstructed muscles of *Australopithecus afarensis* (specimen AL 288-1) to maintain erect and/or crouched midstance walking postures, addressing long-standing debates about habitual limb posture. We created a musculoskeletal model of an australopith and human, incorporating 36 muscles in the pelvis and lower limb. Australopith muscular parameters were estimated and seven unique models were produced; these either represented a 'simple', isometric approach (n=4 variants) incorporating force and fibre length only, or a Hill-Type muscle model (n=3 variants), in which each muscle's fibre length, pennation angle, tendon slack length and maximal force were calculated based upon different input variables. Models were positioned into erect and crouched midstance walking postures. Static simulations investigated the influence of posture on the maximally sustainable vertical ground reaction force (vGRF). All australopith variants produced similar simulated muscle activation patterns for an erect limb, with activation variability for the crouched limb. The simple variants were unable to support >1x body weight, thus the Hill-Type variants are optimal. Comparative results imply different muscle group recruitment between species needed to sustain midstance postures at maximally applied vGRFs. In the human, the hip muscles were the most heavily recruited (both postures) but in the australopith, it was the knee and ankle which limited maximal vGRF exertion (erect; all joints for crouched). Overall, we conclude that AL 288-1 was an efficient, erect biped.

This work was supported by a Leverhulme Trust Early Career Fellowship (grant number: ECF-2021–054) and by the Isaac Newton Trust, University of Cambridge, both awarded to ALAW.

Archaic variation is structured by ancestry in living admixed individuals

KELSEY E. WITT[1,2], ALYSSA FUNK[3], LESLY LOPEZ[4] and EMILIA HUERTA-SANCHEZ[1,2]

[1]Center for Computational and Molecular Biology, Brown University, [2]Ecology, Evolution, and Organismal Biology, Brown University, [3]Department of Molecular and Cellular Biology, Brown University, [4]Department of Quantitative and Systems Biology, University of California-Merced

Gene flow from archaic hominins such as Neanderthals and Denisovans has introduced alleles that have proven to be adaptive for modern human populations, and many of these have allowed specific populations to adapt to unique environments. Many living individuals are admixed, and have genomes that are mosaics of multiple ancestries, which can make it challenging to identify these population-specific archaic variants. Here, we use the admixed American populations from the 1000 Genomes Project dataset to understand how archaic ancestry is distributed across the genomes of admixed individuals. We subdivided the admixed American individuals' genomes into African, European, and Indigenous American ancestry tracts, and assess whether archaic ancestry is more commonly found in tracts of a certain ancestry. We find that archaic ancestry is very low in African ancestry tracts compared to European or Indigenous American ancestry tracts, and that Denisovan ancestry is highest in tracts with Indigenous American ancestry. We also use the Indigenous American ancestry tracts to identify genes that may have been adaptive specifically in Indigenous American populations, and find multiple candidate genes for adaptive introgression, including some that have been identified as adaptive in other studies. Our work highlights the importance of incorporating admixed genomes into the study of human population history and archaic introgression.

This work is supported by NIH grant 1R35GM128946-01, awarded to Emilia Huerta-Sanchez.

Quantifying Multivariate Human Growth: Using a Gaussian Copula to explore the dependency structure of human growth traits

CHRISTOPHER A. WOLFE and KYRA E. STULL

Anthropology, University of Nevada, Reno

Human growth and development reflect the holistic phenotype of an individual at a certain point along their life course. This phenotype is the external expression of combined genetic and environmental factors and is inherently multivariate – encompassing numerous measurable traits. However, contemporary research lacks the analytical toolkit necessary to quantify the multivariate growth phenotype. The current study quantifies the multivariate relationships between 61 growth traits using 1,317 individuals from the Subadult Virtual Anthropology Database. The traits used are common markers of human growth and development, including long bone lengths and breadths, epiphyseal fusion, and dental development. To model the underlying dependency structure, the vector of growth traits is fit to a Mixed Discrete-Continuous Gaussian Copula within the Stan language environment. A copula is a multivariate cumulative distribution function that models the inter-correlation structure between random variables. Results show that the dependency structure is mutable both across ontogenetic modules and throughout the ontogenetic window. Traits within similar ontogenetic modules (e.g., long bone growth vs. dental development) display higher degrees of inter-trait dependence, but such relationships weaken as growth slows and ceases. The results prove that growth traits do not develop independently but are shaped as part of a larger high-dimensional structure that varies in tandem across ontogeny – providing further evidence that the human body is a joint biological unit that should not be distilled into facile univariate analyses. Multivariate models such as copulas provide a novel means to further explore and quantify the complexity of human phenotypic variation.

This research was funded by two federal grants (NIJ 2015-DN-BX-K409 - and NIJ 2017-DN-BX-K144)

Variation in the rotational profile of the lower limb in industrial era modern humans.

JESSICA S. WOLLMANN, MICHELLE E. CAMERON and BENCE VIOLA

Department of Anthropology, University of Toronto

The rotational profile of the lower limb includes femoral torsion, tibial torsion, and talar neck angle (TNA), which collectively affect the mobility of the hips, the rotation of the knees, and the angle of the foot during walking and standing. All three measures are likely developmentally plastic, but little research has explored how these measures vary between individuals or how they relate to each other within an individual. Here, we examine how femoral torsion, tibial torsion, and TNA vary with biological factors, such as age, sex, body mass, and bone length. We also examine symmetry between the right and left leg and how these measures relate to each other within an individual. Bilateral data were collected from 45 (M = 37, F = 8) industrial era individuals from the J.C.B. Grant Collection. A t-test was used to compare males and females. Correlations were used to evaluate bilateral symmetry, intra-individual relationships between variables, and relationships between the rotational profile and biological factors. There were no differences between males and females for any aspect of the rotational profile. The right and left leg were reasonably symmetric within an individual. Femoral torsion and tibial torsion were not correlated, but tibial torsion was positively, although weakly, correlated with TNA. Tibial torsion was negatively correlated with age and body mass. Femoral and tibial torsion were not correlated with bone length. Future studies will explore the effects of activities such as intense terrestrial mobility and horseback riding on the rotational profile.

Arthur Keith's changing views about early hominins

BERNARD A. WOOD[1] and PAIGE MADISON[2]

[1]CASHP, GWU, [2]History, North Carolina State University

This contribution focuses on how Arthur Keith's three-stage (hylobatian, troglodytian, and plantigrade) scenario for the evolution of modern human upright posture, which he outlined in the first of his 1923 Hunterian Lectures, helped shape

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

his response to the discovery of what we now call fossil hominins from southern Africa in the second quarter of the 20thC. Our analysis is based on Keith's published works and his comments to the press, supplemented by archival records from the Royal College of Surgeons of England, including personal letters and notebooks. We consider how Keith's background, education, and experience may have influenced his immediate reaction, and rather different subsequent response, to the discovery of the Taung(s) child. Tracing his perspective across a quarter of a century as it was recorded in his published works, lectures, and letters to Raymond Dart and others, we also consider how the same factors may have influenced his evolving response to the subsequent discovery of a larger sample of early hominins from Kromdraai and Sterkfontein. Using the centenary of Keith's Hunterian Lectures as an opportunity to dissect an important chapter in paleoanthropology's history, our analysis also 1) reflects on the origin and evolution of Keith's concept, and 2) uses this historical case to derive lessons for practicing paleoanthropologists around the requirement to balance theoretical commitments with the need to respond to new and novel evidence.

A Social Autopsy of Maternal and Fetal Mortality Rates from the Milwaukee County Poor Farm Cemetery (1882-1925)

KATHARINE C. WOOLLEN, COLE N. WHITE and JENNIFER F. BYRNES

Anthropology, University of Nevada, Las Vegas

The United States has one of the highest maternal and infant mortality rates of any developed country, particularly affecting minoritized groups. A social autopsy framework is used to understand the overarching social, economic, and political conditions that contributed to these deaths throughout American history. During the 19th-early 20th centuries in the United States, poorhouses provided refuge for single mothers, and were maternity homes for young, pregnant, unwed women. One such location was the Milwaukee County Poor Farm Institutional Grounds. Archival data from the *Register of Burials at the Milwaukee County Poor Farm Cemetery* (RBMC) was analyzed for deaths attributed to pregnancy-related complications in women along with overall fetal mortality. In total, 6/119 (5.04%) young and 3/147 (2.04%) middle-aged adult females died from pregnancy-related complications; these were attributed to abortion complications and puerperal infections. No significant difference was detected between young and middle-aged females (p=0.194). From the Milwaukee County Poor Farm Cemetery (MCPFC), 192 burials were estimated to be female, of which 23 (12%) were young and 62 (32.3%) middle-aged adults. A total of 707 fetal (<40 weeks gestation) deaths were recorded in the RBMC. From the MCPFC, 142 fetal remains were excavated. Poverty is a strong predictor of birth outcomes in the past and present, resulting from inadequate reproductive education and birth control access. Utilizing archival and bioarchaeological records of maternal and fetal deaths uncovers invisible societal fissures in America's historical social foundation, revealing the historical reverberations of differential mortality in the present.

Quantifying the effects of urbanization on ancient Georgian populations with the oral microbiome

STERLING WRIGHT[1], LAURA WEYRICH[1] and MAKA CHKADUA[2]

[1]Anthropology, Penn State University, [2]Geology, Georgian National Museum

Urbanization is a significant cultural phenomenon that impacts the health of local populations in many contexts, especially in facets related to the spread of infectious diseases. Current bioarchaeological analyses compare health differences between rural and urban populations by measuring the expression of skeletal stress markers. However, quantifying the effects of urbanization on ancient human populations remains a challenge. Because ancient oral microbiomes have been shown to be associated with past lifestyles, they may also reflect effects of urbanization. Here, we investigated the ancient DNA in dental calculus of individuals from ancient Georgia dating to the Bronze Age (1,500 BCE-500 BCE), Antique period (499-399 CE), and Middle Ages (300 CE-599 CE). Rich archaeological assemblages associated with these individuals indicate that urbanization intensified from the Bronze Age to the Middle Ages, and paleopathological analyses concluded that each cultural period could be correlated with various skeletal markers, such carious lesions and antemortem tooth. Our results support these findings as they indicate that oral microbiome composition is correlated with cultural periods and skeletal pathologies. MapDamage2 and SourceTracker (v.2.0) were used to authenticate the ancient DNA and microbial signatures. Our analyses reveal that ancient oral microbiomes can provide additional empirical evidence when investigating archaeological questions related to the impact of urbanization on human health.

Factors influencing locomotion and mechanical energetics in growing wild sifakas (*Propithecus verreauxi*)

ROSHNA E. WUNDERLICH[1], NICHOLAS HESLEP[1], NJARATIANA A. RAHARINORO[2], GABRIEL NICULESCU[3] and RICHARD R. LAWLER[4]

[1]Department of Biology, James Madison University, [2]Mention Zoologie et Biodiversité Animale, Université d'Antananarivo, [3]Department of Physics and Astronomy, James Madison University, [4]Department of Sociology and Anthropology, James Madison University

Collection of fine-grained locomotor and energetic data on long-lived wild arboreal primates is hampered by technological difficulties and unreasonable personnel requirements for simultaneous behavioral data collection across age classes and environments. We employ inertial sensors to address these challenges and explore ontogenetic aspects of locomotion and energetics in sifaka. Sifaka juveniles achieve locomotor independence early (6-8 months) but continue long-bone growth until age 5. This creates mechanical and energetic challenges when juveniles travel with adults. We instrumented 8 wild sifaka (3 yearlings, 3 subadults, 2 adults) in 4 social groups with tri-axial accelerometers for 1.5-8 weeks and collected simultaneous continuous behaviors on focal pairs. We quantified overall dynamic body acceleration (ODBA, proxy for mechanical energy expenditure), peak accelerations, leap counts, and activity budgets. We used linear mixed models to examine the effects of age, social group and environment on the observed variation. We developed a machine-learning algorithm to identify behavioral context and locomotion from the sensors using time-matched behavioral data collection. ODBA varied more across groups and habitats than among age categories. Acceleration peaks were highest in yearlings, who need to produce higher take-off forces with their shorter limbs. Our machine learning algorithm successfully classified contexts and most locomotor behaviors >95% of the time. Our results provide a method for using accelerometers to identify behaviors and quantify mechanical energy expenditure. Empirically, numerous factors influence locomotor mechanics and energetics, and larger samples will be necessary to isolate the effects of age class and environment.

This research was supported by the Leakey Foundation.

The effect of sex on risk of mortality in two Ottoman-era populations from Hungary

SAMANTHA L. YAUSSY

Department of Sociology & Anthropology, Utah State University

After seizing the cities Buda and Pest from the Kingdom of Hungary (part of the Habsburg Monarchy) in 1541, the Ottoman empire transformed the capital and surrounding territories into a crucial part of the border defense system along the Habsburg-Ottoman front. To examine how mortality during Ottoman occupation was selective with respect to sex, this study analyzes data from two skeletal samples dated to the 16th-17th centuries: Fonyód-Bézsenypuszta (n = 55) and József Nádor Tér (n = 69). Whereas the József Nádor Tér sample is composed of individuals who lived in the cities of Buda and Pest during the Ottoman period, the Fonyód-Bézsenypuszta sample consists of pastoralists called "vlachs" who lived on the border of Ottoman territory and served as auxiliary military forces for

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

the empire. In this study, sex (in adults aged 18+ years) was modeled as a covariate affecting the Gompertz model of mortality. The results indicate that sex had an effect on the risk of mortality within the Fonyód-Bézsenypuszta sample but not the József Nádor Tér sample. Within the Fonyód-Bézsenypuszta sample, males faced a significantly higher mortality risk compared to females ($p < 0.007$). Increased risk of mortality among males in the Fonyód-Bézsenypuszta sample was likely due to the dangerous position occupied by the vlachs as vassals to the Ottoman government, as young adult males in this community were more likely to be involved in violent border skirmishes compared to females and individuals living in the capital city.

This research was funded by an AABA Cobb Professional Development Grant.

Changes in Brain Anatomy as a Consequence of Normal Endocranial Shape Variation in Modern Children

SAMANTHA E. YAWITZ[1], JESSICA M. CRONIN[2], CHLOE PHELY-BOBIN[3], ABIGAIL H. SORENSON[4], GRACE A. SELECKY[1], EMIELYN DAS[5], HANNAH NAIRN[6], REBECCA S. JABBOUR[7] and GARY D. RICHARDS[8]

[1]Department of Molecular and Cell Biology, University of California, Berkeley, [2]Department of Integrative Biology, University of California, Berkeley, [3]Department of Political Science, University of California, Berkeley, [4]Division of Computing, Data Science, and Society, University of California, Berkeley, [5]Department of Cognitive Sciences, University of California, Berkeley, [6]Department of Public Health, University of California, Berkeley, [7]Department of Biology, Saint Mary's College of California, [8]Department of Biomedical Sciences, A.A. Dugoni School of Dentistry

Previously we assessed normal endocranial shape variation in a small, age-restricted sample of modern human children. Here we present the results of our evaluation of a larger sample with more landmarks (71% and 82% increase, respectively), with the latter more closely approximating individual neural structures, and a slight increase in the age range. External reorganization of neural structures is detailed by lobe, and the consequent internal changes are discussed.

CT-scans of normal 5.0-7.9-year-old skulls (n=70) were taken (helical mode, standard kernel) and reconstructed as isosurfaces (0.3 mm isotropic voxels). Ages represent averages of all teeth and are based on the degree of crown/root calcification. Endocranial shape and structural changes were evaluated based on a principal components analysis, employing Procrustes-aligned shape variables in Morphologika2. To assess overall shape variation, we employed 62 landmarks, while variable numbers of landmarks were used to assess individual lobes or regions. Endocranial reconstructions from isosurfaces were size-adjusted based on the geometric mean.

PC1 (16.4%) defines a dolichocephaly-brachycephaly axis, with the most significant changes involving compression of the occipital lobe and cerebellum, midparietal lobe expansion, and superior elevation of the posterolateral parietal-occipital lobe transition. PC2 (11.2%) involves anteroposterior compression of the endocast and parasagittal uplifting and flattening along the superior frontoparietals. PC3 (8.3%) involves an anterior frontal lobe extension, occipital lobe/cerebellum clockwise rotation, and parasagittal flattening.

Understanding normal variation in endocranial shape in modern children is important for interpreting brain evolution in fossil Homo but also for evaluating potential impacts of shape change on neural function.

Student Opportunity Fund, University of California, Berkeley

Hominoid shoulder ancestral states and evolutionary rates estimated from chronophylomorphospace reconstruction

NATHAN M. YOUNG

Orthopaedic Surgery, University of California San Francisco

How hominoid postcranial diversity evolved remains heavily debated due to a limited and often contradictory Miocene ape fossil record. A promising approach to this question is to use geometric morphometrics to quantify shape variation of key anatomical regions and reconstruct ancestral nodes from time-calibrated molecular phylogenies. Here, this "chronophylomorphospace" method is used to model scapula shape in representatives of all living hominoid genera and generate testable predictions of their evolution, including estimates of ancestral states, evolutionary trajectories and rates, and timing of character transformations. This model is further informed by examples from the hominin fossil record, including *Australopithecus sediba* (MH2, 1.98Ma) and the recently described australopithecine "Little Foot" (StW 573d, 3.67Ma). Reconstructed morphospace supports a scenario in which *Pongo* retains primitive features of the ancestral hominoid shoulder condition, while hylobatids and African apes evolved more derived cranial spine/glenoid orientations in parallel. Supporting this idea, gibbons display significant diversity, with basal lineages *Nomascus* and *Bunopithecus*exhibiting blade morphologies predicted to be intermediates to the ancestral ape condition. Fossil hominins are consistent with a rapid and concerted history of directional selection on lateralization from an African ape-like ancestor while retaining a characteristic hominine supraspinous shape. Together these results indicate that living hominoid shoulder diversity reflects a combination of primitive traits, parallelism, and lineage-specific homology consistent with more complex interpretations of their forelimb evolution. Future challenges remain to confirm or refute these model predictions with additional fossils and to isolate the primary selective and/or functional signals represented by estimated shapes and evolutionary trajectories.

This research was supported by grants from the Cora Du Bois Charitable Trust and the National Science Foundation (BCS-1518596).

Colonized Knowledge and the WEIRD in Forensic Anthropology and Beyond

NANDAR YUKYI

Department of Anthropology, University of Nevada, Reno

In the recent years, there has been an increase in discussions on diversity, equity, and inclusion (DEI) initiatives in "Western" academia and other colonial professional spheres, including anthropology. In these discussions, questions of what to learn from them and how to move forward have been often emphasized. However, in order to effectively discuss how to move forward, it is crucial to look back onto patterns of effects that past colonial practices have power structures in anthropology. Indeed, a common thread is that WEIRD (Western, educated, industrialized, rich, and democratic and a euphemism for white) anthropologists have remained on top of the power structure created by the legacy of colonialism. The current study presents two bibliometric studies: the first surveying 793 forensic anthropology (FA) journal articles from 2015 to 2019 to analyze WEIRD vs. non-WEIRD contexts that the top contributors in the field originate from, and the second on 329 Southeast Asian (SE Asian) archaeology journal articles from 2012 to 2022 to understand the dynamics of international collaborations in this region. Results from both studies showed that FA authors from WEIRD contexts (73% of the authors assessed) or from Western countries doing research in SE Asia (76% of the authors) are the predominant knowledge producers in both fields. These bibliometric studies highlight the underrepresentation of non-WEIRD scholars and local scholars conducting research in their own countries in recent academic literature. Being aware of these disparate patterns is one of the first steps to dismantle the colonization of knowledge in anthropology.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Platyrrhine proximal humerus morphology reflects phylogeny and locomotor differences related to glenohumeral joint function

LIAM M. ZACHARY[1] and JUSTIN T. GLADMAN[2]

[1]Anthropology, University of Arkansas, [2]Shared Materials Instrumentation Facility, Duke University

Kinematic studies of locomotor performance and electromyographic studies of muscle activation patterns suggest that differences in glenohumeral joint function exist between primates that employ orthograde postures during suspensory locomotion and primates that utilize a variety of pronograde locomotor behaviors including leaping and quadrupedalism. Platyrrhines are a particularly suitable primate group to test this hypothesis because suspensory and more generalized arboreal quadrupedal taxa are present within a single primate radiation. Here, we investigated shape variation in the proximal humerus using 3DGM to assess the relationship between suspensory locomotion and glenohumeral joint function in platyrrhine primates. Twenty-five 3D landmarks were recorded on the proximal humerus in a phylogenetically diverse sample of platyrrhines (n=284). Results of GM analyses suggested that there are functional differences in the glenohumeral joint of suspensory platyrrhines, supporting findings from other lines of evidence. Principal components analysis of Procrustes aligned coordinates showed separation between suspensory taxa and more quadrupedal taxa. Additionally, pair-wise permutation tests indicated significant morphological differences between suspensory atelines and platyrrhines that rely on pronograde movement patterns. Shape differences were visualized as thin-plate spline deformations, which demonstrated a rounded and globular humeral head in orthograde taxa and a humeral head that was more oval in outline with a flattened superior articular surface in pronograde taxa. These shape differences suggested greater glenohumeral joint mobility in suspensory taxa. Proximal humerus shape was significantly correlated with rates of suspension in platyrrhines, but this relationship was insignificant when phylogeny was considered, highlighting the challenges of disentangling functional and phylogenetic signals.

Testing for divergent selection on complex traits in humans: challenges and opportunities

ARSLAN A. ZAIDI[1,2], JINGUO HUANG[3] and MARK SHRIVER[3]

[1]Genetics, Cell, and Developmental Biology, University of Minnesota, [2]Health Informatics, University of Minnesota, [3]Anthropology, Pennsylvania State University

Detecting adaptation to climate in humans is a challenging problem. Traditionally in anthropology, hypotheses of climate adaptation were tested by looking for correlations between the trait and relevant environmental variables (e.g., skin pigmentation and UV exposure). Such trait-environment correlations, however, can arise even in the absence of adaptation because of direct effects of the environment on the phenotype as opposed to genetic changes in response to the environment. Thus, trait-environment correlations are not in and of themselves sufficient evidence of local adaptation and must be supported by a correlation between the environment and the genetic variation underlying the trait of interest.

Here, we first describe how environmental confounding challenges the inference of genetic variation across diverse populations. Using extensive population genetic simulations, we show how recently admixed populations can be used to disentangle genetic and environmental effects on the phenotype. Our innovation over previous approaches lies in the use of local ancestry as opposed to genotype to estimate the effect sizes of trait-associated loci. This avoids confounding by subtle environmental effects, which we have previously shown, are notoriously difficult to correct in genome-wide association studies. We show that, in principle, this approach can be used to accurately infer the extent to which phenotypic differences between populations are due to genetic differences.

We contextualize our findings within the broader field of anthropological genetics, present limitations of current approaches, including ours, and present an optimistic outlook for the future as genetic and phenotypic data from admixed populations becomes increasingly available.

This work is supported by National Institute of General Medical Sciences award K99GM137076 to Arslan Zaidi.

Age differentiation in the mortuary rites of early Saxon Great Chesterford

SONIA R. ZAKRZEWSKI and ANN-KATHRIN SCHMIDT

Archaeology, University of Southampton

This study investigates the concept of social ageing and the perception of age in a rural early Saxon assemblage. Age, as part of identity, may be reflected in the mortuary rite. Gender distinction of graves, such as with weaponry, is well known in contemporary cemeteries, but the age demarcation is less well studied.

The skeletal remains of 160 individuals were studied. Not all could be reliably aged using dental development, skeletal developmental and/or transition ageing methods. Of those that could be aged, 41 were infants aged less than 1 year, 16 were children aged 1-7 years, 6 were older children (≤15 years), 24 were youths/young adults (≤20 years), 28 were adults aged 20-40 and 25 were mature individuals aged over 40.

Despite burial disturbance, clear age thresholds were identified in furnishings. Significant differences were found in the relationship with many grave goods, including knives (x^2=32.3, p<0.001) and brooches (x^2=26.9, p<0.001). Indeed, infants were never buried with personal equipment, e.g. knives, brooches or weaving tools. Younger individuals, aged under 20, were occasionally found with simple brooches; radiate and applied brooches were only found in prime aged adults, whereas square-headed and saucer brooches were only found in the mature individuals.

At Great Chesterford, individuals had to cross an age threshold in early childhood to be seen as full members of society, with infants not considered as such. Adulthood also had age differentiation. Pathology had no effect on female burials, but furnishing differences may be seen in males with and without spinal pathology.

The occupational history of Denisova Cave

ELENA I. ZAVALA[1,2], ZENOBIA JACOBS[3,4], BENJAMIN VERNOT[2], MICHAEL V. SHUNKOV[5], MAXIM B. KOZLIKIN[5], ANATOLY P. DEREVIANKO[5], ELENA ESSEL[2], CESARE DE FILLIPO[2], SARAH NAGEL[2], JULIA RICHTER[2], FREDERIC ROMAGNE[2], ANNA SCHMIDT[2], BO LI[3,4], KIERAN O'GORMAN[3], VIVIANE SLON[6], JANET KELSO[2], SVANTE PAABO[2], RICHARD G. ROBERTS[3,4] and MATTHIAS MEYER[2]

[1]Molecular and Cell Biology, University of California, Berkeley, [2]Genetics, Max Planck Institute for Evolutionary Anthropology, [3]Centre for Archaeological Science, University of Wollongong, [4]Australian Research Council Centre of Excellence for Australian Biodiversity and Heritage, University of Wollongong, [5]Institute of Archaeology and Ethnography, Russian Academy of Sciences, Siberian Branch, [6]Department of Anatomy and Anthropology, Tel Aviv University

Located in the Altai Mountains, Denisova Cave is an important site for human evolution history. It is comprised of three chambers that cover a time span of over 300,000 years with Pleistocene sediments that contain four different archaeological assemblages. There have been extensive excavations at the site resulting in the identification of hundreds of faunal remains, lithics, and skeletal remains of Neandertal and Denisovans and the offspring of a Neandertal mother and Denisovan father. However, the association of each hominin group to the different archaeological assemblages has been debated. In this study we collected 728 sediment samples from the Main, East and South chambers across all Pleistocene layers. We enriched each for both mammalian and human mitochondrial(mt) DNA. We identified ancient mammalian mtDNA in 685 and ancient human mtDNA in 175 samples. With this dataset we

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

were able to reconstruct the occupational periods of different hominin groups and provide the first genetic evidence of ancient modern humans at the site. In addition, we identified changes in the abundances of different large mammals as well as the types of hyaenas and bears at similar time periods as climatic shifts in the region. In this presentation we will place the findings of our study within the context of previous and recent studies on the cave.

Funding for this project was provided by the Max Planck Society

Assessing orangutan habitat quality and the conservation value of a secondary forest within Gunung Palung National Park, Borneo, Indonesia

VICTORIA R. ZDANOWICZ[1], TRI WAHYU SUSANTO[2,3], BETH BARROW[3], TATANG MITRA SETIA[2] and CHERYL D. KNOTT[1,3,4]

[1]Biology, Boston University, [2]Biology, Universitas Nasional, [3]Gunung Palung Orangutan Conservation Program, [4]Anthropology, Boston University

Rates of primary forest degradation and deforestation in Borneo exceed the rest of the world's tropical forests. For critically endangered Bornean orangutans (*Pongo pygmaeus wurmbii*), habitat loss threatens the stability of their remaining populations. About 75% of all wild orangutans live outside protected areas, and yet our understanding of how and if Bornean orangutans utilize land beyond the primary forest is limited. With rates of forest loss and fragmentation on the rise, there is a need to assess the value of human-modified landscapes in the conservation and long-term survival of orangutans. We investigated orangutan habitat quality within the Gunung Palung National Park (GPNP) landscape, focusing on the conversation value of a secondary forest with a history of logging. With temporally matched census and phenology data from intact and disturbed sites, we assessed forest diversity, structure and composition, and the patterns of key orangutan feeding trees. Though site diversity did not significantly differ, our analyses revealed significant variance in forest structure and composition, with lower proportions of large feeding trees and fewer epiphytes and lianas in the degraded forest. Still, critical orangutan foods were abundant in the disturbed forest, including a disproportionate percentage of invasive species orangutans are known to seek out. Orangutans navigate a range of habitats in response to changes in local feeding ecology. Thus, the presence of such resources, considering historical disturbance, elucidates the under-researched role of secondary forests in the long-term survival and conservation of Bornean orangutans across a regional matrix of habitat type and quality.

NSF BCS-1638823, USFWS F18AP00898, F19AP00798, F22AP00733-00, Conservation Food and Health Foundation, Disney Conservation Fund, Sea World Busch Gardens, Ocean Park Conservation Fund, National Geographic Society 86238C-21; Leakey Foundation

Ontogeny of impact loading in quadrupedal chimpanzees and gorillas

ANGEL ZEININGER[1], DANIEL SCHMITT[1], HERMAN PONTZER[1], DAVID RAICHLEN[2], KEVIN G. HATALA[3] and ROSHNA E. WUNDERLICH[4]

[1]Evolutionary Anthropology, Duke University, [2]Department of Biological Sciences, University of Southern California, [3]Department of Biology, Chatham University, [4]Department of Biology, James Madison University

Paleoanthropologists have debated for over a century associations between human bipedalism and its potential terrestrial or arboreal origins. The anatomy and mechanics of human bipedalism are generally viewed as emerging after our divergence from the human/chimpanzee last common ancestor, rather than having deeper evolutionary roots. One essential feature of human/hominin bipedalism is a foot capable of withstanding the vertical impact transient (IT) that occurs when the heel strikes the ground. IT magnitude is determined by impact velocity, the effective foot mass (M_{eff}) that decelerates to zero at impact, and the time over which the foot decelerates. While ITs are well-studied in human bipedalism, and noted in bipedal chimpanzees, they have never been investigated in detail in African ape quadrupedalism. Using force and kinematic data from an ontogenetic series of chimpanzees (n=3; 8, 10, and 18 years) and gorillas (n=6; 6, 9, 24, and 35 years), we calculated IT magnitude, impulse, loading rate, M_{eff}, and knee angle during quadrupedal steps. Across ages, gorillas had an extended knee at heel strike and impact peak, and a consistent human-like heel-only heel strike. While an IT was present in all gorilla steps, it was absent in some chimpanzee steps. In gorillas and chimpanzees, IT magnitude and impulse were highest in the youngest individuals and decreased with age, while loading rate followed the inverse trend. Ontogenetic patterns and aspects of human impact loading are present in African apes suggesting that human heel strike mechanics could have evolved before bipedalism, possibly in a quadrupedal ancestor.

Research supported by the National Science Foundation Grant BCS-1517561

Use of Laser-Induced Breakdown Spectrometry (LIBS) in sorting commingled human remains

KATIE ZEJDLIK[1], KRISTEN LIVINGSTON[2,3], GRACE MEYERS[1], JONATHAN D. BETHARD[4] and MATTHIEU BAUDELET[2,3,5]

[1]Anthropology & Sociology, Western Carolina University, [2]National Center for Forensic Science, University of Central Florida, [3]Chemistry, University of Central Florida, [4]Anthropology, University of South Florida, [5]The College of Optics and Photonics, University of Central Florida

Commingling of human remains can result from mass disasters, conflicts, epidemics, mortuary ritual, or even curation mishap. Sorting, or reassociation, of large-scale commingling is challenging and requires time, space, and the practiced ability to recognize the indicators necessary for reassociation of remains, especially when the bones are fragmented. Laser-Induced Breakdown Spectroscopy (LIBS) is an atomic spectroscopy method that uses a focused laser to sample materials at the microscale and excite the subsequently atomized matter in the generated micro-plasma, resulting in an elemental profile. It requires no sample preparation, is visually non-destructive, and can detect low atomic weights such as carbon, hydrogen, nitrogen, and oxygen. Portable LIBS is therefore a potentially useful tool for reassociating commingled remains beyond the capacity of other elemental methods, such as the more popularly used portable X-ray fluorescence (XRF). This presentation is a pilot study examining the utility of LIBS analysis for sorting human bones from twelve individuals. Six males and females with an average age of 70 years were sampled from the John A. Williams Documented Human Skeletal Collection at Western Carolina University. Results showed that using chemical data reduced from 23000 variables to 200 principal components, linear discriminant analysis gives a 90% or higher accuracy in assigning a bone to its known individual. The average classification accuracy was 95%. The next phases of this project will expand the sample size to 60 individuals and include a comparison of human accuracy via a reassociation test using trained, forensic and bioarchaeological anthropologists.

This project is supported by Award No. 15PNIJ-21-GG-04151-SLFO, awarded by the National Institute of Justice, Office of Justice Programs, U.S. Department of Justice.

Mountain and lowland gorillas have different rates of craniodental lesions

JOHN A. ZEMAN[1], CLAIRE E. TERHUNE[2], SIOBHÁN B. COOKE[3,4] and CLAIRE A. KIRCHHOFF[1]

[1]Biomedical Sciences, Marquette University, [2]Department of Anthropology, University of Arkansas, [3]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, [4]New York Consortium in Evolutionary Primatology Morphometrics Group

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

Mountain (*Gorilla beringei*) and lowland gorillas (*G. gorilla*) have been recognized as distinct species relatively recently. Thus, few studies have explicitly evaluated species-level differences in skeletal lesions and other hard tissue measures of morbidity. We contrasted prevalence of craniodental lesions in mountain versus lowland gorillas and tested for associations between lesion types. We examined adult crania (n= 76 *G. beringei*, n=82 *G. gorilla*) for skeletal signs of antemortem tooth loss (AMTL), TMJ osteoarthritis (TMJ OA), alveolar recession, pulp cavity exposure, dental abscesses, and other trauma using standard criteria. We then used nonparametric tests to evaluate lesion co-occurrence and species differences. Our results suggest many lesion types co-occur in both species. Both *G. gorilla* and *G. beringei* showed significant co-occurrence between TMJ OA and pulp cavity exposure and abscesses. Both species also showed associations between AMTL and pulp cavity exposure as well as between alveolar recession and pulp cavity exposure. In addition, *G. gorilla* showed associations between TMJ OA and AMTL, alveolar recession, and trauma, as well as associations between AMTL and alveolar recession, and between alveolar recession and abscesses. There were no sex differences in *G. gorilla*, but AMTL in *G. beringei* differs by sex. Between-species comparisons likely show that *G. beringei* have a higher prevalence of TMJ OA (47% compared to 27% in *G. Gorilla,* p=0.009) and alveolar recession (22% vs. 12%, p=0.049). The significant differences in dental lesion types between species provides more evidence for the ecological and behavioral differences between gorilla species.

NSF BCS-1551766 (CET); NSF BCS-1551669 (SBC); NSF BCS-1551722 (CAK)

Two Cases of Ankylosing Spondylitis in Central Plains, China, Western Han (3rd Century BCE – 1st Century CE)

XIAOYA ZHAN, JING SHAO, YINGPEI ZHU and HUI-YUAN YEH

Department of History, School of Humanities, Nanyang Technological University, Nanyang Techonological University

Two individuals show osseous changes that are consistent with ankylosing spondylitis at Dapuzi Cemetery, Xi'an, Shaanxi, China. Burial goods and burial practices indicate that this cemetery was mainly occupied during the Western Han Dynasty (3rd Century BCE – 1st Century CE). Ten thoracic vertebrates and connected ribs of M55, a young adult (16–20 years old), are fused together, while the cervical vertebrates show great degenerative changes. The sacroiliac joints show features of ankylosis. Shoulders and hip joints also present significant degenerative changes. M112, a female in her 30s, has similar joint changes and has a "bamboo spine," which is often observed in the final stage of ankylosing spondylitis. The prevalence of ankylosing spondylitis in the observed samples is 2.3 % (2/86) which is higher than the prevalence of it in mainland China today (~0.4%). We hope this study could improve our understanding of ankylosing spondylitis in ancient Chinese populations.

This study is funded by the Creativity and Excellence Programme and NAP Grant from Nanyang Technological University, Singapore. Hui-Yuan Yeh is the recipient of both grants.

An open-source photogrammetry pipeline for acquiring 3D biological models

CHI ZHANG[1], STEPHEN MATHER[2] and A. MURAT MAGA[1,3]

[1]Center for Developmental Biology and Regenerative Medicine, Seattle Children's Research Institute, [2]Center for Information Technology, Oberlin College and Conservatory, [3]Department of Pediatrics, University of Washington

Accurate and efficient 3D digitization is crucial for data collection and analysis in biological and forensic anthropology. Although microCT scanning remains the gold standard for capturing the geometry of specimens, modality cannot capture the surface texture, which can provide important information such as the coloration of bones that could give taphonomic or forensic insights. Here we present an affordable and highly flexible structure-from-motion (SFM) photogrammetry pipeline based on open-source tools and a regular DSLR camera for acquiring accurate 3D models with realistic texture. SFM photogrammetry is a relatively new technique that registers 2D images for reconstructing camera positions. It then generates a dense point cloud for detailed meshing and texturing. Our pipeline is based on the open-source package OpenDroneMap (ODM), which is commonly used for landscape and architecture modeling based on aerial photography. Our sample comprises sixteen *Aplodontia rufa* (mountain beaver) skulls. Photos were taken automatedly by syncing the shutter of the camera with a turntable. Using models derived from microCT scans of the samples as the reference, our results show that the geometry of the models derived from ODM is sufficiently accurate for metric and morphometric analysis. (e.g., measurement errors are usually around or below 2%, and morphometric analysis captures consistent patterns of shape variations). The surface texture is also highly realistic. Overall, our pipeline of photogrammetry can provide a convenient, affordable, and flexible tool for the 3D digitization of human remains in the lab, museum, and field for research and education.

Reproduction of Cayo Santiago Rhesus Colony based on the Patrilineal Family Trees: The Missing Patterns

QIANG Q. ZHAO[1], TERRY B. KENSLER[2], DEBBIE GUATELLI-STEINBERG[3], LUCI ANN P. KOHN[4], GEORGE FRANCIS[5] and QIAN WANG[5]

[1]Computer Science, Mercer University, [2]Caribbean Primate Research Center, University of Puerto Rico Medical Sciences Campus, [3]Department of Anthropology, The Ohio State University, [4]Department of Biological Sciences, Southern Illinois University Edwardsville, [5]Department of Biomedical Sciences, Texas A&M University School of Dentistry

The rich history and records of rhesus monkeys on Cayo Santiago (CS) provides a detailed history of family relationships, facilitating extended genetic analyses of residents' reproductive history. According to datasets from two recent censuses in 2013 and 2020, 10949 distinct animals are identified with matrilineal traces and information about natal social group and most recent group assignment. This collaborative project aims to build a database to manage existing data and new data to be collected. A unified ID code is generated for each subject to preserve individual privacy (e.g., their CS tattoos) and provide a common identifier to match a subject record (as from the census dataset) with possible catalog entries, as well as measurements, scan images, behavioral evaluation ratings to be collected during the current research effort. Studies on the CS rhesus population have so far been based mostly on matrilineal lines that can be traced back to 77 founders. Sire information started to become available with the adoption of DNA-based technologies. A custom analysis system with database graphical user interfaces (GUI) is under development using standard computer programming languages (including Java, Python, and SQL). This system can construct both matrilineal and patrilineal family trees. Researchers in this collaborative team started to use these tree structures to trace various pathological or behavioral phenomena with family relationships. Initial analytical results based on a "big-data" approach revealed male reproduction patterns (including peak time span, number of descendants, male-female interaction, and migration between social groups) that can be compared with related records.

NIH 5P40OD012217 NSF #1926528, 1926481, 1926402, and 1926601

Genome Wide Investigation of High-Altitude Adaptation in Tibetan Monpa

KIMBERLY T. ZHU[1], PALOMA S. CONTRERAS[2], SUDIPTA GHOSH[3], TOM D. BRUTSAERT[4] and ABIGAIL W. BIGHAM[1]

[1]Anthropology, University of California, Los Angeles, [2]Anthropology, University of Michigan, Ann Arbor, [3]Anthropology, North-Eastern Hill University, Meghalaya, India, [4]Department of Exercise Science, Syracuse University, Syracuse

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

High-altitude hypoxia, or low oxygen availability experienced at elevations over 2,500 meters above sea level, presents one of the strongest selective pressures acting on humans over the course of our evolutionary history. Genetic investigations of high-altitude adaptation have been well-documented in high-altitude indigenous populations in the Andes and Western Himalayas, revealing multiple genetic signatures of positive selection. The indigenous Monpa population from the Tawang district of Arunachal Pradesh in Northeastern India have historically resided at high altitude in the Eastern Himalayan Mountains (3,800m above sea level). However, their pattern of genetic adaptation to high-altitude hypoxia has not been explored. To do so, we performed a genome-wide selection scan using SNP genotype data from 49 Tibetan Monpa individuals. We applied three tests of positive selection including the Locus Specific Branch Length (LSBL), XP-nSL, and iHS. These tests identified evidence of positive selection at several loci involved in the body's response to hypoxia, particularly in the hypoxia inducible factor (HIF) pathway. We then then performed a gene-set enrichment analysis to detect overrepresented biological pathways in our results. Together, our findings provide novel insights into the genetic basis of adaptive evolution among Tibetan Monpa and contribute to understandings of convergent evolution as well as adaptation to high-altitude hypoxia.

Reconstructing the genetic history of the Late Iron Age "Celtic" groups from north and south of the Alps (4th -1st century BCE) (CELT.U.D.ALPS)

STEFANIA ZINGALE[1], ZITA LAFFRANCHI[2], ALICE PALADIN[1], LISA MEISELEDER[1], SANDRA LÖSCH[2], GABRIELE ARENZ[2], LUCIANO SALZANI[3], IRENE DORI[4], FELIX MÜLLER[5], VANESSA HAUSSENER[5], MARC-ANTOINE KAESER[6], GÉRALDINE DELLEY[6], ROSSANA CARDANI VERGANI[7], LUISA MOSETTI[7], VALENTINA COIA[1], MARCO MILELLA[2] and ALBERT ZINK[1]

[1]Institute for Mummy Studies, Eurac Research, Bolzano, [2]Department of Physical Anthropology, Institute of Forensic Medicine, University of Bern, [3]Soprintendenza per i Beni Archeologici del Veneto, Settore territorio, Sede di Padova-Nucleo di Verona, Padova, [4]Soprintendenza Archeologia, Belle Arti e Paesaggio per le province di Verona, Rovigo e Vicenza, [5]Bernisches Historisches Museum, Bern, [6]Laténium, parc et musée d'archéologie, Neuchâtel, [7]Ufficio dei Beni Culturali, Repubblica e Cantone Ticino, Bellinzona

From the Late Bronze Age onwards, shared elements of the so-called "Celtic" culture linked different human groups which were distributed across Europe. During the Late Iron Age (LIA, 4th – 1st centuries BCE), these groups were involved in migration processes and settled in the Italian Peninsula after crossing the Alps. Although these movements are archaeologically documented, the genetic history of LIA "Celtic" groups from north and south of the Alps remains unexplored.

In this paleogenomic study, we aim to address: i) if the relative homogeneous "Celtic" culture is also reflected in their genomic makeup, ii) how the genetic relationships between the studied "Celtic" groups and other ancient and present-day populations from Europe are characterized. For this, we carried out molecular analyses on 136 skeletal remains from 13 LIA archaeological contexts from modern Switzerland and Northern Italy. The genetic sex determination of 84 individuals resulted in 45 XX and 39 XY, including 29 subadults. With the additional support of mitochondrial DNA, we detected biological relatedness among individuals within two different Swiss archeological sites, and another case in one of the North-Italian sites. Comparative analysis shows that LIA individuals from Switzerland and Northern Italy are not clearly differentiated, suggesting genetic affinity among them. Moreover, their genomic diversity overlaps with those of present-day populations. However, our data suggest genetic discontinuity between LIA individuals from Northern Italy and present-day populations from the same geographic area. Conversely, the comparison with published data suggests a stronger genetic affinity among Iron Age groups from Europe.

This research was supported by a Swiss National Science Foundation grant to Marco Milella and Albert Zink (grant number: 10531FL_197103 / 1).

ötzi, the Iceman - new insights into health, diet and disease of the 5300-year-old glacier mummy

ALBERT R. ZINK

Institute for Mummy Studies, Eurac Research

The Tyrolean Iceman, commonly known as ötzi, is the world's oldest glacier mummy and one of the best investigated ancient human remains in the world. Since the discovery of the 5,300-year-old Copper Age individual in 1991, in the Eastern Italian Alps, a variety of morphological, biochemical, and molecular analyses have been performed that revealed important insights into his origin, his life habits, and the circumstances surrounding his demise.

In recent years, new radiological investigations, the sequencing of the complete genome and nanotechnological investigations have added further interesting findings about the life and death of the Iceman. By using highthroughput sequence analysis, his genetic ancestry, phenotypic characteristics and diseases predispositions could be inferred. In addition, genetic evidence for a virulent *Helicobacter pylori* strain was detected in his stomach and a comparative whole-genome analyses of the 5,300-year-old bacterium revealed new and important insights into the evolution of this pathogen.

By using a combined multi-"omics" approach, a molecular fingerprint of the Iceman's diet preceding his death was obtained. The analysis revealed a remarkably high proportion of fat in his diet, supplemented with dried wild meat, cereals and with traces of toxic bracken. The detection of the Iceman's stomach content further provided the unique opportunity to study the intestinal flora of a Copper Age individual. The results appear to confirm a loss of diversity in modern populations with a westernized lifestyle. The most important and latest scientific findings regarding the Iceman are discussed with consideration of the perspectives and limitations in modern mummy research.

Investigating the Relationship Between Vertebral Neural Canal Size Variation and Mortality Risk Among Modern Documented Americans

CAROLINE L. ZNACHKO

Anthropology, University of Tennessee, Knoxville

Vertebral neural canal (VNC) size has been used as an indicator of childhood stress exposures to test the Developmental Origins of Health and Disease hypothesis in bioarchaeological samples. However, bioarchaeological demographic parameters are often unknown and estimated. This project examines the relationship between VNC size variation, self-reported childhood socioeconomic status (SES), and mortality among modern documented Americans. Adults (N=115) from the UT and TXST Donated Skeletal Collections with well-preserved thoracic and lumbar vertebrae were examined. Maximum VNC anteroposterior and transverse diameters, sex, stature, SES (lower, lower-middle, middle, upper-middle, upper), and age were recorded. Redundancy analysis was used to model standardized VNC size variation with explanatory variables and an ANOVA tested for significance (α=0.05) in RStudio. While sex and stature were not significant predictors, SES was ($p<0.00$) with lower SES exhibiting significantly smaller VNC diameters than other statuses. A Cox Proportional Hazards model examined the relationship between VNC sizes and age. Overall, negative regression coefficients indicate larger anteroposterior and transverse diameters have a lower risk for mortality with significant differences in the middle thoracic anteroposterior and lumbar transverse diameters. Including SES as a covariate reveals lower and lower-middle SES have an increased risk of mortality with smaller VNC diameters, while middle to upper groups have mixed risk. Results suggest that childhood SES related stress exposures among modern Americans, as exhibited by smaller VNC sizes, influence

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

mortality risk in accordance with previous studies. Future incorporation of covariates like cause-of-death could further reveal how small VNC size relates to life history.

This project was, in part, funded by the Grady Early Endowment Fellowship and Graduate Research Support Fellowship at Texas State University.

Using visual technologies to develop novel strategies for engaging with communities in paleogenetics

JAIME ZOLIK[1], LAURA POTT[1], JOSÉ L. SANTA CRUZ ALCALÁ[2], CLAIRE MAASS[3], SAMANTHA PORTER[4] and MARIA NIEVES-COLÓN[1]

[1]Department of Anthropology, University of Minnesota Twin Cities, [2]Lead Archaeologist, Apacheta Consultores, [3]Forensic Anthropologist, Defense POW/MIA Accounting Agency, [4]Liberal Arts Technologies and Innovation Services, University of Minnesota Twin Cities

Paleogenetics research involves the permanent destruction of ancestral remains. Therefore, it is important that researchers collaboratively discuss laboratory processes with descendant and stakeholder communities. Here we describe the application of visualization technologies to actively engage and meet the interests of stakeholder community partners in our pilot ancient DNA (aDNA) project in *La Quebrada*, Peru. The collaborative goals of this project are to use aDNA to investigate the genetic diversity and kinship patterns of enslaved African and Afro-descendant peoples buried in an unmarked cemetery of a 18th century *hacienda* in coastal Peru. During three consultation events held in September 2021, May 2022, and September 2022, descendant community members voiced their interest in learning more about how we extract and analyze the aDNA of their ancestors' remains. To meet the community's requests we used four different visualization technologies during pilot laboratory work in summer 2022: photography, videos, animations, and photogrammetry. For example, by wearing GoPros over personal protective equipment, our team recorded clean laboratory procedures for sampling and DNA extraction of teeth from 30 individuals. We compiled the recordings into short videos using iMovie. We found that community members reacted positively to these forms of media when we showed them during our September 2022 consultation. We are continuing to optimize these engagement methods and assess their efficacy at science communication. By sharing our experiences, we demonstrate that visualization technologies open novel pathways for biological anthropologists to engage and involve communities in the research process.

This work was funded by Rust Family Foundation for Archaeological Research, American Association of Biological Anthropologists Cobb Professional Development Program, and University of Minnesota Department of Anthropology Wilford Funds Award

Adjustment of subsistence strategy -entheseal changes of the ancient population in the Houtaomuga siteÔºåNortheast China

RUIQI ZOU

School of Archaeology, Jiln University

Entheseal changes are skeletal markers formed where a muscle, tendon, or ligament attaches to the bone cortex, often used in the behavioral reconstruction of ancient populations. This study aims to affirm the possible relationships between entheseal expression and physical activity, as well as the feasibility of generating osteoarchaeological markers, found within the skeletal collection of the Houtaomuga site in Da'an, China. Based on the presence of settlement and millet cultivation, materials were categorized as early period (12900-2250 BP) and late period (2250-2050 BP). Using the Mariotti method, 23 postcranial skeletal entheseal changes of sixty-three individuals were visually examined. Results showed that frequency and severity differed between early and late adolescents and between males and females. Males exhibited higher levels of entheseal robustness and more significant entheseal robustness on the right side, while females showed asymmetry in entheseal robustness on both sides. The distribution of entheseal robustness in the early and late populations was basically the same. Still, the late populations bore less activity stress than the early populations. In conclusion, the results of the study show that the ancient inhabitants of Houtaomuga always maintained the subsistence pattern of fishing, hunting, and gathering, but the overall reduction of the activity pressure of the Houtaomuga population in the late stage convinced us of the emergence of a certain degree of sedentary life. This change in subsistence strategy effectively responded to the late Holocene climate change in the northeast and prevented the society from collapsing.

Associations between human host characteristics, health over the life course, and vulnerability to persistent late stage syphilis infection

MOLLY K. ZUCKERMAN[1], CASSANDRA M. DEGAGLIA[2], KERRI WIDRICK[1], FABIAN CRESPO[3], SHARON N. DEWITTE[4], LAUREN NICHOLS[1], MUNEEBAH UMAR[1], AMANDA WISSLER[4] and ALEISHA REYNOLDS[1]

[1]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Department of Anthropology, Tulane University, [3]Department of Anthropology, University of Louisville, [4]Department of Anthropology, University of South Carolina

Within diverse research domains, most research on acquired syphilis (*Treponema pallidum pallidum*) has investigated its origin and antiquity, leaving many epidemiologically, clinically, and paleopathologically germane questions about the common infection relatively under-addressed. Here, we partially, preliminarily address one of the most pressing questions: Which host characteristics, focusing on chronic physiological stress (stress) and inflammatory phenotype (IP), are associated with greater vulnerability to late stage infection *vs.* infection resolution following early stage (primary, secondary)? LEH, indicative of early life stress, periodontal disease (PD), indicative of a hyper-IP (HIP) and adult stress, and dental caries, potentially indicative of limited immunological infection control, are assessed in several samples to accommodate diverse theoretical and material limitations involved in skeletal analyses of syphilis. These include: archaeologically derived, post-Medieval English individuals with skeletal evidence of late stage syphilis (n=33) coupled with control, non-pathological individuals (n=111); and individuals with antemortem syphilis diagnoses from historical documented collections (Robert J. Terry Anatomical Collection: n=18; Hamann Todd Osteological Collection (HTOC) (n=85). Preliminary results from logistic regressions reveal significant differences in frequencies of LEH (46%; p=.05, p<.1), caries (82%; p=.04), and PD (63%; p=.03) in the pathological *vs.* control sample, while the HTOC and Terry individuals, respectively, show high frequencies of LEH (83%), caries (89%; 100%), and PD (94%; 100%). Combined and interpreted through the Developmental Origins of Health and Disease (DOHaD) paradigm, these suggest associations between early life stress, systemic HIP, adult stress, weakened immune responses, and vulnerability to late stage syphilis.

NSF Senior: Reconstruction of host immunological status, host immune response, and heterogeneity in frailty to acquired syphilis (Award: 1946203), NSF EAGER: Identification of specific pathogens in human dental calculus (Award: 1643318)

Inferring geographic origins from individuals buried along the *Camino de Santiago* pilgrimage route: Insights from the Silo of Charlemagne cemetery

ANDREA M. ZUREK-OST[1] and EMMA J. BONTHORNE[2]

[1]Anthropology Department, University of North Carolina at Chapel Hill, [2]Kellogg College, University of Oxford

The Silo of Charlemagne is a medieval cemetery located in Orreaga/Roncesvalles, Navarre (northern Spain), an area which has long served as a gateway to the Iberian Peninsula for those crossing the Pyrenees. This crossroads has played an integral part in mobility through historical Europe as the traditional first stop along the religious pilgrimage route *el Camino de Santiago*. Historic records and recent archaeological investigations conducted by Aditu Arkeologia indicate that throughout the centuries, this subterranean cemetery structure has served as a repository for the remains of both local and nonlocal individuals,

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License

including religious pilgrims and soldiers from nearby military campaigns. This project investigates the importance of Orreaga/Roncesvalles as a nexus in historic Iberia for locals and nonlocals through stable isotope analysis.

Human molars from individuals interred in the Silo of Charlemagne were sampled for strontium ($^{87}Sr/^{86}Sr$) and oxygen ($^{18}O/^{16}O$) isotope analysis (n = 17). Results were compared to published strontium and oxygen values from western Europe, as well as local faunal samples. Strontium and oxygen maps for geographic origin assignment were created using the RStudio package *assignR*, resulting in probability assignment isoscapes for each individual.

Individuals buried in the Silo of Charlemagne constitute a diverse sample, with 76.5% (n =13) falling outside of the local range. Historic records support the hypothesis that both pilgrims and soldiers from other areas of Europe, such as France, would have been interred in the cemetery. These results support the assertion that the Silo of Charlemagne was an important mortuary facility for historic mobility.

This research was supported by the University of North Carolina at Chapel Hill Graduate School Summer Research Fellowship, Department of Anthropology Kupferer Fellowship, and Research Laboratories of Archaeology Mooney Fellowship.

Should we reconsider what we know about physical activity patterns in hunter-gatherers? Recent evidence of past populations from the southern extreme of South America

RODRIGO ZÚÑIGA THAYER[1] and JORGE SUBY[2]

[1]Departamento de Arqueología, IMHICIHU-CONICET, Ciudad de Buenos Aires, Argentina, [2]Facultad de Ciencias Sociales, INCUAPA-CONICET, Universidad Nacional del Centro de la Provincia de Buenos Aires, Quequén, Buenos Aires, Argentina

Since the 1970's, high physical activity patterns have been reported in skeletal remains of ancient hunter-gatherer. However, present models often propose a homogeneity that may not reflect the wide behavioral and environmental diversity linked to this type of populations. The aim of this work is to explore the variability of physical activity patterns in hunter-gatherer societies, through the study of skeletal human remains of marine and terrestrial hunter-gatherers that inhabited Patagonia Austral (southernmost extreme of America) during the late Holocene.

Results from morphological (i.e., entheseal changes, upper limb length asymmetry and femoral robusticity) and pathological variables (i.e., osteoarthritis, osteochondritis dissecans, patella bipartite and Schmorl's nodes) were taken into account, considering their possible relationship with terrestrial and maritime economies. Maritime hunter-gatherers showed higher frequencies of entheseal changes in the upper limbs and robusticity of the lower limbs, bipartite patella, and osteoarthritis of the spine than terrestrial hunter-gatherers. Instead, they showed low prevalence of OCD and Schmorl's nodes.

Physical activity patterns may show notable differences among hunter-gatherers, associated with adaptive responses to environmental and cultural stressors. Moreover, the development of pathologies and morphological changes are possibly related to different mechanical pressures, required as part of subsistence activities. These data suggest the need of new models that do not over-simplify the consequences of physical stress in hunter-gatherer societies. Some biases must be considered, due to the small number of skeletons that is generally included in hunter-gatherer samples. However, further comparisons among ancient hunter-gatherer population could offer new insights to its physical stress patterns.

This paper has been supported by the National Council for Science and Technology (CONICET-Argentina) and Grant PICT 0191-2016 (National Agency for Science and Technology, Argentina).

Unique growth pattern and long-lasting isolation – do they affect dental morphology in the Baka pygmies?

PETRA G. ŠIMKOVÁ[1,2], GERHARD W. WEBER[1,2,3], FERNANDO RAMIREZ-ROZZI[4,5] and CINZIA FORNAI[1,2,6,7,8]

[1]Department of Evolutionary Anthropology, University of Vienna, [2]Human Evolution and Archaeological Sciences HEAS, University of Vienna, [3]Core Facility for Micro-Computed Tomography, University of Vienna, [4]URP2496 Pathologies, Imagerie et Biotherapies Orofaciales, Dental School, Montrouge, Universite Paris Cite, [5]Eco-anthropologie (EA), Museum national d'Histoire naturelle, CNRS, Universite de Paris, [6]Vienna School of Interdisciplinary Dentistry – VieSID, Klosterneuburg, [7]Centre of Clinical Research, University Clinic of Dentistry Vienna, Medical University of Vienna, [8]Institute of Evolutionary Medicine, University of Zurich

The Baka pygmies are unique in their growth pattern, characterized by a decreased rate during infancy resulting in short stature, and also due to early tooth eruption compared to other African populations. They identify themselves as 'Pygmies' (gk. pygmē) to emphasize their distinctness from their closest neighbors, the Bantu populations, who immigrated from western-central Africa several thousand years ago. We aimed at comparatively investigating the Baka's deciduous second molars (dm2s) to contribute to the understanding of dental variation in this human group.

We analyzed high-resolution µCT scans from 60 upper and 59 lower dm2s from individuals of various geographical origins, including 55 teeth from the Baka individuals. Using Geometric Morphometrics on five sets of 3D landmarks, intra- and inter-populational variation of the sample was assessed. Two-Block Partial Least Squares analysis was used to investigate the covariation between upper and lower dm2s. Size differences were assessed based on the natural logarithm of Centroid Size.

According to our results, populations overlapped largely based on their dm2 morphology. The Baka's lower dm2s showed the highest range of variation, interesting mostly their distal region, and crown height. Conversely, upper dm2s morphology varied the most in Europeans. We observed a high shape covariation between upper and lower dm2s (r1=0.82). The Baka and South Americans showed the largest dental sizes within our sample. Despite the Baka's long-lasting isolation with low-level non-pygmy populations admixture, the shape of their dm2s does not allow to distinguish them from other populations.

26927691, 2023, S75, Downloaded from https://onlinelibrary.wiley.com/doi/10.1002/ajpa.24731, Wiley Online Library on [19/12/2023]. See the Terms and Conditions (https://onlinelibrary.wiley.com/terms-and-conditions) on Wiley Online Library for rules of use; OA articles are governed by the applicable Creative Commons License