Check for updates

PROGRAM OF THE

91ST ANNUAL MEETING OF THE AMERICAN ASSOCIATION OF BIOLOGICAL ANTHROPOLOGISTS

MARCH 23 – APRIL 1, 2022

To be held

Denver, Colorado and Online

AABA Scientific Program Committee

Leslea J. Hlusko, Chair

Donovan Adams
Francisca Alves Cardoso
Eduardo Amorim
Benjamin Auerbach
Karen Baab
Heather Battles
Jonathan Bethard
Michelle Bezanson
Tara Cepon-Robins
Susanne Cote
Elisabeth Cuerrier-Richer
Miguel Delgado
Victoria M Dominguez
Amanda Ellwanger
Kori Filipek
Rebecca George
Rebecca Gilmour
Jesse Goliath
Kathleen Grogan
Lauren Halenar-Price
Angela Harden
Kevin Hatala
Amber Heard-Booth
Morgan Hoke
Jennifer Hotzman
Kent Johnson
Erin Kane
Saige Kelmelis
Brittany Kenyon-Flatt
Kristina Killgrove
Marc Kissel
Krystiana Krupa
Susan Kuzminsky
Myra Laird
Nathan Lents
Christopher Lynn
Heli Maijanen
Melanie Martin
Lumila Paula Menéndez
Alison Murray
Christina Nicholas
Heather Norton
Cara Ocobock
Rob O'Malley
Marin Pilloud
Thomas Rein
Kathryn Reusch
Terry Ritzman
Gwen Robbins Schug
Julienne Rutherford
Krithivasan
Sankaranarayanan
Lauren Schroeder
Maja Šešelj
Eric Shattuck
Michelle Singleton
Tanya Smith
Elizabeth St Clair
Katie Starkweather
Bethany Usher
Caroline VanSickle
Catalina Villamil
Cara Wall-Scheffler
Kerryn Warren
Karen Weinstein
Julie Wieczkowski
Teresa Wilson
Xinjun Zhang

AABA Meetings Director

Lori Strong, Burk & Associates, Inc.

Contributed Sessions Planning Committee

Francisca Alves Cardoso
Karen Baab
Jonathan Bethard
Tara Cepon-Robins
Susanne Cote
Elisabeth Cuerrier-Richer
Victoria M Dominguez
Amanda Ellwanger
Jesse Goliath
Lauren Halenar-Price
Jennifer Hotzman
Kent Johnson
Saige Kelmelis
Marc Kissel
Krystiana Krupa
Myra Laird
Nathan Lents
Christopher Lynn
Heli Maijanen
Christina Nicholas
Heather Norton
Cara Ocobock
Kathryn Reusch
Terry Ritzman
Gwen Robbins Schug
Eric Shattuck
Michelle Singleton
Elizabeth St Clair
Catalina Villamil
Kerryn Warren
Julie Wieczkowski
Xinjun Zhang

Program Assistant
Catherine E. Taylor

2021-2022 AABA Executive Committee

Steven R. Leigh
President

Anne L. Grauer
Past President

Leslea J. Hlusko
Vice President and Program Chair

Graciela Cabana
Treasurer

Sheela Athreya
Secretary

Trudy Turner
Editor, *American Journal of Biological Anthropology*

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

Shara Bailey
Professional Development

Chelsey Juarez
Student Programs

Kristi Lewton
Membership

Julienne Rutherford
History and Honors

MESSAGE FROM THE VP & PROGRAM CHAIR

2022 Abstract Issue

This volume consists of accepted abstracts submitted for presentation at the 91st Annual Meeting of the American Association of Biological Anthropologists hosted in two venues: in Denver, Colorado, from March 23-26, and online on the Pathable platform from March 28 -April 1. A total of 784 abstracts were submitted by the October 15, 2021 deadline. Each abstract was subjected to peer-review by at least two members of the program committee, with reviews completed by December 1, 2021. The committee recommended rejection for just over 1% of the abstracts. Authors of accepted abstracts were notified on December 8, 2021. Four abstracts had been withdrawn by January 23, 2022.

The 2022 AAPA abstract issue includes 770 peer-reviewed scientific papers presented in alphabetical order by the last name of the first author. Of these, 610 are scheduled to be presented during the in-person portion of the program in Denver. The online part of the 2022 program includes 311 abstract presentations, with 173 presenters choosing to present in both parts of the program. Once again, our program is truly international, with scientists from all over the world including Africa, Asia, Australia, Europe, Latin America, and the Middle East. We are pleased to be joined by our partner organizations: the American Association for Anthropological Genetics, the Dental Anthropology Association, the Human Biology Association, the Paleoanthropology Society, and the Paleopathology Association,.

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 (143 abstracts) are included in this year's program: six podium presentations will take place in Denver and be live-streamed onto the Pathable platform, five poster symposia that will also be in the Denver program, and two symposia will be exclusive to the online program. There are 627 contributed abstracts. By subfield, these include Bioarchaeology (n=91, ~15%), Dental Anthropology (n=43; ~7%), Education in Biological Anthropology (n=16; ~3%), Forensic Anthropology (n=44; ~7%), Functional Anatomy & Tissue Biology (n=90, ~14%), Genetics & Genomics (n=55; ~9%), Human Behavior (n=17; ~3%), Human Biology (n=72; ~11%), Paleoanthropology (n=94; ~15%), Primatology (n=105; ~17%).

Acknowledgements and Appreciation

My sincere thanks to everyone who helped organize the 2022 meetings. I am immensely grateful to the 67 talented, generous, and dedicated members of our Program Committee, who conducted and completed reviews thoughtfully, thoroughly, and expeditiously. We also thank the 32 members of the Program Committee who additionally took on the task of organizing the contributed sessions for both the Denver and the Online programs. I also want to express my deep gratitude to the nine members of the Advance Team who met in Denver to set up that program, who stepped up when I was unable to travel to be there in person to lead the effort: Steve Leigh, Lori Strong, Anne Grauer, Heide Rohland, Anna Warrener, Caley Orr, Michala Stock, Gwen Robbins Schug, Kristi Lewton, and the student volunteers: Catherine Morgan, Alexandria Kennedy, Bridget McGann, Ellie Berg, and Jamie Ernewein.

The 2022 annual meeting is another unprecedented conference format for AABA, combining an in-person and an online format. Many people stepped up to create this new format and keep our scientific community together in the midst of this third year of the global Covid-19 pandemic. Thanks are due to our extraordinary business partners, Lori Strong and her team (from Burk & Associates), as well as Ed Hagen (our webmaster and app developer). Our program assistant, Catherine Taylor, has been invaluable, as have the Officers and other members of the Executive Committee. A very special thanks goes to AABA President Steve Leigh and AABA Past President Anne Grauer for their leadership in envisioning and supporting this new meeting format in this third incredibly challenging year of the pandemic.

Leslea J. Hlusko
AABA Vice President and Program Chair

ABSTRACTS

Comparison of Temporal Cortex Cytoarchitectural Variability Across Primates

ISHAN S. ABDULLAH[1], ALEX R. DECASIEN[2,3], CHRISTOPHER TAYLOR[4], GWYNETH MCNIFF[1], AMY LONGTIN[1], VICTORIA BARONE[1], ADAM SNYDER[1], ADITYA LOGANATHAN[1], ZAHRA WAHED[1], ZOE PIPA[1], CHRISTINA HEROLD[5], KATRIN AMUNTS[5,6] and CHET C. SHERWOOD[1]

[1]Department of Anthropology, The George Washington University, [2]Department of Anthropology, New York University, [3]Section on Developmental Neurogenomics, National Institute of Mental Health, [4]Data Science Program, The George Washington University, [5]C. & O. Vogt-Institute of Brain Research, University Hospital Düsseldorf, Medical Faculty, Heinrich Heine University of Düsseldorf, [6]Institute of Neuroscience and Medicine INM-1, Research Center Jülich

Primates with larger brains tend to possess a greater number of distinct cortical areas, but there are limited data from systematic quantitative analysis of cytoarchitectural variation across the cortex of different species. The current study aimed to determine if brain size covaries with cellular distributions across the cortical surface. Greater cytoarchitectural differentiation might indicate increased modularity of cortical function. Our preliminary sample included coronal histological sections of the temporal lobe from *Indri indri, Lagothrix lagotricha, Saguinus midas, and Saimiri sciureus.* The temporal lobe contains cortical areas that function in higher-order auditory processing and visual object recognition. The cortex was sampled from ~200 equidistantly-located sites in each brain from sections representing the entire rostrocaudal axis of the temporal lobe. From each site, characteristics of cellular distributions were quantified using image analysis procedures to obtain data on vertical changes from the top of layer II to bottom of layer VI in: 1) the proportion of cell profiles versus neuropil space (grey level); and 2) the size distribution and density of cell profiles. Results showed that the coefficient of variation in cortical grey level increased with brain size (rho=0.95, P=0.05). Variation in cell profile sizes tended to decrease, but not significantly (rho=-0.80, P=0.20). We found no consistent rostrocaudal gradient of variation in these aspects of cytoarchitecture across temporal lobe sections in the sample. Further analyses will incorporate a greater range of primates. These studies will contribute to our understanding of developmental mechanisms in shaping primate cortical structure.

Same-sex sexual behavior in wild woolly monkeys (*Lagothrix lagotricha poeppigii*)

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

[1]Department of Anthropology, University of Texas at Austin, [2]Department of Anthropology, Miami University, [3]Tiputini Biodiversity Station, College of Biological and Environmental Sciences, Universidad San Francisco de Quito

Studies of sexual behaviors and reproductive strategies have often focused on interactions between different-sex dyads, potentially underestimating the frequency of same-sex sexual behavior (SSSB) among animal species. However, SSSB is ubiquitous across the animal kingdom, and, among primates, there are a variety of species that commonly display SSSB (e.g., bonobos, macaques, capuchins). Here, we present novel data on same-sex mounting behavior, one type of SSSB, in wild woolly monkeys (*Lagothrix lagotricha poeppigii*) living in a pristine tropical rainforest in the Ecuadorian Amazon. Between 2014 and 2018, we recorded data on sexual behaviors among adult and subadult individuals in four neighboring social groups. Of 279 observed cases of mounting, five (1.8%) were among same-sex dyads (four female-female and one male-male). Interestingly, all five cases involved at least one subadult individual, suggesting that in woolly monkeys SSSB may be used as an experimental or learning strategy for subadults prior to reaching sexual maturity as adults. However, further investigations are needed to better understand the function of SSSB in woolly monkeys. With this study, we hope to grow the comparative data set to better understand the function of non-conceptive sexual behaviors, including SSSB, among animals including primates.

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.

Meat Sharing in Savanna-Dwelling Chimpanzees at Fongoli, Sénégal

ANGELA ACHORN[1], STACY LINDSHIELD[2], PAPA IBNOU NDIAYE[3] and JILL D. PRUETZ[4]

[1]Department of Anthropology, Texas A&M University, [2]Department of Anthropology, Purdue University, [3]Département de Biologie Animale, Université Cheikh Anta Diop de Dakar, Senegal, [4]Department of Anthropology, Texas State University

Humans form social groups that are larger, more complex, and more cooperative than those of any other vertebrate taxa, which begs the question of how this level of social organization emerged. Food sharing is often considered to be a component of this large-scale cooperation and is hypothesized to have played a crucial role throughout our evolutionary history. To understand the function of food sharing among our early hominin ancestors, we can turn to our nonhuman primate relatives for insight. In this study, we examine the function of food sharing within the Fongoli chimpanzee community, a population of western chimpanzees (*Pan troglodytes verus*) in southeastern Sénégal. We test four non-mutually exclusive hypotheses that have been used to explain patterns of food sharing: kin selection, generalized reciprocity, sharing-under-pressure, and food-for-mating opportunities. We analyzed food sharing events (n=484) resulting from hunts, along with data on estrous swellings, copulations, prey size, rank, age-sex class, and kinship to determine which variables predict likelihood of food sharing during this study period (2006-2019). When we tested the predictions of each hypothesis independently, we found support for kin selection, generalized reciprocity, and food-for-mating opportunities. However, when we examined the effects of all variables combined, we found that reciprocity was the strongest predictor of whether or not an individual shared food, with food possessors being more than twice as likely to share with individuals who had previously shared with them. We discuss the significance of these findings from a savanna-dwelling chimpanzee population that systematically hunts vertebrate prey with tools.

The readability of bioanthropological abstracts and the implications for science communication

DONOVAN M. ADAMS[1], KELLY C. MCGEHEE[1] and CLAIRA E. RALSTON[2]

[1]Anthropology, University of Central Florida, [2]Anthropology, University of Nevada, Las Vegas

Abstracts provide summary information for research and may be the only accessible source of information due to lack of journal access or conference proceedings. Therefore, it is important for abstracts to be clear and concise for effective communication among colleagues and to the public. The present research examines the readability (i.e., processing and comprehension) of abstracts and the implications for science communication.

Abstracts between 2010-2021 from nine bioanthropological journals and two conferences (American Association of Biological Anthropologists and Anthropology abstracts from the American Academy of Forensic Sciences) were examined for temporal, forum, and topic trends in readability. The R package *quanteda.textstats* was used to calculate readability formulae and the Tool for the Automatic Analysis of Lexical Sophistication was used to assess natural language processing features.

Preliminary results suggest the average expected reading level for anthropological abstracts is college graduate, with language choice generally more similar to academic corpora than to fiction or news corpora. Conference abstracts demonstrate a statistically significant trend toward increasing sentence complexity, though academic-based language may be decreasing. Forensic-based venues often showed the greatest complexity, while the *American Journal of Human Biology* and *International Journal of Osteoarchaeology* showed the lowest complexity.

Initial results suggest: 1) accessibility of anthropological abstracts for a public audience is limited, with measures suggesting college education is expected for effective comprehension; 2) conference abstracts are increasingly structurally complex but word-choice may be tending towards greater accessibility; and 3) while there are differences in readability between topics, concerns for accessibility are disciplinary-wide.

Geometric morphometric and predictive modeling of the adult human pubic symphysis for implementation in fossil reconstruction

MAYOWA T. ADEGBOYEGA[1], SARA JHANJAR[1] and TIMOTHY D. WEAVER[1,2]

[1]Anthropology Department, University of California, Davis, [2]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

The pubic symphysis is a secondary cartilaginous joint that connects the left and right pubic bones to complete the anterior margin of the pelvic aperture. Because the pubic bone is often fragmentary and cartilage is not preserved in fossil remains, we rely almost entirely on studies of modern humans to understand pubic symphysis morphology.

In this study, we investigated the morphology of the articular surfaces of the pubic bones in 103 adult humans (52 male; 51 female), ages 20 to 96 who have undergone CT imaging in the University of California Health system. We employed geometric morphometrics and multivariate linear regression analyses to determine the predictive capabilities of sex, age, height, and size on pubic symphysis shape. We trained several models on our dataset including two-stage models that treated height and size as mediator variables and accounted for the indirect effects of age and sex on them. We then conducted mean squared error tests using leave one out cross validation to assess which model best predicts the shape of the pubic symphysis. Our goal was to identify models that can improve fossil pelvic reconstructions by helping us better infer the shape of missing elements of the pubic symphysis. The model containing sex alone yielded the lowest mean squared error value (0.02708) however, the other models yielded relatively higher but very similar mean squared error values (0.02720 – 0.02727). The similarities suggest an inconsequential effect of the mediator variables – height and centroid size – on pubic symphysis shape.

The Legacy and Disposability of Brown Bodies: The Bioethics of Skeletal Anatomy Collections from India

SABRINA C. AGARWAL

Anthropology, University of California Berkeley

As contemporary bioarchaeologists struggle to cultivate a postcolonial practice, the need for a code of professional ethics guiding the use of human remains acquired illegally or under expanded repatriation policies has dominated the discourse. However, the ethical responsibility of scientists working with skeletal anatomical legacy collections has received little attention. India was the primary global red market source of human skeletons for almost 150 years, with an estimated peak of 60,000 skeletons/year exported prior to the ban in 1985, the majority obtained by illegal theft/murder/coercion. While the mass exportation of human skeletons since the ban has ceased, India continues to illegally traffic skeletal remains for anatomical study. These human remains continue to train generations of biomedical practitioners and biological anthropologists globally, with hundreds of thousands of red market skeletons in the classrooms of Western countries today. In this paper I trace the history of the commodification of Indian bodies that began with British colonization that was set in slow genocide and violence. From my positionality as both a bioarchaeologist and an Indian brown body, I discuss how biopower maintained docility to extract the legacy of skeletons and the historic complicity of biological anthropologists to use the vulnerable and marginalized for scientific gain. I explore why bioarchaeologists continue to use and maintain this legacy of thousands of generations of bodies to be used solely as objects of anatomical landmarks, and why this type of reflexive analysis of our praxis continues to be critical to transform and decolonize our discipline.

This abstract is part of the symposium, Ethics in the Curation and Use of Human Skeletal Remains

A comparative isotopic approach to early Colonial Indigenous diet – El Japón, Xochimilco, Mexico

EDGAR ALARCÓN TINAJERO[1,2], LAURIE J. REITSEMA[1], JORGE A. GÓMEZ-VALDÉS[3] and LOURDES MÁRQUEZ MORFÍN[3]

[1]Department of Anthropology, University of Georgia, [2]Center for Applied Isotope Studies, University of Georgia, [3]Posgrado en Antropología Física, Escuela Nacional de Antropología e Historia

Early Colonial documents from central Mesoamerica testify to the raising of European livestock and planting of European crops alongside native ones soon after Spanish contact in the 16th century. The extent to which Indigenous people, especially of the rural commoner class, may have consumed newly introduced foods is less known. Carbon and nitrogen stable isotope analysis of 74 skeletal samples representing 16th-17th century individuals from El Japón – an Indigenous farming hamlet in the Xochimilco area – provide insight into individual diets in the context of a rapidly transforming Mesoamerican world. Carbon isotope ratios ($\delta^{13}C$) in bone collagen in this study average -8.07 ‰ PDB (SD 0.55), while nitrogen isotope ratios average 8.96 ‰ AIR (SD 0.50). $\delta^{13}C$ in bone apatite averages -2.59 ‰ PDB (SD 0.69). Both apatite and collagen isotopic ratios are consistent with individuals from Mesoamerican communities where maize agriculture was central. Relying on a multi-tissue stable isotope model to reconstruct past diets, we identify similarity to relatively smaller precontact agricultural communities and distinguish El Japón from more urbanized Mesoamerican communities and North American communities of differing subsistence strategies. Consistency with precontact communities indicates persistence in local food sources and foodways in the southern Basin of Mexico decades after Spanish contact and colonization.

Supported by UGA: Graduate School Dean's Award; Department of Anthropology Brian Daniel Gumbert Archaeological Graduate Research Award, Melissa Hague Field Study Award, and Janis Faith Steingruber Student Travel Award

A test of the Coimbra method of recording entheseal changes as applied to the foot skeleton

MALORIE E. ALBEE

Department of Anthropology, The Ohio State University

Prior studies have indicated that entheseal changes throughout the skeleton are largely reflective of age and body mass with mixed results concerning activity patterns. To add to this debate, this study tests the effectiveness of employing the new Coimbra method to record entheseal changes of the calcaneus (Calcaneal tendon enthesis), hallucal metatarsal (*Peroneus longus* m. and *Tibialis anterior* m. entheses), and fifth metatarsal (*Peroneus brevis* m. enthesis) to understand past activity patterns. Presence and severity of entheseal changes was scored for 71 adults (28 born pre-1950, 43 born post-1950) from the William M. Bass Donated Skeletal Collection, and these scores were contrasted according to age, sex, stature, body mass, temporal period, and occupation. Spearman's rank correlations show that age has the greatest impact on changes for the Calcaneal tendon enthesis, the *Peroneus brevis* m. enthesis, and the *Tibialis anterior* m. enthesis. Stature is the largest contributing factor to changes of the *Peroneus longus* m. enthesis. Moreover, ANCOVA tests show that several aspects of the entheses observed are more severe in the pre-1950 sample, even when accounting for demographic covariates. Differences according to occupation are less

clear; Calcaneal tendon enthesis Zone 2 erosion (p=0.0081) is statistically different between occupational standing ranks even when accounting for covariates, but the highest entheseal scores are observed among the lowest rank. These findings support prior studies that established age as a major contributor to entheseal changes but show that temporal period, stature, and occupation also contribute to entheses formation in the foot.

The evolution of early hominin food production and sharing

INGELA ALGER[1,2], SLIMANE DRIDI[1], JONATHAN STIEGLITZ[1] and MICHAEL L. WILSON[3,4,5]

[1]Institute for Advanced Study in Toulouse, University of Toulouse Capitole, [2]Toulouse School of Economics, TSE-R CNRS, [3]Anthropology, University of Minnesota, [4]Ecology, Evolution and Behavior, University of Minnesota, [5]Institute on the Environment, University of Minnesota

In striking contrast to the individualistic foraging of other primates, humans engage in collective foraging, with a sexual division of labor and widespread sharing of plant and animal foods. Evidence that hominins relied on extracted plant foods (e.g., roots and tubers) before animal foods became a major dietary component prompts a need to consider how extracted plant food sharing may have shaped hominin evolution. Here we propose a novel theoretical model of food production and sharing among early hominins (~6–2.5 mya), prior to the emergence of frequent scavenging, hunting and cooking. We examine how diverse mating systems (monogamy, polygyny, and promiscuity) may have shaped production and sharing of plant foods. We hypothesize that extracted plant foods were vulnerable to theft, and that male mate guarding protected females from food theft. Our mathematical model finds that females extract foods, and share them with males, only when: i) extracting, rather than collecting, plant foods pays off energetically; ii) risk of food theft is substantial; and iii) males guard females. Males extract foods whenever they are sufficiently high in value, but share these foods with females only under promiscuous mating and no mate guarding. These results suggest that if early hominins had mating systems with pair-bonds (monogamous or polygynous), sharing of extracted plant foods may have occurred long before scavenging, hunting and cooking. This incipient sexual cooperation may have enabled hominins to expand into more open, seasonal habitats, and provided a foundation for the subsequent evolution of unique human life history traits.

Institute for Advanced Study Toulouse (IAST) funding from the French National Research Agency (ANR) under grant ANR-17-EURE-0010 (Investissements d'Avenir program).

Art, Orality, and Migration: The roles of *NF1*, mnemonics, and somatic adaptation in the hominin biocultural toolkit

ANDREA J. ALVESHERE[1], LYNNE KELLY[2] and VINCENT M. RICCARDI[3]

[1]Sociology and Anthropology, Western Illinois University, [2]Arts, Communication and Critical Enquiry, LaTrobe University, [3]Director, The Neurofibromatosis Institute

Two decades after the discovery of the unique hominin variant of the *FOXP2* language gene, much more has been revealed about the emergence, expansion, and comingling of both hominin populations and hominin genetic variants. Recently, identification of a unique hominin variant of the *NF1* gene, and revelations about the importance of art (including objects, music, dance, and story) in the knowledge systems of oral ("non-literate") societies, have together exposed additional interconnected pieces of the human evolutionary puzzle. Current understanding of *NF1* gene function is primarily derived from study of the autosomal dominant disorder, Neurofibromatosis Type 1 (NF1), caused by a germline or early embryonic mutation of the *NF1* gene that disrupts the function of its protein product, neurofibromin. This causes progressive development of neurofibromas (benign proliferative lesions of the nerve sheath), involving somatic mutation of the remaining functional allele. Persons with the NF1 disorder also often face challenges with attention/focus, spatial reasoning, executive function, prosodic interpretation, and musicality. Each of these skill areas are optimized in the presence of two fully-functional human-type *NF1* alleles. These skills are also central to the knowledge systems of oral societies, especially in memorizing and passing on accurately (sometimes for millennia) vast quantities of life-sustaining information on resources, dangers, and strategies for navigation, cooperation, and survival. This study presents current evidence for the mechanics of, and relationships between, candidate genetic, somatic, and cultural elements of the extraordinary intellectual toolkit that enabled non-literate humans to populate or traverse every biome on Earth.

The effect of diet on the gut microbiome of humans and non-human primates

KATHERINE R. AMATO[1], ELIZABETH K. MALLOTT[2], ZACH DICKSON[3], SAM LONG[4], MELANIE KUCH[4], PAULA D'ALMEIDA MAIA[1], LAURA DIAKIW[5], MARIA FERNANDA DE LA FUENTE[6], PAUL A. GARBER[7,8], MICHAEL GURVEN[9], MORGAN HOKE[10,11], CHRISTOPHER KUZAWA[1], THOMAS MCDADE[1], ROBIN NUSSLOCK[12], ALICIA RICH[13], NICOLA SCHIEL[6], CHRISTOPHER A. SCHMITT[14], BENJAMIN TRUMBLE[15] and HENDRIK POINAR[16]

[1]Anthropology, Northwestern University, [2]Biological Sciences, Vanderbilt University, [3]Biology, McMaster University, [4]aDNA Center, McMaster University, [5]na, Olderkesi Wildlife Conservancy, [6]Biology, Federal Rural University of Pernambuco, [7]Anthropology, University of Illinois at Urbana-Champaign, [8]Program in Ecology, Evolution, and Conservation Biology, University of Illinois at Urbana-Champaign, [9]Anthropology, University of California at Santa Barbara, [10]Anthropology, University of Pennsylvania, [11]Population Studies Center, University of Pennsylvania, [12]Psychology, Northwestern University, [13]Biology and Earth Science, Otterbein University, [14]Anthropology, Boston University, [15]School of Human Evolution and Social Change & Center for Evolution and Medicine, Arizona State University, [16]Department of Biochemistry and Biomedical Sciences, McMaster University

Among other factors, a shift toward a low-fiber diet across human evolution is believed to have increased energy availability and allowed the emergence of energetically expensive traits such as relatively large brains. However, reduced dietary fiber has also been associated with chronic disease, particularly in the context of modern humans consuming industrialized diets. The gut microbiota (GM) degrades dietary fiber to generate short-chain fatty acids, which can be used by hosts for energy and influence metabolism and inflammation. Therefore, variation in host fiber consumption can affect host physiology via impacts on the GM. However, given human evolutionary diet patterns, we hypothesize that the GM-diet relationship is unique in humans. To address this hypothesis, we assessed GM composition and functional potential in populations of humans (Bolivia, Peru, Philippines, U.S.) and non-human primates (*Papio Anubis, Chlorocebus aethiops, Callithrix jacchus*) with qualitative differences in fiber intake. GM diversity was lower in human, baboon, and vervet populations consuming more industrialized diets with less fiber ($F_{10,249}$ = 46.2, p<0.01). Firmicutes relative abundances were lower in humans overall and lower in all primates consuming more industrialized diets. In contrast, Bacteroidetes relative abundances were higher in humans overall. They did not vary with diet in humans, decreased in response to an industrialized diet in baboons and increased in both vervets and marmosets. Our data suggest that while some diet-GM dynamics are shared across primates, others vary as a function of both the specific diet being consumed as well as host ecological niche and evolutionary history.

Microbiome data generation and analysis were funded by the Wenner Gren Foundation and CIFAR.

Biological distance in east Yorkshire, England: a preliminary analysis

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

[1]Department of Anthropology, University of Alaska Anchorage, Anchorage, AK, 99508, [2]Research Centre in Evolutionary Anthropology and Palaeoecology, School of Biological and Environmental Sciences, Liverpool John Moored

University, Liverpool, UK., Liverpool John Moores University

Dental anthropological study of the Iron Age inhabitants of east Yorkshire, England, particularly its applicability in estimating biological affinities among these populations, has been generally overlooked. The present study provides a preliminary analysis of the population history and demographic dynamics among these groups. Specifically, the key hypothesis to be tested is whether the spread of Celtic material culture throughout east Yorkshire was accompanied by concomitant biological change. The Arizona State University Dental Anthropological System was used to record 36 crown, root, and intraoral osseous traits in 190 dentitions from two samples of two regional populations, Rudston Makeshift and Wetwang Slack. These data were then compared using principal components analysis and the mean measure of divergence statistic to yield intersample phenetic affinities, and identify the traits driving inter-sample variation. Biological distance estimates suggest the following: 1) phenetic heterogeneity is evident among samples, to indicate greater genetic diversity among populations than previously believed; 2) population continuity is not supported; 3) the Rudston and Wetwang Slack populations retained a degree of genetic divergence and cultural autonomy; 4) the spread of Celtic artifacts throughout east Yorkshire may have been the result of a cultural transition. Simply put, the comparative results suggest these groups represent biologically distinct populations. Thus, the hypothesis is not supported. Therefore, the spread of Celtic material culture among populations in east Yorkshire may have been accompanied by little to no biological interaction, while greater genetic diversity among populations possessing regionally diverse Celtic material culture is implied.

Investigations of Cultural Identity during the Hellenistic Period: A Bioarchaeological Analysis of the Human Skeletal Remains from Kaman-Kalehöyük

CHERYL P. ANDERSON

Anthropology, Boise State University

The goal of this research was to perform a bioarchaeological analysis of the Hellenistic period (ca. 300-100 BCE) human skeletal assemblage at Kaman-Kalehöyük in central Anatolia (present-day Turkey). In particular, the aim was to reconstruct the paleodemography of the human skeletal remains excavated from 11 pits at the site and to assess whether these individuals displayed evidence of trauma. These data, along with information about the burial context, were used to test the hypothesis that the sample at Kaman-Kalehöyük is consistent with other Celtic Galatian burial assemblages. In particular, the burial context and skeletal data from Kaman-Kalehöyük are compared to published data from Gordion in central Anatolia, which has been interpreted as a possible example of Celtic Galatian ritual sacrifice.

The results of this research show that the minimum number of individuals interred in these pit burials is 28, which includes individuals from all age categories and equal numbers of female and male adults. This paleodemographic profile is very similar to that found at Gordion, with fewer infants and a higher percentage of adults. The burial context is also consistent with other Celtic Galatian sites, including Gordion. Evidence for perimortem trauma was not observed on any of the skeletal remains but antemortem trauma was found on three individuals (10.71%), including one adult with extensive healed injuries on the skull and postcranial skeleton. Possible explanations for the burial practices and demography observed in the Hellenistic period pit burials at Kaman-Kalehöyük include ritual activities and/or inequalities associated with low social status.

Ankle Joint Functional Morphology in the *Paracolobus mutiwa* Specimen KNM-WT 16827

MONYA ANDERSON and THOMAS CODY PRANG

Anthropology, Texas A&M University

During the Plio-Pleistocene, the Turkana Basin was home to at least 4 large-bodied colobine species: *Cercopithecoides williamsi, Cercopithecoides kimeui, Paracolobus mutiwa,* and *Rhinocolobus turkanensis.* Except for *R. turkanensis,* all display postcranial morphology consistent with some degree of terrestriality. *Paracolobus mutiwa* is also distinguished by having small tarsals relative to the robusticity of their long bones and compared to earlier species like *P. chemeroni*. This suggests that although they some features with terrestrial cercopithecines, *P. mutiwa* likely possessed unique ankle morphology derived for these more terrestrial colobines.

Here we present preliminary comparative analyses of astragalar and calcaneal morphology of *P. mutiwa* (KNM-WT 16827). The cercopithecid sample includes astragali (N = 288) and calcanei (N = 298) representing 171 extant colobines, 98 extant cercopithecines, 13 fossil colobines, and 6 fossil cercopithecines. Our quantitative analyses are focused on 13 linear metrics, 12 functionally relevant indices, and body mass estimates.

In *P. mutiwa,* the astragalus displays a typically colobine distally wide trochlea, but resembles terrestrial cercopithecines in its high lateral trochlear margin and narrow talocalcaneal facet. Compared to extant colobines, the calcaneus displays a large talar articular plane, long calcaneal tuberosity, and prominent peroneal tuberosity. The calcaneus also more resembles large colobine fossil specimen from the Omo Valley (L895-1) than *P. chemeroni,* especially in its proportions relative to long bone dimensions. Overall, the ankle joint morphology of *P. mutiwa* reflects a positional repertoire distinct from fossil and extant terrestrial cercopithecines and arboreal colobines.

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.

Characterization of DNA methylation change with age in the hippocampus of rhesus macaque

TANNER J. ANDERSON[1], ELISABETH A. GOLDMAN[1], MAILI SMITH[1], SAM WARD[2], BRETT A. DAVIS[2], NOAH SNYDER-MACKLER[3], STEVEN KOHAMA[4], LUCIA CARBONE[2,5] and KIRSTIN N. STERNER[1]

[1]Department of Anthropology, University of Oregon, [2]Department of Medicine, KCVI, Oregon Health & Science University, [3]Center for Evolution & Medicine, School of Life Sciences, Arizona State University, [4]Division of Neuroscience, Oregon National Primate Research Center, [5]Division of Primate Genetics, Oregon National Primate Research Center

Unlike chronological age, biological age is affected by genetic and environmental factors. Mechanisms that regulate the rate of biological aging are not entirely known but the epigenome (e.g., DNA methylation) is thought to play an important role. To better understand age-related epigenetic changes in the hippocampus, one of the first brain regions affected by the aging process, we characterized DNA methylation change with age in 96 banked hippocampus samples from rhesus macaques aged 3 to 35 years (corresponding human ages ~9 to 105 years) using reduced representation bisulfite sequencing (RRBS). We found the most differences in methylation between the brains of juvenile (3-5 years) and older individuals (>20 years) (n=67 differentially methylated regions [DMRs], FDR < 0.1). Preliminary characterization of these DMRs suggest that nearly all (64 of 67) become hypomethylated with increasing age. Interestingly, one of the three DMRs hypermethylated with age was annotated to miR-193a, a microRNA that functions as a tumor suppressor. Using these samples, we also generated an epigenetic clock that accurately predicted age in leave-one-out cross validation (Pearson's r = 0.9; median absolute difference = 2.44 years), highlighting its utility as a biomarker of biological aging. Characterizing how the epigenome changes with age in the hippocampus will help identify how behavioral,

lifestyle and environmental factors interact with molecular mechanisms to shape the pace of aging and aging-related disease in the brains of long-lived primate species, including our own.

This research was funded by the University of Oregon and Oregon Health & Science University Collaborative Seed Grant program and by ONPRC support (P51 OD 011092)

Misidentification of Hispanic individuals during death investigations: the impact of identification errors on research questions in anthropology and public health

NICOLLETTE S. APPEL[1,2], HEATHER H.J. EDGAR[1,2], KEITH HUNLEY[1] and SHAMSI DANESHVARI BERRY[3,4]

[1]Department of Anthropology, University of New Mexico, [2]Office of the Medical Investigator, University of New Mexico, [3]Department of Biomedical Informatics, Western Michigan Homer Stryker MD School of Medicine, [4]Department of Pathology, University of New Mexico

Vital records include governmentally gathered information on deaths, including demographic variables such as age, sex, race, and ethnicity. They are used to understand trends in public health, such as changes in death rates due to motor vehicle accidents, homicide, and substance abuse. These records can reveal patterns of health disparities related to neighborhood effects, rural/urban risks, and racial and ethnic inequity. In New Mexico, the death investigators and medical examiners assign the information that goes into each individual's record, which is then compiled in larger datasets and made available for public health research. Errors in these records can affect inferences researchers make about causes health disparities.

Here, we examine the accuracy of vital records related to Hispanic ethnicity by comparing the information in death investigation reports to reports made by next of kin (NOK) in telephone interviews, using data from the New Mexico Decedent Image Database (n = 2209; nmdid.unm.edu). This comparison revealed that investigators underestimate Hispanic deaths in the state. Overall, for each individual that NOK identified as Hispanic, investigators misidentified them 34% of the time. For 20% of cases, investigators did not record individuals as Hispanic when NOK did. In 6% of cases, investigators described individuals as Hispanic when NOK did not. Despite this high error rate, statistical analyses showed that neither average age at death nor proportions of manners of death differed between investigator- and NOK-identified Hispanics. Inaccuracies in the assignment of race and ethnicity in vital records can influence broader anthropological and public health research.

Life expectancy over time and death seasonality among captive former biomedical research chimpanzees

DREW M. ARBOGAST[1], JOHN J. ELY[2,3,4], W. SCOTT MCGRAW[1] and DOUGLAS CREW[1]

[1]Anthropology, The Ohio State University, [2]Founder, MAEBIOS, [3]Anthropology, George Washington University, [4]Veterinary Sciences, UTMD Anderson Center, Keeling Center for Comparative Medicine

An accurate assessment of longevity and mortality is vital to the study and conservation of any species. Recent reports on a retired U.S. population of captive former biomedical research chimpanzees provided life tables, survival statistics, ages at death, current age-sex composition, population projections, and future animal care cost projections. However, the accuracy of such information is often confounded by time and the size and age of the population. We analyzed 2,249 individuals observed between 1900-2014 to determine whether life expectancy changed over time and whether a seasonal pattern in mortality existed. Results indicated a dramatic increase in median age at death beginning around 1985, rising from 15.2 years in 1985 to 30.3 years in 2000 to 36.2 years in 2014. Furthermore, season of mortality was unevenly distributed among the 1,190 observed deaths. Percent of deaths was greatest during the winter months of December, January, and February (n=338), followed by autumn (Sep-Nov, n=321), spring (March-May, n=272), and summer (Jun-Aug, n=259, x^2=14.54, df=3, p<0.001). Our study demonstrates that the use of age at death alone in chimpanzee life history analyses can be misleading, as it is likely that captive populations have not yet reached their full aging potential. Life expectancy estimates may be influenced by improved husbandry practices over time, but they may also be an artefact of population aging and more individuals living out their lives. Population development and seasonal variation need to be thoroughly considered when making management or conservation decisions based on age of death analyses.

Partially funded by NIH Grant RR08083 to JJE. Thanks to Manuel Moro, Ph.D., for CRU approval, and to Raven Jackson-Jewett, D.V.M., for advice and assistance.

Theorizing the Genomic Archive as Method for an Abolitionist Science

SAMANTHA M. ARCHER

Department of Anthropology, University of Connecticut

In their 2019 *Current Anthropology* article, "Patchy Anthropocene: Landscape Structure, Multispecies History, and the Retooling of Anthropology," Tsing et al. argue for a recalibration of the tools of anthropology in order to develop a "symbiogenetic relationship" between anthropologists and their allies, including biologists and ecologists (Tsing et al. 2019:S188). A "patchy anthropology" comes alongside other recent calls for a radical reconfiguration of the anthropological discipline, including the theorization of an "abolitionist anthropology" (Shange 2019) and "The Case for Letting Anthropology Burn" (Jobson 2020).

While calls for paradigm shifts in the anthropological discipline are not new, the recent proliferation of theoretical concepts that call upon anthropologists to think beyond disciplinary boundedness in order to agitate and retool the way we know and learn within the discipline lend themselves well to the biological anthropologists' toolkit.

In this paper, I will demonstrate how a reconceptualization of genomic and molecular anthropological data as archival is one way we unsettle the subjective-objective binary that, despite calls for a critical biocultural anthropology and interdisciplinary scholarship in biological anthropology (Fuentes 2010, Leatherman and Hoke 2016, Leatherman and Goodman 2019), persist in our discipline. In order to go beyond mere scholarly collaboration that stops where subjective theory ends and objective data begins, we need an abolitionist, patchy, mixed-methods anthropology that leans into the subjective nature of all data and allows for a radical reconfiguration of how we make meaning from it – regardless of whether it is collected in the field, the museum, or the laboratory.

New cercopithecid fossils from Hadar

JULIA L. ARENSON[1,2], IRENE E. SMAIL[3], STEPHEN R. FROST[4] and CHRISTOPHER C. GILBERT[1,2,5,6]

[1]PhD Program in Anthropology, The Graduate Center, CUNY, [2]New York Consortium in Evolutionary Primatology, [3]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [4]Department of Anthropology, University of Oregon, [5]Department of Anthropology, Hunter College, CUNY, [6]Division of Paleontology, American Museum of Natural History

Cercopithecid primates are present at many Neogene fossil sites in the Middle and Lower Awash Valleys of Ethiopia, including four taxa from the Hadar Formation deposits at Hadar. The Sidi Hakoma, Denen Dora, and Kada Hadar monkey communities are dominated by *Theropithecus oswaldi* cf. *darti*, while *Parapapio* cf. *jonesi*, cf. *Rhinocolobus turkanaensis*, and *Cercopithecoides meaveae* are rare among the faunal collections. Here we present several new specimens from the Hadar Formation that add to the non-*Theropithecus* cercopithecid sample, including comparative analyses of a nearly complete male mandible allocated to cf. *Rhinocolobus* (A.L. 1001-4) from the Kada Hadar Member with a sample of 200 extant colobinans and African fossil colobines. Although similar to *Rhinocolobus*specimens in symphyseal and corpus proportions, A.L. 1001-4 is somewhat smaller and less robust than other *Rhinocolobus*

males, has a broader P_4 and M_2, and a wider lateral eminence. The symphysis lacks a median mental foramen, consistent with cf. *R. turkanaensis* from the Afar Basin and unlike material from the Turkana Basin. As the most complete cf. *Rhinocolobus* from the Afar, this specimen adds considerably to the hypodigm and provides a better assessment of variation in this genus between the older Afar and younger Turkana samples. Other notable new Hadar specimens include a juvenile *C. meaveae* mandible (A.L. 173-28) and a poorly preserved mandible referred to cf. *Parapapio* cf. *jonesi* (A.L. 1541-1), both from the Denen Dora Member. Collectively, these specimens indicate greater continuity of the monkey fauna through time within the Hadar Formation than previously recognized.

This project was funded by the NSF (#BCS-2018093; #BCS-1926163; GRFP #40F79-02 04), Leakey Foundation, Wenner Gren Foundation (RG#8523; HF#8928), PSC-CUNY Faculty Research Award Program, Hunter College, and University of Oregon.

Quantitative assessment of the influence of the glenoid *labrum* in the morphology of the glenoid cavity of the scapula in hominoids

JULIA ARIAS-MARTORELL[1,2], GEORGINA RAVENTÓS-IZARD[1], AROA CASADO[3], JUAN FRANCISCO PASTOR[4], SALVADOR MOYÀ-SOLÀ[1,5,6] and JOSEP Mª POTAU[3]

[1]Paleoanthropology and Paleoprimatology, Institut Català de Paleontologia Miquel Crusafont, [2]School of Anthropology and Conservation, University of Kent, Canterbury, CT2 7NR, UK, [3]Unit of Human Anatomy and Embryology, Faculty of Medicine, University of Barcelona, c/Casanova 143 08036, Barcelona, Spain., [4]Museo Anatómico, Departamento de Anatomía y Radiología, Facultad de Medicina, Universidad de Valladolid, c/Ramón y Cajal 7, 47005, Valladolid, Spain, [5]Institució Catalana de Recerca i Estudis Avançats (ICREA), Passeig de Lluís Companys 23, 08010 Barcelona, Spain., [6]Unitat d'Antropologia Biològica (Departament de Biologia Animal, Biologia Vegetal i Ecologia), Universitat Autònoma de Barcelona, 08193 Cerdanyola del Vallès, Barcelona, Spain

The glenoid cavity of the glenohumeral (shoulder) joint is characterized, in vivo, by the presence of a fibrocartilaginous rim around its perimeter, i.e., the glenoid *labrum*. Previous qualitative assessments of the *labrum* indicate that there are differences in the morphology of the glenoid cavity when the *labrum* is present, especially in humans, which might affect functional aspects of the glenohumeral joint not previously contemplated. In this study, we used quantitative techniques (2D and 3D geometric morphometrics and linear measurements) to characterize the morphology of the glenoid cavity of a sample of humans (N=8), chimpanzees (N=10) and cercopithecoids (N=14), recorded both with and without *labrum* to assess effects it might have in the depth, surface area and shape of the glenoid cavity. Results indicate that the *labrum* adds a significant amount of surface area and depth in humans without affecting the overall shape of the glenoid. In chimpanzees, the *labrum* only adds depth to the glenoid but not surface area. These findings indicate that the glenoid *labrum* increases the contact between the glenoid cavity and the proximal humerus in humans and chimpanzees, possibly acting as a stabilization mechanism of the glenohumeral joint. Conversely, the presence of *labrum* in cercopithecoids does not increase the available surface area of the glenoid or its depth, but it increases their variability with regards to shape. Overall, results indicate that there might be a need to re-evaluate the locomotor inferences made from the skeletal morphology of the glenoid cavity both in extant and fossil hominoids.

Funded by Generalitat de Catalunya (AGAUR BP-H2020 MSCA-Cofund #801370 to JAM), MINECO (Spain) and the EU (FEDER) (CGL2014-52611-C2-2-P to JMP), and the University of Barcelona (APIF-UB 2016/2017 to AC).

Evolution and lifestyle effects on sex differences in the human immune system

AUDREY M. ARNER[1], BENJAMIN MUHOYA[2,3,4], CHARLES WAIGWA[4,5], FRANCIS LOTUKOI[4], JULIE PENG[3], VARADA ABHYANKAR[3], JOSEPH KAMAU[5,6], C. J. METCALF[2], JULIEN F. AYROLES[2,3] and AMANDA J. LEA[1]

[1]Department of Biological Sciences, Vanderbilt University, [2]Department of Ecology and Evolution, Princeton University, [3]Lewis Sigler Institute for Integrative Genomics, Princeton University, [4]Mpala Research Centre, Nanyuki, Kenya, [5]Department of Biochemistry, School of Medicine, University of Nairobi, [6]Institute of Primate Research, National Museums of Kenya

The "Pregnancy Compensation Hypothesis" posits that sex differences in the mammalian immune system is an evolved, adaptive trait explained by selection on female immunity during pregnancy, during which increased immunomodulation is required to both tolerate the fetus and continue to stay healthy. In humans, post-industrial changes in reproductive ecology are expected to exacerbate these sex differences, as lower parity leaves female immune systems under-stimulated. Yet, robust tests of how lifestyle change impacts immune system sex differences are rare. To address this gap, we collected interview, genome-wide blood gene expression (n=459), and immune cell type data (n=658) from traditional Turkana pastoralists as well as individuals of the same genetic background that have recently moved to cities. We found that lifestyle alters sex differences in immune function, such that monocyte, neutrophil, basophil, and eosinophil counts exhibit distinct male-female differences in pastoralist versus urban settings. However, despite urban lifestyles being associated with overall reductions in female parity, we did not find evidence that these reproductive changes explain sex x lifestyle effects on immune cell counts. We are currently following up on these results 1) at the molecular level, by using our gene expression data to identify genes with exacerbated male-female differences in urban relative to pastoralist environments and 2) across species and contexts, by using comparable datasets from non-human primates, other subsistence-level human populations, and human cohorts in the U.S. Overall, our work provides insight into how sex differences in health are impacted by the sociocultural and ecological changes that accompany lifestyle transitions.

Parsing out functional signals: The influence of phylogeny on the primate first metatarsal

IRISA D. ARNEY[1], JASON S. MASSEY[2] and ZANA R. SIMS[3]

[1]Department of Medical Anatomical Sciences, Western University of Health Sciences, [2]Department of Anatomy and Developmental Biology, Biomedicine Discovery Institute, Monash University, [3]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

The hallucal metatarsal (MT1) supports locomotor and positional behaviors in primates and has been the focus of work investigating the evolution of bipedality and grasping abilities in fossil primates. The degree to which the morphology of articular facets and plantar diaphyseal curvature reflect function across all primates, however, has been understudied and is explored herein.

We used 3D geometric morphometric methods to explore MT1 shape in relation to function and phylogeny. Ninety MT1 surface meshes were downloaded from Morphosource to generate a broad sample of extant anthropoids that encompass a range of locomotor repertoires. Sliding semi-landmark patches were placed on articular facets, and one curve was fitted along the plantar midline diaphysis. Landmark coordinates underwent a generalized Procrustes analysis before subsequent analyses.

A principal component analysis of the whole dataset reveals 67.24% of the variance is contained within the first two PCs. PC1 separates hominoids from all other primates but is highly correlated with centroid size (R^2=0.65). While a discriminant analysis performed on the proximal facet correctly identifies knuckle-walkers and bipeds, no such differentiation is found among other anthropoids. The distal facet showed some clustering by locomotor category, and a discriminant analysis performed well for most groups. To account for the effects of phylogeny on the patterns observed, a phylogenetic PCA was performed. Results demonstrate no significant patterns, and previous clusters dissolve.

We find that, while some aspects of MT1 morphology discriminate among locomotor regimes, not accounting for phylogeny may misrepresent the true locomotor signal when characterizing fossil remains.

Nutritional status of school-aged Haitian children living in the Dominican Republic

SHAHNA L. ARPS

Department of Sociology and Anthropology, University of Toledo

Monitoring of school-aged children's nutritional status in the Dominican Republic is limited, particularly in Haitian immigrant communities. While rates of malnutrition have generally decreased in children under age five, socioeconomic disparities in nutritional status persist due to the economic insecurity and social marginalization Haitian families experience. To examine current trends in older children and adolescents, anthropometric assessments of 117 children ages 3 to 17 were carried out in urban/peri-urban communities around Puerto Plata in the Cibao Norte region. Height, weight, mid-upper arm circumference, and skinfold thickness (triceps and subscapular) were measured and compared to international references. Z-scores were calculated to classify children as stunted (5.1%), thin (2.6%), overweight (5.1%), and obese (3.4%) based on World Health Organization categories. Most children fell within the normal ranges for anthropometric indicators; however, undernutrition and overnutrition did co-occur in this population and will likely complicate nutritional interventions. While the literature has emphasized risks for undernutrition in Haitian immigrant communities, overweight and obesity were more prevalent in this study, suggesting that low-resource communities are experiencing the nutrition transition in the Dominican Republic. The larger percentages of overweight and obese children may be related to urban/peri-urban residences in particular. Current migration trends in the Dominican Republic are largely urban, so identifying this shifting pattern of risks toward obesity is critical for the development of appropriate health interventions and public health policy in the country.

This research was funded by the University of Toledo.

The thermoregulatory imperative and recent human evolution: climate, selection, and population history

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

[1]Dept. of Anthropology, The University of Tennessee, [2]Dept. of Biology, Sacred Heart University, [3]Dept. of Anatomy, Cell Biology, and Physiology, Indiana University School of Medicine

This abstract is part of the symposium, *The weight of the evidence: A session to honor the legacy of Chris Ruff*. Starting thirty years ago, Chris Ruff published a series of papers wherein he argued body shape and limb proportions of humans and their ancestors reflect, in part, adaptation to climate. He demonstrated that this "thermoregulatory imperative" was a manifestation of surface area to volume ratios in body form, a product of limb segment ratios, as well as width of the body and body mass as demonstrated through the cylindrical model. Subsequent decades of research have reinforced this pattern ecogeographically and temporally.

Researchers point to this body of work as evidence for responses to directional selection in body shape and size. However, while the morphological patterns correlate with climate and geography, both these correlations and the cylindrical model are untested hypotheses about the evolutionary forces that shaped body form.

We present a meta-analysis of our data, which include population structure, climatic variables, and latitude in multi-trait evolutionary models, in addition to studies of morphological integration to test these hypotheses. Collectively, we conclude that directional selection alone does not explain ecogeographic variation in body shape. Rather, some traits—namely body breadth and body mass—may have evolved in response to selection motivated by climate, while other traits like limb dimensions are complicated by population history. Moreover, we demonstrate that these traits cannot respond independently to evolutionary forces, and to best understand their evolution we must examine them collectively within explicit evolutionary models.

Intrapartum and Postpartum Home-to-Hospital Transfers in the United States

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

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

For most of human evolution, births occurred at home with support from trusted community members. While the evolutionary mechanisms underlying human birth complications are debated, they occur in a small number of births and can endanger maternal-newborn health. In the U.S., birthing people may have the option to undergo home-to-hospital transfer for advanced biomedical care. However, legal and financial barriers can complicate such decisions to the detriment of maternal-newborn health. The goal of this research is therefore to examine national, regional and temporal trends in U.S. home-to-hospital transfer rates using the Midwives Alliance of North America (MANA) Stats 4.0, a secondary anonymized dataset containing U.S. home and birth center data from 2012-2018 (n= 47,883 births). We find that national intrapartum and postpartum maternal transfer rates are 8.97% (SD=0.345, range= 8.33%-9.31%) and 2.12% (SD=0.243, range= 1.69%-2.37%), respectively. The national newborn transfer rate is 1.40% (SD=0.116, range=1.23%-1.42%). Minor yearly fluctuations in these national transfer rates occur with no discernable time trends. However, we observe regional differences in maternal intrapartum transfer rates, with the highest in New England, the Pacific Northwest, Alaska, and Hawaii, and the lowest in the Midwest, Great Lakes, and mid-Atlantic regions. Regional differences in home birth attitudes and legalization status can influence home-to-hospital transfer rates. While homebirth is generally a low-risk endeavor in the U.S., efficient transfer systems are needed to address potential complications.

Interdisciplinary approaches provide insight into structural violence and acute bacterial infections in an individual from the Terry Collection

RITA M. AUSTIN[1,2,3,4], MOLLY K. ZUCKERMAN[5], TANVI P. HONAP[1,2], HEDWIG LEE[6], GEOFF K. WARD[6], CHRISTINA WARINNER[7], KRITHIVASAN SANKARANARAYANAN[1,8] and COURTNEY A. HOFMAN[1,2,3]

[1]Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, [2]Department of Anthropology, University of Oklahoma, [3]National Museum of Natural History, Smithsonian Institution, [4]Frontiers in Evolutionary Zoology, Natural History Museum of Oslo, [5]Department of Anthropology and Middle Eastern Cultures, Mississippi State, Mississippi State University, [6]Departments of Sociology and African and African American Studies, Washington University in St. Louis, [7]Department of Anthropology, Harvard University, [8]Department of Microbiology and Plant Biology, University of Oklahoma

This abstract is part of an invited symposium, *Ethics in the Curation and Use of Human Skeletal Remains*. Through an interdisciplinary, humanizing osteobiographical approach, this presentation reveals direct and unprecedented insight into antemortem, end-of-life, and death circumstances of an individual from the Robert J. Terry Anatomical Collection. In showing how the embodied experiences and context of structural violence impacted this individual, we also highlight the historic, long accepted, and dehumanizing treatment of anatomical collections in research. This osteobiography focuses on a 23-year-old Black male (St.LI), who died in 1930s St. Louis, Missouri, by synthesizing genetic analysis of dental calculus with contextualized information from documentary and skeletal evidence.

St.LI exhibits osteological evidence of lifelong hardship and systemic poor health (e.g., chronic oral infections, probable tuberculosis, trauma, activity markers). Metagenomic sequencing recovered three pre-antibiotic era pathogen

genomes (*Klebsiella pneumoniae*, *Acinetobacter nosocomialis*, and *Acinetobacter junii*), which likely contributed to the recorded cause of death, "lobar pneumonia". Documentary evidence confirms St. LI died in a segregated, infamous hospital, and was subject to harsh chemical treatment postmortem for skeletonization following anatomization. Cumulatively, results reveal a personalized narrative of historic processes of structural violence endured by individuals and that supported the production of anatomical collections reliant upon marginalized communities for their creation. This history necessitates that historic documented collections no longer be considered or conceptualized as neutral within scientific contexts and that humanization efforts for these collections be prioritized, including reorientation of research frameworks and goals utilizing these collections towards more ethical strategies.

Funding sources included the National Science Foundation (NSF BCS-1643318) and a Smithsonian Institution Pre-Doctoral Research Fellowship.

Frontal sinus morphology as a forensic identification method: a comparison of intra-observer scores between scout radiographs and 3D skull images

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

Department of Anatomy, Des Moines University

In forensics, frontal sinus identification studies utilize antemortem and postmortem samples of the same imaging modality; in practice, this may not be available. The goal of this preliminary study is to assess whether basic frontal sinus features can be observed consistently across image modalities (CT vs radiograph).

This study incorporates scout radiographs and translucent digital crania (rendered from CT scans) from two sources: postmortem individuals (with soft-tissue) from the New Mexico Decedent Image Database (NMDID; n=30) and dried crania from the Smithsonian Institute (SI; n=20). First, sinus presence/absence (P/A) was established, with presence above the supraorbital line. If present, the following variables were recorded: P/A intersinus septum, P/A right/left sinus, and arcade number.

McNemar tests on P/A data and Wilcoxon tests on count data indicate no significant differences between image modalities for either sample (all p-values >0.05). However, the SI sample had higher consistency for the inter-sinus septum than NMDID (SI p=1.000; NMDID p=0.250). This is likely a result of the presence of soft tissue in the NMDID sample. Sinus P/A for both samples performed with high agreement (p=1.000).

Overall, results of this study indicate utilizing different image modalities should not alter assessments of basic frontal sinus morphology. However, presence of brain tissue may make some traits (e.g. intersinus septum) difficult to see. This study provides preliminary support for mixed-modality comparisons. Future research should be conducted on larger sample sizes and additional variables (e.g., intra-sinus septa) to assess how they are affected by changes in diverse image modalities.

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.

Comparative analysis of the Early Pleistocene *Homo* fossils from Gona, Ethiopia

KAREN L. BAAB[1], MICHAEL ROGERS[2], EMILIANO BRUNER[3] and SILESHI SEMAW[3,4]

[1]Department of Anatomy, Midwestern University, [2]Department of Anthropology, Southern Connecticut State University, [3]Centro Nacional de Investigación sobre la Evolución Humana (CENIEH), [4]Stone Age Institute and CRAFT Research Center

We present two virtual reconstructions of hominin fossils from Gona, Ethiopia that expand the early Pleistocene *Homo* record from east Africa. The initial description depicted a physical reconstruction of the relatively complete DAN5/P1 calvaria, dated to 1.5-1.6 Ma, and illustrated the left and right hemi-maxillae and some post-canine teeth. Here we present a virtual reconstruction of the nearly complete face for DAN5/P1 that includes the nasal aperture, orbits, supraorbital and infraorbital regions and anterior palate. The combined calvaria and face of DAN5/P1 represents one of the best-preserved early *Homo* crania in the East African fossil record, rivaling specimens such as KNM-ER 1813 and KNM-ER 3733 for completeness. The more fragmentary BSN12/P1 fossil, dated to 1.26 Ma, consists of four fragments that were pieced together to form a superior vault. We generated three slightly different reconstructions to account for uncertainty in the position of the lateral supraorbital fragment. These reconstructions enabled direct comparison of the superior vault shape in BSN12/P1 and DAN5/P1 within a broader Pleistocene *Homo* context.

Geometric morphometric analysis suggests that calvaria shape in the Gona fossils aligns with African *Homo erectus*, but is also similar to other small-brained and early *Homo* species. Similarly, the shape of the face (particularly the upper face) of DAN5/P1 differs from early *Homo* fossils in the same direction do as other *Homo erectus*. These results, when viewed alongside discrete features in DAN5/P1 and BSN12/P1 shared with *Homo erectus*, lead us to tentatively confirm the original attribution of the Gona fossils to *Homo erectus*.

Major funding provided by Leakey Foundation, EU Marie Curie, MINECO and the Ministry of Science, Innovation & Universities, Spain. Additional support came from NSF, Wenner-Gren Foundation and National Geographic Society.

Strengthening comparisons of ancient and modern human oral microbiomes: Accounting for variations in sample type

ALYSSA C. BADER[1,2], LAURA S. WEYRICH[3], JOYCELYNN MITCHELL[4], BARBARA PETZELT[4] and RIPAN S. MALHI[5,6]

[1]Anthropology, University of Colorado Boulder, [2]Culture and History, Sealaska Heritage Institute, [3]Anthropology, The Pennsylvania State University, [4]Treaty Office, Metlakatla First Nation, [5]Anthropology, University of Illinois at Urbana-Champaign, [6]Carl R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign

Human dental calculus has been proven to preserve ancient bacterial DNA for thousands of years, providing a window into the co-evolution of humans and their oral microbiomes. The ability to directly compare oral microbial profiles from ancient dental calculus with those of living populations is critical to understanding how the microbiome has changed in response to biocultural factors throughout human history. However, methodological challenges exist. For example, ancient oral microbiomes reconstructed from dental calculus may be compared to modern microbiomes extracted from more accessible sample types like saliva or gumline swabs. Because diverse microbial communities occupy the various environmental niches within the mouth, researchers may falsely attribute taxonomic variation stemming from biases in sample type to change over time or biocultural differences between ancient and living populations.

Here, we present the results of a two-tiered comparison of human oral microbial profiles, collected from ancestral and descendant Indigenous communities via a community-collaborative research partnership. First, we demonstrate the taxonomic composition of the oral microbiome sampled from the descendant community (gumline swabs, n=17) differs significantly from the microbiome of the ancestral community (dental calculus, n=45, PCoA p=0.001). Second, we compare genomic libraries constructed from two sample types, (1) gumline swab and (2) dental plaque, collected simultaneously from 11 participants. The taxonomic composition of these sample types differs significantly (PCoA, p=0.021), driven by Firmicutes, Proteobacteria, and Actinobacteria (LDA).

Understanding how the taxonomic composition of these sample types varies can guide direct comparisons of ancient and oral microbiomes, leading to more informative interpretations.

NSF BCS 1732263; NSF SMA 1911813

Osteoarthritis of thoracic vertebrae among modern humans with respect to sex and age K. Lauren Bagwell and Frank L'Engle Williams

K. LAUREN BAGWELL[1] and FRANK L'ENGLE WILLIAMS[2]

[1]Department of Anthropology, Louisiana State University, [2]Department of Anthropology, Georgie State University

Osteoarthritis is a common disorder associated with the aging process and will affect nearly all adults over the age of fifty. Extensive research has been conducted on the effect osteoarthritis has on the peripheral joints, while the spine has been less studied. This study examines osteoarthritis of thoracic vertebrae for differences with respect to age and between males and females. Thoracic vertebrae of 98 individuals (28 females and 27 males 50-55 years of age ["older"], and 23 females and 20 males 70-75 years of age ["elderly"]) of the William M. Bass collection from the University of Tennessee Knoxville were scored for severity and extent of lipping, porosity, and eburnation of the superior and inferior surfaces of thoracic bodies (i.e., 144 observations per individual) using Buikstra and Ubelaker's (1994) non-metric system. Mann-Whitney test was used for statistical analysis. Results show that in both females and males, elderly adults generally have significantly higher scores for lipping, porosity, and eburnation than older adults. The principal result for comparison between sexes is that males have significantly higher scores than females for lipping among both older and elderly adults. Results suggest that severity and extent of osteoarthritis increase with advancing age in both sexes among those 50 years of age and older, and the sex difference in osteoarthritis may imply differences in occupational labor, particularly among those 50-55 years of age.

New Upper Paleolithic human remains from Ksar Akil (Lebanon)

SHARA E. BAILEY[1,2], ALEJANDRA ORTIZ[1] and CHRISTIAN A. TRYON[3,4,5]

[1]Center for the Study of Human Origins, New York University, [2]New York Consortium in Evolutionary Primatology, [3]Department of Anthropology, University of Connecticut, [4]Human Origins Program, National Museum of Natural History, [5]Department of Anthropology, Harvard University

New archival research at the Peabody Museum of Archaeology and Ethnology uncovered photographs and radiographs of a previously undescribed individual from the Early Upper Paleolithic (early Ahmarian) levels of Ksar Akil (Lebanon), one of the few circum-Mediterranean archaeological sites with early fossils of *Homo sapiens*. Few human fossils exist from this area and time period, and the skull and associated post-crania of the juvenile known as 'Egbert' from Ksar Akil are now lost. We provide an analysis of photographs and first-generation casts of Egbert's dentition and the first description of the "new" individual, which was found adjacent to Egbert during the 1938 excavations and only noted briefly in initial publications. The "new" individual consists of dental/mandibular material only. Like Egbert, it is from level XVII or XVIII, conservatively dated from ~39-43 ka. Archival photographs suggest a juvenile of 7-9 years, similar to that estimated for Egbert. Unambiguously assigned to *H. sapiens*, the teeth of Egbert and the new individual are remarkably "modern". The upper and lower deciduous first molars are bicuspid; the upper deciduous second and permanent first molars possess reduced hypocones and square occlusal outlines. The lower first permanent molars are four-cusped, a rare trait even among recent *H. sapiens*. Its presence in two contemporaneous individuals at Ksar Akil suggest a possible locally distinctive population marker for groups in the Levant at this time, and thus one possible line of evidence useful for studies seeking to understand the demographic history of early *H. sapiens* groups in Eurasia and elsewhere

Archival research was undertaken during a workshop sponsored by the Radcliffe Institute For Advanced Study, Harvard University.

Confronting taphonomic challenges from excavation through curation of human remains

BRENDA J. BAKER

Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona State University

Recovery of human remains from archaeological contexts is affected by the pitfalls of preservation, and by excavation techniques and expertise of excavators. Little attention has been paid to the biocultural taphonomic factors affecting remains once removed from the ground and the challenges of working with legacy collections. The ways in which remains are transported from the field to lab and their long-term storage area, how they are stored, extent of collection organization, degree to which excavation records and human remains are documented, and how the collections were managed and maintained over time have substantial impact on our ability to assess and contextualize them. Using examples drawn from fieldwork and study of human remains from Cyprus, Egypt, Sudan, and the United States, these human-induced taphonomic factors are confronted. Inadequate expertise and poor planning for storage and ongoing care of biological remains often lead to missing or damaged elements, mixing, loss of provenience information, and limited accessibility of collections. Best practices are discussed, even where locally available materials are limited. Continuing to press project directors to ensure that experienced bioarchaeologists are included in fieldwork, while also urging funding agencies and antiquities organizations to require such expertise for all projects likely to encounter human remains during excavation is imperative. Furthermore, training in bioethics and in the curation and management of human remains collections must be incorporated into coursework at both undergraduate and graduate levels to counter negative effects of biocultural taphonomic factors and improve ethical treatment of human remains at all stages.

Tracing demographic histories through time using ancient DNA in Chilean Fuego-Patagonia

CHRISTINA M. BALENTINE[1,2], MARTA ALFONSO-DURRUTY[3], AUSTIN W. REYNOLDS[4], MIGUEL VILAR[5,6], FLAVIA MORELLO[7], MANUEL SAN ROMÁN[7], LAUREN C. SPRINGS[8] and DEBORAH A. BOLNICK[2,9]

[1]Department of Integrative Biology, University of Texas at Austin, [2]Department of Anthropology, University of Connecticut, [3]Department of Sociology, Anthropology, and Social Work, Kansas State University, [4]Department of Anthropology, Baylor University, [5]Department of Anthropology, University of Maryland, [6]National Geographic Society, [7]Instituto de la Patagonia, Universidad de Magallanes, [8]Department of Anthropology, University of Texas at Austin, [9]Institute for Systems Genomics, University of Connecticut

Historically, hunter-gatherers living east and west of the Andean foothills of southern South America (Fuego-Patagonia) practiced different subsistence strategies. To the east, the wide open and relatively dry *pampas* presented a climate ideal for Terrestrial hunter-gatherers who depended on terrestrial animals (e.g., *Lama guanicoe*). In contrast, Marine hunter-gatherers who lived on islands in the western archipelago, a colder and wetter environment, mainly subsisted on marine resources (e.g., seals and shellfish). Archaeological evidence dates Terrestrial hunter-gatherers' presence in Fuego-Patagonia to at least ~10,500 BP, whereas Marine hunter-gatherers' presence dates to ~6,500 BP and is associated with highly specialized tools that have only been observed in the archaeological record after this time. Genetic analyses of some ancient Fuegian-Patagonians have supported the hypothesis that Marine hunter-gatherers migrated into the region after Terrestrial hunter-gatherers, around 6,500 BP (7,500 calBP), while analyses of other individuals suggest that Marine hunter-gatherers descended from the earlier Terrestrial hunter-gatherer groups.

Here, we test these hypotheses by analyzing newly collected genome-wide data from n=46 ancient Chilean Fuegian-Patagonian individuals belonging to Marine, Terrestrial, and Mixed-economy archaeological sites dating to 6,895–304 calBP. We explored basic population structure among these hunter-gatherer groups using PCA and ADMIXTURE. We calculated π, pairwise-F_{ST}, and *f*-statistics, and developed demographic simulations to further examine genetic relationships among the groups. The results of this study shed light on local demographic patterns of ancient southern South American groups, which in turn provides more insight into broader population histories of South America.

This study was funded by FONDECYT (Chile), National Geographic Society, National Science Foundation, and Wenner-Gren Foundation. C. M. Balentine is supported by an NSF Graduate Research Fellowship.

The external and internal morphology of a hominin vertebra from 'Ubeidiya, Israel and its implication to early homo evolution

ALON BARASH[1], MIRIAM BELMAKER[2], OMRY BARZILAI[3] and ELLA BEEN[2,4,5]

[1]Azrieli Faculty of Medicine, Bar Ilan University, [2]Department of Anthropology, University of Tulsa, [3]Archaeological Research Department, Israel Antiquities Authority, [4]Department of Sports Therapy, Ono Academic College, [5]Department of Anatomy and Anthropology, Tel-Aviv University, Tel-Aviv, Israel

'Ubeidiya, Israel, is one of a few out-of-Africa sites with evidence of early Pleistocene Hominin remains. Here we discuss a juvenile vertebra (UB-10749) from stratum II-23 uncovered in 1966, recently rediscovered among the faunal remains.

UB-10749 is a complete vertebral body. We employed several qualitative and quantitative methods to determine its taxonomic affinity, serial allocation, age-at-death and predicated adult height and weight. Comparing UB-10749 to other large mammal present at 'Ubeidiya, revels it most closely resembles a hominoid. Further analysis places UB-10749 well within the genus *Homo and* identify it as pre-sacral 2 or 3 vertebra (L3-L4). While linear measurements estimate the age at death as 11-15 years, geometric morphometric shape analysis estimates the age as 6-10 years. The ossification level of UB-10749, visible under the microscope and a µCT scan shows that the vertebral arch did not ossify, and that there are no signs of endplate ossification, comparable to a 3–6 years old modern human. Thus, while size suggests an age equivalent to a modern human adolescent, the ossification pattern corresponds to a modern human child. Assuming UB-10749 was 6–10 years old at death, its adult size would have been about 180cm and 65Kg.

Based on these predications, UB-10749 does not resemble small-bodied hominins such as *H. habilis* or *H. georgicus* and instead exhibits biological affinities to east African large-bodied early Pleistocene hominins, such as penecontemporaneous KNM-WT 15000, suggesting more than one out-of-Africa dispersal event.

This research was funded by NSF proposal 1851613 to M.B.

Can language-training shape ape brains? Koko and Michael compared to other gorillas

NICOLE BARGER[1,2,3], PENNY PATTERSON[4], CHRISTA NUNES[4], KEVIN KEEL[5], CHERYL D. STIMPSON[6,7], AUSTIN K. BEHEL[1], JOSEPH M. ERWIN[1], PATRICK R. HOF[8] and CHET C. SHERWOOD[1,3]

[1]Anthropology, The George Washington University, [2]Anatomy, Howard University College of Medicine, [3]Center for the Advanced Study of Human Paleobiology, The George Washington University, [4]The Gorilla Foundation, [5]Pathology, Microbiology, & Immunology, University of California, Davis School of Veterinary Medicine, [6]Henry M Jackson Foundation for the Advancement of Military Medicine, [7]Uniformed Services University, [8]Nash Family Department of Neuroscience, Icahn School of Medicine at Mount Sinai

Nearly 50 years of research indicates that great apes can be taught to communicate using elements of human language. Yet, the effects of lifelong language enrichment on ape brains remain unexplored. We present the first analysis addressing whether brain structure varies among apes with and without language-training. Starting in infancy, the gorillas Koko and Michael were trained using a modification of American Sign Language, which they utilized for decades prior to postmortem brain MRI scanning. We observed no difference in overall brain size compared to sex-matched conspecifics (*Gorilla gorilla gorilla*; n = 14). However, running an exploratory one-sample t-test on a published brain structure volume dataset (Barks et al., 2015), we found Michael's frontal and temporal cortices are each nearly 20% larger and the remaining cortex 57% smaller compared to the other gorillas, when factoring out brain size. Given frontal and temporal lobes contain homologues of Broca's and Wernicke's language areas, this suggests language-training may affect relevant functional territories. To test this, we measured volumes from T2 MRIs using the Amira software suite for the frontal operculum (Broca's area homologue), the superior temporal gyrus and planum temporale (both containing Wernicke's area homologue), the precentral (primary motor), and transverse (primary auditory) gyri in Koko, Michael, and 14 conspecifics. Additionally, we are incorporating data from these individuals into a broader exploratory dataset comparison to include subcortical structures. Further analyses of these data will reveal whether, and to what extent, language homologues and motor control areas are modified in Koko's and Michael's brains.

This project is supported by the AABA's Cobb Professional Development Grant.

Indigeneity within datasets: DNA sequences journeys and genomic representations about the Karitiana (Yjxa) people

CARLOS ANDRÉS BARRAGÁN[1] and JAMES R. GRIESEMER[2]

[1]Department of Science & Technology Studies STS, University of California, Davis, [2]Department of Philosophy, University of California, Davis

In this talk we analyze the practices and processes through which blood samples from some members of the Karitiana people, an indigenous group in the Western Amazon (Rondônia, Brazil), were transformed into digital DNA sequences, datasets, and increasingly are reused for analytical and comparative purposes in multiple human evolutionary and biomedical studies. We track the sometimes disembodied but interconnected social lives of tissue, digital data, and Karitiana donors in order to pose important questions about contemporary bio-mapping technologies and indigeneity—understood here broadly as ways of being "indigenous" through time and space. We offer a model about how the materiality of human genomic data enables and silences certain forms of representation (scientific, cultural, and political), while compromising both the epistemic and bioethical robustness of human population genomics. We use our model to (*a*) make an argument about the need to produce similar efforts for each of the other 51 populations represented in the HGDP-CEPH Diversity Cell Line Panel, and (*b*) propose to explore a mode of governance of genomic datasets between indigenous communities (like the Karitiana) and life-scientists that we call *informed co-participation.* In this framework, past DNA donors and their descendants play an active role in sanctioning the re-use of stored digital bio-data for new purposes, and also in re-assessing provisional results and population metadata according to their self-fashioned notions of indigeneity. This is a much-needed strategy for testing the contemporary robustness of datasets and the cultural assumptions that make them more "real" and less epistemic objects.

This presentation summarizes content from an article draft based upon work supported by the U.S. National Science Foundation (NSF) under Grant No. SES-1849307-0.

Educational, but Ethical? The Tension within Historic Skeletal Collections

JENNIFER A. BARRON

Department of Anthropology, Texas State University

In an ongoing study of viewership of a historic skeletal collection housed at the Forensic Anthropology Center at Texas State, visitors are asked about their first impressions of a historic pathology collection on display. This study is the first step in a larger dissertation research project regarding the best practices for historic human skeletal collections that lack an ethical provenience. The early data suggests a strong tension between the fascinating and educational component of the collection and an aversion and discomfort to the display of the collection. This study is the first quantitative evaluation of its kind.

The Real Deal? Validation of a Dental Calculus Model Using FTIR

BJØRN PEARE BARTHOLDY[1], SHIRA GUR-ARIEH[2] and AMANDA G. HENRY[1]

[1]Department of Archaeological Sciences, Leiden University, [2]The Leon Recanati Institute for Maritime Studies, University of Haifa

Dental calculus is increasingly used by researchers looking at diet in past populations. These studies employ a range of methods including microscopy, and DNA and protein extraction. Despite the promise of these methods little attention has been given to the potential biases associated with the accumulation of dietary compounds into dental calculus during the lifetime of an individual. Our recently-developed oral biofilm model has the potential to elucidate these biases by growing *in vitro* dental calculus in a controlled environment. Here we report on one validation test of the system, which explored whether our model calculus mineralizes in a manner similar to actual calculus. FTIR was conducted on multiple samples across 25 days of model calculus growth. Results show an overall increase in the inorganic component relative to organic over the course of the experiment. This is especially evident in the hydroxyapatite peak at 1040 and doublet at 605 and 565 wavenumbers (cm^{-1}), and a reduction in intensities of the peaks at 1546 and 1654 wavenumbers (cm^{-1}). IR splitting factors (IRSF) ranged from 2.38–3.30, indicating a similar level of crystallinity to modern human-derived calculus samples (IRSF 3.46–3.76). The final model calculus consisted mainly of carbonated hydroxyapatite, the principal component of real calculus, although with a higher organic component than the comparative modern samples. This and prior validation of the model dental calculus suggests that it is a viable method to supplement the analysis of fossil dental calculus.

This research has received funding from the European Research Council under the European Union's Horizon 2020 research and innovation program, grant agreement number STG–677576 ("HARVEST").

Human origins in Southern Africa: Reflections on the influence of scientistic narratives on society

STELLA BASINYI and REBECCA R. ACKERMANN

Department of Archaeology, Human Evolution Research Institute (HERI), University of Cape Town

Archaeological narratives and the heritage program in southern Africa are developed from a foundation laid by a hegemonic group of white men who traversed the African soils studying "the African". They engaged in both physical and ethnographic research on indigenous people, for purposes of understanding the African past and their ancestors, sculpting scenarios of what past hunter gatherer societies might have been and looked like. Therefore, colonial ideologies remain engraved in human origins research and narratives of the African past. This study explores how indigenous societies have been affected and influenced by these constructed narratives by asking: Who owns, constructs, and controls the narratives of the African past, and who does not and why? Qualitative case study research design was employed, with data collected through open-ended, semi-structured, in-depth interviews. Thematic analysis was implemented to identify themes and patterns within the data. Results from the Makgadikgadi region in Botswana, an area central to a recent "Palaeo-wetland human origins" hypothesis promoted by international scientists (e.g. Chan et al 2019), indicate that hegemony persists. Paleoanthropological narratives have lasting impact on people outside the discipline, especially the descendants from populations who have been othered, managed and produced by science. Heritage spaces are symbolic platforms in which communities interact and connect with their pasts and origins yet are portrayed in ways that tend to fixate these communities in an abstract image of the African past. Scientists must stop narrating human origins stories that equate living Africans and so-called foraging societies with early humans.

This work was supported by the National Science Foundation of South Africa and the University of Cape Town #AdvancingWomxn 2021 grant

Ontogenetic variability in collagen fiber orientation at the midshaft femur of Virunga mountain gorillas (*Gorilla beringei beringei)*

KAILIE M. BATSCHE[1], SHANNON C. MCFARLIN[2], KEELY ARBENZ-SMITH[2], KIRSTEN GILARDI[3], THADÉE MUHIRE[4], TARA S. STOINSKI[4], ANTOINE MUDAKIKWA[5], RICHARD MUVUNYI[5], BIN HU[6] and TIMOTHY G. BROMAGE[6]

[1]Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine, [2]Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, [3]Gorilla Doctors, UC Davis Wildlife Health Center, [4]Karisoke Research Center, Dian Fossey Gorilla Fund International, [5]Department of Tourism and Conservation, Rwanda Development Board, [6]Departments of Biomaterials and Biomimetics, New York University College of Dentistry

The preferred collagen fiber orientation (CFO) within bone influences its resistance to loading in tension and compression. CFO studies thus have the potential to reveal form-function relationships between the adaptive response of bone and locomotor behavior. Within Virunga mountain gorillas, behavioral studies have indicated that juveniles are more arboreal than adults until 2-3 years of age. This study examines whether there is consistent age and spatial variability in CFO at the midshaft femur of Virunga gorillas that reflects their locomotor repertoire. As preferred CFO influences bone strength, we address whether the distribution of CFO will change with age in accordance with the observed shift in behavior.

100-micron sections of midshaft femora from gorillas (N=15) of known age were prepared for circularly polarized light (CPL) imaging, following established illumination standards. CPL images were converted to grayscale in Fiji® and binned using an 8-bit color look-up table. Percent area represented by LUT bins (%LUT) was analyzed to test for age differences among whole cross-sections, and across concentric rings, radial sectors, and the anterior-posterior cortex within cross-sections, using Kruskal-Wallis and Friedman's ANOVA.

While no significant age differences were found in CFO, there is a predominance of longitudinally-oriented collagen across all ages. Significant regional variation in CFO was found within cross-sections for two age groups analyzed separately ($p<0.0001$). Younger individuals (<3 years) show more variation in %LUT values, indicating a more variable pattern of CFO. This analysis provides preliminary evidence of regional differences of CFO which may reflect load distribution associated with locomotion.

Funding: NSF (BCS-0852866, BCS-0964944, BCS-1520221), National Geographic Society CRE (8486-08), The Leakey Foundation, Rwanda Development Board, DFGFI, GWU, 2010 Max Planck Research Award to TGB.

ABSTRACTS

Genetic Evidence for Heat Adaptation in Mexican Mayans

VINCENT M. BATTISTA[1,2], KIMBERLY T. ZHU[3], OBED GARCIA[4], KATARINA EVANS[5], MARÍA INCLÁN[6], MELISA KIYAMU[8], TOM BRUTSAERT[7], MARK SHRIVER[9], LAUREL PEARSON[9] and ABBY BIGHAM[3]

[1]Clinical and Translational Epidemiology Unit, Massachusetts General Hospital, [2]Biological Anthropology, University of Michigan, [3]Department of Anthropology, University of California - Los Angeles, [4]Department of Biomedical Data Science, Stanford University, [5]Department of Anthropology, Queens College (CUNY), [6]Department of Political Studies, Centro de Investigación y Docencia Económicas, [7]Department of Exercise Science, Syracuse University, [8]Departmento de Ciencias Biologicas y Fisiologicas, Universidad Peruana Cayetano Heredia, [9]Department of Anthropology, Pennsylvania State University

The abilities to regulate body temperature and hydration levels have long been a focus in the study of human evolution. There is ample evidence of evolutionary adaptation to sub-zero temperatures in circumpolar groups, but evidence for derived adaptive responses to heat stress are lacking. In environments such as tropical rainforests, high temperatures and humidity create heat indexes in excess of 55˚C (131˚F), which can lead to dehydration, heat stroke, and even death. To determine whether populations from hot, tropical regions of Abya Yala ("the Americas") show genomic evidence of natural selection in response to high ambient temperatures, selection scans were conducted using SNP data derived from Mexican Mayan study participants (N = 65) living in Chiapas, Mexico. Combining haplotype and frequency-based tests of selection, these data were used to test the hypothesis that Mexican Mayans have undergone recent evolutionary changes in genes that might offset the stress of high ambient temperature. Compared to related populations (Han Chinese, Peruvian Quechua), our analysis reveals strong selective sweeps centered on genes that are putatively adaptive to high temperature stress. These include genes in implicated in water/salt homeostasis pathways (*NEDD4L*), lipid metabolism (*PPARG*), heat shock protein binding (*HSPA12A*), vasodilation (*BDKRB2),* and thyroid function (DUOX family). Such results point towards a scenario under which a suite of adaptive changes -- involving cellular, vascular, and metabolic responses to heat -- are locally-adaptive to humans from lowland forests of Mesoamerica.

Don't bite off more than you can chew: A behavioral analysis of premolar use in capuchins during feeding

SARAH E. BAUMGARTEN[1], MYRA F. LAIRD[2], KRISTIN A. WRIGHT[3], BARTH W. WRIGHT[4], ROBERT S. SCOTT[5], CALLUM F. ROSS[6], ADAM VAN CASTEREN[7], MARIANA DUTRA FOGAÇA[8,9] and DAVID S. STRAIT[1]

[1]Department of Anthropology, Washington University in St. Louis, [2]Department of Integrative Anatomical Sciences, University of Southern California, [3]Department of Biomedical Science, University of Missouri, Kansas City, [4]Department of Anatomy, Kansas City University of Medicine and Biosciences, [5]Department of Anthropology, Rutgers University, [6]Department of Organismal Biology and Anatomy, University of Chicago, [7]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, [8]Neotropical Primates Research Group, São Paulo, Brazil, [9]University of Veterinary Medicine Vienna, Vienna, Austria

In vivo experiments suggest that variation in feeding behavior may have a greater effect on craniofacial loads, stresses and strains experienced by the skull than variation in food material properties (FMPs). While studies of FMPs are becoming increasingly common, less is known about precisely how primates process different types of food. Yet, it has been hypothesized that the ingestion of foods using the premolars may have been a selectively important behavior in early hominins. Here we quantify feeding behaviors involving the premolars in a population of wild tufted capuchins (*Sapajus* libidinosus) that consume mechanically challenging foods. Video data of a wild *S. libidinosus* were analyzed to 1) assesshow *S. libidinosus* use their premolars during feeding, 2) investigate whether different behaviors are associated with ingesting different foods, and 3) assess how premolar use varies between foods.

We analyzed a total of 239 instances of ingestive behaviors. Our results indicate that simple bites are the most common (74% of all bouts). Torquing food objects anteriorly and pulling them laterally were regularly observed (11 and 10%, respectively). Feeding on tough tubers elicited all the above modalities of premolar use. Torquing of food objects superiorly and inferiorly was used to forcefully tear tough seed exocarps. Twisting of bromeliad stems was also observed. ~20% of all premolar feeding bouts involved upper limb forces, suggesting those forces should be incorporated into biomechanical assessments of skull form and its relationship to feeding adaptations.

This research was supported by grants from the National Science Foundation's Biological Anthropology directorate (NSF-BCS- 1440541, NSF-BCS-1440542, NSF-BCS-1440545, NSF-BCS-1627206, NSF-BSC-2051326).

Transitioning from biosphere to geosphere: Assessing diagenesis of bone stable isotope values to understand taphonomic trajectories

MELANIE M. BEASLEY

Department of Anthropology, Purdue University

Stable isotope analyses of archaeological bone have become an increasingly common research avenue for interpreting human behavior in the past. The aim of this study was to explore a classic taphonomic problem: how does the geosphere alter biogenic isotope values when bone ceases to be regulated by physiological mechanisms in the biosphere? This study examines patterns of bone diagenesis through analysis by infrared spectrometry of bone bioapatite samples in relation to organic preservation quality indicators at multiple archaeological sites with varied taphonomic histories. To test the assumption that if the organic phase of bone is preserved, then the mineral bioapatite phase will also be unaffected by postmortem alteration, the crystallinity (IR-SF, a measure of crystallinity) and carbonate content (C/P) were calculated from FTIR spectra for 454 bone apatite samples with corresponding extracted collagen samples from the same modern, historic, and prehistoric humans. In the absence of physiological chemistry regulating the reprecipitation and void filling by exogenous ions, geochemistry processes regulate the formation of apatite crystals in the burial environment (geosphere). The prehistoric bone samples in this study exhibit extreme regional and within-site variation in diagenesis trajectories based on the variation in IR-SF and C/P values observed relative to collagen quality indicators. The lack of predictive patterning between bone bioapatite and collagen diagenesis suggest that the burial context and site formation are critical to understanding the biphasic taphonomic trajectories in bone. In bone, the preservation of the organic phase is not indicative of the preservation of the inorganic phase.

A new small hominoid from the early late Miocene of Bavaria (Germany.)

DAVID R. BEGUN[1], ANDREW C. HOLMES[1], ADRIAN TRÖSCHER[2], GABRIEL FERREIRA[2], JÉRÔME PRIETO[3], THOMAS LECHNER[2,4] and MADELAINE BÖHME[2,4]

[1]Department of Anthropology, University of Toronto, [2]Senckenberg Centre for Human Evolution and Palaeoenvironment, Tübingen, [3]Department für Geo- und Umweltwissenschaften, Ludwig-Maximilians-Universität München, [4]Department of Geosciences, Eberhard-Karls-University of Tübingen

Hammerschmiede is best known as the *Danuvius* hominine locality. Its exceptionally rich vertebrate fauna contains nearly 140 species from three different levels. All *Danuvius* fossils come from the 11.62 Ma old HAM 5 level, deposited rapidly in a rivulet with minimum transport. Three teeth from HAM 5 are consistent in size with larger pliopithecoids but differ morphologically from any pliopithecoid and from *Danuvius*. The unworn M^2 crown is unlike pliopithecoids and *Pliobates*, having a reduced, smooth cingulum and buccal style and being narrower relative to length.

Crista are less strongly developed, cusps less compressed and basins broader and shallower. However, the cingulum and style distinguish it from *Danuvius* and all European hominines. The I^2, which is missing its apex, is unlike pliopithecoids in being thickened at the cervix with a taller shoulder and a more convex lingual surface. The P^4 fragment lacks the typical pliopithecoid cristodonty and deep basins. These specimens do not match *Danuvius* or any pliopithecoid in morphology. They most likely represent a small hitherto unknown European late Miocene ape. If so, this taxon increases the diversity of late Miocene catarrhines in Europe, more in line with species diversity in the early and middle Miocene of Africa. More fossils are needed to resolve this question. Given the small sample we refrain from naming a new taxon and instead assign this sample to Hominoidea indet.

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).

Looking at violence: Assessing the ability of imaging technology to interpret violence from trauma caused by projectile points along skeletal remains

ALEXANDER F. BELANGER

Department of Geography and Anthropology, Louisiana state University

Analyzing violence within ancient populations is crucial to understanding the relationships present at a given location and time. Skeletal remains and trauma are valuable tools in analyzing this possible violence. Not only is the type of trauma and its location important, but the type of weapon that caused the trauma is equally essential. Current methods of trauma analysis range from traditional methods such as physical observations to more technological approaches using complex imaging technology. This research tests the ability of radiological and 3D imaging technology to capture the nature of projectile point wounds present on skeletal remains using data from previously published papers totaling twelve cases with varying types of imaging methods. Publications were selected based on the shared research objectives of analyzing the nature of the trauma resulting from interpersonal projectile point violence. These publications use an array of imaging technology to analyze prehistorical and historical human populations in tandem with related literature to assess the possible interpersonal violence present in the selected populations. The results suggest that radiological and three-dimensional imaging technology are helpful tools when researching violence within populations while providing valuable digital data sets to researchers. These data sets increase access to the skeletal assemblages through digital means while retrieving more data from the skeletal material. Additionally, the enhanced data from skeletal collections afford researchers more confidence in the conclusions being made. The ability to interpret interpersonal violence is significantly heightened with the ability to use radiological and three-dimensional imaging technology.

The hair microbiome of wild lemurs: functional insights from shotgun metagenomics

RACHEL B. BELL[1], RICHARD R. LAWLER[2], JOELISOA RATSIRARSON[3], JEANNIN RANAIVONASY[3], REBECCA LEDUC[4] and JASON M. KAMILAR[1,5]

[1]Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst, [2]Department of Sociology and Anthropology, James Madison University, [3]Agroecology, Biodiversity and Climate Change Department, ESSA, University of Antananarivo, [4]Department of Biology, University of Massachusetts Amherst, [5]Department of Anthropology, University of Massachusetts Amherst

Nonhuman primates are covered in hair that provides an environment for a rich array of microbiota, yet the hair microbiome is critically understudied. Furthermore, the limited knowledge we currently have on the hair microbiome comes from targeted gene sequencing (e.g. 16S sequencing), which provides little direct information on the functional potential of the microbiome and does not capture the full taxonomic diversity of microbial communities. Therefore, in this study we seek to characterize the functional profile of the hair microbiome in wild lemurs using shotgun metagenomic sequencing. Given initial results from 16S rRNA sequencing showing differences in microbial diversity across body regions, we also compare microbial diversity and functional genes between different regions of hair. Microbiome samples were collected from the head and lower back hair of wild Verreaux's sifaka (*Propithecus verreauxi*) at Bezà Mahafaly Special Reserve in Southwest Madagascar. Samples were processed through 16S rRNA and shotgun metagenomics bioinformatics pipelines. We find that the sifaka hair microbiome exhibits both unique and shared functional characteristics when compared to shotgun metagenomic studies of other mammal microbiomes. The results of our study highlight the value of hair microbiome research on wild nonhuman primates. Conducting research in wild primates allows us a relatively unperturbed view of microbial diversity and functions existing in the environmental setting in which they have developed. Furthermore, the hair microbiome may modulate the cutaneous immune system. Characterizing the functional profile of the hair microbiome may therefore provide valuable insights into the relationship between the hair microbiome and host health.

This research is funded by the University of Massachusetts Amherst Predissertation Grant, Dissertation Fieldwork Grant, and Natural History Collections Summer Scholarship; the Leakey Foundation, and the NSF Graduate Research Fellowship Program.

Intentional burial or natural deposition? A taphonomic approach to the interpretation of isolated human skulls

SILVIA M. BELLO[1], LUCILE CRÉTÉ[1] and SIMON A. PARFITT[1,2]

[1]Dep Earth Sciences, The Natural History Museum, London, UK, [2]Institute of Archaeology, University College London, London, UK

Humans have the unique characteristic among organisms of deliberately and culturally disposing of their dead, a behaviour expressed in a variety of ritualistic and funerary manipulations. The human skull is probably the anatomical element more commonly manipulated after the death of the individual in ways that include peri- and post-mortem decapitation, skull caching, secondary deposition, decoration of skulls and modifications of skulls to make masks and skull cups. It is also not unusual, however, to find isolated skulls for which it is difficult to unequivocally determine the nature of the deposition, either intentional or natural. We collated descriptions for 90 isolated skulls from sites in Africa, Europe, Near East and Asia, from approximately 2 million to 20,000 years BP. Among these, 11 skulls are from deposits with evidence of human occupation, suggesting a possible intentional deposition. We also collated information from archaeological and ethnographic sources relating to over 40 human skulls intentionally modified into skull-cups. We evaluated and compared the state of preservation (completeness and breakage patterns) of the isolated skulls found in natural deposits, with those found in cultural deposits and with skulls modified into skull-cups. Results suggest that the pattern of preservation is remarkably similar among these three categories. We therefore conclude that the state of preservation alone cannot be used to determine intentionality, and only the archaeological context and the presence of humanly induced modifications can help to determine the deliberate deposition of isolated skulls.

We are indebted to the Calleva Foundation for supporting our work.

Prey size economics, ethnography, and the human trophic level

MIKI BEN-DOR

Department of Archaeology, Tel Aviv University

Large prey should have been preferred targets of hunters during the Pleistocene because of their higher fat content, energetic return, biomass density, and the lack of need for projectile technology in their acquisition. Biases in the ethnographic record and interpretation of the zooarchaeological record obscure large prey's criticality to humans.

Realizing the full value of large prey to Paleolithic humans may help discover the significance of large prey decline throughout the Pleistocene as a driver of key Paleolithic phenomena as adaptations to cope energetically with the prey size decline. However, recent papers have argued that: <ol> There was no prey size decline in Africa between the Acheulian and the MSA   Large animals didn't bring a higher energetic return   Humans could not acquire very large fauna "at-will".   Using regionally specific zooarchaeological data from Africa and the Levant, I will show that indeed there was a pronounced decline in prey size, not only during the Late Quaternary Megafauna Extinction but much earlier between the Acheulian and the MSA/MP in Africa and the Levant.

An actualistic prey acquisition case study from the Hadza will show that large animals are their preferred prey and those very large animals are severely underrepresented in Archaeological sites, and simple technologies are required for their acquisition and dispatch. I will also comment on the problematic use of ethnographic hunting returns, achieved with guns, dogs, and bows and arrows to predict Pleistocene energetic returns.

The Holocene population history of the Florida region: an assessment of dental nonmetric traits

DANIEL BENITEZ[1], ALISON A. ELGART[2] and MIGUEL E. DELGADO[3]

[1]Department of Anthropology, University of Kentucky, [2]Department of Social Sciences, Florida Gulf Coast University, [3]Division Antropologia, Facultad de Ciencias Naturales y Museo, Universidad Nacional de La Plata

The Holocene population history of pre-Hispanic populations in Florida has remained elusive because previous bioarchaeological research has focused on specific periods and regions, skeletal collections are poorly preserved, and the use of alternative lines of evidence such as aDNA is not possible. Considering that teeth are the best-preserved remains within the archaeological record and that they are reliable proxies to trace human evolutionary history, the aim of the present study is to investigate the diachronic pattern of population affinities of the Florida region by using dental nonmetric traits as well as model-bound and model-free approaches. In this study, we included 23 skeletal samples ranging from the Paleoindian to European Contact periods in which 28 dental traits were scored following the ASUDAS method. We used the R-matrix method, biodistances (*D2* and MMD) and correlation matrix analyses to evaluate distinct population history scenarios, the levels of biological diversity by region and period, and the role of evolutionary forces shaping the patterns of dental diversity. Our results show a complex regional population history, varying levels of biological diversity (F_{ST} total 0.162; F_{ST} by period 0.120 and F_{ST} by region 0.095) and the differential role of gene drift and gene flow. The pattern of biodistances suggests spatial, temporal, and cultural differentiation across the Holocene. These results are integrated into a robust population history model that can be tested through the use of other lines of evidence. Importantly, the present research sheds light on the biocultural relationships established among Florida pre-Hispanic populations over millennia.

Genetic Ancestry Testing and the Politics of Blackness in Afro-Caribbean Communities

JADA BENN TORRES

Anthropology, Vanderbilt University, Vanderbilt Genetics Institute, Vanderbilt University

A series of studies published in the early 2000's highlighted the genetic ancestry of both ancient and contemporary peoples from Puerto Rico. These studies revealed substantial Indigenous ancestry among Puerto Ricans and elicited discussions about the continuity of Indigenous peoples on the island. While activists, the media, and other stakeholders celebrated these findings, there were others that noted anti-Black sentiment interwoven into discourses regarding the Indigenous legacies of Puerto Ricans. Accordingly, this type of genetic work was understood by some to be another instance where African-derived contributions to Puerto Rico were downplayed or otherwise marginalized. It was within this context that my collaborators and I initiated a community-engaged study in conjunction with the Corporación Piñones se Integra (COPI), to consider the genetic and cultural identities of self-described Afro-Puerto Ricans.

While highlighting some of the more recent findings of this ancestry work, I specifically comment on how these results have been received by community members. Drawing on a recent weekend long event in which COPI celebrated its nearly 20-year presence in the community with a delegation of Garifuna peoples from New York, I reflect on how discussions about genetic ancestry testing and anthropology more broadly, create opportunities to reimagine the connections between Caribbean communities and to think more critically about how genetic perspectives may work to shape notions of Blackness across the African diaspora. I conclude with ideas about how merging community engagement with genomic studies can be a dynamic factor in shaping scientific approaches to studies of minoritized populations.

The presented research was generously supported with funding from the Office for Equity, Diversity and Inclusion and the College of Arts and Science at Vanderbilt University.

When does a body become a thing? The transformation from person to object in the treatment of human remains

CAROLINE BENNETT

Department of Anthropology, Te Herenga Waka Victoria University of Wellington

This abstract is part of the symposium *Ethics in the Curation and Use of Human Skeletal Remains*, co-organized by: Carlina de la Cova, Siân Halcrow, and Gwen Robbins Schug

The collection and display of human remains is common across the globe: in museums, university collections, memorials, and catacombs. As objects they hold symbolic power as well as practical use. For ancient remains, their place as archaeological artefacts rather than forensic remains places them in a category of material object; a tool for living humans to understand their past, to be examined and stored alongside other recovered objects. However, these were once living humans, embedded in social networks of kin and community with associated systems of knowledge and understanding. Drawing on anthropological research on the treatment of human remains after genocide, conflict, and disaster, this presentation will consider, when does a body become a thing? At what point does it change from being a human with related needs for care and consideration, to an object open to curation and display? What is the politics that influence this transformation, and how does it fluctuate over time?

The potential Impact of a sacralized fifth lumbar vertebra on auricular surface aging

KRISTA E. BENNETT

Geography and Anthropology, Louisiana State University

Sacralization of the fifth lumbar vertebra changes the biomechanics of load transmission through the pelvic region and can result in morphological changes of the auricular surfaces of the sacroiliac joint (Singh et al., 2014; Tague, 2009). This study investigates if differences in age progression of the auricular surface of the ilium can be identified in individuals with sacralization of the fifth lumbar vertebra. A total of 156 paired sacra and ilia aged 29 to 96 years, from the William Bass Donated Skeletal Collection were randomly selected for examination. Os coxae were scored using the Buckberry and Chamberlain (2002)

age estimation method of the auricular surface of the ilium. Sacra were evaluated for presence and degree of sacralization of the fifth lumbar vertebra. For this study, full sacralization was scored when both transverse processes were fused with the alae of the sacrum, thus altering the morphology of the auricular surface. Results found 21 (13.46%) individuals showed partial or full sacralization of the fifth lumbar vertebrae, with 12 (57%) of those individuals showing full sacralization. The age-at-death of those individuals with full sacralization fell within the assigned age range estimates; however, the Buckberry and Chamberlain age range intervals are broad, and many individuals' actual ages fell at the older end of the age range intervals. These results suggest the Buckberry and Chamberlain aging method is reliable with full sacralization, however, it should be used with caution as changes in biomechanical loading can increase stress and degeneration to the joint surfaces.

Cooperation in the face of conflict: the effect of between-group competition on cooperation and oxytocin in capuchin monkeys

MARCELA E. BENÍTEZ[1,2], STELLA R. MAYERHOFF[2,3] and SARAH F. BROSNAN[2,3,4]

[1]Department of Anthropology, Emory, [2]Language Research Center, Georgia State University, [3]Department of Psychology, Georgia State University, [4]Neuroscience Institute, Georgia State University

A common pattern in human social behavior is that we are highly cooperative with group members when competing with an outgroup, even at a cost to ourselves. This phenomenon, known as parochial altruism, may have been an important factor in the evolution of cooperation, yet we know little about how conflict influences cooperative decision-making in nonhuman primates. If parochial altruism is an important factor in the evolution of cooperation, other cooperative primates should, like humans, increase cooperation in the face of between-group conflict. Here, we examined whether socially-housed capuchin monkeys (*Sapajus apella*) cooperated more often when competing against another social group and the underlying hormonal mechanism that may promote increased cooperation during conflict. Using a tug-of-war based bar pull apparatus, we found that capuchins were more likely to cooperate for inequitable, but not equitable food rewards in the presence of another group. Furthermore, a preliminary analysis (n=23 samples) suggests that urinary oxytocin was higher after competing with another group (M=124.28 pg/mg) compared to the no competition control (M=21.95 pg/mg) but only, again, when outcomes were inequitable. These results mirror studies in humans, supporting the hypothesis that both parochial altruism and the biological underpinnings of these behaviors are evolutionarily conserved in the primate taxa.

This research was funded by the GSU Brains & Behavior Seed Grant and the National Science Foundation (SBE 1919305)

Ethical challenges of institutional bioarchaeology: A case study of a 19th century asylum context

JACQUELINE M. BERGER, PH.D., RPA

Center for Health Equity, Education, and Research, Boston Medical Center

Current scholarship regarding institutional contexts is rapidly expanding, and often seeks to address the treatment of previously disadvantaged and/or marginalized groups, and their place in the bioarchaeological record. In concert with these advances, bioarchaeologists have progressively begun to acknowledge and grapple with the ethical dilemmas inherent to the discipline, namely the treatment and usage of human remains for scientific study, the construction of memory and historical narratives, and the responsibility of the researcher to living stakeholders. These issues are further heightened in institutional bioarchaeology, demanding that scholars interrogate how to responsibly and ethically conduct research on the remains of marginalized individuals who have lost their agency postmortem. The present study explores these challenges through the example of the Siena Craniological Collection (SCC) from Siena, Italy, which contains patients of the *L'Ospedale Psichiatrico San Niccolò* (San Niccolò Psychiatric Hospital - SNPH). Demographic and osteological analyses of the SCC, with particular focus on a sample of patients from the SNPH (*n* = 130), were conducted using both associated archival material and skeletal collection remains. Results of these analyses reveal that SNPH patients were primarily lower socioeconomic status individuals who were institutionalized, and subsequently anatomized, without their consent. With these results in mind, the present study interrogates current ethical approaches in bioarchaeology, explores the ethical challenges unique to institutional contexts through a review of the SNPH sample, and offers suggestions for those interested in conducting ethical investigations of institutional contexts, especially within the novel framework of the bioarchaeology of mental illness.

Support for research and analysis provided by the University of South Florida Department of Anthropology Dissertation Completion Fellowship.

Differential effects of climate on the ranges of five primate species along an elevational gradient

ANDREW B. BERNARD, ZONGQI YU and ANDREW J. MARSHALL

Department of Anthropology, University of Michigan

Climate is a major driver of environmental change, and field studies of extant primates are crucial to understanding climate's role in the evolution of primate adaptations. We know little, however, about how and why changing climate affects species, and whether these effects are consistent among species. One leading hypothesis predicts that populations will shift their ranges to track changes in their habitats, a pattern observed for many non-Primate taxa. We tested this hypothesis for five sympatric primate species by modeling 14 years of bimonthly censuses across an 18-1100 m.a.s.l. elevational gradient in Gunung Palung National Park (GPNP), Indonesian Borneo. We built generalized linear models to model the elevation of primate observations (*Pongo pygmaeus* [n=869], *Hylobates albibarbis* [n=3739], *Presbytis rubicunda* [n=4595], *Macaca fascicularis* [n=2231], and *Macaca nemestrina* [n=259]) as a function of time, temperature, and rainfall. Despite site-wide increases in both maximum monthly temperature (+0.26C) and average monthly precipitation (+16.4mm) from 2007 to 2020, we found no meaningful elevational shift in the distributions of any species over time. There were, however, differences among species in whether and how climate related to their distributions: for example, while elevations of gibbons, red leaf monkeys, and orangutans were not predicted by temperature or precipitation, minimum monthly temperature was a reliable predictor of the elevation of pig-tailed and long-tailed macaques. Changes in climate at GPNP may not yet be substantial enough to induce populations to shift, but our results have critical implications for understanding how abiotic factors differentially impact the distributions of sympatric species.

Funding for A.B. provided by the Leakey Foundation and Rackham Graduate School, University of Michigan.

Prehistoric socio-territoriality in Malawi: multi-isotopic perspectives on the behavioral ecology of Late Pleistocene foragers

ALEX BERTACCHI[1], STANLEY H. AMBROSE[2], JULIA I. GIBLIN[3], ANDREW M. ZIPKIN[4], JESSICA C. THOMPSON[1] and POTIPHAR KALIBA[5]

[1]Department of Anthropology, Yale University, [2]Department of Anthropology, University of Illinois at Urbana-Champaign, [3]Department of Sociology, Criminal Justice, and Anthropology, Quinnipiac University, [4]School of Human Evolution and Social Change, Arizona State University, [5]Ministry of Tourism, Culture and Wildlife, Republic of Malawi

The exploitation of dispersed and gregarious ungulates is believed to have favored high residential mobility and non-territorial land use systems in human foraging groups. Recent aDNA studies suggest that in northern Malawi these open systems gave way to more regionalized behavior between 50,000-17,000 years ago. Behavioral ecological models of human territoriality predict that such a shift would involve a subsistence focus on dense and spatiotemporally predictable resources. In northern Malawi these conditions may be met through specialized hunting of grazer herds during dry-season aggregations in waterlogged grasslands (dambos). We conducted multi-isotopic analyses of herbivore tooth enamel ($\delta^{13}C$ and $\delta^{18}O$: n = 86; $^{87}Sr/^{86}Sr$: n = 51) from archaeological sites in northern Malawi spanning the last 30,000 years to characterize vegetation, rain seasonality and the mobility patterns of prey species. Our results indicate that the environment became more humid between the Terminal Pleistocene and the Early Holocene. Zebras included some browse in their diets during the dry season and sourced their water from ^{18}O-depleted (less evaporated) sources compared to all other herbivores. This suggests competition and niche partitioning between equid and bovid grazers. Intra-tooth sequential samples suggest that most of the zebras were migratory, but with a possible shift to more local territories after the Last Glacial Maximum. A single zebra from the Terminal Pleistocene appears to be non-migratory. Further analyses will clarify whether a transition from opportunistic/dispersed to specialized/localized hunting is recorded in the fossil record.

This research was funded by the Yale Institute of Biospheric Studies.

Accounting for evolutionary relatedness in biomechanical data

MICHAEL A. BERTHAUME[1] and SARAH ELTON[2]

[1]Division of Mechanical Engineering and Design, London South Bank University, [2]Department of Anthropology, Durham University

Biomechanical data within a comparative framework is analysed either independently of phylogeny or in a phylogenetic framework. Analysing data independently of phylogeny treats species as the units of analysis and assumes biomechanical data is statistically independent of the species themselves. Analysing data in a phylogenetic framework assumes the variation in biomechanical data under neutral selection is correlated with the variation the underlying molecular / genetic data captured in the tree. We test the latter assumption and ask if existing phylogenetic methods can accurately detect phylogenetic signal in biomechanical data. Nine muscle force and lever arm characters were varied with a constant mutation rate and used to calculate bite force/mechanical advantage for each generation. A pure-birth model with 100 random uniformly distributed speciation events created 101 extant species after 3,333 generations. Two sets of evolutionary simulations (100 runs each) were run to create hypothetical clades, where characters were varied under unconstrained (Brownian motion) or constrained (log-normal) neutral selection, the latter ensuring continuous parameters stayed positive. In both sets of simulations, phylogenetically independent contrasts (PICs) showed character states were consistently uncorrelated with biomechanical data. In the constrained simulations, Pagel's lambda and Blomberg's K (phytools, R) correctly predicted neutral selection in 97/100 runs. In the constrained simulations, lambda and K implied non-neutral evolution occurred in 34/100 runs. Our results imply variation in biomechanical data is poorly correlated to the underlying genetic / molecular tree data, and existing phylogenetic methods only consistently yield correct results when physiological, anatomical, and mechanical constraints are ignored.

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 slippery relationship between eccrine gland density, sweat production and heat dissipation in humans

ANDREW W. BEST[1], DANIEL E. LIEBERMAN[2] and JASON M. KAMILAR[3,4]

[1]Department of Biology, Massachusetts College of Liberal Arts, [2]Department of Human Evolutionary Biology, Harvard University, [3]Department of Anthropology, University of Massachusetts Amherst, [4]Graduate Program in Organismal and Evolutionary Biology, University of Massachusetts Amherst

Humans have a highly derived eccrine sweat gland density, ten times that of other apes. This unique trait is thought to be linked with increased physical activity and ranging during hominin evolution. However, the relationship between intraspecific variation in eccrine density and ability to dissipate heat is unexplored. Here we present data on functional eccrine gland density (FED) collected using pilocarpine iontophoresis to induce sweating, vinyl polysiloxane impression material to record sweat droplets, computer-assisted sweat impression analysis, and gauze to collect sweat. We found no correlation between FED and sweat production in a sample of 72 volunteers. Sweat production and FED were also unrelated in a sample of 8 heat-acclimatized endurance athletes cycling in a warm metabolic chamber. Indirect calorimetry revealed that heat dissipation quotient was not associated with FED even after accounting for effects of body fat, age, body surface area/body mass, and heat production per kg. Taken together these results suggest that, within the range of variation observed in our sample, neither sweat production nor evaporative cooling capacity are the product of functional eccrine density. Thus, gland-level attributes such as sweat production and sodium reabsorption per gland likely have a much larger influence on whole-body sweat production, evaporative cooling and water loss. In this view, low FED within the range of contemporary variation may not incur heat dissipation nor water loss penalties as adaptation or plasticity in gland-level characteristics are sufficient to match evaporative cooling capacity to demand.

Funding for this research was provided by The Leakey Foundation, The Wenner-Gren Foundation, and the University of Massachusetts Amherst Graduate School.

Sex estimation of os coxae using DSP2 and MorphoPASSE software: A validation study of an American sample

ELIZABETH A. BEWS

Department of Anthropology, University of South Florida

The os coxae is the most sexually dimorphic skeletal element in the body. For that reason, the pelvis is the most reliable indicator of an individual's biological sex in bioanthropological contexts. Recently, two new methods for sex estimation have been developed: Diagnose Sexuelle Probabiliste Version 2.0 (DSP2) and MorphoPASSE. DSP2 estimates sex based on ten pelvic measurements, while MorphoPASSE relies on the scoring of eight morphological traits. The reliability of both methods has been independently tested, however, there has been no study comparing the accuracy of the two methods for sex estimation. The goal of this study is to compare the accuracy of the DSP2 and MorphoPASSE systems in the identification of os coxae from 147 documented skeletal individuals (122 male and 25 female) drawn from the University of Iowa Stanford Collection (UI-SC). DSP2 had an accuracy of 96% and MorphoPASSE had an accuracy of 93%, with no statistically significant difference in the accuracy of the two methods (p=0.818). In the study sample, DSP2 and MorphoPASSE had the same error rate for males, while MorphoPASSE had a higher error rate for females than DSP2. Interestingly, there was no overlap in the individuals for which MorphoPASSE and DSP2 estimated sex incorrectly. Results suggest that both MorphoPASSE and DSP2 can be used separately, or in combination during the process of sex estimation by biological anthropologists

The relationship between zygomatic arch morphology and diet in closely-related primates

MAYA BHARATIYA[1,2], HALLIE M. EDMONDS[3,4] and GABRIELLE A. RUSSO[1]

[1]Department of Anthropology, Stony Brook University, [2]Griffith Centre for Social and Cultural Research, Griffith University, [3]Department of

Biological Sciences, Northern Arizona University, [4]Center for Evolution and Medicine, Arizona State University

Comparative studies have shown that primates known to consume biomechanically tough and/or hard foods have larger temporal fossae than primates that consume biomechanically softer foods. The former group also possesses relatively more robust zygomatic arches and exhibits increased cortical bone relative to total subperiosteal bone in the anterior zygomatic root to facilitate efficient mastication. However, less is known about potential phylogenetic constraints on the internal and external morphology of the zygomatic arch. This study builds on previous work by evaluating if closely-related primates that differ in diet toughness and hardness diverge in functionally informative aspects of zygomatic arch morphology. Species from three genera were analyzed: 1) *Gorilla gorilla* and *Gorilla beringei*, 2) *Pongo pygmaeus* and *Pongo abelii*, and 3) *Macaca* spp. (seed eating macaques, non-seed eating macaques, and bamboo eating macaques). External and internal zygomatic arch morphology was quantified from linear measurements derived from 3D landmarks and cross-sectional data obtained from CT scans. Metrics did not statistically differ between species of *Gorilla* or *Pongo*, which might be explained by dietary variation among populations within each of these species. Seed eating macaques possess relatively more robust zygomatic arches with larger temporal fossae than other macaque groups. Relative cortical area distributions were highest in macaques that consume bamboo, and lowest in seed eating macaques, suggesting that loading regimes vary within biomechanically challenging diets. These results support the utility of external zygomatic arch morphology as an indicator of diet type that may be informative for interpreting the primate fossil record.

Mechanobiology of sesamoid formation as a model for endochondral ossification in the skull

HENNA D. BHRAMDAT and DAVID J. DAEGLING

Anthropology, University of Florida

Sesamoid bones ossify endochondrally. While endochondral ossification correlates with somatic growth and maturation, the role of mechanical stimuli on bone formation remains unresolved. This study employs a sesamoid model of endochondral ossification to investigate the potential role of mechanobiological signals in the appearance and growth of ossification centers, with a view toward developing theoretical applications to the primate basicranium.

We constructed a finite element model in R based on the structure of a pisiform within the flexor carpi ulnaris tendon (FCU-t). The sesamoid was assigned material properties of hyaline cartilage initially, and the FCU-t properties were based on in situ observations from the literature. A macaque growth model was used to simulate increased load over time as a function of body mass (German et al. 1994, AJPA, 93:373-380). A load case of uniaxial tension from the FCU-t was applied over 150 iterations, representing sequential growth intervals. The mechanical signal was defined as shear strain, with those elements of the sesamoid anlage exposed to yield strain being assigned higher values of shear modulus prior to the subsequent iteration. Spatial and temporal pattern of ossification was inferred from the resulting stiffness distributions.

The model produces a sesamoid with heterogeneous stiffness, with alternating periods of material stasis and active ossification. Assuming the metabolic processes underlying endochondral ossification are similar throughout the body, and accounting for presumed differences in load cases, shear stresses provide a potent – yet inconstant – stimulus in the etiology of bone formation in the basicranium.

An Early Life Course Analysis of Ancient Maya Individuals Using Dietary Stable Isotopes

JACK A. BIGGS

Department of Anthropology, Michigan State University

Stable carbon and nitrogen isotope analyses permit an important perspective for dietary studies in bioarchaeology. However, samples often only encompass a specific period in an individual's life, giving an incomplete view of their early years. This study applied a serial and multi-tooth sampling method of dentine from cave, rockshelter, and residential burials of the ancient Maya from central Belize. Each site type represents a different aspect of the ancient Maya mortuary program and social structure. Caves were spiritually charged spaces with restricted access (for both ritual and mortuary activities), rockshelters were commonly used as communal and unrestricted burial spaces by rural agricultural groups, and residential burials represent a semi-restricted and urbanized burial space where inclusion was likely based on group or familial relation. A combination of bioarchaeological, ethnohistoric, and ethnographic resources were used to create a Maya social age classification system. Informed by these chronological and social age boundaries, tooth dentine was sectioned using a Buehler IsoMet Precision Saw, such that each dentine section encompassed the dietary history of a particular social age (e.g. early childhood or adolescence). Each individual is represented by nine dentine sections from three teeth (encompassing infancy through early adulthood and allowing for overlap between tooth classes). The combination of isotopic ratios across all dentine sections per individual reveals a more complex and nuanced dietary history per individual that has not been seen or investigated in the Maya region.

The metabolic demands of the human brain: and how we got it wrong

BENJAMIN T. BIKMAN

Department of Cell Biology and Physiology, Brigham Young University

The brain is among the highest metabolic rate organs in the body. This extreme metabolic demand is largely met by only two metabolic fuels—glucose and ketones. While brain ketone use is largely unregulated and unrestricted, glucose use by the brain is partly regulated by the hormone insulin. By containing insulin-dependent glucose transporters, compromised brain insulin signaling leads to a possible "energy deficit" wherein the brain is unable to obtain sufficient energy to meet its energetic needs. This phenomenon is reflective of an increasingly prevalent condition known as insulin resistance. To make matters worse, as the body and brain are becoming insulin resistant, the elevated insulin levels that accompany this condition inhibit hepatic ketogenesis, depriving the brain of ketones. Ultimately, it is in this circumstance of brain energy deprivation where the human body finds itself. The remarkable prevalence of insulin resistance, including of the brain, is an adaptation to the environment we have created—one of near-constant consumption of foods that create a metabolic storm. The solution, then, is to adjust eating habits that reflect those of earlier generations; namely, one that allows for proper insulin signaling and periods of ketogenesis.

Age Estimation with Bone Histomorphometry from the Human Ilium

ANNIE BILLINGS and ASHLEY C. SMITH

Department of Anthropology, University of Toronto

During a forensic assessment of skeletal material, anthropologists are often called upon to estimate the age of unknown individuals using the skeleton. By looking at micro-features such as bone remodeling activity, age can be estimated using histological methods. In the past, the majority of these methods relied primarily on long bones, specifically the femur and clavicle. However, it is important to have alternative bones to rely on, such as the ilium, due to potential damage of the commonly used elements. In this study, the authors estimated the validity of using the iliac crests as a marker for age estimation. Twelve iliac crest biopsy samples, consisting of individuals ranging from 30 to 63 years of age were used. The authors estimated the age of individuals by using three previously published equations for age estimation using the clavicle. The clavicle age

estimation equations were chosen as the amount of cortical bone thickness is similar to those of the ilium. Regression analysis found that all three equations had a low positive linear relationship between actual age and estimated ages of individuals. Pearson's correlation coefficient values of all three equations suggest there was a non-significant difference between the equation results and our study. To conclude, the study performed adequately and would require further testing to determine the proper accuracy of age estimation methods involving the ilium. However, it is foreseeable that age estimation using the ilium could have the potential to be used in the field if more specific formulae were developed.

Anti-racist genomics: responding to scientific racism in the 21st century

KEVIN A. BIRD

Department of Horticulture and Ecology, Evolution, and Behavior Program, Michigan State University

Recent advances in genomics and the widespread availability of public databases have fueled a resurgence in scientific racism. Authors have claimed polygenic scores provide evidence a significant portion of differences in cognitive ability between Black and white populations are caused by genetic differences, frequently attributing these differences are due to natural selection. I outline the conceptual and methodological problems with methods like Genome-Wide Association Studies and polygenic scores perpetuated in mainstream research that facilitate racist misuse. I then directly challenge racist hypotheses about racial IQ differences, partially addressing methodological concerns and cautiously interpreting the polygenic-score analyses. I apply methods to detect genetic differentiation and polygenic selection that address biases in polygenic scores, testing the claim that genetic differences explain cognitive gaps and that divergent selection occurred between populations with African and European ancestry. I provide evidence inconsistent with divergent selection and genetic differences driving the Black-white gap in cognitive ability.

I am supported by NSF-GRFP DGE-142487.1. I also thank the MSU-IMPACTS program's travel grant for making it possible for me to present here.

An accessory to developmental stress: the relationship between Linear Enamel Hypoplasia (LEH) and molar cusp expression

ERIN C. BLANKENSHIP-SEFCZEK[1,2], ALAN H. GOODMAN[3], MARK HUBBE[2], JOHN P. HUNTER[4] and DEBBIE GUATELLI-STEINBERG[2]

[1]Cultural and Social Studies, Creighton University, [2]Anthropology, Ohio State University, [3]Anthropology, Hampshire College, [4]Evolutionary Ecology and Organismal Biology, Ohio State University

Morphological features of the Arizona State University Dental Anthropology System (ASUDAS) are central to biodistance studies, in part because of their high heritability. However, recent studies suggest that stress during development may influence accessory trait expression. To further assess the relationship between developmental stress and variation in accessory cusp expression, the present study makes use of dental casts (n=73) collected from a nutritional supplementation study conducted in rural Mexico during the 1970's. Previous work on this sample revealed that supplemented and non-supplemented groups differed in molar trait expression. The present study asks whether there is a relationship between variation in stress experience and molar trait expression across individuals in this sample, using linear enamel hypoplasia (LEH) as a marker of individual stress. LEH data were collected during the original study. From the casts, presence and size of upper molar cusp 5 (C5) and Carabelli's cusp were recorded. Using Fisher's Exact tests, we analyzed the relationship between LEH presence on incisors and canines in developmental zones and the presence of each of the two molar traits. For C5, there was a significant association between the absence of canine LEH and presence of C5 (p=0.005), while for Carabelli's cusp, there was a significant association between canine LEH and the presence of Carabelli's cusp (p=0.021). These results suggest that developmental stress may affect occlusal and peripheral accessory cusps differently. These results also suggest that it might be useful to account for developmental stress in biodistance studies that include data on accessory cusp expression.

This research was funded in part by the Department of Anthropology Clark Spencer Larsen Award and the Ohio State University Alumni Grants for Graduate Research and Scholarship.

Biomechanical advantage of the early *Homo erectus* shoulder for stone toolmaking: a musculoskeletal modeling approach

ALICIA BLASI-TOCCACCELI[1,2], GUILLAUME DAVER[1], MICHEL BRENET[3], SANDRINE PRAT[4], LAURENT HUGUEVILLE[5], SONIA HARMAND[6,7], JASON LEWIS[6] and MATHIEU DOMALAIN[2]

[1]PalEvoPrim (UMR CNRS 7262), Université de Poitiers, [2]Pprime (UPR CNRS 3346), Université de Poitiers, [3]PACEA et INRAP GSO (UMR 5199), Université de Bordeaux, [4]MNHN/CNRS/UPVD (UMR 7194), Alliance Sorbonne Université, Musée de l'Homme, [5]ICM, Institut du Cerveau et de la Moëlle épinière, [6]Turkana Basin Institute and Department of Anthropology, Stony Brook University, [7]CNRS (UMR 7055), Université Paris Nanterre

While the emergence of stone toolmaking by hominins is commonly perceived as a major milestone during human evolution, it is unclear whether stone tool production has promoted or benefited from specific forelimb anatomical changes. Here, we investigated whether the peculiar traits of the shoulder of early *Homo erectus* (*ca.* 1.8-1.5 Ma), characterized by short clavicle, low humeral torsion, and broad thorax, could have affected performance of free-hand stone knapping. Clavicular, humeral, and thoracic metric data from extant humans and the most complete early *H. erectus* shoulder remains (i.e. skeletons from Dmanisi I and KNM-WT 15000 skeleton from West Turkana), were used to implement early *H. erectus* characters from a *H. sapiens* shoulder musculoskeletal model. Forelimb kinematics and electromyographic data of a knapping expert producing flakes using free-hand percussion technique served as input of a biomechanical simulation to compute joint moments and muscle forces. Our results indicate that the shorter clavicle and lower humeral torsion of early *H. erectus* (relative to *Homo sapiens*), which are the two most impacting parameters, provide biomechanical advantage. Conversely, the *H. sapiens* shoulder presents mechanically less propensity for stone flaking because of generally higher joint moment and muscle force production for the same outcome. In an evolutionary context, morphological comparisons with other fossil hominin and extant hominoid species highlight the potentially selective value of clavicle length and the co-opted nature of humeral torsion in early *H. erectus* for stone flaking.

Agence Nationale pour la Recherche (ANR-12-CULT-0006, ANR-17-CE27-0005), Région Nouvelle Aquitaine (CPER-FEDER P-2017-BAFE-68), LOComotion des HOminines fossiles par SImulation musculo-squelettique du Membre thoracique (AAPR2020-2020-8624210).

Bye-bye binary: collaborative, gender-expansive strategies for identification of Trans Does

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

[1]Department of Anthropology, Idaho State University, [2]Department of Anthopology, University of New Hampshire, [3]Department of Anthropology, Texas Tech University, [4]Trans Doe Task Force, Redgrave Research

Construction of the biological profile is fundamental to uncovering a decedent's identity. However, overreliance on sex estimation discounts the importance of gender as a fundamental component of living identity. Skeletal morphology alone cannot inform about gender, but biological sex estimates in combination with other contextual information can be used to construct *biocultural* profiles that consider identity more holistically. While bioarchaeologists have engaged with gender theory for decades, few forensic anthropologists view sex as nonbinary and fewer have experience with transgender and gender-expansive (TGE) and skeletal indicators of

gender-affirming procedures. This is concerning, as TGE individuals experience fatal violence at highly disproportionate rates. Incorporation of queer theory and holistic practices can guide efforts to eradicate biological reductionism and reduce harm in cases involving TGE individuals.

Here, we introduce the multi-disciplinary work, practices, and data mining strategies of the Trans Doe Task Force (TDTF), which advocates a harm reduction model to cultivate culturally-informed and gender-expansive approaches to identifying LGBTQ2S+/TGE victims. Successful TDTF case examples will be used to demonstrate the utility of implementing these strategies as part of collaborative efforts uniting the experiential knowledge of advocates with the osteological and sociocultural knowledge of anthropologists. These strategies were applied contrasted with current medicolegal practices that may serve to impede identifications by failing to consider gender identity and the unique needs of TGE cases. Collaborative initiatives between anthropologists and other forensic professionals along with LGBTQ2S+ community advocates yielded better results when dealing with the challenges of identifying TGE victims.

Dental health and self-reported childhood socioeconomic status in the William M. Bass Donated Skeletal Collection

LYDIA G. BLIZZARD[1] and HALEY HORBALY[2]

[1]Department of Anthropology, Binghamton University, [2]Department of Anthropology, University of Tennessee, Knoxville

Research on health disparities in modern populations has established that an individual's socioeconomic status (SES) determines their participation in dental services, with lower SES groups exhibiting reduced engagement in such services. While this association between SES and health care is established for living populations, it is unknown whether this pattern is observable in a skeletal population. This study assesses whether this trend is evident in the dentition of 186 randomly selected donors in the Bass Donated Skeletal Collection (WMB). Antemortem documents include self-reported childhood SES, which were scored on a scale of one (low income) to four (high income). Individuals were evaluated for dental work and dental pathology on a presence/absence basis. Analysis shows that almost all individuals (92.6%) had dental work present, while just over half (60.6%) exhibited dental pathology. Cochran-Armitage tests indicate a significant relationship between the presence of dental pathology and SES ($p<0.01$); specifically, higher SES groups exhibit a higher prevalence of dental pathology. Interestingly, no statistically significant relationship is observed between dental work and SES, nor between dental work and dental pathology ($p>0.01$). These findings may indicate a limited relationship between SES and dental care in the WMB; alternatively, childhood SES may not reflect adult SES and therefore fails to predict engagement with dental care in this sample. This study highlights the difficulty of integrating self-reported antemortem data with skeletal evidence to infer social standing or health as biological anthropologists are often tasked to do.

Development of an Excel spreadsheet for the Skeletal Heath Index and application to a modern marginalized individual

KARA D. BOND and OSBJORN M. PEARSON

Department of Anthropology, University of New Mexico

This research addresses methods for interpreting and documenting skeletal trauma and disability in bioarchaeology and forensic contexts. We quantifying pathologies applying the Skeletal Health Index (Steckel, Sciulli, and Rose (2002). A health index from skeletal remains. The Backbone of History, Cambridge University Press, pp.61-93.) and its QALY (quality-adjusted- life- years) calculations. The health index was developed to compare past societies; we developed the Excel spreadsheet to operationalize it and applied it to a man's skeleton from the Maxwell Museum of Anthropology's Documented Collection (#154 [85.26.2.]). This individual has traumatic injuries, dental loss, osteoporosis, degenerative joint disease, and infection. He died from blunt force trauma when he was struck by a car. The skeletal lesions inform an osetobiography of this individual's life. Computation of the Health Index produced a QALY score of 16.25. Only 7 of the 65 ancient sites evaluated by Steckel et al. (2002) have a lower QALY, which places this individual's set of pathologies in a broader context. This contemporary application emphasizes how difficult life was in ancient societies with similar QALY scores. The intent is to encourage others to apply the spreadsheet and the skeletal health index to better contextualize skeletal evidence of disability, trauma, and quality of life. This system can be applied to forensic and bioarchaeology cases. The Excel spreadsheet is available on the first author's academia.edu page.

Evidence for δ^{66}Zn values as indicators of meat consumption in the Taï chimpanzees

RENEE D. BOUCHER[1], KLERVIA JAOUEN[2], JULIA RIEDEL[3], CHRISTOPHE BOESCH[3,4], ROMAN WITTIG[3,4] and VICKY M. OELZE[1]

[1]Department of Anthropology, University of California, Santa Cruz, [2]Géosciences Environnement Toulouse, Observatoire Midi Pyrénées, [3]Department of Primatology, Max Planck Institute for Evolutionary Anthropology, [4]Taï Chimpanzee Project, Swiss Centre for Scientific Research in Côte d'Ivoire

The stable isotope ratios of Zn (δ^{66}Zn) have been closely linked to trophic position (herbivore, omnivore, and carnivore) in a variety of animal species, with the potential to use δ^{66}Zn values to indicate breastfeeding. In Taï National Park, Côte d'Ivoire, previous studies on dietary intakes from hunting resulted in conflicting interpretations of how infrequent meat consumption is reflected in light stable isotopes. Therefore, it remains unclear if infrequent meat consumption will be reflected in the δ^{66}Zn values of a mainly frugivorous primate, such as the chimpanzee (*Pan troglodytes*). First, we examine if δ^{66}Zn values could be a reliable indicator of trophic enrichment due to meat consumption in adult and adolescent chimpanzees (n = 26) where there is observed hunting and meat eating. Second, we test if the Zn isotopes of subadult chimpanzees (n = 7) fractionate relative to the ratios recorded for their respective mothers (n = 6) indicating nursing. We analyzed δ^{66}Zn values in chimpanzee dental enamel samples from the Taï Chimpanzee Collection via MC-ICP-MS. We found that male chimpanzees, known to consume more meat than their female counterparts, are significantly lower in δ^{66}Zn values relative to females, suggesting trophic enrichment. Subsequently, in δ^{66}Zn values, breastfeeding chimpanzees (n = 3) were marginally higher, whereas in-utero chimpanzees (n = 4) were indistinguishable relative to their respective mothers. We suggest that δ^{66}Zn analysis has the potential to indicate infrequent meat consumption in wild primates, with likely less interference from environmental factors than other isotope systems within the food web.

University of California, Santa Cruz

New dental remains of the Miocene small-bodied catarrhine *Pliobates cataloniae*

FLORIAN BOUCHET[1], CLÉMENT ZANOLLI[2], SERGIO ALMÉCIJA[1,3,4], JOSEP FORTUNY[1], JOSEP M. ROBLES[1], AMÉLIE BEAUDET[1,5,6], SALVADOR MOYÀ-SOLÀ[1,7,8] and DAVID M. ALBA[1]

[1]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, [2]PACEA, UMR 5199 CNRS, MCC, Université de Bordeaux, [3]Division of Anthropology, American Museum of Natural History, [4]New York Consortium in Evolutionary Primatology, AMNH, [5]Department of Archaeology, University of Cambridge, [6]School of Geography, Archaeology and Environmental Studies, University of the Witwatersrand, [7]Life & Medical Sciences, Institució Catalana de Recerca i Estudis Avançats, [8]Unitat d'Antropologia Biològica, Departament de Biologia Animal, Biologia Vegetal i Ecologia, Universitat Autònoma de Barcelona

Pliobates cataloniae is a small-bodied catarrhine from the Miocene of NE Iberian Peninsula. Originally described as a stem hominoid, it has been considered a pliopithecoid by other authors. This species was only represented by the holotype, which consists of a female partial skeleton including the upper cheek teeth from Abocador de Can Mata locality ACM/C8-A4 (Vallès-Penedès Basin). Here we report additional dentognathic remains of *P. cataloniae* from the nearby and

roughly coeval (11.6 Ma) locality ACM/C5-D1. The new sample includes a male left maxillary fragment with P3/–M1/, a right maxillary fragment with M1/–M2/, a left I/2, and a female left lower canine. Due to the less advanced degree of wear and the more completely preserved P3, the new maxillary fragments enable a more accurate description of *Pliobates* cheek tooth morphology than the holotype, while the incisor and canine represent the first evidence of its lower dentition. As noted in the original diagnosis, the upper cheek teeth differ from those of other small catarrhines, but more closely resemble dendropithecids than pliopithecoids. Additional similarities with dendropithecids are present in the P3 and the lower teeth, reinforcing the contention that *Pliobates* might be more closely related to African dendropithecids than Eurasian pliopithecoids. Ongoing detailed descriptions and comparisons of the external and internal morphology of the *Pliobates* dentition will hopefully clarify further its systematic status, with relevant implications for catarrhine evolution and paleobiogeography.

AEI (PID2020-116908GB-I00, PID2020-117289GB-I00), Generalitat de Catalunya (CERCA Programme and Consolidated Research Groups 2017 SGR 086 and 2017 SGR 116), MCIN (PRE2018-083299), IdEx Université de Bordeaux/GPR Human Past, French CNRS.

Variation of the Pubis Across Populations: A Geometric Morphometric Analysis

FATIMAH BOUDERDABEN[1], MITCHELL ROSELIUS[2] and KATE SPRADLEY[1]

[1]Anthropology, Texas State University, [2]Sales, Critical Systems Inc.

When attempting to estimate the identity of unknown human remains, forensic anthropologists must generate a biological profile. This profile is composed of an estimation of sex, age, ancestry, and stature. Sex is one of the first assessments completed and is arguably the most important. Many different methods of sex estimation have been developed. The most accurate of these methods involve the assessment of the pelvis, where the strongest degree of sexual dimorphism is found in modern humans. These methods have become standardized over time. However, standardized metric and nonmetric assessments of sex are not as accurate when applied to populations that are not black or white. Degrees of sexual dimorphism are different when comparing individuals from differing population affinities. Therefore, it is important to assess sex while considering ancestry to effectively assess the validity of the sex estimation practices of forensic anthropologists.

This study compared the morphology of the ventral surface of the pubis between two different modern populations. 3D images were taken of 198 left innominates and semilandmarks were placed along the pubis. A General Procrustes analysis was done to control for shape differences. Finally, a principle component analysis and canonical variate analysis were run in MorphoJ based on 40 landmarks.

It was found that there was considerable overlap between the two populations when discriminating by sex and an overall 7% error rate was found based on the principle component analysis.

The first author is financially supported by the National Science Foundation through the Graduate Research Fellowship Program.

Dietary Influences on Oral Microbial Composition in Murine Models: Implications for Human Health and Evolution

GRACE B. BOWLAND[1] and LAURA S. WEYRICH[1,2]

[1]Department of Anthropology, Pennsylvania State University, [2]Huck Institutes of the Life Sciences, Pennsylvania State University

Oral microbiota are involved in the development and progression of non-communicable diseases (NCDs), such as obesity, diabetes, cardiometabolic disease and cancer. The composition of oral microbiota may be shaped by a variety of different lifestyle factors, including diet, which may influence health outcomes. However, it remains unclear how specific dietary inputs influence oral microbiota composition and diversity. As murine models are a valuable way to examine how different diets influence microbiota in controlled environments, we examined oral microbiota in C57BL/6 mice (n=125) to assess the effects of dietary energy density (characterized as low, medium, and high) and macronutrient composition (fats, carbohydrates, and proteins) on oral microbiome composition and diversity. Using 16S rRNA gene sequencing and analysis, we did not find significant shifts in number of species associated with different diets. However, preliminary analyses did reveal significant compositional shifts in mice with low energy density diets. Additionally, all macronutrients significantly contributed to differences in microbial community composition, and distinct taxa and composition shifts were attributed to decreases in protein and increases in fats and carbohydrates. Further analyses will examine how shifts in specific macronutrients may act in tandem (i.e., fats and carbohydrates vs. only fats or only carbohydrates) on oral microbiota and explore functional signatures associated with compositional changes. Our results suggest that large scale shifts in diet can influence the oral microbiome, which may have implications for human health and our understanding of how the microbiome contributes to mammalian evolution.

Old questions, new methods: testing hypotheses for canine dimorphism in the evolution of anthropoid primates using phylogenetic analyses

LUCYNA A. BOWLAND, ASHLY N. ROMERO and CHRISTA D. KELLY

Anthropology, University of Arkansas

Numerous hypotheses have been proposed to explain selective pressures affecting the evolution of canine dimorphism in anthropoid primates. However, these hypotheses have yet to be tested using the novel phylogenetic techniques commonly employed in other biological analyses. Here we used the R-package OUwie to test new phylogenetic analyses against traditional methods found in a meta-analysis of the anthropological literature to better explain the selective pressures affecting the evolution of canine dimorphism. OUwie estimates the rate of evolution for continuous traits while measuring the effect of selective regimes on the traits in question. We chose three selective regimes hypothesized to affect the evolution of canine dimorphism. We then obtained maxillary canine height measurements for a broad comparative sample of extant anthropoid primates (n=67 species) from the available literature and standardized canine height using a measure of cranial size to account for the large variation in primate body size. The rate of canine height evolution was evaluated separately for males and females since sexual dimorphism results from either changes acquired independently in males or females or from changes occurring in both sexes. We analyzed the likelihood of the effect of each selective regime on canine size evolution against the null assumption that canine size variation occurred because of random drift using multiple models found in the OUwie package. Preliminary results indicate that most selective pressures acting on the evolution of canine height differentially affect males and females, but that mating system strongly affects canine height evolution in both sexes.

'Social metabolism' and biocultural anthropology: A concept at the intersection of adaptability and political-economic analyses

JARED M. BRAGG

Department of Anthropology, Kenyon College

A key challenge for biological anthropologists interested in forging 'biocultural syntheses' is developing theories that balance both evolutionary-adaptative and social-structural determinants of human variation.

In this paper I discuss an interdisciplinary concept referring to resource use and exchange between humans and their environments, the idea of a

'social metabolism,' assessing its potential to forge connections between political-economic and adaptive frameworks in human biology research.

Departing from previous utilizations of this notion in fields such as environmental sociology, I develop the concept of social metabolism with reference to the database and theoretical perspectives of biological anthropology. Evidence from the comparative study of the life history of the genus *Homo*, energetics of human reproduction, and human behavioral ecology leads to the provisional conclusion that a social metabolism might be considered a fundamental characteristic of the human adaptive complex.

To explore the extent of analogical overlap of the 'biological' and 'social' utilization of the term metabolism, these data are contextualized within an integrative theoretical perspective drawing from economic anthropology and archaeology, with a special focus on areas related to social process and cultural evolution. Establishing conceptual congruence among these levels of analysis is crucial to maintaining the linkage between adaptive and political-economic frames.

These lines of evidence and theory suggest that social metabolism is best conceived as an emergent 'level' of organismic integration and adaptation. Transformations in human relations have led to alterations in biological parameters such that certain social configurations are presupposed by the developmental systems of individual members of our species.

Estimating *Pan* demography from nucleotide site patterns

COLIN M. BRAND[1,2], FRANCES J. WHITE[3], ALAN R. ROGERS[4] and TIMOTHY H. WEBSTER[4]

[1]Bakar Computational Health Sciences Institute, University of California San Francisco, [2]Department of Epidemiology and Biostatistics, University of California San Francisco, [3]Department of Anthropology, University of Oregon, [4]Department of Anthropology, University of Utah

Introgression appears increasingly ubiquitous in the evolutionary history of various taxa, including humans. However, accurately estimating introgression is difficult, particularly when there are many parameters and when models are misspecified. Here, we compare previously proposed models for the genus *Pan* by analyzing nucleotide site patterns. Using this approach, we can focus on deep time and estimate parameters simultaneously. We used 71 genomes representing all five extant *Pan* lineages and a human sample, as an outgroup, to calculate site patterns from 52 million SNPs across all 23 autosomes. Next, we constructed 118 models using previously proposed introgression events, calculated the site patterns for each model, generated model parameters, and assessed their fit to the observed data. We found a single best fit model that included two introgression events: one from bonobos into the ancestor of eastern and central chimpanzees and another from western chimpanzees into eastern chimpanzees. We estimate these admixture proportions to be 0.006 and 0.214, respectively. Further, we find an older divergence for the chimpanzee common ancestor at 987 ka. These results support previous findings of gene flow between bonobos and chimpanzees as well as between the two lineages that occupy the ends of the chimpanzee range. This second event indicates that the current and past ranges of at least two chimpanzee subspecies were different. Our study suggests that introgression played a role in the evolution of bonobos and chimpanzees but to a lesser extent than in humans.

Hundreds of *Colobus* fossils from the Late Pleistocene of the Afar Rift, Ethiopia

MARIANNE F. BRASIL[1,2], TESLA A. MONSON[3], CATHERINE E. TAYLOR[2,4], RYAN M. YOHLER[2,4] and LESLEA J. HLUSKO[2,4,5]

[1]Berkeley Geochronology Center, [2]Human Evolution Research Center, University of California Berkeley, [3]Department of Anthropology, Western Washington University, [4]Department of Integrative Biology, University of California Berkeley, [5]Centro Nacional de Investigación sobre la Evolución Humana (CENIEH)

Modern colobines span a broad range of the African continent and present a wide array of morphological and behavioral diversity. However, our understanding of morphological evolution in the recent history of colobine lineages has been limited by a sparse later Pleistocene fossil record. Here, we add significantly to the record of this group by describing a large sample of colobine fossils (n=360) recovered from Late Pleistocene sediments in the Middle Awash study area of Ethiopia. We described this sample relative to extant colobines and a fossil sample from Asbole, Ethiopia (ca. 600,000 ka) using linear dental, cranial, and postcranial metrics, as well as qualitative features. We also recorded the sex, ontogenetic, and taphonomic characteristics of this sample. On the basis of morphological affinities to extant and fossil *Colobus*, we referred 360 individuals to *Colobus* cf. *guereza*. The majority of individuals are of young- and middle-adult age. Owing to a small degree of dental sexual dimorphism, sex could not be estimated for most individuals. Among the seventy-nine individuals that preserve evidence of animal modification, carnivore damage is most frequent and is often seen in combination with insect and/or rodent damage. Morphologies intermediate to the Asbole *Colobus* sample and extant *Colobus guereza* suggest a phyletic relationship among these time-successive samples. By filling in the gap between the Middle Pleistocene fossils from Asbole and the modern taxa in the Afar Region of Ethiopia, this large new sample of *Colobus* fossils offers novel insights into the last half million years of colobine evolution.

MFB supported by: the John Templeton Foundation; UC Berkeley's Chancellor's Fellowship and Portuguese Studies Program. CET supported by: NSF DGE-1752814. Travel supported by: Human Evolution Research Center at UC Berkeley.

Detecting skeletal perimortem sharp force trauma on postmortem computed tomography images in forensic anthropology

SANDRA BRAUN, LARA INDRA, SANDRA LÖSCH and MARCO MILELLA

Department of Anthropology, Institute of Forensic Medicine, Bern, Switzerland

Postmortem computed tomography (PMCT) is nowadays part of the analytical toolkit of forensic anthropologists. When investigating presence and type of skeletal sharp force lesions, however, the usefulness of tomographic data is not clarified. Similarly, scanty data are available about the statistical association between soft tissue and bone lesions, with potential biases when trying to reconstruct violent scenarios from skeletal traumatic patterns. Here, we tackle these issues by studying sharp force trauma in a sample of 41 individuals analyzed at the IRM Bern. All individuals died following exposure to sharp force trauma; information for all individuals include autopsy and forensic radiology reports, and PMCT. Two forensic anthropologists with different radiological training investigated sharp force lesions on PMCT. We then compared the results among observers, and with those from the original autopsy and radiology reports. Intra- and interobserver agreements were moderate to perfect, intermodality agreements were substantial. Agreement with forensic examinations was rather low, with the lowest errors obtained on the 2D modality. Out of a total 623 soft tissue injuries, 71 (11.4%) penetrated to the bone, with individual frequencies averaging 26.1%. All bone lesions in suicides concentrated on the thorax and were executed with large knives. Bone lesions in homicides, associated with a variety of sharp tools, were most frequent on the thorax, followed by the head and neck and the upper extremities. Our study provides new data for forensic and archaeological reconstructions based on skeletal traumatic patterns. They also highlight important methodological issues facing this type of studies.

Protocols and observer error rates for odontometric data collection on 3D virtual subadult crania

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

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

To better understand the vast range of skeletal variation across the globe, biological anthropologists are turning to databases of radiographs and computed tomography (CT) scans. However, the use of such images rather than dry bones requires slightly different data collection protocols and an understanding of how these newly developed protocols will affect observer error. For this study, a protocol is presented for the collection of cervical and maximum crown dimensions from deciduous and permanent teeth on CT scans. Intra- and inter-observer error were assessed via Technical Error of Measurement (TEM) and relative TEM (rTEM). Data were collected on deciduous and permanent teeth reconstructed from full-body or head and neck CT scans of 11 deceased individuals from the United States aged between 1.46 and 19.99 years deriving from the Subadult Virtual Anthropology Database (SVAD).

Intra- and inter-observer TEM and rTEM values were overall low for permanent and deciduous teeth, and for crown and cervical measurements. The highest rTEM values were observed for cervical measurements, ranging from 0.442% to 4.48% (interobserver) and from 0.00% to 5.76% (intraobserver). In comparison, rTEMs for crown measurements were below 3%. Bland-Altman plots show that 95% of deciduous and permanent measurement differences fell within a +/-1 mm confidence interval and no significant bias was identified. Errors are slightly higher than those reported in other studies, but still fall within an acceptable range. These results indicate that the developed protocols enable observers to obtain reliable odontometric data from 3D CT scans. The protocols are freely accessible online.

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

Collagen Denaturalization in Porcine Femora: Maceration and its Effect on Co/NCo Ratios

EMILY BROOKS[1], THERESA DE CREE[2] and DR. KATELYN BOLHOFNER[3]

[1]SHESC Department of Anthropology, ASU, [2]Coroner's Office, Northampton County, PA, [3]School of Mathematical and Natural Sciences, ASU

Collagen is the most abundant organic component in bone. Collagen will degrade faster after death than its inorganic counterparts, because of collagen's characteristics it could be an indicator for the postmortem interval (PMI). Collagen to Non-Collagen ratios (Co/NCo) have been investigated as a PMI indicator in *Sus scrofa* and human models.

Due to these properties, it could be utilized forensically. Maceration is a common procedure in forensic anthropology to clean partially fleshed remains for analysis. As such, it is important to determine if the maceration process significantly denatures collagen. Collagen denaturalization begins around 150˚F and collagen becomes random coils around 500˚F. Maceration processes vary between facilities, but bones can be exposed to temperatures as high as 400˚F. Therefore, it is hypothesized that the maceration process could decrease collagen content in bone.

Porcine femora were sampled prior to and after the maceration process. Samples were embedded in epoxy resin and thin sectioned. These were then stained using the Chondrex Sirius Red Fast Green Staining Kit. Microscopic images were taken and imported into MATLab to determine red and green color values. Color values from the bone samples were compared before and after maceration and subjected to a student's T test to determine if differences were statistically significant.

The preliminary sample showed that the difference in the Co/NCo ratios and collagen content was insignificant. However, non-collagenous content did show a statistically significant difference between pre and post maceration samples (P= 0.038). Further testing will be conducted to determine if the difference persists.

An analysis of the five young *Homo naledi* juveniles recovered from the Rising Star Cave System, South Africa

JULIET K. BROPHY[1,2], DEBRA R. BOLTER[2,3,4], JOHN HAWKS[2,5] and LEE R. BERGER[2]

[1]Geography and Anthropology, Louisiana State University, [2]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand, [3]Department of Anthropology, Modesto Junior College, [4]Department of Anthropology, California State University Stanislaus, Turlock, [5]Department of Anthropology, University of Wisconsin-Madison

A third locality, U.W. 110, containing *Homo naledi* remains was recently identified within the Rising Star Cave System, South Africa. A single, young juvenile was recovered, consisting of 6 teeth and 28 cranial fragments. Based on the eruption stage of the first permanent molar, this addition makes a total of five known young *H. naledi* juveniles, including one from the Lesedi Chamber and three from the Dinaledi Chamber. This research describes the fossil material attributed to each individual as well as further unassociated, deciduous teeth. The dentition is compared across the three localities and to other southern African hominins of similar maturational age. The results suggest that the deciduous teeth are remarkably consistent at Rising Star in their metric and non-metric traits such as evincing Carabelli's traits, dental chipping, and crown outline shape. The new maxillary dm2s from U.W. 110 are also consistent with previous results with measurements that fall outside the size range of *Australopithecus robustus*, *Australopithecus africanus*, and southern African *Homo* sp. and a quadrangular crown outline shape that is similar to other *Homo* species. These findings supports previous conclusions about the strong dental morphological homogeneity during development. The growing number of young individuals recovered from the Rising Star Cave System allows us to gain a better understanding of their variation, or lack thereof, and provides a basis to estimate broad ranges for age at death of the individuals.

Funding provided by National Geographic Society, Lyda Hill Foundation, South African National Research Foundation, Centre for Excellence in Palaeosciences, University of Witwatersrand, Vilas Trust, Fulbright Scholar Program, Louisiana State University

Examination of a parallel laser apparatus to measure growth and flanges of wild Bornean orangutans (*Pongo pygmaeus wurmbii*)

ELLA R. BROWN[2,4], TIMOTHY G. LAMAN[5], ERIN E. KANE[1,2], FAYE S. HARWELL[1,2], TRI WAHYU SUSANTO[2,6] and CHERYL D. KNOTT[1,2,3]

[1]Department of Anthropology, Boston University, [2]Gunung Palung Orangutan Conservation Program, [3]Department of Biology, Boston University, [4]Department of Anthropology, University of Michigan, [5]Museum of Comparative Zoology, Harvard University, [6]Biology Faculty, Universitas Nasional

Laser photogrammetry allows for remote measurements by using projected lasers with a known separation as a reference within a photo. Despite its value for investigating body size and growth of wild animals, such studies remain rare, particularly for arboreal animals. We constructed a novel laser photogrammetry device from commercially-available parts, and measured the forearm lengths and flange widths of 16 wild Bornean orangutans (*Pongo pygmaeus wurmbii)* in Gunung Palung National Park, Indonesia. Our objectives were to validate our method and report preliminary measurements and growth rates. We measured forearm lengths in three different ways to see which returned the most consistent results, and re-checked the laser spacing with calibration photos after each session. We estimated error with repeatability, accuracy, and inter-observer reliability measures, tracked the forearm growth of three immature females, and examined the ratio of flange size to forearm length for four adult males. The longest forearm measure was the most repeatable (CV = 1.64%), and was similar to flange repeatability (3.50%). Accuracy was high (error = 0.25%), and inter-observer error low (3.74%). Laser spacing increased with distance to the subject, but we corrected for this using the calibration photos. Females grew at -1.37mm/month over the course of one month to 1.07mm/month over the course of five. For adult males, flange width and forearm length did not increase in tandem. We discuss issues encountered, and

hope this accessible method can expand the use of laser photogrammetry and be used to further investigate wild orangutan growth and males' unique bimaturism.

National Science Foundation BCS-1638823, US Fish and Wildlife Service #F19AP00798 and F18AP00898, Disney Conservation Fund, LSB Leakey Foundation, ARCUS Foundation, and Conservation, Food and Health Foundation

Faculty preferences for fieldwork experience in graduate program applications

MICHELLE BROWN[1,2], CHRISTOPHER SCHMITT[3], LAURA C. LOYOLA[4], LEO R. DOUGLAS[5] and MARY E. BLAIR[6]

[1]Department of Anthropology, University of California, Santa Barbara, [2]Department for the Ecology of Animal Societies, Max Planck Institute of Animal Behavior, [3]Department of Anthropology, Boston University, [4]Spatial Sciences Institute, University of Southern California, [5]Liberal Studies, New York University, [6]Center for Biodiversity and Conservation, American Museum of Natural History

Prospective graduate students in biological anthropology are often advised to seek out fieldwork opportunities before applying to graduate programs. However, such experiences tend to be prohibitively expensive and may prevent members of under-represented groups from pursuing careers in anthropology. To understand why advisors place such a strong emphasis on acquiring fieldwork experience and to determine what alternatives might be acceptable, we conducted a survey of US faculty (N = 128 individuals) in PhD-granting anthropology programs. The majority of advisors (74%) preferred candidates with prior fieldwork experience and had accepted such candidates as graduate students (97%), yet only 44% habitually provided such opportunities for current or recent college students. Fewer than half of advisors cared about the type of fieldwork experience (e.g., field school versus internship) or whether it was within their sub-field, but the majority (65-80%) felt that independent research was the best indicator of future success as a scientist. Most (89%) felt that such experiences were unique and could not be replaced with other types of research exposure; the only activity associated with some of the same skills as fieldwork was long-term experience in a foreign country. There is no indication that the preference for fieldwork experience has diminished, despite a growing awareness of how it restricts the diversity of future cohorts of biological anthropologists. We propose that a national funding mechanism is needed to help recent college graduates obtain fieldwork experience.

We are what we chew: Diet-induced morphological changes in the mandible

LUCY E. BRUEMMER and MAJA SESELJ

Department of Anthropology, Bryn Mawr College

With the introduction of agriculture, the diet of humans underwent a significant shift from harder foods that required more masticatory effort (meats, nuts) to softer foods (grains, cooked vegetables). Since the Industrial Revolution, our diets have undergone another shift caused by eating highly processed foods that demand even less of our masticatory apparatus, resulting in overcrowding, impactions, and malocclusions. In this study, I explored how mandibular growth during subadulthood may reflect different diets using six mandibular measurements. Measurements were collected from seven different skeletal samples from Africa, Asia, Europe, and North America (N=371) from different time periods, and analyzed using linear regression models and ANOVA. Dietary hardness was approximated on an ordinal scale based on historic, ethnographic, archaeological, and stable isotope data for different samples.

The results indicate that a harder diet is correlated with morphological changes during ontogeny, specifically in greater measurements of anteroposterior condyle length, mandibular ramus width/height in samples with harder diets. Surprisingly, there were no significant differences among the samples for mandibular length, condylar breadth, or mandibular corpus thickness. The morphological changes during ontogeny detected here complement past research using linear measurements and provide evidence of plastic responses in the mandible, particularly when doing cross-population comparisons in early versus late subadulthood. These results suggest that plastic response in the mandible is likely mediated by diet, pointing to potential dental and clinical applications for intervention and treatments of orthodontic issues caused by soft diets.

We are what we chew: diet-induced morphological changes in the mandible

LUCY E. BRUEMMER and MAJA ŠEŠELJ

Anthropology, Bryn Mawr

With the introduction of agriculture, the human diet underwent a significant shift from harder foods that required more masticatory effort (e.g., wild-collected plant and animal foods) to softer foods (e.g., grains). Since the Industrial Revolution, our diets have undergone another shift caused by eating highly processed foods that demand even less of our masticatory apparatus, resulting in overcrowding, impactions, and malocclusions. In this study, we explored how mandibular growth during subadulthood may reflect different diets using six linear mandibular measurements. Measurements were collected from seven different skeletal samples from Africa, Asia, Europe, and North America (N=371) from different time periods, and analyzed using linear regression models and ANOVA. Dietary hardness was approximated on an ordinal scale based on historic, ethnographic, archaeological, and stable isotope data for different samples.

The results indicate that a harder diet is correlated with morphological changes during ontogeny, specifically with greater measurements of anteroposterior condyle length, mandibular ramus width and height in samples with harder diets. Surprisingly, there were no significant differences among the samples for mandibular length, condylar breadth, or mandibular corpus thickness. The morphological changes during ontogeny detected here complement past research using linear measurements and provide evidence of plastic responses in the mandible, particularly when doing cross-population comparisons in early versus late subadulthood. These results suggest that the plastic response in the mandible is likely mediated by diet, pointing to potential dental and clinical applications for intervention and treatments of orthodontic issues caused by soft contemporary diets.

Wenner-Gren Foundation for Anthropological Research Dissertation Fieldwork Grant; National Science Foundation DDIG 0925861; Center for the Study of Human Origins at New York University; New York Consortium in Evolutionary Primatology

Repetitive Kneeling in a Byzantine Monastic Community

BRIANNA A. BRYAN[1], SUSAN G. SHERIDAN[2] and CHRISTOPHER D. LYNN[1]

[1]Department of Anthropology, University of Alabama, [2]Department of Anthropology, University of Notre Dame

In this study, we investigated the enthesopathies (pathologies of the places where ligaments or tendons meet bones) of the monastic skeletal collection of Byzantine St. Stephen's (5th and 6th century AD). Studying entheseal changes in commingled remains can reveal general cultural patterns of health within the population. A commingled collection of monks recovered from the site of Byzantine St. Stephen's basilica is known to have performed repetitive kneeling activities (genuflection) hundreds of times per day. Based on the historical documents and past research, we predicted that there would be enthesopathies on the lower limbs that reflect this repeated kneeling activity. To test this hypothesis, we scored the lower limb enthesopathies based on robusticity, osteolytic, and osteophytic formations, which utilized a combination of accepted scoring methods. We categorized and scored a total of eight insertion sites on the femur, patella, tibia, fibula, and calcaneus, as these areas would most likely highlight the muscle usage of the monks during genuflection. There was a total of 281 femur fragments, 227 tibia fragments, 79 patella fragments, 71 fibula fragments, and

218 calcaneus fragments for a total of 876 bone fragments scored. Regarding the nature of the repeated activity, we predicted that enthesopathies will highlight bilateral differences on the five different bones based on the genuflection stance (left leg forward, right leg back). Overall, there were several enthesopathies on the bones scored; however, bilateral differences were not heavily prevalent.

A novel method for collecting primate orbital volume in 3DSlicer

EMILY R. BRYSON[1], VALERIE B. DELEON[1] and TIMOTHY D. SMITH[2,3]

[1]Department of Anthropology, University of Florida, [2]School of Physical Therapy, Slippery Rock University, [3]Department of Anthropology, University of Pittsburgh

This project proposes a novel method for the collection of orbital volume (OV) in the open-access post-processing software 3DSlicer. Traditionally, OV has been collected by 1) physically filling the orbit of cadaveric specimens/dry skulls, 2) collecting 2D measurements, and 3) by using 3D segmentation software on digital reconstructions of the skull to measure the orbital cavity. Previous literature has highlighted the need for a consistent and anatomically informed way of closing the anterior orbital aperture. The current lack of consistency may affect volumetric measurements, introducing error into studies of shape and size of the orbit. The semi-automatic method proposed here efficiently closes the anterior aperture by mapping a curved plane to user-defined points representing the fluctuating depth and projection of the orbital margin. An iterative semi-automatic segmentation of the cavity is then conducted to collect orbital measurements (e.g., volume).

A step-by-step workflow is presented here along with solutions to common sources of potential error such as the nasolacrimal canal and incomplete orbital walls. A measurement error study was conducted using multiple species of anthropoid primates. The orbit was segmented in three separate trials. Because of the range of species sizes, error was evaluated using a coefficient of variation (CV). For the dependent variables *orbit surface area* and *aperture circumference*, CV was well below 1% for all individuals. For *orbit volume* and *aperture area*, CV ranged up to 1.7%. This semi-automated method for segmenting the orbital cavity increases efficiency and repeatability and is freely available through the open-source software 3DSlicer.

Funded by the National Science Foundation (BCS-1830894 and BCS-1830919)

Entheseal changes and joint degeneration of upper limb bones in males and females in medieval Giecz, Poland

EMMA T. BRZEZINSKI[1,2] and AMANDA M. AGNEW[1,2]

[1]Department of Anthropology, The Ohio State University, [2]Skeletal Biology Research Lab, The Ohio State University

Entheseal changes (ECs) and degenerative joint disease (DJD) in the upper extremity are often used as evidence of physical activity and handedness, and thus serve as indicators of behavioral patterns in past populations. The purpose of this research was to characterize ECs and DJD in upper limb bones in a medieval Polish population to identify patterns in sexual division of labor.

The sample included clavicles, humeri, and radii representing adult males (n=89) and females (n=53) from the early medieval (11th-12th c.) cemetery site, Gz4, in Giecz, Poland. Most entheses demonstrated a significant right-bias in both the sex-pooled sample and in each sex ($p<0.003$), except the conoid tubercle for females (chi-square test, $p=0.194$). Generally, side differences in ECs were not significantly related to sex, except the radial tuberosity (chi-square test, $p=0.027$), where males are ~5 times less likely to be scored "right" than females (nominal logistic regression, $p=0.041$). No relationship between side and DJD presence/absence was observed in the sex-pooled population or each sex (chi-square test). However, females demonstrated significantly lower odds of having DJD than males in the medial and lateral clavicle (68.3%, 48.2%), the distal humerus (43.7%), and the distal radius (58.9%) (binary logistic regression, $p<0.05$). This suggests that males may have engaged in more strenuous activities involving the upper limb. In addition, differences in radius ECs suggest sex-specific functional loading in the forearm distinct from the rest of the upper extremity, consistent with previous directional asymmetry findings in this sample.

A macaque model for the effects of admixture on body size

LAURA T. BUCK[1,2], DAVID C. KATZ[3], REBECCA ROGERS ACKERMANN[4,5], LESLEA J. HLUSKO[6,7], SREE KANTHASWAMY[8] and TIMOTHY D. WEAVER[2]

[1]School of Biological and Environmental Sciences, Liverpool John Moores University, [2]Department of Anthropology, University of California Davis, [3]Cell Biology and Anatomy, University of Calgary Cumming School of Medicine, [4]Department of Archaeology, University of Cape Town, [5]Human Evolution Research Institute, University of Cape Town, [6]Department of Integrative Biology, University of California Berkeley, [7]Centro Nacional de Investigación sobre la Evolución Humana (CENIEH), [8]School of Mathematical and Natural Sciences, Arizona State University

Recent advances in genetics have shown that hybridisation occurred during human evolution, yet its morphological impact remains underexplored. Ancient DNA is a powerful tool but given the conditions required for its preservation, it is best used in combination with fossil morphology. Studies of non-human primates have suggested a signature hybrid morphology, which could be used to diagnose hybrids in the hominin fossil record. This signature may include extreme size, high levels of variation and markers of developmental instability, but how phylogenetic distance and admixture proportion affect these characteristics is unknown. Non-mammalian studies suggest extreme morphotypes are more likely in early generation hybrids and with greater divergence between parents. To understand the hominin fossil record, we must study admixture in taxa that approximate hominin hybridisation as closely as possible. Here, we use proxy taxa (Chinese and Indian *Macaca mulatta*) with comparable divergence time (in generations) to *Homo sapiens* / Neanderthals. Our sample is large, multigenerational and of known hybridity. Measuring crown-rump and limb lengths, we investigate the relationship between admixture and size variation, discussing these and further results. In contrast to previous studies in more phylogenetically disparate taxa and with more early generation hybrids, we find no individuals of extreme size, nor greater variation in hybrids than in full-bred taxa. We suggest that hybridisation between closely related taxa, such as Neanderthals and *H. sapiens*, may lead to more subtle morphological patterns than previously anticipated. However, investigation of the role of phenotypic, as well as phylogenetic, divergence is required.

This research was funded by grants #1623366 and #1720128 awarded by the National Science Foundation (USA) and The Leakey Foundation.

A noble childhood? Exploring the diet and health of high status individuals from medieval Stirling Castle, Scotland, through isotope analysis of incremental dentine

JO BUCKBERRY[1], JULIA LEE-THORP[2], HANNAH KOON[1], CHELSEA LANDON[1], CATHY BATT[2] and JULIA BEAUMONT[1]

[1]Archaeological and Forensic Sciences, University of Bradford, UK, [2]Research Laboratory for Archaeology and the History of Art, Oxford University, UK

Stirling Castle was a key garrison of the Scottish Wars of Independence, 1296-1328 and 1332-1357AD. In 1997, excavations at Stirling Castle revealed a lost royal chapel and eight burials that were radiocarbon dated to the 14th and early 15th centuries. Evidence of interpersonal violence, a preponderance of blunt-force injuries and scurvy within the sample suggests they may relate to the documented sieges of Stirling Castle. The significant burial location within a royal castle combined

with extremely high rates of developmental conditions suggests they may be high-status. This paper presents isotope analysis of incremental dentine, undertaken to investigate the childhood health and diet of this exceptional group of individuals, and highlights the importance of multi-tissue isotope analysis in bioarchaeology.

Previous carbon and nitrogen isotope analysis of bone collagen indicated these individuals ate a mixed diet, with isotopic ratios similar to other medieval British populations. New isotopic analysis of incremental dentine was undertaken for all individuals with surviving teeth (N=6). The only individual where we could assess evidence of weaning appears to have been breastfed. Two individuals revealed dietary shifts, from a low status terrestrial based diet to a higher status diet with increased protein and fish. Significantly, four of the individuals revealed opposing co-variance of C and N isotope ratios, indicative of physiological stress during childhood and adolescence. It appears that even the wealthy were not immune to the challenges of medieval life.

This research was funded by Historic Environment Scotland

Migrant Mortality and Survivorship in Ancient Teotihuacan: Isotopes and Survival Analysis

GINA M. BUCKLEY[1], REBECCA STOREY[2] and LINDA R. MANZANILLA[3]

[1]Archaeometry Laboratory, University of Missouri Research Reactor, [2]Department of Comparative Cultural Studies, University of Houston, [3]Instituto de Investigaciones Antropológicas, Universidad Nacional Autónoma de México

The ancient city of Teotihuacan (AD 1-550) in central Mexico was the most populous urban center in Mesoamerica during the Classic period and a multi-ethnic hub that attracted migrants from across this region. While past bioarchaeological research at this great urban center has examined population health as a whole at the neighborhood level, it has yet to be observed how the health and well-being of migrants compared to that of native-born residents. Understanding the impact of migration on health is important because past paleodemographic research across the globe has suggested that migrants moving into urban areas may have faced elevated risks of disease and mortality. This presentation uses data from strontium and oxygen isotopes to identify migrants in three neighborhoods across the city – Tlajinga, La Ventilla, and Teopancazco – and applies Kaplan-Meier survival analysis and Cox proportional hazards analysis to estimate if migrants faced elevated risks of mortality and greater reductions in survivorship than native Teotihuacanos.

This project was funded by the National Science Foundation (NSF) Dissertation Improvement Grant (BCS-1927690), and the Proyecto Arqueológico Tlajinga Teotihuacan (PATT) funded by the NSF (BCS-13212447).

Within-group sperm competition influences testes size in Verreaux's Sifaka (*Propithecus verreauxi*)

GABRIELLE L. BUENO and REBECCA J. LEWIS

Department of Anthropology, University of Texas at Austin

Sexual selection predicts that males invest in sperm competition when females mate with multiple males. Because group composition facilitates access to mates, we hypothesized that variation in within-group mate competition influences investment in sperm competition. Verreaux's sifaka (*Propithecus verreauxi*) live in both single and multimale groups, allowing us to test the effect of within-group sperm competition on testes size using linear-mixed effects models. We predicted that dominant males living in multimale groups have larger testes than males in single-male groups. Within multimale sifaka groups, dominant males have higher testosterone levels than subordinate males due to either reproductive suppression or alternative mating tactics and are thus predicted to have larger testes. We collected testes mass and body weight from 24 adult male sifaka at Kirindy Mitea National Park in western Madagascar from 2006 to 2019 (n = 57 measurements). Consistent with expectations, we found that dominant males in multimale groups had significantly larger absolute ($p=0.016$) and relative ($p=0.0015$) testes mass than males in single-male groups. Within multimale groups, dominant males had significantly larger absolute ($p<0.0001$) and relative ($p<0.0001$) testes mass than subordinate males. Males that transitioned between multimale and single male groups exhibited the same pattern. Sperm competition is typically examined via interspecific comparisons of testes size and mating system. Our results demonstrate that (1) males flexibly respond to the current level of within-group sperm competition, and (2) through dominance, within-group contest competition impacts male investment in sperm competition.

National Science Foundation SBE#1719654, The Leakey Foundation, Primate Conservation, Inc., The University of Texas-Austin, private donations

Lemuroid Teeth vs. Lorisoid Teeth: Different Ways to go for Gums

ANNE M. BURROWS[1,2], SERGI LÓPEZ-TORRES[3,4,5], KEEGAN R. SELIG[4,5] and MARY T. SILCOX[6]

[1]Physical Therapy, Duquesne University, [2]Anthropology, University of Pittsburgh, [3]Biology, University of Warsaw, [4]Vertebrate Paleontology, American Museum of Natural History, [5]Primatology, New York Consortium in Evolutionary Primatology, [6]Anthropology, University of Toronto Scarborough

Gummivory is a rare dietary niche among primates but is found in some strepsirrhines. This dietary niche may have also been an important adaptation of early primates, so finding a dental signature for gummivory is desirable. Lorisoid gummivores have toothcombs that are resistant to bending in the sagittal plane, along with smaller lower molars than in lorisoids that do not depend upon gums. Our understanding of dentition in gummivorous lemuroids remains incomplete. The present study focuses on the toothcomb and molars in lemuroids that include large percentages of gums in their diets. We also include lemuroids that gouge tree bark routinely, even though they do not consume large amounts of gums, because the demands on the anterior teeth are likely to be similar. We used sliding, digital calipers to take select measurements from the toothcombs and upper/lower last molars of various species. Because body sizes vary tremendously among lemuroids, we scaled all measurements by the geometric mean of each specimen, then statistically compared scaled means using a one-way ANOVA ($p<0.05$). Results show that lemuroids have no similarities in dental signatures for gummivory to lorisoids. Gummivorous and gouging lemuroids had significantly lower toothcomb bending-resistance and larger last molars than non-gummivorous lemuroids. These 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. Continuing work on gummivory in lemuroids, including collecting novel behavioural data, and studying toothcomb wear trajectories, should elucidate this question.

Sex-based differences in absolute and scaled frontal sinus volumes among humans

LAUREN N. BUTARIC and COLE T. AMUNDSON

Department of Anatomy, Des Moines University

The frontal sinus is often applied in forensic contexts; however, patterns of its variation remain poorly understood. For example, while genotypic females typically possess smaller frontal sinuses— presumably due to overall smaller body sizes— sex-based differences in relative frontal sinus size remain unknown. This preliminary study utilizes CT scans of 140

individuals (76M/64F) across four morphologically distinct groups (Australians; sub-Saharan Africans; Arctic Inuits; Central Europeans) to test whether sex-based differences in frontal sinus volume remain once scaled for size. Frontal sinus volumes were segmented from CT scans, and frontal bone size was calculated via the geometric mean of three distances: right-left frontomalare orbitale; nasion-bregma; and right-left temporale. Individual frontal sinus volumes were scaled via respective frontal bone size. Absent sinuses (5F/1M) were included as "0ml." Independent T-tests indicated females present with significantly smaller sinuses for both absolute (Means: Female=4.1715ml; Male=6.9616ml; t=3.67; p<0.001) and scaled volumes (Female=0.0144; Male=0.1725; t=3.0055; p=0.003). Analyses of covariance (ANCOVA) were conducted to further investigate how frontal bone size and sex relate to frontal sinus volume. An initial ANCOVA indicated a non-significant interaction (F=0.166; p=0.685); an ANCOVA without the interaction indicated a significant effect of sex (F=6.774; p=0.010). These results suggest that, unlike the maxillary sinus, both absolute and scaled frontal sinus size are significantly smaller in females. This finding adds to literature suggesting that ontogenetic mechanisms underlying variation for the paranasal sinuses likely differ, which could have implications for their use in forensic identifications and other fields (e.g., paleoanthropology).

This project was supported by the National Institute of Justice (Award No. 2020-75-CX-0013) and an IOER grant (Award No. 3-19-01).

Disrupting genomics as disrupting scientism

GRACIELA S. CABANA[1], LINDSAY A. SMITH[2], FRANCISCO DI FABIO ROCCA[3], BÁRBARA MAZZA[4] and MARCELA M. MENDOZA[5]

[1]Department of Anthropology, University of Tennessee, Knoxville, [2]School for the Future of Innovation in Society, Arizona State University, [3]Departamento de Antropología, CONICET, Universidad Maimónides, [4]Instituto Nacional de Antropología y Pensamiento Latinoamericano (INAPL), CONICET, Universidad de Buenos Aires, [5]Global & International Studies, Western Michigan University

The field of genetics originated as a bounded space for "the study of heredity." As such, genetics has exerted undue power over other fields of knowledge, especially those considered to be apart from the physical body, such as "the mind," society, culture, and "the environment." This epistemic separation of nature/culture has since guided academic knowledge production and impacted individuals and societies in fundamental ways.

We discuss how genomics, as a technologically and computationally intense iteration of genetics, exaggerates the artificial separation between nature/culture. We do so from the perspective of our ongoing collaborative project in Argentina, in which we are studying Argentine individuals' discourses of self and national via a multi-method approach in which we collect genomic data to inform and enrich ethnographic data. Throughout the project we continually developed ways to maintain, if not elevate, the authority of the social science aspects of the project. However, those efforts were often overwhelmed by publics' allure of genetics.

In this presentation, we provide examples of those experiences to demonstrate the ways in which genomics presents a special challenge to the long-standing phenomenon of "scientism" – or the belief that scientific knowledge has a universal claim to truth (Ingold 2013). We argue that this intensified form of scientism challenges anthropology to take even more seriously calls to retheorize biology. Would finally adopting frameworks of "cultural biology" (Goodman 2014) or biosociality as "human becomings" (Ingold & Pálsson 2013) enable an anthropological disruption of not only "the genome" but of the overdetermination of science itself?

Supported by the National Science Foundation (NSF-SES-1344185) and the Latin American & Iberian Institute, University of New Mexico.

Scurvy and its presence in an Early/Middle Transition (500-200 B.C.) California Shell Mound Cemetery

ALYSON C. CAINE[1,3], CHRISTOPHER CANZONIERI[2] and DANIEL SHOUP[3]

[1]Anthropology and Heritage Studies, University of California, Merced, [2]Bioarchaeology, Basin Research Associates, [3]Bioarchaeology, Archaeological/Historical Consultants

Non-adult scurvy is rarely observed in individuals under the age of four months and when present is the result of maternal deficiencies in utero (Brickley & Mays, 2019). While rare, infants have been recorded with scurvy in clinical research and archaeological research of indigenous populations of the Americas (Crandall, 2014). Excavations at a shell mound cemetery site that date to the Early/Middle Transition Period (500-200 B.C.) recovered multiple infants and children with skeletal alterations indicative of scurvy. This research presents these individuals and considers the etiology of scurvy in infants and children at this Indigenous Californian shell mound cemetery in Alameda, California.

Seven non-adults, ranging from 38 weeks to 2 years at the time of death, exhibited characteristic skeletal alterations of scurvy (vitamin C deficiency). Variable distributions of bony changes were observed, including deposits of reactive bone and abnormal porosity at the greater and lesser wings of the sphenoid bones, squama and petrous portion of temporal bones, mandible, maxilla, scapulae, and periosteal new bone formation at the diaphysis of long bones, including the humerii, radii, ulnae, and tibiae. Radiographic analysis exhibits further skeletal alterations characteristic of scurvy, including thinning of the cortical bone, generalized osteopenia, scurvy line, and the white line of Frankel. These seven individuals represent 54% of the infants (n=13) and 22% of individuals under the age of ten at the time of death (n=32). Two of the infants were also recovered with adult females; however, adults did not show evidence of macroscopic skeletal alterations of scurvy.

Andean populations adapted to high-altitude hypoxic environments use thoracic ventilation more than lowlanders to breathe while walking and running

WILLIAM É. CALLISON[1], MELISA KIYAMU[2], FRANCISCO C. VILLAFUERTE[2], TOM D. BRUTSAERT[3] and DANIEL E. LIEBERMAN[1]

[1]Department of Human Evolutionary Biology, Harvard University, [2]Laboratorio de Transporte de Oxigeno, Universidad Peruana Cayetano Heredia, [3]Department of Exercise Science, Syracuse University

Despite sustained aerobic activity requiring up to 10-fold higher rates of air intake, human populations living in high-altitude, low-oxygen (hypoxic) environments remain physically active. While these populations have been found to have larger chest and lung volumes, how their thoraxes actively help increase ventilation is unknown. Here we show that thoracic contributions to ventilation during sustained aerobic activity at high altitude derives from a combination of adulthood acclimatization, developmental adaptation, and population-level adaptation to aerobic demand in hypoxic environments. Spirometry, heart rate, and rib-motion measurements were collected during walking and running on a treadmill in Quechua individuals in Peru born and living at sea-level (~150 m) versus high altitude (>4000 m) and in lowland individuals living at sea-level in Boston (~35 m). We found that Quechua individuals, regardless of altitude of birth and testing environment, increase thoracic volume 1.8-2.9 times more than Boston lowland participants by expanding the thorax 1.1-1.5 times more dorsoventrally and 1.4-2.0 times more mediolaterally ($p<0.05$). Further, Quechua individuals who live in or had developmental exposure to hypoxic environments have 5-7% deeper chests that result in 1.3-1.6 times greater increases in thoracic ventilation at a corresponding percent of maximum heart rate relative to age-matched Quechua individuals born and living at sea-level ($p<0.05$).

Increased oxygen demand due to environment, aerobically demanding activities, or a combination of both, has helped shape the form and function of the human thorax.

Funding for this project was provided by the Wenner-Gren Foundation for Anthropological Research Dissertation Fieldwork Grant #9805.

Percentage of Collapsed Vertebrae Found Within a Skeletal Sample of Individuals Aged Fifty-Five and Older

JAYLA D. CAMPBELL

Department of Geography and Anthropology, Louisiana State University

Research regarding percentage of a population presenting a collapsed vertebra is limited within the field. It is important to collect this data, especially within older populations, to assess collapse patterns and use findings to advance medical treatment. Within a modern skeletal collection fifty-five years of age and older at Southeast Texas Applied Forensic Science Facility, it was predicted that at least 25% of individuals will present at least one collapse. 4% were Hispanic, 2% were African, 1% were Native American, 1% were Asian, and 2% were of unknown decent with the rest being of European decent. A mean age of 66 and a median age of 63.5 was found for the sample of 100 individuals. Calipers were used to collect anterior and posterior measurements of vertebral bodies from the first thoracic to the fifth lumbar vertebra, with each individual having fifteen to eighteen vertebral bodies. The greatest instances of collapse occurred within thoracic vertebrae with the highest occurrences in the seventh, eighth, and eleventh thoracic vertebrae, which is consistent with previous research. A total of 135 collapsed vertebrae were found throughout the sample occurring within 60% of the sample size, a significant increase from the original prediction. Within the individuals presenting the collapse, the mean age was 67.1 with a median age of 65 indicating that a collapse is most likely to be found in individuals ten years older than our minimum sampled age. From the data we can accept the hypothesis because the findings were 35% greater than expected.

The impact of walking posture on skeletal structure in the femoral epiphyses of *Rattus norvegicus*

AMERICA M. CAMPILLO[1], SHARON KUO[1], ADAM D. FOSTER[2] and TIMOTHY M. RYAN[1]

[1]Department of Anthropology, Pennsylvania State University, [2]Department of Anatomy, School of Osteopathic Medicine, Campbell University

Bone responds to mechanical loads through growth. This skeletal response to external loading has been important for reconstructions of past behaviors in extinct taxa. However, uncertainty still exists regarding the extent to which habitual locomotor patterns such as bipedalism or quadrupedalism are reflected in bone morphology. This study assesses the effects of different locomotor postures on bone structure of the femur in a rodent model (*Rattus norvegicus)*. The study individuals come from a previously-executed experiment (Foster, 2019) that utilized a treadmill-mounted harness system to induce bipedal walking postures in rats over 12-weeks. The sample included individuals from two experimental groups plus a control: fully-loaded bipedal walking, quadrupedal walking, and no exercise controls. Femora were microCT scanned at a resolution of 20µm and the external shape was analyzed and compared among groups using auto3dgm (Boyer et al., 2015) to assess the impacts of differences in hip postural angle on external bone shape. In both the proximal and distal femur, the no activity controls grouped together along PC1 (73% and 84% of the variation, respectively), and the fully loaded bipedal and quadrupedal groups overlapped. However, in the distal femur the fully loaded bipedal and quadrupedal individuals grouped closer together along PC1 whereas in the proximal femur, there was less separation among activity groups. These results suggest that the distal femoral epiphysis responds more to changes in hip postural angle than the proximal epiphysis. However, subsequent trabecular bone analyses may be more informative when analyzing locomotor changes than external morphology.

National Science Foundation (BCS 1153863), The Force & Motion Foundation, and the School of Anthropology at the University of Arizona

Investigation into robust methods for noninvasive detection of Simian Immunodeficiency Virus

TESSA H. CANNON[1], RAJNI KANT SHUKLA[2], CHRISTOPHER MADDEN[3], VANESSA HALE[3] and W. SCOTT MCGRAW[1]

[1]Department of Anthropology, The Ohio State University, [2]Department of Veterinary Biosciences, The Ohio State University, [3]Department of Veterinary Preventive Medicine, The Ohio State University

Human immunodeficiency virus (HIV) was originally introduced into human populations through zoonotic transmission of the simian lentiviruses infecting African primates, collectively referred to as simian immunodeficiency viruses (SIV). SIV occurs naturally in over 40 primate species in sub-Saharan Africa and these viruses have crossed species barriers on multiple occasions, leading to the spread of HIV-1 and HIV-2. Humans continue to be exposed to these RNA viruses through handling and consumption of primate bushmeat, so it is important to investigate wild-living nonhuman primate populations to determine approximate SIV prevalence and understand viral shedding in natural hosts. Here, we seek to identify the most robust "field-friendly" methods for storing and testing primate fecal samples for SIV (e.g. without freezing or refrigeration). Fecal samples from mandrills (*Mandrillus sphinx*) housed at the Columbus Zoo and Aquarium were inoculated with three known concentrations of inactivated SIV virus and preserved in four different storage buffers. SIV RNA was then extracted from samples at four time points across 12 weeks to determine the efficacy of each buffer for detecting SIV virus in primate fecal samples over time. Quantitative reverse-transcription (RT)-PCR was used for detection and quantification of viral RNA. By identifying significant differences in SIV detection and quantification between buffers and storage times, our results provide evidence for robust "field-friendly" methods to detect SIV in non-invasive fecal samples. These methods will be used to complete the first quantification of SIV viral load in fecal samples from wild sooty mangabeys (*Cercocebus atys*) from the Taï Forest, Côte d'Ivoire.

This work was made possible by an Infectious Diseases Institute Trainee Transformative Grant awarded to Tessa Cannon and Rajni Kant Shukla at The Ohio State University.

Tracing human mobility in Late Prehistoric Eastern Sudan (V-II millennium BCE)

GIUSY CAPASSO[1,2], FEDERICO LUGLI[3], ALESSANDRA SPERDUTI[4,5] and ANDREA MANZO[2,5]

[1]Department of Cultural Heritage, University of Padua, Italy, [2]Italian Archaeological Expedition to Eastern Sudan, (IAEES), [3]Department of Cultural Heritage, University of Bologna, Italy, [4]Bioarchaeology Service, Museum of Civilizations, Rome, Italy, [5]Department of Asian, African and Mediterranean Studies, University of Naples "L'Orientale", Italy

The dynamics of human settlement in Late Prehistoric Eastern Sudan have been the object of extensive research by the 'Italian Archaeological Expedition to Eastern Sudan' (IAEES), leading to the discovery of three different necropolises, yielding nearly 200 tombs dated to a wide chronological period ranging from the 5th to the 2nd millennium BCE.

Here we present the result of strontium isotope ($^{87}Sr/^{86}Sr$) analyses of human dental enamel, aiming to trace human mobility in the area from a diachronic perspective. Dental enamel of first or second permanent molars was sampled from 8 individuals from site UA50 (5th millennium BCE), 8 from site UA53 (4th-3rd millennium BCE) and 57 from the site K1 (3rd-2nd millennium BCE). The $^{87}Sr/^{86}Sr$ ratio was determined through multicollector inductively coupled plasma mass spectrometry (MC-ICPMS) analyses.

While during the 3rd-early 2nd millennium BCE most individuals show homogeneous, most likely local Sr signals, in the 5th millennium BCE and from the 2nd millennium BCE onwards mobility is likely to

be more pronounced. No significant differences in individual Sr signature are present between sexes. Furthermore, the results indicate that the diachronic change in funerary rituals attested at the K1 site – that appears in the more recent Gash Group graves (2500-1800 BCE) and in the Jebel Mokram ones (1800-1500 BCE) – might not be related to individual migratory phenomena.

The study was funded by ISMEO (International Association for Mediterranean and Oriental Studies), University of Naples 'L' Orientale', and the Italian Ministry of Foreign Affairs.

The Developmental Impacts of Natural Selection on Human Pelvic Morphology

TERENCE D. CAPELLINI[1], MARIEL YOUNG[2], DANIEL RICHARD[3], MARK GRABOWSKI[4], BENJAMIN AUERBACH[5], BERNADETTE DE BAKKER[6], JACO HAGOORT[7], PUSHPANATHAN MUTHUIRULAN[8], HELEN KURKI[9], LIA BETTI[10] and KRISTI LEWTON[11]

[1]Human Evolutionary Biology, Harvard University, [2]Human Evolutionary Biology, Harvard University, [3]Human Evolutionary Biology, Harvard University, [4]Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University, [5]Department of Anthropology, The University of Tennessee, [6]Department of Medical Biology, Section Clinical Anatomy & Embryology, University of Amsterdam, [7]Department of Medical Biology, Section Clinical Anatomy & Embryology, University of Amsterdam, [8]Human Evolutionary Biology, Harvard University, [9]Department of Anthropology, University of Victoria, [10]Centre for Research in Evolutionary, Social and Inter-Disciplinary Anthropology, University of Roehampton, [11]Department of Integrative Anatomical Sciences, University of Southern California

Bipedalism is a key adaptation that allowed for crucial behavioral shifts in human evolution. At the crux of bipedalism is the pelvis. Compared to African-ape pelves, human pelves, notably ilia, has been reduced in height, expanded in breadth, and curved parasagittally. Underlying pelvic adaptations are changes in the developmental regulation of genes. As most gene regions exhibit functional pleiotropy, regulatory sequences impact phenotypes in highly specific anatomical domains and timepoints. However, our understanding of pelvic developmental genetics is poor, especially in humans. We took an multidisciplinary approach to address this shortcoming. We first phenotypically examined human and ape pelves to assess morphological variation and evolvability, finding marked changes to human pelvic traits. Next, we used developmental biology and demonstrate that the unique human pelvic morphology emerges in its cartilaginous form by eight-weeks gestation, showing how selection shaped prenatal development. We then use transcriptomics and epigenomics to characterize cartilage cells extracted from human gestational pelvic elements and reveal its developmental genetic architecture. By taking an evolutionary perspective, we find notable evidence of ancient selection on regulatory sequences involved in pelvic-specific development, particularly for the ilium, and on sequences functional across the pelvis, the latter indicative of complex polygenic selection. We find that past selection has drastically reduced genetic variation across living humans specifically in ilium sequences, but in ilium morphology, serving to connect genome-wide regulatory patterns to phenotypic ones. Overall, our findings reveal key insights into the developmental genetics of a fundamentally critical human trait complex, the pelvis.

The authors received funds from Harvard University (Dean's Competitive Award) to conduct human studies, and from NSF (BCS1518596) to conduct mouse studies.

Relative limb strength in the 3.67 Ma hominin skeleton, StW 573 ("Little Foot"), and its implications for the role of arboreality in hominin evolution

KRISTIAN J. CARLSON[1,2], TEA JASHASHVILI[1,3], JASON L. HEATON[2,4,5], TRAVIS R. PICKERING[2,5,6], M. LORING BURGESS[7], LAUREN SARRINGHAUS[8,9], AMELIE BEAUDET[10,11,12], ROBIN H. CROMPTON[13], DOMINIC STRATFORD[11], KATHLEEN KUMAN[11], RONALD J. CLARKE[2] and CHRISTOPHER B. RUFF[14]

[1]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [2]Evolutionary Studies Institute, University of the Witwatersrand, [3]Department of Geology and Paleontology, Georgian National Museum, [4]Department of Biology, Birmingham-Southern College, [5]Plio-Pleistocene Paleontology Section, Department of Vertebrates, Ditsong National Museum, [6]Department of Anthropology, University of Wisconsin, Madison, [7]Osteology & Paleoanthropology Department, Peabody Museum of Archaeology & Ethnology, Harvard University, [8]Department of Evolutionary Anthropology, Duke University, [9]Department of Anthropology, University of Michigan, Ann Arbor, [10]Department of Archaeology, University of Cambridge, [11]School of Geography, Archaeology and Environmental Studies, University of the Witwatersrand, [12]Department of Anatomy, University of Pretoria, [13]Department of Musculoskeletal and Ageing Science, Institute of Life Course & Medical Sciences, University of Liverpool, [14]Center for Functional Anatomy and Evolution, Johns Hopkins School of Medicine, Johns Hopkins University

The ca. 3.67 Ma adult skeleton known as 'Little Foot' (StW 573), recovered from Sterkfontein Member 2 breccia in the Silberberg Grotto, is remarkable for its morphology and completeness. Both humeri and femora are preserved, making it the earliest such hominin example. Cross-sectional geometric (CSG) properties of these long bone diaphyses allow inferences into limb use and behavior because of plastic responses to loads incurred by diaphyses during life. Here, we analyzed CSG properties from regions of interest along left humeral and femoral shafts and evaluated them relative to one another and relative to body size estimates. We compared StW 573 proportions to those of other hominins and extant great apes. Results confirm StW 573 is more like chimpanzees and Western lowland gorillas than modern humans or other *Homo* taxa in relative femoral-humeral strength. In fact, StW 573 is modestly more African ape-like in this regard than *Australopithecus afarensis* (A.L. 288-1). Humeral strength relative to estimated body size firmly places StW 573 amongst most other australopiths for which comparable data are available and also amongst African apes, which tend to exhibit comparatively stronger humeri than modern humans or other *Homo* taxa. In contrast, StW 573 femoral strength relative to estimated body size is intermediate between that of African apes and *Homo*. While many StW 573 morphologies imply the adaptive importance of terrestrial bipedal gaits, limb bone CSG properties, reflecting in-vivo behavior of this 3.67 Ma individual, irrefutably indicate that arboreal activities formed a selectively advantageous part of its locomotor repertoire.

We thank the DSI-NRF of South Africa, The Palaeontological Scientific Trust (PAST), the University of the Witwatersrand, and the University of Southern California for funding this research.

Gut microbial plasticity in animal domestication and human industrialization

RACHEL N. CARMODY[1] and ASPEN T. REESE[2]

[1]Department of Human Evolutionary Biology, Harvard University, [2]Department of Biological Sciences (Ecology, Behavior & Evolution), University of California San Diego

Domesticated animals and industrialized humans have experienced rapid, profound changes in diet, environment, and social interactions that have shaped the gut microbiota. Sequencing the gut microbiota of domesticated and wild mammals plus humans from industrialized and non-industrialized populations, we confirmed strong gut microbial signatures of domestication and industrialization, and we observed parallel changes in gut microbiota profile across these distinct processes. In mice and canids, wild-domesticated differences in the gut microbiota and its functional potential could be partially reset by swapping diets between members of a wild-domesticated pair, suggesting that domestication-associated differences in the gut microbiota were driven by ecological selection as well as host-specific factors. To probe whether gut microbiota changes could have benefited the host under domesticated conditions, we transplanted gut microbial communities from wild and domesticated mice fed wild or domesticated diets into gnotobiotic mice fed wild or domesticated diets, assessing the physiological implications of differences in donor microbiota, donor diet, current diet, and their complex interactions. Taken together, our results suggest that gut microbial plasticity could have facilitated host adaptation to the ecological changes associated with domestication.

Whether similar gut microbiota changes have assisted humans in adapting to industrialized lifestyles, or whether gut microbial plasticity has instead increased host-microbiome-environment mismatch with deleterious consequences for human health, remains unclear. Elucidating when, why, and how gut microbial plasticity affects host response to ecological change has critical implications for our understanding of past, present, and future human health.

This study was supported by the William F. Milton Fund and Dean's Competitive Fund for Promising Scholarship at Harvard University.

Female geladas accelerate weaning in larger groups – possibly to reduce infanticide risk

SOFIA C. CARRERA[1], ALICE BANIEL[2,4], JACOB FEDER[3], NOAH SNYDER-MACKLER[4], THORE BERGMAN[1,5], JACINTA BEEHNER[1,6] and AMY LU[2]

[1]Department of Psychology, University of Michigan, [2]Department of Anthropology, Stony Brook University, [3]Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, [4]Center for Evolution and Medicine, Arizona State University, [5]Department of Ecology and Evolutionary Biology, University of Michigan, [6]Department of Anthropology, University of Michigan

Weaning is a classic example of parent-offspring conflict. Extended nursing provides benefits to infants but comes at a cost to mothers' future reproduction. Accelerated weaning can result from either greater maternal access to resources or exposure to environmental risks. In some cases, accelerated weaning may also serve to protect infants from threats, such as male-mediated infanticide. In wild geladas (*Theropithecus gelada*), the leading cause of infant mortality is infanticide following the arrival of a new breeding male. Male takeovers are more frequent in larger groups, therefore females in larger groups may benefit from accelerating all weanings, even in the absence of an actual takeover event during lactation. Here, we determined the effect of group size on the likelihood of a mother's resumption of cycling, as based on sexual swellings (N = 66) – a commonly used marker of weaning – in a population of wild geladas living in the Simien Mountains National Park, Ethiopia. Removing actual takeover weanings, we nevertheless found that those in larger groups were more likely to resume cycling (i.e., wean) at any given age (HR = 1.4, z = 2.82, $p < 0.01$). Females in large groups do not experience faster maternal reproductive rates (i.e., inter-birth intervals) in this population, therefore we believe the benefits of accelerated weaning may lie chiefly in avoiding sexually selected infanticide.

National Science Foundation (BCS-1945701, BCS-0715179, BCS-1723228, IOS-1255974, IOS-1854359, BCS-1723237, BCS-2010309), Leakey Foundation, National Geographic Society (NGS-8100-06, NGS-8989-11, NGS-1242, NGS-50409R-18), Fulbright Scholars Program, University of Michigan, Stony Brook University, Arizona State University.

Assessing the performance of Advanced Normalization Tools (ANTs) in automating skeletal phenotype extraction from large datasets of 2D images

CHELSEA C. CATALDO-RAMIREZ[1], DAVID HADDAD[2], NINA AMENTA[2] and TIMOTHY D. WEAVER[1]

[1]Department of Anthropology, University of California, Davis, [2]Department of Computer Science, University of California, Davis

Many disciplines have benefited greatly from the recent rise of big data and computational power. However, our ability to extract skeletal phenotypes is typically limited to how efficiently a researcher can manually place landmarks or extract outline data. For large medical imaging databases manual extraction of anatomical data is not feasible because of the time involved. To combat this, we assessed the performance of an existing image registration framework (Advanced Normalization Tools [ANTs]) on automating the extraction of postcranial skeletal metrics from total body DXA scans in the UK Biobank (project 54084). The ANTs pipeline consists of manually landmarking an atlas image and then registering every non-landmarked image (the "moving images") to the atlas through a series of linear and non-linear transformations. At this point the landmarks are propagated from the atlas to each transformed moving image and then inverse-transformed back to the original form of the respective moving image. A set of 23 DXA images were manually landmarked with 35 landmarks each, representing 18 linear distances throughout the skeleton. Each image was then tested as the atlas image to guide landmark propagation onto all other images (n = 506 pairs), and the percent error between manually-derived inter-landmark distances and propagated distances were calculated for each measurement. On average, metrics from the axial skeleton outperformed those from the limbs, and the lower limb outperformed the upper limb suggesting that with further modifications, ANTs can be utilized for automated 2D anatomical data extraction from the thoracic cavity, pelvis, and lower limb.

University of California, Davis

Calcar femorale variation in extant and fossil hominids and its relationship with bipedalism

MARINE CAZENAVE[1], TRACY L. KIVELL[1,2,3], MARTA PINA[4,5], DAVID R. BEGUN[6] and MATTHEW M. SKINNER[1,2,3]

[1]Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, Canterbury, UK, [2]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, [3]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand, Johannesburg, South Africa, [4]Interdisciplinary Centre for Ancient Life, School of Natural Sciences, University of Manchester, Manchester, UK, [5]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, Cerdanyola del Vallès, Spain, [6]Department of Anthropology, University of Toronto, Toronto, Ontario, Canada

The calcar femorale (CF) is a vertical to slightly oblique spur of thickened bone, internal to the lesser trochanter of the proximal femur, considered to be functionally related to bipedal locomotion. It has recently received attention due to its identification in the early hominin *Orrorin tugenensis*. However, beyond its anatomical description in recent humans, among primates the presence of the CF has only been investigated in the rhesus monkey and detected in chimpanzees, one *Australopithecus* and in a Middle Pleistocene *Homo* femur. Using high-resolution microtomography, we investigated the occurrence, 3D morphology and size variation of the CF in a mixed-sex, adult sample of humans, *Pan troglodytes*, *Gorilla gorilla*, *Pongo* sp. and *Papio ursinus*, as well as in a late Miocene great ape (*Rudapithecus*) and five Plio-Pleistocene hominins from southern and eastern Africa (*Australopithecus* and *Paranthropus*). In our analyses, 9/10 humans, 6/10 *Pan*, 6/10 *Gorilla*, 1 captive *Pongo* and none of the *Papio* specimens show a distinct CF. The CF's morphology and dimensions vary across taxa; only its height, systematically higher and extended into the lower part of the lesser trochanter, discriminates humans from the extant nonhuman apes (except for one *Gorilla*). A variably-developed CF occurs in all fossils (including the Miocene *Rudapithecus*) except in one *P. robustus* femur. These results indicate that the CF cannot be reliably considered as a diagnostic trait of habitual bipedal locomotion and emphasizes the need for further investigations on the functional role of this feature.

MC is funded by the Fyssen Foundation. This project has received funding from the European Research Council (grant agreement No. 819960) and NSERC (RGPIN-2016-06761).

Rural Embodiment and Child Health (REACH) Study: Effects of resource access and macroparasite exposure on intestinal inflammation among children from rural Mississippi

TARA J. CEPON-ROBINS[1], ELIZABETH K. MALLOTT[2], ISABELLA C. RECCA[1] and THERESA E. GILDNER[3]

[1]Department of Anthropology, University of Colorado Colorado Springs, [2]Department of Biological Sciences, Vanderbilt University, [3]Department of Anthropology, Washington University in St. Louis

Embodiment Theory describes how external environments and lived experiences shape internal physiology and health. Documented disparities in rates of intestinal inflammation and gastrointestinal cancers between Black and white Americans may be related to embodied experiences of psychosocial stress, unequal access to resources, and exposure to pathogens. Here we test relationships between resource access (household income level, measures of nutritional status [WHO-defined BMI-for-age/Height-for-age z-scores]), macroparasite infection status (measured using 18S rRNA gene amplification/sequencing), and fecal calprotectin concentrations (FC; a biomarker of intestinal inflammation measured using ELISA) among 24 children (ages 6 months to 14 years) from a predominantly Black community in rural Mississippi. Median FC in this sample was 140 ug/g. 83% of children had clinically elevated FC levels (>50 ug/g). Bootstrap linear regression and analysis of covariance tests were used to examine relationships between FC levels and lifestyle, anthropometric, and infection variables. Household income ($p = 0.07$; 95%CI = -86.93, -0.53) and BMI z-scores ($p = 0.02$; 95%CI = -180.92, -10.21) were negatively associated with FC levels. Several macroparasitic infections were discovered, including infections with nematodes ($n = 2$) and platyhelminths ($n = 5$). Children experiencing platyhelminth infections had higher FC ($n = 5$; $p = 0.019$; $\eta p2 = 0.283$), though this appears to be driven by variables related to resource access. These findings suggest that embodied experiences associated with unequal resource access in rural environments may be contributing to elevated rates of intestinal inflammation among children, with implications for the development of chronic health conditions in adulthood.

Support: Boettcher Foundation Webb-Waring Biomedical Research Grant; Dartmouth College McKennan Postdoctoral Fellowship; Dartmouth College Claire Garber Goodman Fund; University of Colorado Colorado Springs

Taphonomy and care of subadults from the Neo-punic Tophet at Zita, Tunisia

JESSICA I. CEREZO-ROMAN[1], BRETT KAUFMAN[2], GLENYS MCGOWAN[3], ALI DRINE[4], THOMAS R. FENN[5], HANS BARNARD[6], RAYED KHEDHER[7], SAMI BEN. TAHAR[8], STACY EDINGTON[9] and ELYSSA JERRAY[10]

[1]Department of Anthropology, University of Oklahoma, [2]Department of the Classics, University of Illinois at Urbana- Champaign, [3]School of Social Science, The University of Queensland, [4]Institut National du Patrimoine, Institut National du Patrimoine, [5]Department of Anthropology, University of Oklahoma, [6]Department of Near Eastern Languages and Cultures, Cotsen Institute of Archaeology, University of California, Los Angeles, [7]Arab Studies, Davidson College, [8]Institut National du Patrimoine, Institut National du Patrimoine, [9]Department of Anthropology, Baylor University, [10]Centre Camille Jullian, Aix-Marseille University

Tophets are Phoenician and Punic sanctuaries where cremated infants and young children were placed in urns and ritually interred, possibly after first being sacrificed. Classical and biblical authors and modern scholars have focused on the presence or absence of ritual sacrifice within these cultures and contexts. This paper explores the posthumous treatment of subadults found in a tophet at the Neo-Punic site of Zita, near modern Zarzis, Tunisia, to reconstruct how the individuals were treated at the time of death and if it is tied to issues of care. This is done by analyzing the biological profile of the individuals, the thermal alterations, and the taphonomy. We did not find direct evidence of sacrifice. Instead, we found evidence suggesting that individuals were buried with care and that systemic health problems likely affected their lives and contributed to their deaths. These results broaden the use of tophets to include individuals that were not likely sacrificed but died due to health issues.

Social strategies of male bonobos during intergroup encounters

LEVEDA CHENG[1,2], LIRAN SAMUNI[1,2], STEFANO LUCCHESI[1,2], TOBIAS DESCHNER[2] and MARTIN SURBECK[1,2]

[1]Department of Human Evolutionary Biology, Harvard University, [2]Interim Group Primatology, Max Planck Institute for Evolutionary Anthropology

In many male-philopatric species, males form strong affiliative and cooperative relationships within the group, but largely hostile relationships between groups. However, maintaining friendly relationships with neighbours can bring benefits, such as increased protection against predation and/or common rivals, and buffer against harsh ecological conditions. Amicable intergroup relationships also form the basis for large-scale cooperation in humans. Consequently, in many small-scaled human societies, conflicts between groups are often resolved through truce-making and peace is maintained through ritualistic behaviour. To better understand the evolutionary origins of the variation in male strategies during intergroup conflicts, we investigated male aggressive and affiliative interactions with in-group and out-group individuals in bonobos, one of our closest living relatives. We followed two neighbouring bonobo groups for over 3700 hours and collected behavioural data during 92 naturally occurring intergroup encounters in the Kokolopori Bonobo Reserve, Democratic Republic of Congo. Although intergroup interactions were largely tolerant, males still incurred costs from intergroup aggressions (e.g., injuries). However, in-group males rarely formed coalitions against out-group males or females. Unlike patterns observed in male-philopatric species, male bonobos did not show a strong in-group bias in affiliation, and they actively groomed with out-group individuals, especially out-group males. Together, our findings provide insights into potential evolutionary scenarios allowing for the development of male social and cooperative networks that extend beyond the group level.

This study was funded by Harvard University, the Max Planck Society, and the Leaky Foundation.

Comparisons in mortality risk between cause of death categories in a subsample of the Terry Collection

COLLEEN M. CHEVERKO

Biomedical Affairs, VCOM-LC

Recent studies have sought to understand differences in morbidity and mortality between attritional and catastrophic burial assemblages to help researchers uncover differences in hidden heterogeneity and selective mortality. These studies rely on assumptions that most individuals in those samples died through similar causes, either during short-term events or long-term attritional patterns. However, most bioarchaeological samples cannot exclude most non-natural causes of death such as accidents that do not leave perimortem skeletal evidence. The purpose of the current paper is to compare early life stress indicators, age-at-death, and cause of death in a subset of 209 individuals of European descent within the Terry Collection to explore the effect of including individuals with documented non-natural causes of death on interpretations made about mortality risk in skeletal samples. Cause of death was condensed into three categories: infectious, degenerative, and non-natural (e.g., accidental or traumatic). Statistics were run separately using a 'full' sample that included all individuals in the sample ($n=209$) and a 'trimmed' sample excluding those with a documented non-natural cause of death ($n=184$). While the age-at-death distribution in the non-natural cause of death sample differed significantly from the 'trimmed' sample (Female: $t=-1.744$, $p=0.04$; Male: $t=3.50$, $p<0.001$), only one statistical test investigating correlations between early life stress indicators (LEH, stature, and body proportions) and adult mortality risk using age-at-death as a proxy differed between the full

and trimmed samples. These results suggest that comparisons between the full and trimmed sample do not significantly impact interpretations being made about mortality risk in this sample.

This work was supported by the Ohio State University Office of Energy and the Environment, a Larsen Travel Award, and a Coca Cola Critical Difference for Women Grant.

Trabecular bone morphology in Holocene and late Pleistocene modern humans

HABIBA CHIRCHIR[1,2], CAROLINE CARTWRIGHT[1], ANNA RAGNI[3] and JEAN-JACQUES HUBLIN[4,5]

[1]Biological Sciences, Marshall University, [2]Human Origins Program, Smithsonian Institution, [3]Biological Sciences, California State University Los Angeles, [4]Chaire de Paléoanthropologie, Collège de France, Paris, [5]Evolutionary Anthropology, Max-Planck-Institute for Evolutionary Anthropology, Leipzig

Research suggests that recent modern humans have gracile skeletons in having low bone volume fraction, BVF. Specifically, that gracilization of the skeleton occurred in the last 10,000 years with animal and crop domestication and an increase in sedentism. Thus, gracilization has been attributed to a reduction in physical activity in the Holocene. However, there has been no thorough sampling of Pleistocene hominins due to limited access to fossil specimens. Additionally, there are results suggesting that hunter-gatherers are as robust as other non-human primates. Therefore, our study investigates gracilization of BVF in late Pleistocene humans and recent (Holocene) modern humans with different subsistence strategies to improve our understanding of the emergence of gracility. We predict that Upper Paleolithic humans exhibit greater BVF than recent humans. We measured BVF in femora, humeri and metacarpals of Upper Paleolithic hominins- Dolni Vestonice, Ohalo II, Barma Grande- and recent humans including agricultural populations, foragers, and hunter-gatherers using microCT imaging. We found significantly lower ($p<0.05$) BVF in the humeri of agricultural groups than in the Upper Paleolithic hominins and the hunter-gatherers. The Upper Paleolithic femora exhibit a greater BVF mean than the agricultural, but are not significantly different. The metacarpal BVF did not show significant differences across groups however, they did not include Upper Paleolithic samples. Overall, results support our prediction that Upper Paleolithic humans are robust compared to recent humans and highlight the variation in gracility in human groups among diverse subsistence strategies. Therefore, sampling of recent humans with different subsistence methods is still needed.

Sex Estimation for Commingled Sub-adults: Comparison of morphological and proteomic methods

CECELIA CHISDOCK, MAXWELL LANDER and SUSAN GUISE SHERIDAN

Department of Anthropology, University of Notre Dame

While methods of skeletal sex estimation are improving, blind spots in their effectiveness still exist- namely sub-adults and poorly preserved/commingled collections. We applied morphological and proteomic sex estimation methods to a small sample of commingled sub-adults from St. Stephen's monastery (5th-7th c. CE, Jerusalem) to compare their applicability in such circumstances. Each individual was represented by >½ of a mandible (n=7). Teeth were sampled for proteomic sex estimation using liquid chromatography-mass spectrometry to detect sexually dimorphic amelogenin proteins in enamel. All individuals were successfully analyzed, five identified as male (AmelY present) and two as female (no AmelY detected) though the samples' low quality of recovered proteins makes this tentative. Morphological features assessed (preservation permitting) included: chin protrusion, anterior dental arcade shape, gonial eversion, mandibular corpus shape, and symphyseal base shape. When considered individually against the proteomic data, arcade shape shows the highest agreement (5/6, 83.3%)- all others fell below 50%. When considered as a combined sex estimate only 3/5 samples (60%) agreed with proteomic results. Further, some features did not preserve well enough to be utilized (gonial eversion), while others proved difficult to identify even with sufficient preservation (shapes of the corpus and symphysis). While sample size is limited, these results lend credence to the proteomic method for sex estimation in fragmented and sub-adult collections, though identification of females needs refinement. Comparatively, morphological estimates had varying success in previous studies and continue to demonstrate this trend, making their application tenuous, especially when preservation is low.

National Science Foundation Graduate Research Fellowship Grant No. 1841556; University of Notre Dame Institute for the Study of Liberal Arts Graduate Student Research Award and Senior Thesis Grant

The impact of precipitation and humidity on East Asian skeletal variation

ELIZABETH O. CHO[1,2], LIBBY W. COWGILL[2] and GREGORY E. BLOMQUIST[2]

[1]Center for Anatomical Sciences, University of North Texas Health Science Center, [2]Department of Anthropology, University of Missouri

Asia, with its diverse range of climates, remains poorly represented in the study of human ecogeographic body proportions. The monsoon is a significant environmental force in East Asia with two distinct phases. The southwest winds of the summer component cross the equator bringing heavy rain during the warmer months of the year while the winter's northeastern winds bring cold, dry air from Siberia during the coldest months. Previous assessment of Asian body form and minimum temperature during the monsoon's winter phase has found body size to conform with Bergmann's rule while limb length patterns did not follow Allen's rule. These analyses found that Southeast Asians are small overall, possibly due to the greater selective pressure of living in a humid climate which is exacerbated by the monsoon's summer component. Reduction in body size could allow for better thermoregulation as the climate conditions are not conducive to heat dissipation via sweat evaporation. For this study, cranial, nasal, pelvic, limb, hand, and foot measurements were gathered on male (N=460) and female (N=439) individuals from 13 collections across East Asia. Osteometric data and proportional indices were combined with matched autosomal SNP data, precipitation, and humidity data using linear mixed model analysis to evaluate the selective pressure of these climatic factors specifically associated with the monsoon. The influence of both climate variables was found to vary depending on the region of the body assessed, further supporting the need to assess the body as a whole and highlighting the complexity of climatic adaptation.

NSF Biological Anthropology DDRIG (#1847486) and Wenner-Gren Dissertation Fieldwork Grant (#9693)

Infant black and white colobus gut microbiome associations with age and social contact

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

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

The primate gut microbiome is influenced by host demography, behavior, diet, environment. These factors lead to varying microbial composition across individuals, groups, and populations. The development of the primate gut microbiome during infancy is less understood. We collected behavioral data and characterized gut microbial communities in infant black and white colobus monkeys (*Colobus vellerosus*) across 4 social groups from Boabeng-Fiema Monkey Sanctuary, Ghana. Colobus infants ranged in age (2 -18 months) and data were collected during the same season over multiple years. Using 16S rRNA barcoding of the V4 hypervariable region, we found variation in gut microbial alpha diversity across this age cohort (measured via Shannon Index; range: 6.19-8.30). Infant age was highly predictive of this variation when accounting for social group ($p<0.01$) and alpha diversity increased with

infant age. However, a large degree of variation was unexplained by demographic factors alone. We also found varying levels of allomaternal care across infants, measured via number of social partners (range: 4-12) and rates of non-maternal handling and care behaviors. The number of social partners and degrees of social contact influences the diversity of microbes an infant is exposed to via social contact. We will use this variation in social contact to determine how strongly social transmission of microbes shapes infant gut microbiomes. Exploring the relationship between social interaction and gut microbial diversity and composition in infant primates during this critical window of growth and development could have implications for adult gut microbial diversity and ultimately primate health and immune function.

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

Seasonal Variation for Parasitic Infection among Yucatec Maya Children

LAUREN CHRISTOPHER[1], AMANDA VEILE[1] and KAREN KRAMER[2]

[1]Anthropology, Purdue University, [2]Anthropology, University of Utah

Microbial and parasitic exposures are high for many small-scale farmers in low-income regions. Others have experienced or are navigating an epidemiologic transition associated with greater biomedical care access and the implementation of modernized sanitary infrastructure. These changes impact child health, including the incidence rate of intestinal parasites. We examine the incidence and seasonality of intestinal parasites in children from a small-scale Yucatec Maya farming community. Our goals were: 1) calculate the incidence proportion of intestinal parasitic infection, and 2) determine seasonal patterning for parasitic diagnoses. We accessed data for parasitic infection status, collected monthly for 100 children aged 0-5 years (2007-2014, 2623 observations) as part of the *Oportunidades* government program. We calculated the incidence proportion of cases per total observations and a time series linear regression testing seasonal variation. Incidence proportions for intestinal parasites were low (15 cases across the study duration). In 2008, 2009, 2010, and 2014, 6%, 2%, 4%, and 1% of children were diagnosed with an intestinal parasitic infection, respectively. All cases but one occurred in February, May and June. In 2008 and 2010, this seasonal pattern was statistically significant (p-value < 0.001; p-value <0.005, respectively). We report seasonally variable parasite risks, but parasite incidence declined across the study duration. Maya breastfeeding and caregiving practices may buffer young infants (<2 years) from parasitic infection, and improvements in health care may account for the decline of parasitic infections. Future analyses will focus on the specific parasitic risks for Maya children and potential long-term effects on growth and development.

Funding was awarded by the National Science Foundation Grant #0964031

Advances in Subadult Age Estimation: Evaluating the Performance of the Mixed Cumulative Probit (MCP) on Contemporary Subadults

ELAINE Y. CHU[1], CHRISTOPHER A. WOLFE[1], LOUISE K. CORRON[1], MICHAEL H. PRICE[2] and KYRA E. STULL[1]

[1]Department of Anthropology, University Of Nevada, Reno, [2]Applied Complexity Fellow, Santa Fe Institute

When generating new methods for estimating the biological profile, it is important to consider model accuracy, precision, and generalizability but also whether the algorithm is appropriate for the structure of the underlying data. The MCP algorithm accounts for features that are inherent to biological data and multivariate models, namely heteroskedasticity, mixed (ordinal and continuous) data, missing values, and conditional dependence. Univariate and multivariate models using diaphyseal dimensions, epiphyseal fusion scores, and dental development scores were trained on a sample of 1317 individuals from the United States (U.S.) aged between birth and 21 years-old from the Subadult Virtual Anthropology Database (SVAD). Four-fold cross-validation was used for model selection of six ordinal and two continuous univariate model specifications. Model performance was evaluated for accuracy and precision on 20% of the U.S. sample. An additional 267 individuals from the SVAD South African (Z.A.) sample aged birth to 12 years-old were used to evaluate model generalizability. Heteroskedasticity was identified for most variables. Conditionally dependent models outperformed conditional independent models and multivariate models consistently outperformed univariate models. Accuracy for the U.S. and Z.A. samples ranged between 0.92-0.98 and 0.71-0.97, respectively. Precision, evaluated by root-mean-squared error, ranged from 0.81-7.19 for the U.S. sample and 0.45-4.85 for the Z.A. sample. Accuracy and precision were comparable across the two test samples for diaphyseal dimensions, demonstrating relatively strong generalizability of the MCP models for long bones, over epiphyseal fusion and dental development, with accuracy ranges falling within or improving on those reported for other subadult age estimation methods.

Funding sources: This research was funded by two federal grants (NIJ 2015-DN-BX-K409 and NIJ 2017-DN-BX-K144).

A New Application of 3D Modelling to Comparative Sex Estimation

ELIZABETH CHURCH and CAROLYN RANDO

Institute of Archaeology, University College London

This abstract is part of the invited symposium 'Advances and Challenges in the Identification of Sex and Gender in Human Osteological Contexts'.

As biological anthropology and related fields begin to apply new digital information systems, it is important that these new sources of data are utilized to the fullest potential. Novel approaches have an obligation in research design to be conscientious of the ethical and social responsibilities inherent in osteological and technological data. This research is an investigation into using 3D os coxae models to create a reference database for sex estimation. This technique, called blank-model comparison (BMC), is not reliant on a traditional metric (landmark or electronic measurement) or non-metric (morphological scoring) frameworks. BMC uses a combination of GMM silhouette analysis, cloud-cloud comparison and nearest-neighbor statistical analysis to place an unknown model against a reference model-set, which has been arranged along a scale of internal parameters. The unknown model is seriated into a known position within this scale, and can be estimated as more female, more male or placed with transitional areas displaying combinations of overall population-shape. This is a more flexible and interpretive estimation compared to binary categorizations. An overview of the SfM photogrammetry workflow and editing process is presented, in addition to steps taken to preserve the new digital database. Open-source software was used throughout. The reference database is comprised of specimens from St. Bride's Fleet Street, Spitalfields, Luis Lopes and SIMON Geneva, with the potential for any collection-specific digital database to be added in future.

Examining the role of competition in *Cercopithecus mitis* and *Cercopithecus ascanius* dietary morphology

TESSA CICAK

Anthropology, University of Minnesota

Character displacement, or morphological change in response to competition, is widely documented, but few studies focus on primates. *Cercopithecus mitis* and *Cercopithecus ascanius* are typically frugivorous and often associate in multispecies groups, making them good candidates to test the hypothesis that sympatric primates respond to food competition by utilizing alternative resources, resulting in greater differences in molar shape than their allopatric counterparts. Dental impressions were gathered from *C. mitis* and *C. ascanius* collected from sympatric sites of Kisangani and Akenge, DRC, and allopatric sites of Kunungu, DRC, and Tana River, Kenya. Sympatric specimens overlapped in time and

space and allopatric samples were chosen with regard to climate and forest structure ensuring adequate comparability between allopatric and sympatric sites. Using micro-CT scans of m1-m3 (n=215), Dental Topographic Analysis variables were extracted using MolaR. Dirichlet Normal Energy, Relief Index, and Orientation Patch Count Rotated were calculated for each tooth position. To quantify the effect of sympatry/allopatry on morphology, a displacement statistic was calculated for each DTA variable at each tooth position. Of the 32 analyses, 19 returned larger sympatric vector values suggestive of competition. While none researched significance, 12 of the analyses had $P < 0.5$ indicating the pattern is not random. These results are suggestive of competition induced character displacement in *C. mitis* and *C. ascanius*. Non-random values were especially common in RFI and DNE vector length results. Higher RFI and DNE scores may indicate higher reliance on fibrous foods at sympatric sites where competition is greater.

Supported by NSF (grant no. BSC2018642); The Leakey Foundation; The University of Minnesota Bell Museum; University of Minnesota Graduate School: Thesis Research Travel Grant and Doctoral Dissertation Fellowship

Physiological response to multimedia engagement and domestic fires

LINDSEY E. CLARK[1], ALEX M. SENTS[2], LAUREN A. LANDGRAF[3], MATTHEW PAPPALARDO[2] and CHRIS D. LYNN[2]

[1]Department of Educational Psychology and Neuroscience, University of Alabama, [2]Department of Anthropology, University of Alabama, [3]Department of Philosophy, University of Alabama

TV use in the household is so prevalent that some wonder whether its effects are beneficial or if they are potentially addictive. However, the basic audiovisual sensory components of TV and campfires are strikingly similar, which could indicate that watching television stimulates comparable cognitive mechanisms. Previous research indicates the effects of watching a fire may provoke a hypnotic absorptive state where an individual's perception, memory, and mood are altered by their sensory experiences. Here, we test if the characteristics of small fires such as flickering light and crackling sounds enhance this hypnotic effect. Participants include 54 individuals between the ages of 18 and 40 who were recruited from a university student participant pool. Those in the experimental condition watched clips of fires while we measured relaxation response pre- and post-trial via blood pressure and skin conductance. Covariates, including questionnaires regarding hypnotic absorption, prosociality, and fire fascination were measured before the experimental conditions began. We predicted that relaxation, measured by the change in blood pressure and skin conductance per trial, would occur in the conditions that most resembled a naturalistic small hearth or campfire at night. Additionally, we predicted that those who score higher on absorption, prosociality, and fire fascination would demonstrate higher relaxation responses in these conditions. Preliminary data analyses suggests that differences in blood pressure in the multisensory fire and multimedia conditions indicates a stronger relaxation effect relative to the sound of fire alone or a control condition.

Age Estimation: It isn't easy, but it sure is hard enough

MELISSA CLARK[1], COLLEEN M. CHEVERKO[2], ALLYSON SIMON[3], EMMA M. LAGAN[3] and MARK HUBBE[3,4]

[1]Department of Criminology, Anthropology, and Sociology, Cleveland State University, [2]Biomedical Affairs, Edward Via College of Osteopathic Medicine, [3]Anthropology, The Ohio State University, [4]Instituto de Arqueología, Universidad Católica del Notre

Estimating age-at-death is a critical yet difficult step to studying past lifeways, so bioarchaeologists constantly seek to improve the accuracy and precision of age estimation methods. Efforts at refinement are necessary, but they have produced a suite of methods which could limit the comparability of datasets depending on the method(s) employed. It is therefore necessary to reflexively examine the methods bioarchaeologists are using to estimate age. In this paper, we first compare the use of common age estimation methods, including comparing between traditional methods and transition analysis. Second, we report how frequently each traditional aging method was used between 1990 and 2020 and compare our findings to those of Falys and Lewis (2011). Finally, we build on the work of our colleagues by examining trends in the minimum age at adulthood, age categories, and geographic region of institutional affiliation of the first author. In doing so, we found that transition analysis does not appear to be a major source of variation because it has been used in a relatively small number of studies so far. However, we found significant variation in the type of traditional method used, minimum age at adulthood, and adult age categories, which could impact the comparability of results across studies or researchers. This paper highlights the need for continued discussions about standardization in bioarchaeology and the need for bioarchaeologists to continue avoiding applications of methods derived using reference samples that differ markedly from target samples.

Morphology of the cercopithecoid mandibular P3 and its correlation with sex and diet

SAVANNAH E. COBB[1], CLAIRE A. KIRCHHOFF[2], CLAIRE E. TERHUNE[3], ANDREA R. ELLER[4] and SIOBHÁN COOKE[1,5]

[1]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, [2]Department of Biomedical Sciences, Marquette University, [3]Department of Anthropology, University of Arkansas, [4]Department of Anthropology, National Museum of Natural History, Smithsonian Institution, [5]New York Consortium in Evolutionary Primatology Morphometrics Group

The cercopithecoid "honing facet" on the mandibular third premolar (p3), an elongate enamel extension upon which the upper canines hone, has been well-studied for its correlation with sex and behavior. However, other aspects of cercopithecoid p3 morphology, such as the basin located distal to the protoconid, have not yet been analyzed. Biomechanical inference suggests p3 morphology reflects a functional division of the tooth into a mesial enamel extension adapted for canine honing, and a distal basin adapted for mastication. If so, relative lengths of these sections should correlate with both sex and diet. Linear measures were taken on meshes of cast mandibles from 49 adults, male and female, comprising seven genera (*Macaca, Papio, Cercopithecus, Lophocebus, Nasalis, Colobus, Theropithecus*) and three dietary categories (folivore, frugivore, granivore). Boxplots and Kruskal-Wallis tests show a significant relationship between p3 distal basin length with diet, and p3 honing facet length with sex. Folivores tend to have the largest p3 basins, and across all species, males have relatively longer honing facets than females. A third measure, angle of the protoconid, significantly correlated with both sex and diet. Linear discriminant analyses (LDAs) using all three measures on p3 classified sample taxa by sex and/or diet with 67-86% accuracy. When mandibular canine height and m2 length were added to the LDA, accuracy increased to 84-93%. Linear measures of p3 can provide insight into both sex and diet, which has implications for paleontological study, particularly the evolutionary transition between folivorous colobines and frugivorous cercopithecines.

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

Neandertal newborn noggins & Portmann's Secondary Altriciality

ZACHARY COFRAN[1] and JEREMY M. DESILVA[2]

[1]Anthropology Department, Vassar College, [2]Department of Anthropology, Dartmouth College

Portmann famously described humans as "secondarily altricial," born under-developed and growing up in a rich cultural environment. Altriciality has been invoked to explain humans' high rates of early postnatal brain size growth, which in turn

have been correlated with our slow life history. Previous research has variously concluded that Neandertal brain growth rates were either similar to, or faster than, those of modern humans, with disparate implications for Neandertal life history. To help resolve this discrepancy, we use simulation methods to compare brain growth in of modern humans (N=253) and Neandertals (N=39) from birth to adulthood. Simulations take into account small sample size and uncertainty in fossil brain size and age at death.

The first approach uses resampling to calculate the average annual rate of growth (cm^3/year) between a random newborn and a random individual in the age range of the immature Neandertal sample (1.5–12.0 years). Resampled Neandertal rates fall within the human distribution at all ages. The second approach iteratively fits a curve and asymptote to an ontogenetic series, to estimate the rate and duration of growth. The Neandertal data initially suggest a longer duration of slower brain growth (222 cm^3/ year for 4.23 years) compared with humans (343 cm^3/year for 2.5 years). However, simulations show that the Neandertal values fall well within the human confidence limits when the latter are constrained to a fossil-like sample size and age composition. We discuss these results in light of dental and skeletal evidence for Neandertal growth and life history.

The correlation between sex and ancestry in Greek Cypriots and Cretans using the humerus

SAMANTHA A. COHEN[1], XENIA-PAULA KYRIAKOU[2], JULIETTA GOMEZ[3] and ELENA F. KRANIOTI[4]

[1]Odyssey Field School, Centre for Forensic Anthropology and Bioarchaeology, Cyprus, [2]Department of Justice Studies, Florida Gulf Coast University, [3]Center for Anatomy and Human Identification, School of Science and Engineering, University of Dundee, Scotland, UK, [4]Forensic Medicine Unit, Department of Forensic Sciences, University of Crete, Medical School, 71110, Heraklion, Greece

Migratory patterns that existed since ancient times shaped the culture and genetics of the eastern Mediterranean region. The proximity of the islands of Crete and Cyprus to the Middle East, suggest that some biological overlap might exist that might transpire in the shape of skeletal elements. Thus, reference collections from these islands can play a vital role for the development of identification standards to aid repatriation efforts for Missing persons from armed-conflict and deceased migrants. A total of 232 adult left humeri (119 Cretans; 113 Greek-Cypriots) were used from two contemporary collections. Six measurements were used to calculate two ratios (R1=100*HVD/HumL; R2=100*DBr/HumL) to assess the shape of the humerus. Sex and ancestry equations were created using linear regression analysis. The means between males and females were found statistically significant ($p<0.001$) in both populations. Sexual dimorphism was more pronounced in Cretans. Males exhibited statistically significant differences in three measurements and females in two. R2 was found to differ significantly between subgroups for both sexes. Logistic regressions correctly classified 75% of males and 82.1% of females into the correct population subgroup. Cretans have higher R2 ratios compared to Cypriots in both males and females which indicates more robust distal epiphyses compared to the humeral length. It's concluded that a degree of homogeneity exist between the two populations and differences may be explained in terms of activity or genetics. Given the relatively high classification accuracy of the method, it is concluded that both groups may serve as proxy to neighbouring populations.

Greater variability in rhesus macaque (*Macaca mulatta*) endocranial volume among males

ABIGAIL E. COLBY[1], ALEX R. DECASIEN[2], EVE B. COOPER[3] and JAMES P. HIGHAM[3,4]

[1]Department of Anthropology and Archaeology, University of Calgary, [2]Section on Developmental Neurogenomics, National Institute of Mental Health, [3]Department of Anthropology, New York University, [4]New York Consortium in Evolutionary Primatology, NYCEP

The greater male variability hypothesis posits that males exhibit more physical and behavioral variability than females. This pattern is observed across mammalian species and is especially pronounced in sexually selected traits. Greater variability in males likely reflects some combination of evolutionary mechanisms (e.g. balancing or disruptive selection) and developmental mechanisms (e.g. sexually dimorphic developmental schedules) that produce and maintain inter-individual variability. However, research investigating this phenomenon in brain size and structure is almost exclusive to humans. To address this gap in knowledge, we investigate sex differences in variability and heritability of relative and absolute endocranial volume (ECV) in a pedigreed sample of 542 (300F/242M) rhesus macaques using generalized linear mixed models that control for pairwise relatedness (i.e. an 'animal model'). We found that males display more variable relative ECVs (phenotypic variance: male mean=0.646 [0.578,0.693], female mean=0.503 [0.457,0.540]) and absolute ECVs (phenotypic variance: male mean=0.670 [0.598,0.717], female mean=0.533 [0.481,0.568]). These findings are consistent with research in humans and chimpanzees. However, males do not display significantly lower heritability estimates and sex differences in phenotypic variance are not driven by environmental variance for relative (heritability: female mean=0.658 [0.568,0.778], male mean=0.626 [0.522,0.809]; environmental: female mean=0.171 [0.109,0.211], male mean=0.241 [0.119,0.302]) or absolute (heritability: female mean=0.683 [0.613,0.806], male mean=0.667 [0.578,0.827]; environmental: female mean=0.168 [0.112,0.210], male mean=0.223 [0.115,0.283]) ECV. These results suggest that, in rhesus macaques, greater male variability in brain size is likely driven by balancing or disruptive selection, rather than greater susceptibility to environmental effects during their relatively extended development.

Research supported by NYU.

Assessing intraskeletal and regional variation in pore type morphometry: A pilot of the Pore Extractor 2D ImageJ toolkit

MARY E. COLE[1], SAMUEL D. STOUT[2] and AMANDA M. AGNEW[1,2]

[1]Skeletal Biology Research Lab, The Ohio State University, [2]Anthropology, The Ohio State University

Vascular bone porosity is quantified in anthropological contexts as a proxy of bone quality and fragility. Pore systems result from mechanosensitive bone resorption and remodeling, suggesting that local mechanical loading influences pore morphometry. However, histological microstructural patterning and strain patterning have not been consistently linked. We hypothesized that differentiating cortical pores (remodeling products) from trabecularized pores (endosteal resorption products) would better emphasize strain patterning. We piloted our ImageJ toolkit, Pore Extractor 2D (Cole *et al.* 2021), to characterize all pores from matched midshaft femora, tibiae, and sixth ribs in a small histological sample (n = 9). Linear mixed models tested morphometric responses to fixed effects (bone, anatomical region, pore type) and random effects (individual, age, sex). Aggregate pore morphometry showed no significant intraskeletal variation. However, subdivision by pore type identified significant patterning with sufficient sample power (>80%). Cortical porosity is elevated in the femur and tibia, while trabecularized porosity (R^2 = 32%) and pore density (R^2 = 95.2%) predominate in the rib. Regional subdivision indicated that porosity and pore size metrics are concentrated in the posterior femur (R^2 = 11.7-13.7%) and anterior tibia (R^2 = 12.7-36.6%), with tibial pore size resulting from trabecularization (R^2 = 79.5-83.8%). Similarly, trabecularization drives elevated percent porosity and pore size metrics in the cutaneous cortex of the rib (R^2 = 55.7-79.7%), while cortical pores concentrate pore density in its pleural cortex (R^2 = 91.6%). Regional variation is an important consideration for representing a whole individual using a sampled region of microstructure.

Detangling pubis bone traits in sex estimation: The utility of pubis morphology prior to ventral arc expression

STEPHANIE J. COLE and KYRA E. STULL

Department of Anthropology, University of Nevada - Reno

The ventral arc (VA) is commonly used in adult sex estimation. However, this trait develops secondary to pubis elongation during which increased estrogen levels in pubertal females displace the adductors to the ventral surface of the pubis, resulting in VA formation. Although this process occurs during puberty, the VA may not fully develop until after 20 years of age. Since pubis elongation occurs prior to VA formation, pubis morphology (PM) may assist in estimating sex in lieu of a VA. The goals of this research were to: 1) determine the age at which the VA is consistently expressed, and 2) determine when PM becomes dimorphic. Data was queried from the Subadult Virtual Anthropology Database: A sample of 226 females and 210 males were used to score PM using a 5-point ordinal scale. VA was also scored for females as present/absent. No female expressed a VA until 14 years (61.5%) and rates of VA per annual age group never exceeded 70% except for 19- and 20-year-olds (78.4% and 71.4%, respectively). A PM score of 3 was found to separate the sexes (p=≤0.01). For females, a score of 3 was first expressed by age 9 (20%) and scores ≤3 were expressed at rates exceeding 86.7% for all females older than 14 years. In contrast, not one male exhibited a PM <3. Results indicate the VA should not be used prior to 20 years, while PM can be accurately applied as early as 14 years.

This research was funded by the Forensic Sciences Foundation (Lucas Grant) and the National Institute of Justice (Award 2015-DN-BX-K409 and Award 2020-R2-CX-0024).

Trabecular bone microarchitecture of the radial and femoral distal metaphyses during the period of locomotor behavior development

ANTONY COLOMBO[1,2,3], SHARON KUO[2], GREGORIO MARCHIORI[4], MELANIA MAGLIO[4], LUCIA MARTINI[4], MILENA FINI[4], MATTEO BETTUZZI[5], MARIA PIA MORIGI[5], ALEX IRELAND[3], TIMOTHY M. RYAN[2] and MARIA GIOVANNA BELCASTRO[1]

[1]Department of Biological, Geological and Environmental Sciences, University of Bologna, [2]Department of Anthropology, Pennsylvania State University, [3]Department of Life Sciences, Manchester Metropolitan University, [4]Complex Structure Surgical Sciences and Technologies, IRCCS Istituto Ortopedico Rizzoli, [5]Department of Physics and Astronomy, University of Bologna

Trabecular bone microarchitecture (TBMA) responds to changes in loading, as experienced during locomotion. Although TBMA is particularly useful in the study of primate locomotor behavior, structural changes related to the development of human locomotion are not fully understood.

The goal of this study is to characterize changes in TBMA in upper and lower limbs in a sample of juvenile humans. We selected 26 children from the *Certosa* identified skeletons collection (Bologna University, 0-38 months old) without signs of bone pathology. The distal radial (n=20) and femoral (n=25) metaphyses were µCT-scanned (9-18 µm) and the bone volume fraction (BV/TV), degree of anisotropy (DA), and trabecular thickness (Tb.Th) were quantified in Medtool 4.4 and mapped using Phenotypic Point Cloud Analysis.

Variation in TBMA parameters was observed for both radial (BV/TV) and femoral (BV/TV, DA, Tb.Th) metaphyses. With advancing age, the radius showed, first, a homogenous distribution of BV/TV; then, a more concentric pattern with higher values medially; and finally, a gradient of moderate values, higher posteriorly. Simultaneously in the femur, Tb.Th and BV/TV showed no differences between medial and lateral sides and the TBMA was more isotropic at the periphery. Then, BV/TV, Tb.Th and DA showed differences between lateral and medial sides. Finally, lateral and medial sides presented similar BV/TV and Tb.Th, and the bone is more isotropic at the midline.

These patterns of TBMA variation may relate to the acquisition and maturation of bipedal walking and the associated changes in loading as children transition through stages including pre-locomotion, crawling, and bipedalism.

This project has received funding from the European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie Actions grant agreement No 886380.

Differences in morphological integration of the hominoid postcranium due to landmarking protocol

MARK A. CONAWAY[1,2] and NOREEN VON CRAMON-TAUBADEL[2]

[1]Ecology, Evolution, and Organismal Biology, Iowa State University, [2]Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo

Previous research has shown that landmarking methods can have distinct effects on results of the calculation of integration, possibly depending on the skeletal element of focus. Here, we expand on this research by comparing integration results for multiple taxa and skeletal elements, each landmarked in two different ways. Anatomical and semilandmark data were collected from 3D surface scans of the os coxa, femur, tibia, fibula, scapula, humerus, radius, and ulna of four hominoid and two cercopithecoid taxa. The anatomical and semilandmarking protocols were designed to characterize similar regions of each bone to best facilitate comparison. Integration was calculated using the Integration Coefficient of Variation (ICV) using interlandmark distances and distributions of values generated using a resampling protocol. Comparison of ICV results between landmarking protocols was performed via Mann-Whitney U tests with Bonferroni correction.

Overall, elements characterized with semilandmarks led to significantly higher ICV values than the anatomical protocols. Crucially, the among taxa pattern of magnitudes was largely conserved even when semilandmarks were introduced. However, among skeletal elements, introduction of semilandmarks was disruptive to the pattern of magnitudes. While the two landmarking protocols generated significantly different results for all skeletal elements, the difference between the two protocols was less pronounced for the girdle elements when compared to the long bones. Likewise, the difference between anatomical and semilandmark protocols was, on average, lower for less integrated taxa. Further research will be necessary using other statistics and methods to determine the extent to which this pattern hold true in integration studies more generally.

This material is based upon work supported by the National Science Foundation under grant number BCS-1830745. This research was supported by a grant from the Leakey Foundation.

Urban-rural homogeneity in morbidity and mortality throughout the life course in the southeastern United States.

BRIDGET A. CONE, JALYNN E. STEWART and MEGAN A. PERRY

Department of Anthropology, East Carolina University

The urban northeastern and mid-Atlantic U.S. in the 18th and 19th centuries often is characterized by poor childhood health due to high population density, poor sanitary conditions, and high levels of pollution, in addition to extractive childhood labor practices. While bioarcheological investigations have identified the poor nutrition and high activity levels of enslaved populations in the Southeast, the impact of urban environments in this predominantly agricultural, non-industrialized region remains relatively understudied. This investigation focuses on how early childhood environments impacted morbidity and mortality of one family from the urban southeastern U.S. from the 1850s through the 1970s. Evidence for early life stress in the form of growth disruption and skeletal and dental lesions associated with disease and malnutrition were documented in a minimum of 29 individuals from the Rhem family vault, located in New Bern, North Carolina. These variables were compared to two contemporary samples from land-owning families in rural eastern North Carolina to identify rural and urban

differences in non-adult health, and its impact on health and disease later in the life course. No rural-urban differences in growth and development and their impacts on morbidity and mortality were identified through logistic regression and correlation analysis. One possible explanation for this homogeneity stems from the high economic status of the individuals included in this analysis, which could have buffered potential detrimental effects of urban living. This evidence highlights the complexity of urban and rural health and the necessity of parsing out impacts of economic status on health.

Neonatal hair as a record of maternal and fetal exposures

CA'LA K. CONNORS[1] and ROBIN M. BERNSTEIN[2,3]

[1]Developmental Pathways, Aurora, CO, [2]Anthropology, University of Colorado Boulder, [3]Biological Anthropology Program, National Science Foundation

This presentation is part of the symposium *Integumentary Anthropology: Examining the Exterior*. Biological material comprising the integumentary system, or produced by it, can be analyzed for biomarkers that reveal information about real-time or past biology of the individual from whom it was collected. As a keratinized matrix that preserves concentrations of – among other things – proteins, hormones, and heavy metals in circulation at the time of its growth, hair can be analyzed to interrogate endogenous physiology and exogenous influences on individual biology.

Neonatal hair, grown mostly *in utero*, can provide a window to understand influences on fetal physiology during gestation, including nutrition, environmental exposures, and hypothalamic-pituitary-adrenal (HPA) axis activity. We report on the analysis of neonatal hair elements and hormones in a birth cohort, and explore the relationships between aspects of the maternal and physical environment during pregnancy, and variation in the analytes measured in neonatal hair.

Consent was obtained from parents in the rural West Kiang region of Gambia to collect and analyze a sub-sample of hair shaved during infants' naming ceremony at one week of age (N: 211; 100F, 111M). Hair samples were prepared and analyzed using published enzyme immunoassay and mass spectrometry protocols for measurement of concentrations of cortisol and cortisone, and levels of calcium, copper, iron and sodium, respectively. Monthly rainfall measures, summed across trimesters of pregnancy for each infant, were used together with maternal parity and anthropometry to explore the relative contribution of these factors, across gestation, to variation in neonatal hair hormones and elements.

Sample collection and analysis funded by the Bill & Melinda Gates Foundation (OPP1066932).

Analytical validation of an enzyme immunoassay protocol to quantify hair cortisol concentrations in human hair

PALOMA S. CONTRERAS[1], SHARMI SEN[1], TEERA LOSCH[2] and JACINTA BEEHNER[1,2]

[1]Department of Anthropology, University of Michigan, [2]Department of Psychology, University of Michigan

Cortisol is a steroid hormone that helps mediate energy allocation during challenging conditions. As such, elevations in cortisol can be used as evidence of exposure to adverse environments. After being released by the adrenal gland, cortisol travels through the bloodstream and gets incorporated over time into the hair shaft via passive diffusion. The slow accumulation of cortisol in the hair, in addition to its non-invasive collection and easy storage, has made hair cortisol concentration (HCC) analyses a useful tool to assess long-term exposure to adverse conditions. Yet, despite its widespread use in humans, we failed to find a published validation of human hair cortisol. Here we describe our cortisol extraction from human hair and present our analytical validation of an enzyme immunoassay protocol to measure HCCs. Parallelism was calculated by running a serial dilution of our pool, and we did not find significant differences in the slopes generated by running the standards and our pool (ANOVA: t-value = 0.272, p = 0.792), indicating parallelism had been achieved. Accuracy was calculated by spiking standards with 35 µl of pool and obtained a mean recovery of 71.7% (SD = 12.33). Precision was assessed by running the same sample three times on the plate. We obtained an acceptable coefficient of variation of 12%. The results of our analytical validation, in addition to the high correlation between HCC and average salivary cortisol levels reported by previous studies, provide evidence of the reliability of this measurement as a biological marker of exposure to environmental challenges.

EHAP award, University of Michigan

Paleohistopathology of Treponemal Disease in Human Bone from Taumako, Solomon Islands (700-300ybp)

KAREN M. COOKE[1], HALLIE BUCKLEY[2], REBECCA KINASTON[2], LAWRENCE KIKO[3] and JUSTYNA J. MISZKIEWICZ[1,4]

[1]School of Archaeology and Anthropology, The Australian National University, [2]Department of Anatomy, University of Otago, [3]Archaeology Unit, The Solomon Islands National Museum, [4]School of Social Science, University of Queensland

The application of histology in paleopathological analysis of treponematosis has been limited to case studies and predominantly European individuals. However, histological examination of larger samples of archaeological human skeletal remains can provide insights into biological processes of disease and their effects on bone microarchitecture. This study investigated quantitative changes of bone microstructure in 65 adult individuals from Taumako, Solomon Islands (700-300ybp), a region of historic and continuing treponemal endemicity.

Thin sections prepared from the anterior tibia, a bone commonly involved in treponemal infection, were examined using polarised microscopy to histologically compare individuals with no visible pathology (n=40), and individuals with gummatous lesions indicative of treponemal infection (n=25). In addition to histomorphological abnormalities, individuals with treponemal infection had lower vascularity than those without the pathology (p=<0.001). Furthermore, while Haversian canal area remained consistent across both groups, overall bone porosity significantly increased (p=<0.001) with infection due to an increase in resorptive spaces and trabecularisation of cortical bone.

These results suggest that new and remodelled bone produced in response to long term treponematosis was significantly less vascular and, in being highly porous, was of poorer quality than is typically observed in non-pathological individuals. While reduced vascularity is consistent with the pathophysiology of treponematosis and effects on angiogenesis, increased porosity suggests a remodelling imbalance and increased osteoclastic activity. These are the first reported quantitative changes in bone histomorphometry in response to treponemal infection. They demonstrate our ability to better understand disease response through the lens of palaeohistopathology, beyond that of disease identification only.

Australian Government Research Training Program; Australian Research Council, Discovery Early Career Researcher Award (DE190100068); The Australian National University.

An analysis of morphological evolution in the catarrhine appendicular skeleton using methods from quantitative genetics

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

[1]Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, [2]Department of Ecology, Evolution, and Organismal Biology, Iowa State University

Morphological differences are frequently used in evolutionary studies, but it is often difficult to determine which observed morphological changes are evolutionarily significant. Quantitative genetics provides mathematical frameworks that can be used to identify potential directional selection in morphological evolution. Lande's generalized genetic distance (GGD) is one such framework. Here, we apply Lande's GGD to examine evolutionary processes affecting the catarrhine appendicular skeleton. 45 inter-landmark distances (traits) from eight elements

(scapula, humerus, radius, ulna, os coxa, femur, tibia, and fibula) were analyzed across seven taxa: *Chlorocebus pygerythrus* (n=32), *Gorilla gorilla* (n=35), *Homo sapiens* (n=35), *Hylobates lar* (n=34), *Pongo pygmaeus* (n=30), *Pan troglodytes* (n=34), and *Macaca fascicularis* (n=35). Evidence of strong directional selection was found on the branches from the last common ancestor (LCA) of *Pan* and *Homo* to *H. sapiens*, and from the LCA of hominoids to *H. lar*. Selection gradients and responses were calculated for these branches. Large selection gradients were indicated on the femur, fibula, tibia, os coxa, humerus and radius on the branch leading to *H. sapiens*, and on the tibia, os coxa, humerus, radius, ulna and scapula on the branch leading to *H. lar.* These results are consistent with selective pressure from derived locomotor patterns and support earlier research indicating parcellation of the hominoid upper and lower limb. However, some traits that are assumed to be adaptive – such as the human tibial plateau – had selection gradients inconsistent with the morphological response, indicating these traits may be the result of processes other than direct selection.

This material is based upon work supported by the National Science Foundation under grant number BCS-1830745. This research was supported by a grant from the Leakey Foundation.

Central and peripheral oxytocin and vasopressin concentrations do not differ between two baboon species with divergent social systems (*Papio hamadryas* and *Papio anubis*)

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

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

Primate social systems can be highly diverse, even among closely related species. However, it is unclear if this diversity is mediated by differences in neuroendocrine physiology. Here we focused on the closely related anubis (*Papio anubis*) and hamadryas (*Papio hamadryas*) baboons, who live in polygynandrous mixed-sex groups and multilevel polygynous societies, respectively, and measured whether these marked social and mating differences could be detected as differences in the baseline levels of oxytocin (OT) in the cerebrospinal fluid (CSF), blood plasma, and urine, and arginine vasopressin (AVP) in CSF. We collected biosamples from 84 baboons (38 hamadryas and 46 anubis) and assayed them with ELISA. Using Bayesian multilevel modelling, we found no differences in hormone concentrations between the two species. However, OT levels did vary with demographic variables, such as sex, age, and reproductive state. Specifically, OT levels were generally higher in females than in males, and peripheral OT levels in females were related to pregnancy, providing important biological validation. Levels of OT and AVP as well as OT from different sources (CSF, plasma, urine) were not correlated. In sum, we found no differences in OT and AVP levels between two closely-related baboon species, suggesting other aspects of neuroendocrine physiology are responsible for the stark differences in their social systems.

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.

Is there an energetic threshold during pregnancy?

CÉDRIC CORDEY[1], NICOLE M. WEBB[1,2,3] and MARTIN HAEUSLER[1]

[1]Institute of Evolutionary Medicine, University of Zurich, [2]Department of Paleoanthropology, Institute of Archaeological Sciences, Senckenberg Centre for Human Evolution and Palaeoenvironment, Eberhard Karls University of Tübingen, [3]Senckenberg Research Institute and Natural History Museum Frankfurt

The "Energetics of Gestation and Growth" (EEG) hypothesis posits labor is initiated when the supposedly exponentially growing energetic demands of the fetus exceed the sustained maternal metabolic capacity of about 2.1×basal metabolic rate (BMR). The EGG model offers an alternative explanation for the secondary altriciality of human neonates, i.e., the greater neurological and physical immaturity compared to those of non-human primates. In contrast, the "obstetrical dilemma" attributes our secondarily altricial newborns to pelvic constraints. However, the metabolic threshold argued under the EGG framework is derived from only one study on 12 women from the UK, while data based on athletes suggest a higher maximum sustained metabolic scope at around 2.5×BMR (extrapolated to a 180-day-long endurance event such as pregnancy). Here, we show that the total energy requirements and BMR during pregnancy show considerable variability across diverse geographic and socioeconomic samples, with the maximum energetic requirement of the expectant mother ranging between 1.6 and 2.4×BMR. The higher reported metabolic levels make it unlikely that a threshold is crossed by the energetic demand of the fetus at the time of birth. Additionally, recent gestational weight gain and body composition data of human females indicate that pregnancy does not pose an energetic constraint in humans, nor does the placenta constitute a significant energetic barrier. The benefit of a presumed metabolic ceiling during pregnancy is unclear from an evolutionary perspective and the unique birth difficulties in modern humans thus require multifactorial explanations that consider the possibility of both obstetric selection and metabolic mechanisms simultaneously.

This project was financially supported by the Swiss National Science Foundation (grant 31003A_176319).

Dominance and paternity in male mantled howler monkeys (*Alouatta palliata*) at La Pacifica, Costa Rica

LISA C. COREWYN[1], KARI BROSSARD STOOS[2] and MARY A. KELAITA[3]

[1]Department of Anthropology, Ithaca College, [2]Department of Health Promotion & Physical Education, Ithaca College, [3]Department of Natural Sciences, St. Philip's College

The priority of access model predicts that male primates should be dominant to monopolize access to fertile females and ultimately increase reproductive success. However, in species that live in multi-male/multi-female groups where females engage in polyandrous mating, the positive relationship between dominance rank and paternity predicted by the model is not consistently demonstrated. Mantled howler monkeys (*Alouatta palliata*) have variable group composition, females mate polyandrously, and males sometimes form dominance hierarchies, though studies using genetic markers to determine the relationship between paternity and dominance are rare in this species. We collected behavioral data on nine adult males in two mantled howler monkey study groups (groups 2 &12) at La Pacifica, Costa Rica from January to December 2010. Males in both groups formed linear dominance hierarchies. Dominance was based on agonistic interactions between dyads and calculated using David's score. We collected fecal samples noninvasively from all adult males and 22 infants and juveniles in both groups for later DNA extraction. We genotyped all individuals using 12 previously screened microsatellite markers found to be polymorphic in this population. Paternity was confidently assigned for 17/22 offspring using the program CERVUS. Preliminary results indicate that the dominant male in each group fathered 43% (group 2) and 56% (group 12) of known sampled offspring. These data suggest that while dominant males may father a higher percentage of offspring compared to

subordinates, they nonetheless tolerate subordinate access to fertile females, and subordinate males can successfully employ alternate mating tactics such as sneak copulations.

This research was funded by the Margot Marsh Biodiversity Foundation and the University of Texas at San Antonio, with additionalsupport from Duke University through Kenneth Glander.

Determination of biological sex through the lateral angle – A methodological improvement

MARIA ANA CORREIA[1,2], ALINE OLIVEIRA[1,3], LAURA L. FREITAS[2], LUANA SPÓSITO[2], JOB CARVALHO[2], RUI MURRIETA[2], ANDRÉ STRAUSS[1,2] and RODRIGO OLIVEIRA[2]

[1]Museu de Arqueologia e Etnologia, Universidade de São Paulo, [2]Laboratório de Arqueologia e Antropologia Ambiental e Evolutiva, Universidade de São Paulo, [3]Centro de Antropologia e Arqueologia Forense, Universidade Federal de São Paulo

The internal auditory canal and the medial surface of the petrous bone form an angle – called the lateral angle – that is sexually dimorphic. Previous studies have used this information to determine the biological sex of human osteological remains, usually following a simple rule where females have angles equal or above 45˚ while males have angles below 45˚. This approach, however, reduces biological sex to an all-or-nothing feature and ignores the high variability and overlap between the two sexes. In this study, the lateral angle of 154 Brazilian identified individuals was measured by 3 observers in 3 separate occasions. We found poor inter-rater reliability – intraclass correlation (ICC) = 0.2 – and moderate intra-rater reliability – ICC = 0.5. Despite the low reproducibility, the lateral angle was still significantly different between females (xÃÖ = 44˚) and males (xÃÖ = 40˚), t = 11.0, p < 0.01, with a moderate effect size (d = 0.4). Using a logistic regression, we propose a new method with ~80% correct sex evaluation, allowing space for the indeterminate and making the method more reliable. The lateral angle method is particularly useful in analyses of fragmented remains, considering that diagnostic osteological features are often not preserved in these cases and that the petrous bone preserves well in the archaeological record. Thus, such methodological improvements are necessary as analyses of fragmented remains become more frequent due to an increase of investigations into mass-casualty incidents– e.g., plane crashes, terrorist acts, human rights violations, natural disasters.

Funding provided by São Paulo Research Foundation (FAPESP), through grants 2017/16451-2 (AS), 2020/06729-6 (MAC), 2020/08769-5 (LS), and 2020/08781-5 (LLF)

Correlations of cortical bone geometry and tissue mineral density across ontogeny in great apes

MIRANDA N. COSMAN and MAUREEN J. DEVLIN

Anthropology, University of Michigan

Bone strength is the product of bone tissue mineral density (TMD), bone mass, and composition. Previous studies in non-human apes have primarily focused on bone size and shape, and few have compared ontogenetic patterns of cortical bone geometry and TMD. This study tests the relationship between cortical bone geometry and TMD in *Pan, Gorilla,* and *Pongo* across ontogeny. We predict that: (1) Cortical tissue mineral density will increase with age in all species; (2) There will be tradeoffs between cortical geometry and TMD, such that narrower bones will have higher TMD and wider bones will have lower TMD. Scans from *Pan* (Adult n=29; Subadult n=39), *Gorilla* (Adult n=15; Subadult n=16), and *Pongo* (Adult n=9; Subadult n=12) were collected from the midshaft femur and humerus using a pQCT scanner and analyzed in ImageJ using MomentMacro and grey values to quantify cortical TMD.

Results indicate that in adults, cortical TMD is higher in *Pan* vs. *Gorilla* in both the femur (+9.25%, p=0.0001) and humerus (+9.02%, p= 0.001), but not vs. *Pongo* (NS). From subadults to adults, cortical TMD in the femur and humerus increases in *Pan,* decreases in *Gorilla,* and is stable in *Pongo.* Cortical bone area and total area increase across ontogeny in all species. Thus femoral cortical area is positively correlated with cortical TMD in *Pan* (r^2= 0.23, p=0.01), but not in *Gorilla* or *Pongo*. These results demonstrate species-specific relationships between cortical TMD and cortical bone geometry, which may be useful for reconstructing locomotion in fossil taxa.

Funding for this project was provided by the Leakey Foundation

Assessment of inter- and intraobserver variability in dental measurements

SIERRA S. COTRONA, BROOKE FISHER and BRIAN E. HEMPHILL

Department of Anthropology, University of Alaska Fairbanks

The purpose of this study is to examine inter- and intraobserver variability in dental metrics in a cast collection from Northeast India. Some 50 plaster casts from the Hmar ethnic group were measured by three researchers with varying degrees of experience. The researchers took mesiodistal (MD) and buccolingual (BL) measurements of 28 permanent teeth, except third molars (due to an inclusion protocol that limited participants to 15 – 19 years of age) during three measurement bouts each minimally separated by a 30-day period. Two-way repeated measures ANOVA tests were employed to compare intra- and interobserver repeatability across the three researchers. Threshold values (α) were set at 0.01.

Results yield mostly nonsignificant differences for intraobserver measurements. This is especially the case across bouts two and three relative to bout one. Results obtained from interobserver variation indicate that the researcher has little impact on the measurements obtained for incisor and molar data, or for MD measurements overall. Premolar BL measurements in both upper and lower arcades as well as maxillary canine and molar BL measurements yielded significant differences. This is likely due to slight differences in the orientation of this measurement relative to the long axis of the crown between observers.

Intraobserver variability was found to decrease with increased experience. Inter-observer variability is a problem for premolars as well as maxillary canines and molars that can be resolved with strict adherence to a protocol calling for BL measurements to be taken in a plane parallel to the longitudinal axis of the crown.

This research is based on plaster casts collected with the financial support of a Fulbright Senior Research Fellowship to Brian E. Hemphill.

Revisiting the thermoregulatory imperative in living humans

LIBBY COWGILL[1], SCOTT D. MADDUX[2] and CARA OCOBOCK[3]

[1]Department of Anthropology, University of Missouri, Columbia, [2]Center for Anatomical Sciences, University of North Texas HSC, [3]Department of Anthropology, University of Notre Dame

Over the past thirty years, Chris Ruff's of contributions to the study of human ecogeographic diversity have influenced a wide array of research in biological anthropology exploring the skeletal manifestation of Allen's and Bergmann's rules in both human and fossil groups. In particular, Ruff's introduction of the "cylinder model" for assessing patterns of skeletal variation across time and space has revolutionized work on ecogeographic body proportions. Our recently funded NSF project (#2020096/2020715/2020506) seeks to build upon Ruff's important theoretical contributions by experimentally testing proposed relationships between ecogeographically-patterned variation in human anatomy and thermoregulatory physiology. Specifically, we are using state-of-the-art environmental chamber to quantify the physiological responses of morphologically diverse living participants exposed to controlled environmental conditions simulating three extreme climates: tropical rainforest (hot-humid), subtropical desert (hot-dry), and circumpolar tundra (cold-dry). These physiological data will then be assessed in conjunction with whole-body CT

scans collected from each participant to verify theoretically predicted relationships between skeletal morphology, soft tissue anatomy, and thermoregulatory physiology. Moreover, through an intentional whole-body approach, this study will also help clarify the cumulative contributions of different anatomical regions to overall thermoregulatory function. This project will thus integrate different regions of the body to investigate assertions regarding climatic patterning of body form. Experimental validation of ecogeographic concepts, especially Ruff's cylinder model, will help refine models and scenarios of climatic adaptation during human evolution, permitting more confident assessment skeletal morphology in both modern populations and the fossil record.

National Science Foundation Grants #2020096/2020715/2020506

Human immune variation and the future of sepsis management: Proposal of a non-infectious autoimmune sepsis phenotype

MARIA L. COX[1,2] and J. GRACE SHAW[1]

[1]Department of Anthropology, University of Illinois at Urbana-Champaign, [2]Program in Ecology, Evolution, and Conservation Biology, University of Illinois at Urbana-Champaign

Individuals with autoimmune disorders are at increased risk of developing sepsis and progressing into septic shock due to prior immune dysregulation. Septic shock is not well understood, has a mortality rate around 50%, and is associated with increased risk of death for years after infection clearance. While current diagnostic criteria for sepsis necessitates an infectious agent, studies have found that 15-50% of patients diagnosed with sepsis/septic shock have no found causative infectious agent or infection site. The dysregulated cytokine response that characterizes septic shock is mirrored in the cytokine dysregulation of autoimmunity. It is therefore possible that autoimmune patients are more easily triggered into a shock response from a stimulus that would be easily managed in patients with adequate immune regulation. This variation may contribute to the percentage of patients with no found causative agent, as there may be no severe systemic infection underlying the shock reaction. There are a vast number of overlapping biochemical pathways between sepsis and autoimmunity that support a non-infectious autoimmune sepsis phenotype. We propose expanding the current definition of sepsis/septic shock to specifically include autoimmune patients who present with septic shock with no causative agent found. Due to the nature of sepsis and medical documentation, data collection for this type of project would necessitate a high degree of funding, resources, and medical partnerships. These types of resources are not readily available; therefore, we focus here on providing a strong hypothesis and avenues for future research to address this human variation in immune function.

Paleosyndemics and biosocial reconstruction of past epidemics

FABIAN CRESPO[1] and CLARK S. LARSEN[2]

[1]Anthropology, University of Louisville, [2]Anthropology, The Ohio State University

This abstract is part of the symposium *Biocultural Approaches to Pandemic Studies: Implications for Pandemic Preparedness.* Our presentation proposes taking syndemic theory into the past and show how the multidisciplinary nature of bioarchaeology can help to generate a paleosyndemic model to reconstruct multiple biosocial layers of past epidemics. Syndemic theory refers to two or more epidemics interacting and exacerbating the burden of a disease and embraces the social and environmental conditions that influence and determine the overall health of populations. Our objective is to review bioarchaeological data previously published on plague, tuberculosis, and leprosy, and integrate findings with ecological immunology and our research on experimental immunology. Our experimental data show how immune cells from healthy donors change the expression of inflammatory proteins under conditions involving exposure to different pathogens. The study of immunological shifts should incorporate social and environmental factors in living populations allowing to explore a more holistic understanding of immune competence. We consider the multiple factors that simultaneously influence the immune competence of individuals within a population, including poor oral health, undernutrition, iron deficiency anemia, or elevated parasite load. This multidisciplinary approach facilitates the development of a paleosyndemic model in order to understand the duration of epidemics and endemic infectious diseases in past populations. This approach requires a wider context and the documentation of multiple circumstances that undermine health, social equality, and community stability. For living populations, the record shows variable outcomes in immune competence, ultimately playing a crucial role on differential survival and mortality.

A New 3D System for Categorizing Variation in Middle Meningeal Neurovascular Patterns As Determined from Endocranial Surfaces of 6-8.0 year olds

JESSICA M. CRONIN[1], EMIELYN DAS[2], ANNABEL T. DAVIS[2], GRACE A. SELECKY[3], REBECCA S. JABBOUR[4] and GARY D. RICHARDS[5]

[1]Integrative Biology, University of California, Berkeley, [2]Department of Cognitive Science, University of California, Berkeley, [3]Department of Molecular and Cell Biology, 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, University of the Pacific

Previously we evaluated the middle meningeal neurovascular bundle in children, using the types established by Adachi (1928), a simplification of the Giuffrida-Ruggeri (1913) system. However, Adachi types do not include basal bifurcation(s), and the Giuffrida-Ruggeri system lacks focus on these originating branches and the observed range of variation. Here we focus on the entire course of this neurovascular bundle, including the petrosal and cavernous branches, to provide a revised typing system.

We employed a GE LightScribe VCT scanner to obtain images of 6-8 year old skulls (*N*=69). Developmental ages are based on comparison of crown/root development for each tooth with the Schour and Massler (1941) standards. Middle meningeal patterns were reconstructed with variably sized landmarks to create 3D models of the vascular network. Vascular patterns were seriated and compiled as a set of types with the range of variation noted for each type. We also examined the patterns relative to developmental age.

Because middle meningeal vascular grooves may not be fully preserved in individuals, we compiled our results in three ways. Firstly, the complete pattern from foramen spinosum to sagittal sinus (Types I-IV). Secondly, the pattern for the upper vault (comparable to Adachi and Giuffrida-Ruggeri). Thirdly, the initial branching pattern including the configuration of the petrosal and cavernous branches (Types I-III). We also identify enigmatic frontal/parietal based impressions that differ morphologically from meningeal impressions, but that do not conform to dural sinuses.

This work adds significant new data for delineating the ontogeny of meningeal vascular evolution within *Homo*.

The contribution of Focus Variation microscopy to the analysis of surface incremental lines and enamel defects on archaeological teeth

LUCILE CRÉTÉ[1], LOUISE T. HUMPHREY[1], AMY SCOTT-MURRAY[2] and SILVIA M. BELLO[1]

[1]Centre for Human Evolution Research, Natural History Museum, London, [2]Imaging and Analysis Centre, Natural History Museum, London

Incremental growth lines (perikymata) on the tooth crown surface record the rate and duration of enamel growth, which varies between teeth, individuals, and species. Interruptions to the normal pattern manifest as furrows on the enamel surface and reflect episodes of growth interruption caused by illness and other physiological insults. These enamel defects therefore capture a retrospective record of the timing and frequency

of developmental disruptions. Previous studies have used various imaging techniques to record and measure these defects, such as scanning electron microscopy combined with a measuring microscope or focus variation microscopy. However, these approaches suffered from several limitations, such as the reliance on casts because of the reflective nature of the enamel surface, and the limited scale of the regions scanned due to high processing times when recording data at high definition. We present an improved technique to capture a topographic model of the entire longitudinal profile of tooth crown surfaces and record normal growth increments and enamel defects, using a Focus Variation microscope, the 'Alicona Infinite Focus G5+ system', a system with greater computing power and new software developments allowing quick 3D data capture on reflective or translucent objects. This technique was tested on human teeth from two young adults from the medieval cemetery of Abingdon (Oxfordshire, UK), to track ~6 years of enamel growth in ~9-day increments through each dentition. Our pilot study demonstrates that this technique presents several advantages compared to previous approaches and represents a useful tool for analyses of enamel defects on archaeological teeth.

This research was permitted by funding from the Calleva Foundation, and Departmental Investment Funds from the Natural History Museum (London, UK).

Exploring Maya population history of Central Belize by means of dental morphological analyses

ANDREA CUCINA[1] and GABRIEL WROBEL[2]

[1]School of Anthropology, Universidad Autonoma de Yucatan, [2]Dept. Anthropology, Michigan State University

Central Belize was an important territory in Prehispanic and Colonial times. Located between the Caribbean coast of Belize and the Central Peten region of Mexico and Guatemala, it received economic, political and demic influences from the surrounding regions. Particularly the Guatemalan Peten played an important role in shaping the political and economic character of communities in Central Belize during the Late Preclassic and Classic periods,.

The present study explores population affinities in Central Belize groups through dental morphological traits in a sample of burials from rockshelters and caves in the Roaring Creek and Caves Branch River Valleys. Rockshelter burials are dated to Late Preclassic/Early Classic (~300 BC – AD 300), while mortuary contexts found deep in nearby caves date to the Late/Terminal Classic (AD 500 – 900). Material culture shows both continuity and abrupt transitions in Central Belize through time, so some demic continuity should be expected. Rockshelters' and caves'groups are morphologically distinct from each other in every analysis; the former clusters with Peten populations, while the latter shows morphological affinity with sites located in the more northern territories of the Yucatan peninsula. These morphological affinities contrast with the evidence from material culture, for they show that biological influence from different regions shifted sometime in the Middle Classic (around AD 400 – 500). The differences found between rockshelters and caves, in addition to being chronological in nature, also reflect socioeconomic differences, with the former being commoners and peasants, and the latter being of higher social level (if not also elite).

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

Biocultural interpretations of skeletal and archival indicators of health in enslavement in Barbados

ANDREANA S. CUNNINGHAM[1] and KRISTRINA A. SHULER[2]

[1]Anthropology, University of Florida, [2]Department of Sociology, Anthropology & Social Work, Auburn University

Archival analyses add crucial context to estimations of health in bioarchaeological research, particularly for decedents whose social positionalities are unique in the skeletal record. To that end, qualitative text analysis enables novel interpretation of salient themes in archival data. This study compared osteological and archival indicators of health in enslaved persons in Barbados, using preexisting data from the 1997-1998 archaeological investigations of Newton Plantation burial ground (N=49) and data from qualitative text analyses of runaway slave advertisements in the *Barbados Mercury, and Bridge-Town Gazette* newspaper dating 1807-1816 (N=516).

Rates of infection and traumatic injury and their distribution across sex and body region were recorded for both samples. Correlation between the datasets were tested through descriptive and chi-square analyses. Descriptions of smallpox were observed in the archival data, which is notably not documented among prevalent diseases at Newton Plantation. Chi-square tests revealed systemic descriptors of violence and infection in the archival data that were not represented in the skeletal data, including the high rate of head injuries and infections and the significant relationship of injury in the chest region. There was no significant effect of sex on rates of trauma or infection, although its distribution occurred more commonly on the lower limb in men and the upper limb in women. These results may suggest the unique positioning of runaway enslaved persons relative to Newton Plantation decedents, as runaway persons are known in the historical record to have experienced extreme violence in response to their modes of resistance.

This material is based upon work supported by the National Science Foundation Grant Nos. DGE-1315138, DGE-1842473, and BCS-2041542.

The dental ecology and oral biology of a population of wild *Otolemur crassicaudatus* from the Lajuma Research Centre, South Africa

FRANK CUOZZO[1,2], JOHN K. DALTON[3], MICHELLE L. SAUTHER[3], ADRIAN SW. TORDIFFE[4] and ILANA VAN WYK[5]

[1]Mammal Research Institute, University of Pretoria, [2]Noctturnal Primate Biology Project, Lajuma Research Centre, [3]Anthropology, University of Colorado-Boulder, [4]Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria, [5]Hans Hoheisen Research Station, University of Pretoria

Here we present dental ecology and oral biology data from 10 capture sessions between 2013-2021 from a population of *Otolemur crassicaudatus* from the Lajuma Research Centre in northern South Africa. In this population (n = 82 adults, 36 females, 46 males), there is a high frequency (> 90%) of maxillary canine damage: fractures, decay and/or apical abscesses, often concurrently occurring in single individuals. This pattern shows no sex difference (X^2 = 0.08, p = 0.77) suggesting an ecological, i.e., feeding cause, rather than male bias in maxillary canine damage due to intra-sexual competition as seen among complex social group living non-human primates (e.g., African cercopithecines or Madagascar's ring-tailed lemurs). We suggest that the population-wide pattern of maxillary canine damage is more likely a result of resource acquisition, specifically gouging bark and hard gum from *Valchellia* sp. (formally *Acacia*) trees, especially during the cold winter season in this Afromontane habitat (>1200 meters). Salivary pH does not vary by sex (n = 26 females, n = 26 males; X^2 = 2.40, p = 0.12), with a slightly acidic mean of ≈6.3, suggesting a long-term diet of less acidic foods in this species, in contrast to several Malagasy lemur species that show more alkaline salivary pH, a potential buffer against more acidic diets. As *Valchellia* gums are acidic and accessing this food is connected to high canine damage, this suggests that gum as a major food source may be a more recent addition to the *Otolemur* diet.

The National Science Foundation, USA (BCS 1638833), The University of Colorado-Boulder.

Calcaneal ecomorphology of Bovidae from the Upper Laetolil Beds, Tanzania.

SABRINA C. CURRAN[1], REBECA THORNBURG[2] and CHARLES MUSIBA[2,3]

[1]Department of Sociology and Anthropology, Ohio University, [2]Department of Anthropology, University of Colorado, Denver, [3]Center for the Exploration of the Deep Human Journey, University of the Witwatersrand, Johannesburg, SA

The Upper Laetolil Beds (ULB) of Laetoli, Tanzania (3.8-3.5 Ma) have long been considered to differ from other *Australopithecus afarensis* bearing sites in that they are often reconstructed as having been more open habitats. Recent studies, however, indicate that the ULB habitats were heterogenous in nature, while still being more on the grassland-bushland side of the habitat continuum. Here, we expand the paleohabitat proxies used to reconstruct the ULB to include bovid calcaneal ecomorphology. Extinct bovids from ULB used in the analysis were from the Leakey's collection re-discovered from Dr. Ndessokia collection. Using geometric morphometrics, a comparative training set was created using extant bovids with known habitat preferences. Ten landmarks were digitized for each specimen, placed into a Generalized Procrustes analysis from which Procrustes coordinates were submitted to principal components analysis to reduce the number of variables, which were then submitted to a canonical variates analysis. Fossil specimens were classified into the habitat category for which they had the highest posterior probability of group membership. Specimens from the extant comparative set were correctly reclassified into their known habitat preference 72.3% of the time with cross-validation. Of the six fossil specimens, four were classified as "Open" and two as "Intermediate" with high to very high posterior probabilities. Though the sample size here is small, it does reflect what has been found in other paleoecological reconstructions of the Upper Laetolil Beds, that is, a relatively open character with more complex (mosaic) habitats found throughout.

To SC: Smithsonian Institution Fellowship To CM: University of Colorado Denver, College of Liberal Arts and Sciences CRISP and SITFAC grants

Cognitive foraging patterns in two sympatric species of South African galago

JOHN K. DALTON[1], MICHELLE L. SAUTHER[1] and FRANK P. CUOZZO[2,3]

[1]Department of Anthropology, University of Colorado, [2]Mammal Research Institute, University of Pretoria, [3]Lajuma Research Centre

Given the paucity of information on nocturnal strepsirrhine primate cognition, we present data on cognitive foraging behaviors in two sympatric species of wild South African galagids: *Otolemur crassicaudatus* and *Galago moholi*. Feeding boxes containing banana slices were placed throughout the animals' habitat, and both direct (time on or inside the box) and indirect (time on branches surrounding the box) interactions were video recorded (n = 37). *O. crassicaudatus* spent more time interacting with the boxes than *G. moholi* [225.67 seconds versus 134.50 seconds; U = 192, p = 0.05] and a higher proportion of visit time on direct interactions than *G. moholi* [83.2% versus 51.8%; U = 216, p= 0.006]. Compared to *O. crassicaudatus*, *G. moholi* spent more time on their approach to the box before beginning to eat [77.67 seconds versus 22.11 seconds; U = 53, p = 0.012]. In contrast, *O. crassicaudatus* spent more time investigating the box in the absence of food and after all food was consumed than *G. moholi* (124.52 seconds versus 30.10 seconds; U = 229, p = 0.001]. The results suggest different foraging strategies in these sympatric galagid species. *G. moholi* appears more neophobic with a risk-averse strategy involving higher degrees of caution, and *O. crassicaudatus* exhibits higher levels of curiosity and lower levels of neophobia involving a more risk-tolerant strategy. These varying strategies may reflect the drastically different sizes of *O. crassicaudatus* (1090g) and *G. moholi* (150g) and the resulting differences in predation risk incurred by the two species.

Anthropology Department's Graduate Student Funding Scholarship and the Beverly Sears Grant, University of Colorado-Boulder.

Utilization of the New Mexico Decedent Image Database

SHAMSI DANESHVARI BERRY[1,2] and HEATHER JH. EDGAR[3,4]

[1]Biomedical Informatics Department, Western Michigan University Homer Stryker MD School of Medicine, [2]Pathology Department, University of New Mexico, [3]Anthropology Department, University of New Mexico, [4]Office of the Medical Investigator, University of New Mexico

The New Mexico Decedent Image Database (NMDID) contains 15,242 full body computed tomography (CT) scans and associated data on demographics, health, lifestyle, and cause, manner, and circumstances of death. NMDID is a web-based application that went live in February of 2020, available to bona fide researchers and educators. The CT scans and metadata were compiled from the Office of the Medical Investigator in New Mexico and from next of kin interviews.

As of September 2021, NMDID has 573 approved users from 46 countries. The largest increase in users, after the initial month of activity (86), came in March 2020 (55) as COVID-19 shut down museums and other collections. The data and images have been used for research on projects including biomechanics, COVID-19, traumatic injury analysis, dental development, sarcoidosis in cancer, art, and virtual education. Approved image requests in September 2021 (n=158) were classified into nine categories: forensic anthropology bioprofile (47), computer science/machine learning/automatic segmentation (22), medical research/biomedical informatics (22), anatomy (19), biomechanics (15), evolutionary studies (12), forensic pathology (11), education (6) and other (4). Thirteen peer-reviewed articles (9) and theses (4) from five countries have published using data from NMDID, representing researchers from 6 countries, on topics including biomechanics, health disparities, forensic pathology, forensic anthropology bioprofile, evolutionary studies, and segmentation. This first report on the uses of NMDID indicates its wide applicability and its potential for future scientific contributions.

NMDID is available to bona fide researchers and educators at NMDID.UNM.EDU.

Funded by National Institute of Justice 2016-DN-BX-0144. Statements made are solely the responsibility of the authors.

Somatotype is a better indicator than body mass index to evaluate body composition

SUDIP DATTA BANIK

HUMAN ECOLOGY, Centro de Investigación y de Estudios Avanzados del IPN (Cinvestav-IPN)

Body mass index (BMI) is a measure of body weight that is composed of body fat and fat free mass. It is presumed that in overweight and obese individuals, BMI has positive correlation with body fat. This association has limitations in cases of individuals with high muscle mass like athletes. **Objective**: To compare between adult male judo athletes and non-athletes the interrelationships of BMI with percentage body fat and somatotype. **Methods:** In a cross-sectional study carried out in 2019 in Merida, Yucatan, Mexico, participants were 20- to 25-year-old male university students who were non-elite judo athletes (n = 25) and non-athletes (n = 25). Height, weight, girths, and breadths were measured. BMI, muscle mass (%), body fat (%), and somatotype were calculated. **Results:** Mean values of age and height of athlete and non-athlete participants were not different. BMI had positive association with percentage body fat, endomorphy (relative fatness), and mesomorphy (relative muscularity). The athletes had balanced mesomorph (2.5-5.2-2.6) and non-athletes had endomorphic mesomorph somatotype (4.2-5.4-1.8). Somatotype was found to be a better indicator than BMI that could distinguish the relative distributions of body fatness, muscularity, and leanness among athletes and non-athletes.

Neural, Dural, and Osseous Interactions and Their Impact on Cranial Shape

ANNABEL T. DAVIS[1], GRACE A. SELECKY[2], CHLOE PHELY-BOBIN[1], MEGAN LUI[1], SAMANTHA YAWITZ[2], JEN TACHIBANA[1], JESSICA M. CRONIN[3],

CHRISTINA KAN[1], KAREN LI[4], REBECCA S. JABBOUR[5] and GARY D. RICHARDS[6]

[1]Department of Cognitive Science, University of California, Berkeley, [2]Department of Molecular and Cell Biology, University of California, Berkeley, [3]Department of Integrative Biology, University of California, Berkeley, [4]Department of Public Health, 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

Factors involved in producing cranial shape have been a continuing focus in human biology. It is well known that osseous cranial shape corresponds to a large extent to that of the neural mass. Less widely investigated is the interactive sphere involving the neural mass, dura mater, and osseous cranium. Here we provide preliminary results of our investigation into the relationship between these structures and how these relationships modify brain, and ultimately, cranial shape. We collected data from sagittally-sectioned cadaver heads (N=10) and sagittal slices of anonymized CT scans (N=31; GE LightScribe VCT scanner, helical mode, standard convolution kernel). In both cases, we measured a series of linear dimensions (N=5) and angles (N=9). The former are employed to determine the cranial/cephalic indices and cranial capacity, while the latter document the cranial base (two variants), clival, and foraminal angles. Additionally, we measured the angular relationship between the great vein of Galen-transverse sinus to the cranial base, to document the angle of the straight sinus.

We found that the position and angle of the straight sinus, which defines the junctional midpoint of the falx cerebri and tentorium cerebelli is significantly correlated with the cranial base angle (n-s-ba, $P<0.05$). This relationship is consistent regardless of cranial shape or capacity. Maintenance of this relationship results in a superior displacement of the medulla/pons and impacts ventricular, corpus callosum, pituitary, and optic chiasma shape/position as cranial shape morphs from dolichocephaly to brachycephaly. Cerebral growth is, then, constrained/directed by falx cerebri-tentorium cerebelli position and uplifted basal neural structures.

The Relationship Between Dental Modifications and Dental Pathologies in the Classic Period Maya

MARIE A. DAY and ERIN C. BLANKENSHIP-SEFCZEK

Department of Cultural and Social Studies, Creighton University

Social practices, such as dental modification, are signs of cultural identity and social membership. Individuals who possessed modification often belong to higher social status groups. This may ultimately lead to overall better oral health profiles for individuals with modifications as their higher status is typically associated with greater access to resources than individuals of lower status groups. However, despite overall better oral health, cultural alterations may be affecting the modified tooth in the form of caries formation and dental attrition. This study looked at dentition from Classic period Maya individuals (n=42) from high, middle and lower status groups. We predicted that teeth affected by modification will exhibit more caries and attrition compared to teeth without modification both within and between social groups. Type and location of dentalmodification, caries and dental attrition were recorded following standard protocol methods. Results show that higher status and middle status individuals exhibit the highest frequency of modification on maxillary incisors and canines. Analysis of caries indicate the presence of modification does not affect formation of enamel lesions. While attrition was observed on modified teeth, results suggest this cultural practice did not impact the presence of wear. Contrary to predicted, our findings suggest that while dental modification is an indicator of socioeconomic status, in this population, it did not differentially affect the presence and severity of caries and attrition.

This study was funded by Creighton University's Center for Undergraduate Research and Scholarship Summer Undergraduate Research Fellowship.

Ethical issues and considerations for ethically engaging with the Robert J. Terry, Hamann-Todd, and William Montague Cobb anatomical collections

CARLINA M. DE LA COVA

Anthropology, University of South Carolina

Anatomical collections have been instrumental to the development of medicine, anatomy, and biological anthropology. This is especially true of the Hamann-Todd, Robert J. Terry, and William Montague Cobb anatomical collections, which have played major roles in the creation of human identification methods central to forensic anthropology and bioarchaeology. However, these series were amassed using structurally violent anatomical legislation that specifically targeted the unclaimed poor and marginalized for nonconsensual dissection. This presentation will examine the history and composition of the Hamann-Todd, Robert J. Terry, and William Montague Cobb anatomical collections. Results, based on demographic and paleopathological analysis, will be discussed and reveal how structural violence at the societal and legislative levels resulted in the dissection, curation, marginalization, and silencing of the individuals that comprise these collections. Focus will be placed on how to restore the silenced identities of the individuals within these series and how to ethically engage with anatomical collections in a manner that brings restorative and social justice to the persons that comprise these collections.

This research was funded by the Smithsonian, Indiana University, the University of South Carolina's Provost Office, and the Office of Sponsored Programs at the University of North Carolina Greensboro

Understanding taphonomic processes of collective burials using photogrammetry: a case study from the Maya area

MIRKO DE TOMASSI

Interdisciplinary Humanities, University of California, Merced

Archaeologists and bioarchaeologists dedicated to the study of pre-Hispanic Maya funerary practices face difficulties due to both cultural and natural circumstances. Distinctive funerary depositional and post-depositional secondary activities, in addition to climatic factors, contribute tremendously to the complexity of mortuary contexts in the Maya region. In this paper, I propose to merge 2D and 3D recording data to obtain a comprehensive understanding of the taphonomic phenomena that affect poorly preserved burials (n = 6) at the site of Palenque, Mexico. Employing a detailed archaeothanatological approach, I argue that careful 3D imaging provides additional valuable insight into the formation processes of funerary contexts, especially when it is integrated with traditional 2D data. Photogrammetric analysis can improve our capacity to reconstruct joint articulations of the body and original funerary deposition of the body in situ. Preliminary results of this research elucidate the intentional activities that led to the archaeological arrangement of the grave assemblage. By noticing the degree of articulation and clarifying the pace at which bodies decomposed, these results showcase the depositional sequence of collective burials, with five burials presenting evidence of post-burial activities, and one burial resulting from a single depositional event. These findings are particularly significant because of the cultural and natural factors contributing to the decomposition of corpses in the Maya region. These preliminary results demonstrate the important potential for 3D methodologies in assessing post-depositional disturbances and movements of the body, both for illuminating funerary taphonomic practices and serving as important recording procedures for the future.

The Impacts of Mating System on Sperm Gene Evolution in Primates

REBECCA M. DECAMP[1,2,3], AMBER E. TRUJILLO[5,6], KEVIN M. TILTON[4], MARY E. BLAIR[7], LUCA POZZI[8], TODD R. DISOTELL[9], ANTHONY J. TOSI[10,11],

ANDREW S. BURRELL[5,6] and CHRISTINA M. BERGEY[2,3,4]

[1]Department of Anthropology, Rutgers University, [2]Center for Human Evolutionary Studies, Rutgers University, [3]Human Genetics Institute of New Jersey, Rutgers University, [4]Department of Genetics, Rutgers University, [5]Department of Anthropology, New York University, [6]New York Consortium of Evolutionary Primatology, [7]Center for Biodiversity and Conservation, American Museum of Natural History, [8]Department of Anthropology, University of Texas - San Antonio, [9]Department of Anthropology, University of Massachusetts - Amherst, [10]Department of Anthropology, Kent State University, [11]School of Biomedical Sciences, Kent State University

Primates display a remarkable diversity of social organization, and various mating systems have arisen convergently multiple times during the evolution of the order. Although theories of sexual selection since Darwin have focused on competition for access to mates, a second arena of sexual selection exists for species in which the sperm of several males may compete to fertilize an egg. This sperm competition may lead to sexual selection on sperm-related morphological and functional traits. Genomic analyses promise additional insight into sexual selection in primates, especially as new genomes from diverse primate taxa are made available. Here, we test the hypothesis that parallel selection has targeted genes associated with post-copulatory functions in sperm (sperm motility, sperm-egg binding, and copulatory plug formation) as opposed to genes involved in pre-copulatory functions (sperm composition and assembly). We used whole-genome data from 39 species of primates to test for codon-level selection and branch-level selection across 168 sperm-associated genes and 100 non-reproductive genes. We found that genes associated with sperm had a higher proportion of codons under selection 1 as compared to non-reproductive genes ($p<0.001$), and that post-copulatory genes had a higher proportion of codons under selection as compared to pre-copulatory genes ($p<0.001$). We also found that primate species with multimale mating systems have higher levels of selection in sperm-associated genes than species with monogamous and polygynous mating systems ($p<0.001$). These results support our hypothesis that selection is operating differently on genes affecting pre- and post-copulation sperm function in primates.

Funding for work provided by National Science Foundation (BCS1640500/1640515, BCS1717188/1718715/1718339, and BCS1926105/1926215).

Linking human sex chromosome evolution to patterns of gene co-expression and sex differences in disease

ALEX DECASIEN[1], KATHRYN TSAI[1], SIYUAN LIU[1], ADAM THOMAS[2] and ARMIN RAZNAHAN[1]

[1]Section on Developmental Neurogenomics, National Institute of Mental Health, [2]Data Science and Sharing Team, National Institute of Mental Health

Humans exhibit sex differences in the prevalence and presentation of many medical conditions, which may (in part) reflect evolved sex differences in gene expression. Of particular interest are the gametologues: genes that have retained functional copies on the X and Y chromosomes despite having ceased recombination over evolutionary time. Recent work suggests that gametologue pairs vary in X-Y functional equivalence and tissue-specific patterns of co-expression. However, we currently lack an understanding of: 1) how patterns of gametologue co-expression relate to patterns of co-expression with all other genes ('coupled co-expression'); 2) the drivers of gametologue co-expression variation; or 3) the functional impacts of differential co-expression with X versus Y gametologues. Here, we used a large, published human gene expression dataset (GTEx V8) to characterize gametologue co-expression and coupled co-expression across >40 tissues. These measures were correlated across tissues and pairs ($rho=0.847$; $p<0.001$), with larger deviations among the most sexually differentiated tissues (testes, prostate, mammary). Gametologues that ceased recombination more recently exhibited more similar promoter sequences and promoter sequence similarity predicted average co-expression ($rho=0.681$; $p=0.021$), suggesting that higher co-expression reflects conserved regulatory mechanisms. Finally, genes showing higher co-expression with X or Y gametologues were associated with sex-biased conditions (Y>X: autism, schizophrenia, and ADHD in brain tissues; X>Y: autoimmune disease in many tissues; all $padj<0.001$). This work improves our understanding of how sex chromosome evolution has influenced the human transcriptome and how these mechanisms may contribute to sex differences in disease.

This research was supported by the Intramural Research Program of the National Institute of Mental Health (NIH annual report number ZIA MH002949-04).

Estimating Sex from the Diameter of the Femoral Neck

HANNAH M. DECKER

Department of Anthropology, Northern Illinois University

It is difficult to estimate the sex of a skeleton when an element is fragmented or missing. To circumvent this problem, I examined if it is possible to estimate the sex of a skeleton from only the femoral neck, specifically the supero-inferior neck diameter (SID). I predicted that males have larger SID values than females. I measured 300 adults of mixed ancestry (black and white) and ages (18 – 93 years) at the Hamann-Todd Collection at the Cleveland Museum of Natural History. To calculate measurement error, I remeasured 20 samples three times each, and had two other researchers measure them once: Mean inter and intraobserver errors were 1mm or less. I used the binary linear regression equation of Luna et al. (2021) to determine if SID can be used to estimate sex. Using this approach, I correctly identified the sex of 84% of the skeletons. As predicted, males have larger SID values (33.97 mm ± 2.57 SD) than females (29.62 mm ± 2.11 SD). The results show that the SID measurement provides a high degree of accuracy for estimating the sex of contemporary skeletons in the United States.

A Review of Anatomical Terminology for the Hip Bone

EMILY DEEM[2], NICHOLAS V. PASSALACQUA[1], DIANA MESSER[1], KATIE ZEJDLIK[1] and ALEXANDRA KLALES[3]

[1]Anthropology and Sociology, Western Carolina University, [2]Forensic Sciences, Western Carolina University, [3]Anthropology and Sociology, Washburn University

There is a long history attempting to standardize anatomical terminology of the human body, most recently culminating in publication of the *Terminologia Anatomica*. This volume is dedicated to standardization of anatomical terminology for both clinicians and anatomists. However, there continues to be a lack of consistency in terminology. This paper specifically explores terminological inconsistencies for the hip bone.

Nine terms for the hip bone were selected for investigation: "coxal bone", "hip bone", "innominate bone," "*os coxa*," "*os coxae*," "*ossa coxae*," "*os innominatum*," "*os pelvicum*", and "pelvic bone". Terms were chosen based on their inclusion in the *Terminologia Anatomica*, and/or common usage in anthropological literature. Searches for these terms in publications were conducted using the PubMed, JSTOR, and EBSCO databases.

Results demonstrate differences in terminology used to describe the hip bone both over time and between disciplines. "Innominate bone" was the most frequently used term and second-longest term in use, making it overall the most consistently used. This was followed by "*os coxae*" as the next most frequently used term, and "*os innominatum*" as the term with the longest span of usage.

The terms used to refer to the hip bone reflect a lack of consistency within and between disciplines. Due to the often-interdisciplinary nature of research, it is important to standardize

terminology across and within disciplines. Based on these results we recommend adoption of "innominate bone" as the preferred term for the hip bone.

Highlighting the invisible: Marginalization in 19th and 20th century anatomical and medical anatomical skeletal collections

CASSANDRA M S. DEGAGLIA[1,2], ANONYMOUS RESEARCH PARTICIPANT[2], MOLLY K. ZUCKERMAN[1] and KATHRYN E. MARKLEIN[3,4]

[1]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Division of Biological Anthropology, National Museum of Natural History, [3]Department of Anthropology, University of Louisville, [4]Center for Archaeology and Cultural Heritage, University of Louisville

Anatomical and anatomical medical collections, such as the George S. Huntington and Robert J. Terry (Terry) Anatomical Collections, have been fundamental to methodological and theoretical developments in biological anthropology. However, these collections were created through processes of structural violence and systemic racism, and individuals within them embody evidence of diverse structural violence. This raises profound and not yet fully developed ethical issues regarding their curation and research use. Recent critiques have particularly highlighted how commingling, and the element-based and population-level analyses common to these collections further disembody and dehumanize individuals within them. Here, we explore one possible semi-restorative strategy for research with anatomical collections: Osteobiography, which by focusing on embodied lived experiences, contingency, and contextualization can represent a humanizing counterpoint. We present the case study of an Anonymous Research Participant (ARP) from the Terry Collection, using a life course perspective, ecosocial theory, and an 11-biomarker skeletal frailty index (SFI). Through this lens, we demonstrate how the ARP agentively bears witness to cumulative experiences of chronic physiological stress (i.e. dental caries, AMTL), trauma, metabolic disease (i.e. osteopenia), congenital defects (i.e. spina bifida), and physical overexertion (i.e. enthesophytes, osteoarthritis) (modified SFI: 6) over their life course, immersed within race-based structural violence and poverty, which contributed to increased frailty, progressive treponemal infection, premature death, and postmortem structural violence via involuntary anatomization. In this way, highlighting the individual and their lived experiences through osteobiography may allow us to more ethically engage with them as complete people, with multifaceted histories.

Bilateral asymmetry and sexual dimorphism in the human cranium

ANTONIETTA DEL BOVE[1,2], ANTONIO PROFICO[3], MARINA MELCHIONNA[4], PASQUALE RAIA[4] and CARLOS LORENZO[1,2]

[1]Department of History, University Rovira i Virgili,, Avinguda de Catalunya 35, 43002 Tarragona, Spain., [2]Department of Quaternary and Prehistory, Institut Català de Paleoecologia Humana i Evolució Social (IPHES_CERCA), Zona Educational 4, Campus Sescelades URV (Edifici W3), 43007 Tarragona, Spain., [3]DFG Centre for Advanced Studies "Words, Bones, Genes, Tools", , Eberhard Karls University of Tübingen, Rümelinstr. 23, 72070 Tübingen, Germany, [4]Department of Earth, Environmental and Sciences, University Federico II, 80126 Napoli, Italy.

Largest part of cranial morphological information is symmetric on the left and right side with respect to the midsagittal plane. A certain portion of cranial shape information is attributable to fluctuant asymmetry. Recent advances in geometric morphometrics allow to quantify and map asymmetry on 3D-models . This study intends to compare in a world-wide sample of modern humans (N=181; 89 females and 92 males) the magnitude and pattern of asymmetry in relation to sexual dimorphism. On each cranium, we defined 50 anatomical landmarks and a symmetric patch of 1000 semilandmarks. We found that the 24.02% of the total variance is associated to bilateral asymmetry. The asymmetric component is composed of 28.58% of directional asymmetry and 71.42% of fluctuant asymmetry. Both sexes share the same pattern of asymmetry; on the left side the parietal is expanded on its lateral portion and the pterion region appears to be shrunken. Our findings agree with previous literature on brain lateralization suggesting as the endocranial morphology drives the entire pattern of asymmetry in the human cranium.

This research has received funding from the Martí i Franquès fellowship program, under grant agreement 2020PMF-PIPF-43 managed by Andreu Ollé Cañellas.

Vascularization may underlie sex differences in chest skin coloration in geladas (*Theropithecus gelada*)

PATRICIA M. DELACEY[1], AMY LU[2], THORE J. BERGMAN[1,3], JACINTA C. BEEHNER[1,4] and NOAH SNYDER-MACKLER[5,6]

[1]Department of Psychology, University of Michigan, [2]Department of Anthropology, Stony Brook University, [3]Department of Ecology and Evolutionary Biology, University of Michigan, [4]Department of Anthropology, University of Michigan, [5]Center for Evolution and Medicine, Arizona State University, [6]School of Life Sciences, Arizona State University

The intensity of sexually selected signals should be the highest value that each male can sustain given a set of underlying costs. One problem in sexual selection theory, however, is that we rarely have data on the underlying mechanisms to assess what these costs are. Here we examined the molecular differences in a putatively sexually selected signal in wild geladas – their red chest patch. We expected males to have increased expression of genes related to androgen and estrogen receptors, indicating a hormonal regulation pathway in the chest skin. Using RNA-sequencing of 4mm chest skin biopsies collected from 21 male and 17 female geladas, we found that 10.5% of the 10,226 detectably expressed genes were significantly expressed between males and females (N=1,077, FDR<20%). Contrary to expectations, we did not find significant differences in sex hormone receptor gene expression. However, genes more highly expressed in males were enriched for biological processes associated with blood vessel formation and blood flow (P<0.022). This supports the idea that oxygenated blood flow contributes to variation in redness. Moreover, because redder chests also radiate more heat, increased blood flow to the chest skin may act as a signal production cost for males in the near-freezing temperatures of the Simien Mountains.

National Science Foundation (BCS-2041542, BCS-0715179, BCS-1732231, BCS-1723237, BCS-2010309, BCS-1723228, IOS-1255974, IOS-1854359); Leakey Foundation (AWD015438); National Geographic Society (NGS-8100-06, NGS-8989-11, NGS-1242, NGS-50409R-18); University of Michigan, Arizona State University, Stony Brook University.

Ectochondral bone: the role of membranes in shaping endochondral bones of the skull

VALERIE B. DELEON[1], KATHERYN P. FRANKLIN[1], LAURA K. HAYNES[1], CHRISTOPHER J. VINYARD[2] and TIMOTHY D. SMITH[3,4]

[1]Anthropology Department, University of Florida, [2]Department of Anatomy and Neurobiology, Northeast Ohio Medical University, [3]School of Physical Therapy, Slippery Rock University, [4]Department of Anthropology, University of Pittsburgh

Bone forms through intramembranous or endochondral ossification, and some bones form as a composite of ossification centers. Most texts describe bone in binary terms based on the initial type of ossification centers. In contrast, we emphasize membranes and cartilage interactions in directing ossification and growth of the skull. Previously, we demonstrated the role of cartilage in shaping intramembranous bone of the facial skeleton. Here, we highlight the role of membranes in shaping endochondral bone.

We combined image data from traditional microCT, diffusion iodine contrast-enhanced CT (diceCT), and histology to create 3D models of the skull and key membranous structures in a comparative primate sample including strepsirrhines (e.g., *Galago moholi*), anthropoids (e.g.,

Aotus nancymaae), and tree shrews (e.g., *Tupaia belangeri*) as an outgroup. We compared the extent of bone deposition in newborns to that in older infants to demonstrate how certain features are formed in the membranes attached to endochondral ossification centers, and directly influenced by the soft tissues of associated functional matrices. With an emphasis on the sphenoid, we illustrate the original endochondral centers of ossification and incremental intramembranous growth of features including alisphenoid and orbitosphenoid.

We encourage the use of the historic term *ectochondral bone* to describe intramembranous projections of bone from an endochondral ossification center. In the German literature, this mode of ossification has long been termed *Zuwachsknochen*. Distinguishing ectochondral bone from other appositional bone (e.g., the bone collar forming on the surface of a cartilage model) helps to reinforce different roles each plays in producing skeletal variation.

Funded by the National Science Foundation (BCS-1830894 and BCS-1830919)

The far reaching effects of disease on morphology

HILLARY DELPRETE

History and Anthropology, Monmouth University

This study was developed to test whether tuberculosis, a common cause of death for individuals from the Hamann-Todd collection, can be linked with differences in pelvic morphology. Twenty pelvic measures were collected from 245 individuals from the Hamann-Todd collection along with information on age, date of birth, and cause of death. It is well known that ancestry and sex lead to differences in pelvic measurements so this study sample was subdivided into 4 groups to account for these differences: Black females, Black males, White females, and White males. The most common cause of death for Black females, Black males, and White males was tuberculosis (25%, 22%, and 17.9% respectively). For White females arteriosclerosis was the most common cause of death (10.2%) followed by tuberculosis (6.8%). To test for differences in pelvic measures between individuals who died of TB and individuals who died of other causes, multiple t-tests were run to determine if there were any significant differences in the collected measurements between individuals with and without TB. The results of this study show that Black females significantly differed in the anterior space of the inlet in individuals that died of TB. Further, Black males show significant differences in the anteroposterior diameter of the inlet, depth of pelvis, and the length of the linea terminalis in individuals that died of tuberculosis. No significant differences were noted for White individuals. These results have important implications for our understanding of how cause of death can have far-reaching effects on morphology.

Dating and site formation of the Late Villafranchian mammals from Senèze, France

ERIC DELSON[1,2,3,4,5], KAREN L. BAAB[6], TERENCE D. CAPELLINI[7], SIOBHÁN COOKE[8], SARAH FREIDLINE[9], STEPHEN FROST[10], EVA C. GARRETT[11], WILLIAM E.H. HARCOURT-SMITH[1,2,3,4], RUSSELL HOGG[12], KIERAN MCNULTY[13], TARA PEBURN[12], MICHELLE SINGLETON[14,15], KATHERINE ST. JOHN[16,17,3,4], MICHAEL STEIPER[18,3,4] and JOHN A. VAN COUVERING[2,3,4]

[1]Department of Anthropology, Lehman College/CUNY, [2]Department of Vertebrate Paleontology, American Museum of Natural History, [3]PhD Program in Anthropology, CUNY Graduate Center, [4]NYCEP, (the New York Consortium in Evolutionary Primatology), [5]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, Spain, [6]Department of Anatomy, Midwestern University, Glendale, [7]Department of Human Evolutionary Biology, Harvard University, [8]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, [9]Department of Anthropology, University of Central Florida, [10]Department of Anthropology, University of Oregon, [11]Department of Anthropology, Boston University, [12]Department of Rehabilitation Sciences, Florida Gulf Coast University, [13]Department of Anthropology, University of Minnesota, [14]Department of Anatomy, Chicago College of Osteopathic Medicine, Midwestern University, [15]Life Sciences Section, Negaunee Integrative Research Center, Field Museum, [16]Department of Computer Science, Hunter College/CUNY, [17]Division of Invertebrate Zoology, American Museum of Natural History, [18]Department of Anthropology, Hunter College/CUNY

The Senèze site, located within a volcanic maar in the Haute-Loire district of the Massif Central, has yielded thousands of mammalian fossils including many nearly complete skeletons since it was first reported by Marcellin Boule in 1892. The holotype skull of *Paradolichopithecus arvernensis* and a partial ulna of *Macaca* are the only primates. Senèze is the reference locality for the mammalian MNQ 18 biochron and the late Villafranchian interval of early Pleistocene age. New fieldwork directed by the late Claude Guérin, Martine Faure and Eric Delson from 2001-2006 aimed to clarify stratigraphy, age, paleoenvironment and taphonomy, and an edited volume reporting the results is nearing publication. Many NYCEP PhD students and faculty (co-authors here) participated in the research. Recalibrated to current standards, the published argon-argon dates include 2.07 ± 0.02 Ma above all fossils, 2.12 ± 0.03 Ma below one main fossiliferous horizon (with *Dicerorhinus* and *Eucladoceros* skeletons), 2.14 ± 0.04 Ma below other fossils and 2.19 ± 0.03 Ma above two *Allohippus* skeletons. Short paleomagnetic columns support these ages, suggesting the presence of the Feni subchron (C2A.n1, ca. 2.14-2.10 Ma) within the Matuyama Chron. The base of the section is undated but probably at least 2.0 Ma, with the possibility of the Huckleberry Ridge and Réunion excursions mostly beyond the sampling intervals. Both taphonomic and stratigraphic analyses agree that the most likely mode of skeletal preservation involved animals slipping into the lake and drowning, unable to regain the steep bank, with no evidence of catastrophic action (e.g., fumarole gas).

USA: NSF, National Geographic Society, Leakey Foundation, and PSC-CUNY faculty research program; France: le Ministère de la Culture, le Conseil général de Haute-Loire et le Conseil régional d'Auvergne.

Cortical and trabecular bone covariation in the human tibia

LILY J. D. DEMARS[1], SHARON KUO[1], JAAP P. P. SAERS[2], TEA JASHASHVILI[3,4], MARK R. DOWDESWELL[6], KRISTIAN J. CARLSON[3,5], ADAM D. GORDON[7], JAY T. STOCK[2,8] and TIMOTHY M. RYAN[1]

[1]Department of Anthropology, Penn State University, [2]Department of Archeaology, Cambridge University, [3]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [4]Department of Geology and Paleontology, Georgian National Museum, [5]Evolutionary Studies Institute, University of Witwatersrand, [6]School of Actuarial Sciences, University of Witwatersrand, [7]Department of Anthropology, University at Albany, SUNY, [8]Department of Anthropology, Western University

All skeletal elements are composed of both cortical and trabecular bone. Most research on skeletal variation in humans and other primates has focused on analyzing only trabecular or cortical bone structure. However, these two levels of bone structural organization are known to have distinct material properties and likely respond differently to mechanical loading. The objective of this study is to compare patterns of bone structural variation in the trabecular bone of the distal tibia and cortical bone of the tibial diaphysis among three archaeological groups with distinct subsistence strategies in order to better understand the relative responsiveness and variability of trabecular and cortical bone structure. Trabecular bone was characterized using a whole joint quantification method and between-group comparisons were performed using the point cloud method and Bayesian multilevel modeling [DeMars et al., 2020]. Cortical bone structure was quantified using cross-sectional properties taken at 10% intervals between 30-70% length. ANOVAs were used to compare groups. Trabecular bone structure of the distal tibia generally supports the hypothesis that more mobile subsistence groups have increased trabecular robusticity. However, very few cortical bone cross-sectional geometric properties differ significantly among the subsistence groups, indicating a difference in how

trabecular and cortical bone respond to mechanical loading environments. The results of this study indicate that future research should include analyses of both trabecular and cortical bone structure in order to further our understanding of the relative responsiveness and variability of both tissue types and get a more complete picture of bone phenotype variation.

NSF BCS 1719187, 1719140, 1847806, European Research Council, Grant/Award Number: 617627; RCUK BBSRC, Grant/Award Number: BB/R01292X/1, NSF GRFP No. DGE 1255832

Sociality in a vulnerable primate: broken bones, birth and bipedalism

JEREMY M. DESILVA[1,2] and CATHERINE K. MILLER[1,2]

[1]Anthropology, Dartmouth College, [2]Ecology, Evolution, Environment and Society, Dartmouth College

This abstract is part of the symposium *Building on the legacy of Adolf Portmann: Interdisciplinary approaches to human evolution and development*. Adolf Portmann interpreted human growth and development through a broad taxonomic lens, inviting scholars to compare humans not just to our primate cousins, but to the entirety of the mammalian class and even birds. It is in that spirit that we wonder how the vulnerabilities of bipedal locomotion in early hominins may have promoted prosocial behaviors. Many of our colleagues have reported important data on the frequency of healed fractures in ape long bones. But we propose that a more telling comparison might instead be the long bones of the saltatorial mammals and terrestrial birds who rely on two-legged locomotion. Stephens et al. (2008) found 267 skeletal injuries among 3,021 small New England mammals, but only one instance of a healed fracture in the saltatory jumping mouse. Furthermore, scholars have found healed injuries to be rare (but not absent) among wading birds, and Rothschild and Rühli, (2007) found not a single healed fracture in the lower limbs of 108 wild ratite birds. It is in this context that we find evidence for healed leg bone fractures in Plio-Pleistocene hominins (KSD-VP-1/1, KNM-ER 738, KNM-ER 2596) and the large percentage of vertebral pathologies (e.g. A.L. 288-1, StW 431) so intriguing and potentially informative about the prosocial nature of early hominins. Interpreting these "fragments" as data rather than footnotes helps connect anatomy and behavior as Portmann modeled nearly 80 years ago.

Dietary and body mass correlates of primate tooth root surface area

ASHLEY R. DEUTSCH, VICTORIA A. WHICHARD, GIULIA R. LAGOMARSINO, EDWIN DICKINSON and ADAM HARTSTONE-ROSE

Department of Biological Sciences, North Carolina State University

Primate tooth crown morphology has been studied extensively and has been found to correlate with both diet and body size. Because, during mastication, force is applied to the crown then transmitted through the root before being dissipated into the alveolar bone, body size and adaptations to dietary specialization may also be reflected in tooth root morphology. An examination of mandibular postcanine tooth root surface area (TRSA) across 75 primates reveals both dietary and body size signals. Although dietary signals are present, they differ across taxa, with stronger and more frequent signals present in strepsirrhines relative to haplorrhines and seem to primarily reflect high frequency loading experienced by folivores as well as the constraints of gape when consuming large hard objects. Additionally, TRSA is strongly correlated with body mass at each tooth locus (mean $r^2 = 0.82$) making it potentially useful for the reconstruction of body size in fossils – especially given that this anatomy may be better preserved than the more exposed crowns. While force experienced by maxillary teeth must be the same magnitude as that experienced in the mandible, force directionality and anatomical constraints experienced by maxillary teeth may differ, potentially producing different function TRSA signals. As such, we also compare maxillary and mandibular postcanine TRSA. Additionally, we present analyses of anterior TRSA. Anterior TRSA may reflect independent signals related to incision, grooming or gouging. While each of these regions may independently reveal correlations with diet and body size, comparison across these regions may reveal more specialized functional adaptations.

Funding was provided by the National Science Foundation IOS-15-57125.

NMDID explorations: Expanding diagnostic criteria for structural scoliosis

JENNIFER K. DEWEY

Department of Anthropology, University of Oklahoma

This research seeks to expand the diagnostic criteria for structural scoliosis by assessing the morphometric variation and biomechanical changes of individuals diagnosed with scoliosis in the NMDID (New Mexico Decedent Image Database). The research questions include: (1) Can other skeletal elements in the axial skeleton be used to indicate the presence of scoliosis in a bioarchaeological sample? (2) What morphological changes are consistent with the degree and type of curvature? The sample included 42 individuals (5 - 91 years) with a scoliosis diagnosis, with the database providing information regarding their age, sex, primary cause, and manner of death. The individuals were first evaluated for the degree of curvature by applying the Cobb method; the results were used to sort the individuals into groups by the degree and type of curvature. The second step used volume rendering of the DICOM images to do additional measurements of the axial skeleton in 3D planes. The third step used modeling software to visualize the bone to assess for more subtle changes associated, including changes to the periosteum, entheseal attachment site, and joint surface. Preliminary results indicate multiple elements in addition to the vertebrae are consistent with changes, including the sternum and ribs associated with the flexure. Descriptive statistics will present the frequency of occurrence as organized by degree of curvature, with information from individual life history supported by clinical literature. This approach can serve as a potential model for expanding the diagnostic criteria for assessing scoliosis in dry human remains typically assessed by bioarchaeologists.

Migrant health before, during, and after the 14th-century Black Death in London

SHARON N. DEWITTE[1], JULIA BEAUMONT[2], JANET MONTGOMERY[3], REBECCA REDFERN[4,5] and HADLEY SIBON[3]

[1]Anthropology, University of South Carolina, [2]Archaeological and Forensic Sciences, University of Bradford, [3]Department of Archaeology, Durham University, [4]Centre for Human Bioarchaeology, Museum of London, [5]School of History, Classics and Archaeology, Newcastle University

Bioarchaeological work has revealed evidence of declines in health prior to the mid-14th century Black Death in London, variation in risk of death with respect to frailty during the epidemic, and improvements in health afterwards. This raises questions regarding underlying mechanisms driving these apparent trends in health in the context of increasing social inequalities, urbanization, and repeated famines and plague epidemics. One possibility is that health improved after the epidemic because of the migration of healthy people into London. Studies in modern populations have documented a "healthy migrant effect", i.e., migrants are a sub-population of healthy individuals and thus, at least temporarily, exhibit better health on average than individuals in their sending and receiving populations. We present preliminary findings, using samples from London cemeteries, regarding differences in survivorship, as a proxy for health, between individuals (n = 93) who were local to London vs. those who were non-local (based on strontium isotope values) across four time periods: Early Pre-Black Death (c. 1000-1200), Late Pre-Black Death (1200-1250), Black Death (c. 1349), and

Post-Black Death (c. 1350-1540). Kaplan-Meier survival analysis reveals significantly higher survivorship in non-locals compared to locals across and within all four time periods. This suggests that the health of migrants to London, in general, was better than that of long-term inhabitants of the city throughout the medieval period. Ongoing work with a larger sample will clarify the intersections of health, risks of mortality, migrant status, and sex across the medieval period in general and during the Black Death specifically.

Funding was provided by NSF (BCS-1722491), RCUK, the Wenner-Gren Foundation (#9229), and the University of South Carolina Provost's Office.

Tree Climbing as a Selective Pressure on the Enlarged Human *Gluteus Maximus*

RAE DIAS and DR. ALISON MURRAY

Department of Anthropology, University of Victoria

Differences between humans and non-human apes in the pelvis and key muscle attachment sites are thought to reflect a trade-off between arboreal and bipedal locomotor abilities. Human morphology enables the hyperextension of the hips by the hamstrings necessary for efficient bipedal locomotion, but this morphology was thought to reduce the capacity of these muscles to powerfully extend the hip when in a flexed position typical of arboreal locomotion. This research tested whether the enlarged human *gluteus maximus* (GMAX) may have been shaped by the continued importance of climbing among humans, as it is recruited more than the hamstrings during powerful hip extension. We utilized motion capture, electromyography, and a musculoskeletal 3-D modeling approach to assess the relative function of the GMAX and the hamstrings of a human model and a model whose pelvic morphology had been altered to approximate that of a chimpanzee's over three movement trials: 1) walking, 2) standing from a seated position, and 3) standing from a deep squat. We hypothesized that the human model's GMAX would perform more effectively more than the hamstrings during hip extension and vice versa for the second model, due to functional differences produced by its altered pelvis. Differences in relative muscle activity across the three trials support our hypotheses in general, and implications for the evolutionary significance of the human GMAX are discussed. Results support the need for a paradigm shift in biological anthropology that views a broader range of human locomotive repertoires as of evolutionary significance, beyond terrestrial bipedal locomotion.

Mitochondrial disfunction: key to rates of gout in Polynesia?

RACHEL R. DICKERSON[1], AMARA SHAUKAT[2], MATTHEW BIXLEY[2], MURRAY CADZOW[2], TANYA MAJOR[2], AMANDA PHIPPS-GREEN[2], RUTH TOPLESS[2], NICOLA DALBETH[3], LISA STAMP[4], GLOBALGOUT CONSORTIUM[7], ANNA GOSLING[5] and TONY MERRIMAN[2,6,7]

[1]Anthropology, University of Pennsylvania, [2]Biochemistry, University of Otago, Dunedin, [3]Medicine, University of Auckland, [4]Medicine, University of Otago, Christchurch, [5]Anatomy, University of Otago, Dunedin, [6]Biochemistry, University of Alabama at Birmingham, [7]GlobalGout Consortium, GlobalGout Consortium

Gout is an inflammatory arthritis caused by NLRP3 inflammasome-mediated production of IL-1b in response to monosodium urate crystal. This disease is seen across the world but occurs in particularly high numbers in the Aotearoa New Zealand Māori and Pacific (Polynesian) populations. This high prevalence of gout may be due to the genomics of people with Polynesian ancestry, in particular their mitochondrial genome due to activation of the NLRP3 inflammasome by the mitochondria. Association between gout and mitochondrial DNA (mtDNA) copy number has been found in Aotearoa New Zealand Māori and Pacific (Polynesian) study cohorts but have not been investigated in non-Polynesian groups. We set out to test these previous findings, as well as test a theory that this association was unique to individuals with Polynesian ancestry. To test this hypothesis, we performed a single association test between gout phenotypes and mitochondrial copy number (MCN) in a group containing 4579 genomes from individuals with European ancestry, 1340 genomes from individuals with East Polynesian ancestry (Cook Island and New Zealand Māori), and 816 from individuals with West Polynesian ancestry. MCN was negatively associated with gout in the Eastern Polynesian sample set ($P = 2.9x10^{-6}$). The same negative association was also seen in the Western Polynesian cohort ($P = 3.6x10^{-16}$). However, there was no association in the European sample set ($P = 0.66$). These results indicate that the high rates of gout among individuals with Polynesian ancestry are likely due to mitochondrial disfunction and may be linked to the unique history of Polynesia.

Myological signals of handedness: bilateral asymmetry in the forearm muscles of non-human primates

EDWIN DICKINSON[1,2], MARISSA L. BOETTCHER[1,3] and ADAM HARTSTONE-ROSE[1]

[1]Department of Biological Sciences, North Carolina State University, [2]Department of Anatomy, College of Osteopathic Medicine, New York Institute of Techology, [3]College of Medicine, Medical University of South Carolina

Bilateral asymmetry in the human forelimb has been extensively documented, and is inferred to reflect behavioral lateralization in which a single hand is consistently favored for specific tasks. In extreme cases (e.g., athletes trained in hand-dominant sports), forearm muscle volume is increased by ~15% and maximal grip strength by ~10%. However, the phenomenon of bilateral asymmetry in the forearm musculature rarely receives formal recognition or discussion in nonhuman primates. In this study, we dissect the left and right forearms of 69 specimens across 32 species (including strepsirrhines, platyrrhines, and catarrhines) to examine the extent of bilateral asymmetry across these lineages. In all lineages, both left- and right-hand dominant individuals were recorded but preliminary findings indicate an overall preference towards increasing muscle mass and physiological cross-sectional area (PCSA) force potential in the right forearm (though trends in fascicle lengths were less consistent). Catarrhines (asymmetry $\bar{x}$ = 11%) and strepsirrhines ($\bar{x}$ = 6%) show consistently more asymmetry in mass and PCSA than do platyrrhines ($\bar{x}$ = 1%). Asymmetry is generally highest within the extensor compartment. Qualitative data also demonstrate a surprisingly high frequency of asymmetry in the presence/absence of specific muscles and the degree of fusion between muscle bellies, particularly within the digital extensor muscles. These data underscore the need to further explore asymmetric trends within nonhuman primates; however, more research is required to investigate the extent to which a species' behavioral repertoire (e.g., the frequency with which consistently lateralized tasks are practiced) contributes towards bilateral asymmetry in the forearm musculature.

Funding was provided by the National Sciences Foundation IOS-15-57125.

Variation in retroflexion and cortical geometry along the primate humerus and their consequences for inferring biomechanical performance

BLAKE V. DICKSON[1], ANGEL ZEININGER[1], DANIEL SCHMITT[1] and KEVIN D. HUNT[2]

[1]Department of Evolutionary Anthropology, Duke University, [2]Department of Anthropology, Indiana University

Long bone morphology has long been used in predicting the locomotor capacity of fossil primates. Among primates, long bone curvature (retroflexion) has been associated with terrestrial/arboreal behaviour and differences in cortical cross-sectional geometry have been described among climbers, leapers, and arboreal and terrestrial quadrupeds. Metrics of bone function are universally measured at midshaft which, under a simplified homogeneous beam model, will experience the greatest strain under load. However, more biologically accurate models of bone biomechanics have shown that strain is often distributed away from midshaft. It remains poorly understood how variation in bone curvature controls strain patterns and cortical reinforcement along the diaphysis, which may impact the reliability of biomechanical inference from midshaft measurements. Utilizing the comprehensive bone

morphometrics we investigate how curvature and cortical cross sectional geometry vary along the diaphysis of humeri in a diverse sample of primates representing terrestrial, arboreal, and suspensory species. Curvature and cortical thickness are positively correlated ($p < 0.001$, $R^2=0.69$), though their positions are not: curvature being greatest proximally and thickness being greatest distally ($p<0.001$). Terrestrial primates are the most curved ($p=0.02$), thickest ($p=0.02$), and most variable ($p<0.001$); and quadrupeds have greater curvature and thickness ($p=0.01$), and more variable thickness ($p=0.02$) than suspensory primates. These results suggest that simple beam bending models based on measurements at only midshaft may not be reliable for predicting biomechanical performance of primate humeri, and may be limited in reconstructing locomotor behaviour.

"They're people too": Perspectives on the (dis)embodiment of teaching assemblages

ELIZABETH A. DIGANGI[1], ARIEL GRUENTHAL-RANKIN[1,2] and TESSA SOMOGYI[1]

[1]Anthropology, Binghamton University, [2]Anthropology, Humboldt State University

This abstract is part of the symposium *Ethics in the Curation and Use of Human Skeletal Remains*. The assemblages of human remains in our university laboratories are integral to teaching osteology and are used for comparison during forensic or bioarchaeological work. However, as an outgrowth of the Western scientific tradition of mind/body dualism, human remains in teaching collections are often regarded differently than those in applied contexts. From processing to storage, the personhood of each individual may become abstracted as we handle, manipulate, and digitally scan their bones for teaching purposes. In this way, we may come to view these remains as "specimens" rather than "individuals."

When conducting forensic casework where the goal is identification and/or return, personhood is foregrounded; bodies are seen as whole and the embodiment of the person's lived experience is reflected in their skeletal remains. These individuals are handled reverently throughout the recovery, analysis, and return process. Opposing this is the unceremonious placement of teaching skeletons into locked cabinets or boxes for transport and storage. Such "specimens" are often sterile white, frequently lack provenance information, and may be parsed apart for explanatory and comparative purposes. Each factor contributes to a dehumanization of these remains and a disembodiment of their lived experiences. Here, we draw from our experience as anthropologists on the Carlisle Barracks Cemetery Disinterment Project to explore the dichotomy of "specimen" and "individual", discuss the ethics of anatomical teaching collections, and provide a path toward the reunification of personhood and teaching "specimen."

Impacts of forest fires on orangutan nutrition and health: Insight into how global climate change will affect an endangered ape

ANDREA L. DIGIORGIO[1,2], DANIEL J. NAUMENKO[3,4], CAITLIN A. O'CONNELL[2,5], LAURA KIELY[6], DOMINICK SPRACKLEN[7], TIMOTHY BRANSFORD[8], REBECCA SA. BRITTAIN[2], ALEXA UGARTE[2,9], SRI SUCI U. ATMOKO[10,11] and ERIN R. VOGEL[12,2]

[1]Writing Program, Princeton University, [2]Department of Anthropology, Rutgers University, [3]Department of Anthropology, University of Colorado, Boulder, [4]Institute of Behavioral Science, University of Colorado, Boulder, [5]Department of Anthropology, University of Pennsylvania, [6]Department of Chemical and Environmental Engineering, University of California Riverside, [7]School of Earth and Environment, University of Leeds, [8]Animal Studies Discipline, Eckerd College, [9]Department of Anthropology, New York University, [10]Biology, Universitas Nasional, [11]Primate Research Center, Universitas Nasional, [12]Center for Human Evolutionary Studies, Rutgers University

The rainforests of Southeast Asia are often considered unpredictable and challenging habitats for large, vertebrate frugivores. Confounding this, global climate change models predict increasingly frequent and severe wildfires, particularly in SE Asian peatland tropical habitats. Recent studies have shown that during and after wildfire smoke-periods, orangutans reduce their feeding time and spend more time resting and moving. Similarly, preliminary analyses from Tuanan in Central Kalimantan, Indonesia show that orangutans exhibit inflammation, stress, and negative energy balance during and after smoke periods. Yet we do not know if these physiological responses to smoke periods are a consequence of reduced nutritional intake during the smoke and post-smoke periods. We predicted that because orangutans spend less time feeding and more time resting and moving during smoke periods, they would have reduced total caloric intake. As a consequence, we predicted that during and after smoke periods, orangutans would have reduced estimated lean body mass (ELBM) (as measured by urinary creatinine adjusted by specific gravity.) We used generalized additive mixed models on 538 all-day focal follows and found that contrary to our predictions, total caloric intake was higher during smoke-periods compared to pre-smoke ($p < 0.001$) and post-smoke periods ($p < 0.001$). ELBM was highest during the pre-smoke period and decreased during the post-smoke period ($p = 0.02$). These results highlight that orangutans are able to maintain adequate nutritional intake during the smoke periods, but also suggest that post-smoke periods characterized by extended low fruit availability are detrimental for this endangered ape.

This research was funded by USAID (APS-497-11-000001 to E.R.V.), L.S.B Leakey Foundation (to E.R.V.), National Science Foundation (to E.R.V. BCS-0643122), Rutgers University (to E.R.V), Center for Human Evolutionary Studies (to E.R.V.)

PanDynamics: Disability as a risk factor for and consequence of infectious disease.

JESSICA L. DIMKA

Centre for Research on Pandemics & Society, Oslo Metropolitan University

The consequences of pandemics, especially but not limited to historical ones, are often studied in terms of mortality. However, survival or death are not the only two potential outcomes; long-term disability and other health consequences of illness are also key to understanding the full impacts of pandemics. Underlying health and disability have also been shown to be important risk factors for severe cases and deaths. Combined with social and economic factors, infectious disease and disability thus interact with each other to drive outcomes. I present this syndemic configuration by briefly highlighting research findings, including a) disparities between non-disabled and disabled populations in Scandinavian countries during the 1918 flu, showing for example, lower morbidity (OR 0.39, 95% CI: 0.298-0.516) but higher mortality ($x^2 = 13.983$, $p < .05$) among residents of psychiatric hospitals vs. staff, b) insights from an ongoing systematic review investigating long-term mental health consequences of pandemics, and c) results from a survey administered in Oslo during summer 2021 that show people with disabilities reported lower uptake of several non-pharmaceutical interventions and higher odds of reporting COVID-19 vaccine uncertainty (OR 2.191, 95% CI: 1.268-3.785). Drawing on these examples, I will discuss the need to consider interconnected changes over time, recognizing that pandemics are not one-time events but instead affect the health and disability status of survivors and thus shape the population at risk for the next wave or epidemic. Therefore, anthropologists must develop theoretical and methodological approaches for studying such dynamic, intertwined processes and relationships.

Projects have received funding from European Union's Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie grant agreement No 841925, Oslo Metropolitan University, and the Research Council of Norway.

ABSTRACTS

A diachronic analysis of Mseleni Joint Disease: Environmental conditions and gender-linked domestic practices as risk factors

ELIZABETH S. DINKELE[1], ROBEA BALLO[2], VICTOR FREDLUND[3] and VICTORIA E. GIBBON[1]

[1]Clinical Anatomy and Biological Anthropology, University of Cape Town, [2]Division of Cell Biology, University of Cape Town, [3]Mseleni Hospital, Kwa-Zulu Natal

Mseleni Joint Disease (MJD) is an osteoarthritic condition of unknown aetiology, endemic to a remote community of Southern African Bantu-language speaking people in KwaZulu-Natal, South Africa. The geographic isolation of MJD, with apparent absence of a genetic aetiology suggests a complex combination of environmental, social, cultural and biological risk factors. The aim of this study was to explore environmental conditions and local lifeways as risk factors of MJD. The geographic and demographic distributions of this disease were explored temporally through a meta-analysis and medical record review. Local domestic practices and indicators of social development were evaluated from census publications and socio-ecological surveys. Female gender was associated with a twofold increase in the likelihood of MJD (p=0.03) and in those older than 40 years, the likelihood of MJD increased twofold every 5 years (p≤0.0001). Age confounded the association between MJD and gender, and the likelihood of MJD in women decreased between 1970 and 2019, suggesting a temporal change in a gender-linked risk factor. MJD was geospatially localised to the arid sand-forest bioclimatic zone in settlements further from water access points. The higher prevalence in women and communities further from water sources suggests environmental and/or biological exposures linked to domestic practices of food and water provision are risk factors of MJD. The temporal decline in prevalence with the shift to a predominantly monetary-based economy is further evidence of a domestic practices as risk factors. This work demonstrates complex interactions between geospatial environments, socio-cultural practices and human health.

National Research Foundation, South Africa (Grant No. 115357 and 980000000460), Rare Disease Foundation Microgrant (#2312), The Department of Human Biology, UCT and Gibbon's Internal Research Grant.

The Visible Ape Project: a free, comprehensive, web-based anatomical atlas for scientists and veterinarians designed to raise public awareness about apes

RUI DIOGO[1,2], NICOLE BARGER[1,2,3], JOSE S. MARTIN[4], MARLI RICHMOND[2] and EVE K. BOYLE[1]

[1]Department of Anatomy, Howard University College of Medicine, [2]Center for the Advanced Study of Human Paleobiology, The George Washington University, [3]Department of Anthropology, The George Washington University, [4]Department of Biology, University of Aveiro

A valuable tool for comparative anatomical education and research in biological anthropology, The Visible Ape Project (www.visibleapeproject.com) is a free online resource designed to comprehensively illustrate anatomy and anatomical variation within and between extant ape species. It contains photographs, MRI, CT scans, and 3D models to explore homologies and variations in soft and hard tissues across hylobatids, orangutans, gorillas, chimpanzees, bonobos, and humans. These include detailed, labeled 3D artist renderings of the musculoskeletal system as well as 3D models of the skeletal and central nervous system based on radiological imaging of apes. They can be manipulated or downloaded and 3D printed to explore anatomy interactively, promoting active learning. Additionally, educational material, including information about non-human ape species, lesson plans, and a glossary of evolutionary and anatomical terms, is available on the site in English and Spanish.

Based at a Howard University, a minority serving institution, the Visible Ape Project especially aims to be accessible to and integrate members of communities underrepresented in anthropology and evolutionary biology from K-12 to college classrooms. Accordingly, the VAP incorporates outreach activities to disseminate science and promote awareness of apes, forming partnerships with veterinarians and conservationists in Africa and Asia. In this presentation, we will introduce the website to illustrate how this accessible, evolving resource can support research and education in biological anthropology.

The Visible Ape Project is funded by the NSF-BCS Excellence in Research Grant #1856329.

Shifting the Paradigm in Forensic Anthropology

DENNIS C. DIRKMAAT, PH.D. and LUIS L. CABO, MS

Department of Applied Forensic Sciences, Mercyhurst University

A few years ago, Forensic Anthropology as a discipline considered that forensic archaeology and forensic taphonomy played key roles in the discipline. Clarification of those roles and consideration of how forensic anthropology operates in the real world has resulted in a suggestion that the field effectively consists of two related though distinct subdisciplines. One is focused almost exclusively on the human bones, primarily for creating a biological profile (age at death, sex, stature and ancestry), and highlighting unique morphologies for personal identification attempts. This is completed in the laboratory, often with little or no consideration of context. Scientifically defendable interpretations of skeletal trauma, however are necessarily limited.

The other subdiscipline involves the more common scenario in which law enforcement and medicolegal professionals request the interaction of forensic anthropologists at outdoor crime scenes. A consideration of those requests suggests that the overwhelming expectation is past event reconstruction and specifically the role of humans during the Death Event, and subsequent taphonomic interval (time between emplacement and recovery): efforts we have labeled 'Outdoor Crime Scene Reconstruction.' Skills in osteology (human from non-human, biological profile and human skeletal trauma analysis) are required, as are those in forensic archaeology (locating evidence and notation of spatial distribution), and forensic taphonomy (understanding the modification of the evidence during the taphonomic interval).

The addition of context to our scientific judgments of past events, based on both the bones and importantly, the forensic scene context, thus represents what we consider a paradigm shift.

Mapping *In Vivo* Linear Microcracks Relative to Microstructure in the Human Rib

VICTORIA M DOMINGUEZ[1,2,3,4] and AMANDA M AGNEW[4]

[1]Anthropology, Lehman College, CUNY, [2]Anthropology, The Graduate Center, CUNY, [3]NYCEP, New York Consortium of Evolutionary Primatology, [4]Skeletal Biology Research Laboratory, The Ohio State University

Microdamage in the form of microcracks accumulates when excessive loads are placed on the skeleton, leading to a reduction in fracture resistance. In most cases, these cracks are targeted by bone remodeling, removing the damaged area and replacing it with a secondary osteon, helping to preserve cortical integrity throughout life. Researchers have suggested that microcracks may play a role in fragility and previous work has demonstrated that basal levels of *in vivo* microcrack density show a weak but significant positive relationship with age in the rib. However, *where* cracks occur may be more significant than how many are present. This study takes a preliminary look at the spatial distribution of linear microcracks in the human rib.

The sample consisted of left or right 6th ribs from 30 individuals (15 female, 15 male), aged from 40–99 years (mean=70, sd=17). Pre-processing, *en bloc* staining was used to distinguish *in vivo* from processing microdamage. Linear microcracks, intact and fragmentary osteons, and cortical porosity were mapped using a geographic information systems (GIS) approach to examine relationships between these variables by sex and age. No universal patterns were observed. However, microcracks appear most often on the endosteal border of the pleural surface whereas

they are more evenly distributed throughout the cutaneous cortex. In older samples, microcracks overlap regions with the greatest osteon density, which is expected. Finally, proximity of microcracks to large pores increases with age, likely as an artifact of decreasing bone mass and a possible risk factor for fragility.

Ontogenetic patterns of limb bone robusticity in a Medieval sample

TABITHA DORSHORST, HERZEN REIS and BRIGITTE HOLT

Anthropology, University of Massachusetts Amherst

While most studies of diaphyseal structure in past populations are based on adult samples, the ontogenetic growth process is widely recognized but still poorly understood as a key determinant of limb bone robusticity patterns. Building on recent studies reporting surface-specific cortical changes across the lower limb, we present ontogenetic patterns in upper and lower limb cortical bone in the Medieval sample from Noli (Italy). While sedentary, the Noli population is historically known for strenuous net fishing from an early age, a behavior expected to produce high upper limb mechanical loads.

Humeri and tibiae were imaged at 35% and 50% humeral length, and 20%, 50% and 80% tibial length, using a pQCT scanner. Age estimates (fetal-15 years) were obtained from dental eruption or derived from bone lengths using equations calibrated on Medieval samples. We examined measures of total (TA), cortical (CA), and medullary (MA) areas, strength (Zp), and shape (Zx/Z) using regression and Pearson correlation tests. All area and strength measures for both humerus and tibia increase significantly at all levels, all reflecting periosteal apposition and endosteal resorption. Our results do not show that childhood fishing activities translates to higher humeral cortical gains. Unlike some previous studies, we find no evidence of endosteal contraction in adolescence. The proximal tibia exhibits the expected increased antero-posterior expansion, but a smaller change than observed in higher mobility populations. Interestingly, midshaft tibial shape increases slightly after age 12, but the change is not significant, confirming previous evidence of higher remodeling thresholds for the midshaft tibia.

Bioanthropological analysis of human remains from the Middle Period in the Dulce River basin and Guasayan hills in northwestern Argentina

HILTON D. DRUBE[1,2], FERNANDA MINOTTO[1] and AGUSTÍN TOGO[2]

[1]Facultad de Ciencias Exactas y Naturales, Universidad Nacional de Catamarca, [2]Facultad de Ciencias Médicas, Universidad Nacional de Santiago del Estero

The Middle Period of the archaeological record in northwestern Argentina has been extensively studied in recent decades and significant information has been added regarding the use of landscape, technologies and subsistence strategies during this period of time. Different societies occupied the valleys and mountains as well as the plains in northwestern Argentina in the Middle Period (circa AD. 400-900). One of such archaeological societies is known as Las Mercedes, which spread its occupation mainly in the Dulce River basin and the Guasayan hills in the province of Santiago del Estero. Its patterns of settlement and its distinctive pottery have been profoundly registered. However, bioanthropological data is scant. The aim of this report is to present the results of the bioanthropological analysis of skeletal remains belonging to this particular society. Standard macroscopic and metric methods concerning the study of human remains were used as well as radiological examination. It is important to notice that few individuals have been recovered from Las Mercedes mortuary contexts. As a result, the skeletal sample studied comprises 16 individuals, including 12 adults and 4 subadults, unburied in different sites. Funerary practices included primary and secondary burials. Although all skeletons are incomplete, data obtained shows the presence of dental disease and metabolic conditions affecting these ancient human groups. Cranial modification was present as a cultural practice and preliminary biodistance analysis does not relate these individuals closely with posterior human groups in the area. Additional molecular studies will be used to reveal new information of this past society.

Funding support provided by FHCSyS-UNSE and FACEN-UNCa.

Embodied Resilience: Biocultural Approaches to Understand Experiences of Trans & Gender Diverse People During the COVID-Pandemic in the U.S

L. ZACHARY DUBOIS[1], JAE A. PUCKETT[2], CINDI STURTZSREETHARAN[3], DEBRA A. HOPE[4], RICHARD MOCARSKI[5], ALEXANDRA JAGIELSKI[1], TERRA DUNN[2], JULIA ROHRABAUGH[1], TAYLOR ANDERSON[2] and ROBERT-PAUL JUSTER[6]

[1]Anthropology, University of Oregon, [2]Psychology, Michigan State University, [3]School of Human Evolution and Social Change, Arizona State University, [4]Psychology, University of Nebraska-Lincoln, [5]Psychology, San José State University, [6]Psychiatry and Addiction, University of Montreal

During 2020-2021, over 100 million people contracted Coronavirus (COVID-19) and over 2.5 million have died. Physical distancing/quarantine have contributed to poor health and well-being for many, but the burden of COVID-19 disproportionally impacts marginalized communities, including transgender and gender diverse (TGD) people. This on-going longitudinal study launched prior to the pandemic includes a diverse sample (N=158) of TGD people in Oregon, Michigan, Tennessee, and Nebraska. The study examines TGD lived experience, resilience, and embodied health within varied contexts. Data collection at baseline and month 12 include interviews, surveys, and multiple biomarker samples followed by a year of monthly surveys. A biocultural mixed-methods approach enabled high retention and multiple-levels of data collection capturing dynamic interactions and embodied experience. Participants range from 19-70 years old (M = 33.06; SD = 12.88) with 27.2% identifying as trans men/men, 26% identifying as trans women/women, and remaining identifying as genderqueer/nonbinary with 30% of participants identifying as people of color. At baseline, 64% scored lower than the mean for physical health of the general population and 52% had heightened/acute inflammation (CRP). Reported pandemic experiences include loneliness (62%) and changes in income/housing/employment (42%). Written responses (n = 1,143) from surveys reveal pandemic-specific challenges including heightened marginalization stress (e.g., misgendering) when quarantining. Contributors to resilience included experience overcoming past challenges, limiting media exposure, time in nature, and connecting with others. Findings make visible lived experiences of TGD people and our strategies for building resilience while underscoring how pandemic challenges exact a disproportionate toll on this population.

Characterizing neurons in schizophrenia-associated regions of the rhesus macaque brain

GABRIELLE R. DUGAN[1], TRISH M. ZINTEL[2], KENNETH L. CHIOU[2], CAITLYN H. SPURRELL[4], AISHWARYA A. GOGATE[4,5], LEA M. STARITA[4,6], DIANA R. O'DAY[4], HANNAH A. PLINER[4], SAMUEL E. BAUMAN[7], NICOLE R. COMPO[7], MELWEEN I. MARTINEZ[7], LAUREN J.N. BRENT[8], CHRISTOPHER S. WALKER[9], OLGA GONZALEZ[10], JACK STYLLI[12], ALEX R. DECASIEN[13,15,19], MARTIN O. BOHLEN[11], JAMES P. HIGHAM[13,15], MICHAEL J. MONTAGUE[12], MICHAEL L. PLATT[12,14,16], JAY SHENDURE[17,18,4,6] and NOAH SNYDER-MACKLER[2,3]

[1]College of Engineering, Virginia Tech, Blacksburg, VA, USA, [2]Center for Evolution and Medicine, Arizona State University, Tempe, AZ, USA, [3]School of Life Sciences, Arizona State University, Tempe, AZ, USA, [4]Brotman Baty Institute for Precision Medicine, Seattle, WA, USA, [5]Seattle Children's Research Institute, Seattle, WA, USA, [6]Department of Genome Sciences, University of Washington, Seattle, WA, USA, [7]Caribbean Primate Research Center, University of Puerto Rico, Puerto Rico, [8]Centre for Research in Animal Behaviour, University of Exeter, Exeter, UK, [9]Department of Molecular Biomedical Sciences, College of Veterinary Medicine, North Carolina State University, Raleigh, NC, USA, [10]Southwest National Primate Research Center, Texas Biomedical Research Institute, San Antonio, TX, USA, [11]Neurobiology, Duke

University School of Medicine, Durham, NC, USA, [12]Department of Neuroscience, University of Pennsylvania, Philadelphia, PA, USA, [13]Department of Anthropology, New York University, New York, NY, USA, [14]Department of Psychology, University of Pennsylvania, Philadelphia, PA, USA, [15]New York Consortium in Evolutionary Primatology, New York, NY, USA, [16]Department of Marketing, University of Pennsylvania, Philadelphia, PA, USA, [17]Howard Hughes Medical Institute, Seattle, WA, USA, [18]Allen Discovery Center for Cell Lineage Tracing, Seattle, WA, USA, [19]Section on Developmental Neurogenomics, National Institute of Mental Health

Rhesus macaques are primates with neurological and social similarities to humans that are used as biomedical models for understanding brain organization and function, including factors that influence the onset of neuropsychiatric disorders. Investigating the macaque brain at the single-cell level will allow us to further our understanding of the contemporary cellular complexity of the macaque brain as well as how it has changed over evolutionary time through comparative analyses of rodents and humans. We conducted single-nucleus combinatorial-indexing RNA-sequencing (sci-RNA-Seq3) on 28 brain regions from two macaques (one male and one female). We characterized 90,226 individual neurons, the most affected cell type in schizophrenia, to investigate differences in cell subtype type gene expression between schizophrenia-associated brain regions (SABRs) and non-SABR. Across the SABRs, there were three main excitatory neuron cell types: *RORB*, *FEZF2*, and *THEMIS*. We found groups of cells specific to the SABRs that expressed genes known to be associated with schizophrenia. Specifically, a cluster of hippocampal neurons was characterized by higher expression of *ZBTB20*, a transcription factor associated with abnormal hippocampal development. Additionally, we identified a cluster of cells from the thalamus expressing known schizophrenia-associated genes *PVALB* and *ATP1B1* that were enriched for inhibitory signaling processes, suggesting we may have found a region-specific interneuron subtype in macaques that may be analogous to a disease-associated cell type in humans. Future work will further describe and characterize these cells, as well as expand to comparing these cells to those from non-SABRs.

This work is funded by the following grants: NIMH U01-MH121260, ORIP P40- OD012217, NIA R00-AG051764, NIA R01-AG060931, NIMH R01-MH096875, NIMH R01-MH089484, NIMH R01- MH118203.

Ritual Violence among the Postclassic Maya: Isotopic inference of mobility at the sites of Zacpetén and Ixlú, El Petén, Guatemala

WILLIAM N. DUNCAN[1], ASHLEY E. SHARPE[2], GEORGE D. KAMENOV[3], PRUDENCE M. RICE[4] and JOHN KRIGBAUM[5]

[1]Department of Sociology and Anthropology, East Tennessee State University, [2]Smithsonian Tropical Research Institute, Smithsonian Institution, [3]Department of Geological Sciences, University of Florida, [4]Department of Anthropology, Southern Illinois University Carbondale, [5]Department of Anthropology, University of Florida

We present and compare isotopic signatures that inform on the geographic origins of individuals subjected to ritual violence from two neighboring Postclassic (AD 950–1524) southern lowland Maya sites, Ixlú and Zacpetén. At Zacpetén, at least 37 individuals were buried in a mass grave (Op. 1000) after the site was taken over, when burials were exhumed, violated, and reinterred collectively. At Ixlú, 21 individuals were sacrificed and interred during two construction episodes of a shrine (Str. 2023). Sampled tooth enamel was prepared and analyzed for light carbon and oxygen and radiogenic strontium ratios to assess the structure and formation of these assemblages. The Zacpetén sample (N=65) has a mean $\delta^{13}C$ of -1.1±0.9‰ and $\delta^{18}O$ of -1.8±1.2‰; the Ixlú sample (N=14) has a mean $\delta^{13}C$ of -2.5±1.1‰ and $\delta^{18}O$ of -2.9±0.6‰. The local strontium range for the southern lowlands is well-established (0.7073–0.7083) and the Zacpetén sample (N=51) mean of 0.70794±0.0004 is well within that range, whereas the Ixlú (N=14) mean of 0.709782±0.0028 falls outside that range. Indeed, the six non-local individuals at Ixlú exhibit strontium >0.710, compared to seven non-local Zacpetén samples, all <0.709. The existence of local and non-local individuals among those subjected to ritual violence reflects complex Postclassic social and political circumstances. Conflict between two regional ethnopolities, western Itza and eastern Kowoj, extended into neighboring areas, which were sources of both allies and enemies for sacrifice. Ixlú and Zacpetén, lying between the Itza and Kowoj territories, were periodically overtaken by each group.

Limitations of Current Data and Methods for the Forensic Identification of Black Undocumented Immigrants

ISIS DWYER

Department of Anthropology, University of Florida

Recent shifts in immigration policy and enforcement on a global scale have resulted in a marked increase of Black migrants from Caribbean and African countries to the United States, via passage through Latin America and across the U.S.-Mexico Border. This study examines whether forensic anthropology is currently prepared to support the identification and repatriation of undocumented Black migrants at the U.S.-Mexico border and throughout the country.

A critical review of literature surrounding forensic ancestry estimation methods illuminates a lack of knowledge about regional cranial variation in individuals racialized as Black, especially in the Caribbean and Latin America. This inquiry underscores the need for more comprehensive methods of forensic ancestry estimation, including a thorough examination of cranial variation in contemporary Afro-descendant individuals. An inventory of the current networks of organizational support for the reporting and repatriation of missing migrants also demonstrates a lack of coverage in the countries of origin of Black migrants in the Caribbean and continental Africa, among other institutional barriers to support.

Undocumented immigration in this country is illustrated as a primarily Latinx issue, erasing the ways Black immigrants (including Afro-Latinx individuals) are uniquely impacted at the intersection of anti-immigrant and anti-Black discrimination. The results of this inquiry suggest that forensic anthropology mirrors this erasure through methods that fail to address contemporary cranial variation in Afro-descendant individuals. The current paradigm shift in forensic anthropology towards a population-focused approach to ancestry estimation represents an opportunity to explore innovative solutions in the identification and repatriation of Black undocumented immigrants.

This material is based upon work supported by the National Academies of Science, Engineering and Medicine Ford Foundation Predoctoral Fellowship.

Morphological variation in the femur of *Theropithecus oswaldi* from Koobi Fora and Olduvai Gorge

LESLEY H. EASON, LUCAS K. DELEZENE and J. MICHAEL PLAVCAN

Department of Anthropology, University of Arkansas

Primate postcranial fossils are assigned to species on the basis of morphology or association with craniodental remains. Several studies also attribute differences in morphology to differences in function. A preliminary step in assessing taxonomic and functional hypotheses is the analysis of morphological variation among extant species. Fossil variation can be referenced against patterns of variation in the extant to evaluate the likelihood of taxonomic and functional hypotheses. Here, we test whether morphological variation of the femur can discriminate among extant papionin species, and whether the patterns of variation can inform on hypotheses about cercopithecoid diversity during the Plio-Pleistocene in eastern Africa. This study evaluates fossil femora attributed to *Theropithecus oswaldi* (KNM-ER 866 and

MCK II) with reference to patterns of variation in the extant. High density 3D point clouds are computed from 3D surface scans of 86 femora representing 9 extant papionin species. Point clouds are scaled to a reference specimen using a ratio of their principal dimensions. Point clouds are aligned using the iterative closest point algorithm. 3D coordinate data are obtained from homologous features. Dimensionality of the data is reduced and variation is compared using principal component analysis. Preliminary results indicate that femoral morphology can discriminate among papionin species. Femoral morphology can also discriminate between extant *Theropithecus* and other papionins. Notably, the two fossils are most similar to extant *Theropithecus,* supporting the genus level attribution. At the same time, resampling procedures reveal a potentially significant degree of variation between the fossils, which may have taxonomic and functional implications.

The Osteological Paradox beyond osteology: Lessons from hair cortisol concentration analysis

KAITLIN E. EAST[1], MEGAN B. BRICKLEY[2], STAN VAN UUM[3], LANA WILLIAMS[4] and TRACY PROWSE[2]

[1]SNA International, [2]Department of Anthropology, McMaster University, [3]Department of Medicine, Western University, [4]Department of Anthropology, The University of Central Florida

Selective mortality is a key issue facing bioarchaeologists. The Osteological Paradox, as set out by Wood and colleagues, posits that skeletal assemblages are comprised of the dead, and do not reflect individual experiences throughout life or the living population. As the interest in applying new techniques from medicine to bioarchaeology increases, the effects of mortality bias on analyses of soft or keratinized tissues, such as hair cortisol concentration (HCC) analysis, remains unexplored. To determine if HCC, used to assess stress experience, is subject to mortality bias, this study explored how the end of life effects HCC.

HCC was analyzed in 40 individuals from the Terry Collection who died between 1923-1960 CE and 40 individuals who died between 2016-2017 CE. HCC was significantly higher in these two samples compared to HCC reported in living, healthy people. HCC was also significantly higher among individuals dying of disease compared to those dying abruptly, and varied significantly in relation to cause of death.

The results indicate increased stress at the end of life. As such, HCC in the dead does not reflect stress experience across the life course or a living population. However, HCC can be used to assess stress experience in the final months of life, which is a period that is often beyond the reach of bioarchaeologists and is poorly understood among still living people. Therefore, studies of soft and keratinized tissues must consider the effects of mortality bias, and may be best suited to the investigation of the end of life.

Biological affinities of human skeletal material in the non-Native American collections of the American Museum of Natural History

HEATHER J.H. EDGAR[1,2], ISIS DWYER[3], ASHLEY S. HAMMOND[4,5] and NELL MURPHY[4]

[1]Anthropology, University of New Mexico, [2]Office of the Medical Investigator, University of New Mexico, [3]Anthropology, University of Florida, [4]Anthropology, American Museum of Natural History, [5]New York Consortium of Evolutionary Primatology

We conducted analyses to estimate the population affinities of a subset (n=46) of the human remains curated by the American Museum of Natural History, as part of its ongoing efforts to better understand the history and composition of the collection. This subset included individuals associated with records indicating affinities from the US or Caribbean, neither Native American or "White." Methods applied drew on traditional craniometric, geometric morphometric, macromorphoscopic, and dental morphological data.

In 22 cases, the estimated population affinity matched those in collections records. For 18 individuals, incomplete preservation prevented affinity estimation. For four individuals, analyses were possible but results were in disagreement, so a consensus estimate could not be reached. These included three individuals described in records as "Black" and one individual described as "Chinese." In two cases, our estimates of affinity disagreed with collections records describing individuals as "Black." These results do not preclude the possibility that the catalog entry is correct. The long, complex history of admixture in the Americas and the persistence of the "one-drop rule" mean that an individual may have descended primarily from one world region (e.g., Europe) but may be culturally affiliated with a group descended primarily from a different world region (e.g., Africa). Additionally, human variation is such that all characteristics of any group can be found distributed in all other groups, albeit often at lower frequencies. This study underscores the challenges in identifying ancestry in historical collections that often lack provenience data.

Quantifying Curves: a geometric morphometric approach to analyze ovarian hormones

DANIEL E. EHRLICH[1,3], MARY P. ROGERS-LAVANNE[4], KATHARINE M.N. LEE[2,3], VALERIE SGHEIZA[2], MEREDITH A. WILSON[2] and KATHRYN B.H. CLANCY[2]

[1]Institute for Social Research and Data Innovation, University of Minnesota, [2]Department of Anthropology, University of Illinois, Urbana-Champaign, IL, [3]Siteman Cancer Center, Washington University in St. Louis, St. Louis, MO;, [4]Carl R. Woese Institute for Genomic Biology, University of Illinois, Urbana-Champaign, IL

We present a novel protocol to align and analyze hormone profiles using a geometric morphometric framework. Controlling for disparate sizes of hormone concentration and cycle length allows Principal Components Analysis to identify the major axes of shape variation and quantify their relative contribution to the overall phenotypic profile. We then use these PC scores to construct a distance matrix for cluster analysis in order to infer phenotypic sub-groups. Permutation testing is used to evaluate significance of phenotypic differences. This method for analyzing hormone profiles is flexible and can easily be adapted to other biomarkers across any time frame.

We demonstrate the method using estradiol profiles of 98 Polish and Polish-American women over the course of one menstrual cycle. In our sample, we found eight major axes of shape variation that contribute to estradiol profiles. These axes together account for just over 75% of variation and yielded three major phenotypes. These groups can each be further divided into 3-4 sub-groups, yielding as many as 10 significantly different phenotypes. Age, cycle length and overall hormone concentration were all investigated as covariates of the hormone profiles. While none were associated with the three major phenotypes, certain shape axes were weakly to moderately correlated with cycle length as well as luteal and follicular phase length. Variation in these traits serves to differentiate some sub-groups within the three major groupings. The presence of anywhere between 3 and 10 phenotypic profiles highlights the need for future work to investigate the processes that drive these shapes.

Research supported by the NSF (BCS-1317140, DDRIG BCS-1732117, DDRIG BCS-1650839, GRFP DGE-1144245), Wenner-Gren Dissertation Fieldwork Grants, APS Lewis and Clark Fund, Beckman Institute CS/AI Award, Sigma Xi & more.

Curating the history of museum collections: Using metadata in research design

ANDREA R. ELLER[1], RITA M. AUSTIN[1,2], STEPHANIE L. CANINGTON[3], COURTNEY A. HOFMAN[1,4,5] and SABRINA B. SHOLTS[1]

[1]Anthropology, National Museum of Natural History, Smithsonian Institution, [2]Biology, Natural History Museum, University of Oslo, [3]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, [4]Anthropology, University of Oklahoma, [5]Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma

Natural history collections prioritize the curation of organismal characteristics, specifically the biology of form (i.e., phenotypic traits). However,

this comes at the expense of other information pertinent to modern ethical and scientific needs. One remedy is the purposeful creation and dissemination of digitally-accessible datasets which include collections' metadata.

We developed and conducted a large-scale survey of human and nonhuman primate (NHP) skeletal collections. Our survey was designed to a) publicly supply archival metadata on the surveyed individuals, b) macroscopically document skeletal preservation and health markers, and c) provide insight for novel investigations regarding environment and health, independent of taxon.

We surveyed 4868 individuals, documenting over 40 variables on geographic area, growth, skeletal health condition, and oral health. Across the total sample, population biases skewed adult (76%) and slightly male (35%, females 33%, unk. 32%). Presence of dental calculus was observed in 35% of the sample, but was differentially distributed among taxa and tooth type. Among NHPs (n=1991, 41% of total sample), about 29% spent time in captivity. Of 875 wild-caught NHPs with known locations, 92% were collected from a human-impacted landscape. This level of data allows future researchers to investigate macro-level questions, and provides curators with direct insight into collection distributions.

Museum-based research in the 21st century faces several challenges: access for researchers, rapidly progressing technological advances, and ethical reconsiderations. Designing research with public availability of data and metadata as a primary goal contributes to closing these gaps, while also inviting innovative approaches to their use and care.

Intergroup encounters among woolly monkeys in Amazonian Ecuador

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

[1]Department of Anthropology, Miami University, [2]Department of Anthropology and Primate Molecular Ecology and Evolution Laboratory, University of Texas at Austin, [3]Tiputini Biodiversity Station, College of Biological and Environmental Sciences, Universidad San Francisco de Quito, Cumbayá, Ecuador

For many group living primates, interactions between neighboring groups may vary from tolerant to hostile. While more aggressive intergroup encounters are often linked to defense over valuable resources, less is known about the factors leading to intergroup tolerance. Here, we characterize the intergroup dynamics of four neighboring groups of woolly monkeys (*Lagothrix lagotricha poepiggii*) – a primate noted to occasionally form tolerant associations with neighboring conspecifics – from Tiputini Biodiversity Station (TBS), Ecuador. Between 2014 and 2015, we recorded 102 intergroup encounters (IGEs). Rates of IGEs were highly correlated with monthly measures of shared space use, with some pairs of groups interacting once every three days and others interacting much more rarely (once every twenty days). Nearly 60% of IGEs were considered "tolerant", where affiliative behaviors (e.g., grooming bouts and copulations) or neutral interactions (e.g., co-feeding) were observed between members from different groups. We found no relationship between the type of IGE and monthly fruit availability. However, IGEs were less likely to be tolerant during the mating season. Finally, despite having access to a dispersed network of kin in which closely related adults may reside in neighboring groups, we did not detect a significant relationship between the number of such relatives shared between groups and the number of tolerant interactions. For woolly monkeys, tolerant IGEs potentially allow individuals to glean information on the location and availability of resources, recruit prospective mating partners, maintain social relationships with dispersed kin, or investigate groups into which they may transfer to in the future.

Funded by NSF BCS-1540403, the Leakey and Wenner-Gren Foundations, the National Geographic Society/Waitt Grants Program, and the University of Texas at Austin

Primates in an urban world

AMANDA L. ELLWANGER[1], LUCY MILLINGTON[2] and JOANNA E. LAMBERT[3]

[1]Department of Cultural and Behavioral Sciences, Georgia State University Perimeter College, [2]Department of Natural Sciences, Manchester Metropolitan University, [3]Program in Environmental Studies and Department of Ecology and Evolutionary Biology, University of Colorado-Boulder

Virtually all ecosystems on earth have been altered by human activity resulting in both ecological and evolutionary impacts on nonhuman species. These effects are most evident in urban centers where sympatric and commensal wildlife must cope with inexorably shifting landscapes and where natural selection is occurring at more rapid and intense rates than in exurban habitats. Here, we explore the effects of rapid urbanization on nonhuman primate species. We adapt a framework from urban ecology to classify primates as urban avoiders (i.e., cannot persist in urban or peri-urban zones), adapters (i.e., edge and "weedy" species), or exploiters (i.e., commensals and synanthropes) to predict how primates navigate changes related to urbanization. We conduct a preliminary analysis focusing on China, India, and Nigeria, as these countries are predicted to experience the fastest urban growth in the next 30 years. We examine 25 genera, comprising 47 species across a diversity of taxa, including galagoes, lorises, colobines, cercopithecines, and hylobatids. We undertake a meta-analysis of data on diet, life history, habitat requirements, conservation status, and phylogenic history to classify these species. The genera were mostly split between avoiders and adapters, with 2 genera labeled as adapters/exploiters. While the effects of slow life histories coupled with range restriction and habitat loss cannot be ameliorated in urban environments, dietary requirements and habitat use (i.e., arboreality) may be incorporated into urban design to promote coexistence (i.e., arboreal corridors, access to refuges within urban areas). Primate flexibility may facilitate coexistence in peri-urban areas, but this warrants further attention.

The impact of seasonal time constraints on grooming relationships and networks of female chacma baboons (*Papio hamadryas ursinus*) in a temperate South African habitat

NICHOLAS W. ELLWANGER[1] and THAD Q. BARTLETT[2]

[1]Department of Geography and Anthropology, Kennesaw State University, [2]Department of Anthropology, University of Texas at San Antonio

Many primate species gain fitness benefits by maintaining grooming bonds with conspecifics. When ecological constraints force a reduction in grooming time, individuals may alter grooming strategies to maintain social bonds. Female chacma baboons (*Papio hamadryas ursinus*) in Hemel-en-Aarde Valley, South Africa, spend significantly fewer hours grooming in winter than in summer. To determine whether and how reduced grooming time impacts female grooming relationships, we compared grooming partnerships and networks of female baboons between winter and summer. We measured grooming dynamics by identifying grooming partners and measuring dyad strength and grooming network characteristics. During the winter, females reduced the number of grooming partners (Z = -3.408, P < 0.001), resulting in a less interconnected grooming network (density = 0.301) than in the summer (0.695). However, dyad strength was not significantly different between seasons (F = 1.84, P = 0.178). Grooming partner identity varied between seasons, and sub-group clustering was lower in the winter than in the summer (Z = -3.408, P < 0.001). These results support the concept that time serves as a significant ecological constraint on female grooming relationships. Females responded to reduced grooming time by decreasing the quantity but not quality of grooming relationships. Reduced grooming network connectivity was not associated with characteristics of a fractured social network, such as clustering. The lack of consistent partner preference between seasons suggests that females

maintain a diversity of grooming partners across the year, potentially to counteract the deleterious effects of time constraints on affiliative behavior and to maintain group stability.

This research was funded by the Department of Anthropology and Office of Global Affairs, University of Texas at San Antonio.

Pandemics in Institutions: A Case Study of Tuberculosis Mortality in the Mississippi State Asylum, AD 1912-1932

TAYLOR A. EMERY and MOLLY K. ZUCKERMAN

Anthropology and Middle Eastern Cultures, Mississippi State University

Tuberculosis, a respiratory infection caused by *Mycobacterium tuberculosis* complex (MTBC), was a leading cause of death in the late-19th and early-20th century US, including Mississippi. Here we explore the impact of epidemic tuberculosis on the institutionalized patient population of the Mississippi State Asylum (MSA), Jackson, MS (AD 1855-1935) compared to the state-level population of Mississippi. Utilizing preliminary data for the years 1915 and 1932 from biennial reports of the Mississippi Department of Health and the MSA, we analyze survivorship in each population. Preliminary analyses indicate that the crude tuberculosis mortality rate was significantly greater within the MSA than in the state population before (1915; $p<0.001$) and after (1932; $p<0.001$) establishment of a state tuberculosis Sanatorium (1918) and public health efforts to combat tuberculosis transmission. Further, while the state-level tuberculosis mortality rate significantly decreased between 1915-1932 (140 per 100,000 to 64.8 per 100,00; $p<0.001$), the MSA's tuberculosis mortality rate simultaneously increased significantly (1028 per 100,000 to 1237 per 100,000; $p<0.001$), despite contemporaneous improvements in medical knowledge of tuberculosis treatment and prevention. Preliminary analysis is limited by a current inability to evaluate age-adjusted mortality rates and the impact of demographic factors (e.g., social race, sex) on tuberculosis mortality rates. Future, more comprehensive analyses (e.g., survival, hazard analysis) may generate higher-resolution pictures of the impacts of pandemic tuberculosis on historical socially vulnerable institutionalized populations, including the interplay of social, economic, political processes within this dynamic.

Stress-related enamel defect prevalence and severity in *Papio ursinus* and *P. anubis*

JIMMY ERKENS[1], JAMAL K. SALAYMEH[1], ESME BEAMISH[2], SHAHRINA CHOWDHURY[3,5,6], LARISSA SWEDELL[4,5,6,7], DEBBIE GUATELLI-STEINBERG[1], W. SCOTT MCGRAW[1] and KATE MCGRATH[1,8]

[1]Department of Anthropology, The Ohio State University, [2]Institute for Communities and Wildlife in Africa (iCWild), University of Cape Town, [3]Department of Anthropology, Brooklyn College–CUNY, [4]Department of Anthropology, Queens College–CUNY, [5]CUNY Graduate Center, [6]New York Consortium in Evolutionary Primatology, [7]Department of Archaeology, University of Cape Town, [8]Department of Anthropology, SUNY Oneonta

Linear enamel hypoplasia (LEH) appears as horizontal grooves around the tooth crown, forming in response to stressors like malnutrition and disease. While LEH defects are very common and conspicuous in hominoids, they are less so in monkeys due to their faster tooth growth, creating often overlooked shallower defects. Here, we analyze the canines and incisors of chacma (Papio ursinus; N=30) and olive baboons (Papio anubis; N=15). We use macrophotography to aid in the identification of defects as localized reductions in enamel thickness and/or disruptions to the normal spacing of growth increments visible on the surface. Defect severity was scored as mild, moderate, or severe. Mann-Whitney-Wilcoxon tests were used to assess species and sex differences. We find that males have more defects than females ($W=157$, $p=0.001$), which is expected given their longer canine formation times and windows of vulnerability to stress. We find no prevalence differences among species ($W=148.5$, $p=0.134$), nor between subsamples of semi-commensal chacma males who spent their early lives inside versus outside national parks ($W=13.5$, $p=0.229$). However, chacma individuals from inside national parks (N=5) exhibit severe defects, while these are absent in all individuals that grew up outside parks (N=4) ($W=18$, $p=0.022$). We hypothesize that baboons with access to anthropogenic foods outside parks are buffered from episodes of food stress in early life that may be more common in the national park setting. Future work will explore associated behavioral datasets and incorporate histological data to provide precise information on the developmental timing of growth disruptions.

Funding provided by The Ohio State University President's Postdoctoral Scholar's Program

A Longitudinal Study of Bone Accrual in Recreational Gymnasts from 4-16 years of age

MARTA C. ERLANDSON, MATTHEW S. CHAPELSKI, BRENDAN ERNST and ADAM DG. BAXTER-JONES

College of Kinesiology, University of Saskatchewan

The size, content, and strength of bone that is accrued during the early years has a profound impact on bone health throughout the lifespan. Bone responds to mechanical loading and stresses from factors such as physical activity. Gymnastics is a unique form of physical activity that creates forces in different locations and of different magnitudes. We have shown that participation in recreational gymnastics at a young age (4-6 years) increases distal radius total bone area (ToA) and total bone content (ToC). The purpose of this study was to examine if the previously reported bone health benefits are maintained as children grew.

Using a mixed-longitudinal design three age cohorts (4-, 5- and 6-years old's) were recruited from recreational gymnastics programs. 126 participants were recruited and serially measured over 10 years (2006-2016). Measures included anthropometrics and peripheral Quantitative Computer Tomography (pQCT) scans of the distal radius and tibia at the 4% and 65-66% bone lengths. Multilevel models were developed to assess trajectories of development whilst controlling for age, sex, weight, and muscle cross-sectional area.

Gymnastics exposure produced a significant independent effect on the distal radius (4%) for ToA ($25.43 \pm 6.95 mm^2$), ToC ($9.58 \pm 2.42 mg/mm$), total bone density ($14.19 \pm 6.46 mg/cm^3$), trabecular density ($13.07 \pm 6.21 mg/cm^3$) and estimated bone strength ($3.17 \pm 1.07 mg^2/mm^4$) with a confidence interval of 95% ($p<0.05$). Gymnastics exposure had no significant effect on the radial shaft or the tibia ($p>0.05$).

Exposure to recreational gymnastics produces long-term benefits to the distal radius, but not the distal tibia.

Dental Microwear Texture Analysis on the Lower Magdalenian "Red Lady" from El Mirón Cave (Ramales de la Victoria, Cantabria, Spain)

ALMUDENA ESTALRRICH[1,2], ANA B. MARIN-ARROYO[1], LAWRENCE G. STRAUS[1,3] and MANUEL R. GONZÁLEZ MORALES[4]

[1]EvoAdapta Group, University of Cantabria, Spain, [2]Department of Anthropology, University of Arkansas, [3]Department of Anthropology, University of New Mexico, [4]Instituto Internacional de Investigaciones Prehistóricas de Cantabria, Universidad de Cantabria-Gobierno de Cantabria-Banco Santander, Spain

El Mirón cave in Northern Spain is a deeply stratified archaeological site covering periods from the Middle Paleolithic to the Middle Ages.

Here, we present the analysis of occlusal molar microwear textures of the Lower Magdalenian human individual, an adult female called "Red Lady" as the skeletal remains were covered in red ochre, dated directly to 15.460 ± 40 BP (uncal.).

Microwear textures were characterized on the facet 9 of the lower left permanent first molar, using white-light confocal profilometry and scale-sensitive fractal analysis.

The results obtained (*Asfc*= 1.208; *epLsar*= 0.0051) indicate a diet rich in meat for the "Red Lady" as the microwear signature variables retrieved are similar to those known for the Fueguians, ethnographically documented meat-eaters from

cold-steppe environments. These results corroborate and complement those obtained previously through isotope analysis, buccal dental wear and faunal remains, implying a wide exploitation of the environment by this woman, and probably by her group.

The variables obtained were compared to previous published data for Upper Paleolithic Modern Humans based on their technological context. The low value obtained for *Asfc* indicate this individual had a diet with low content of abrasives (both dietary or extraneous), different as expected for a Magdalenian individual, and closer to the Gravettian mean value, maybe due to similar use of food preparation techniques.

This research is funded by a H2020-MSCA-IF project No. 891529 (3DFOSSILDIET) to A.E.

The value of aggression in maintaining a multilevel society

KATARINA D. EVANS[1,2], SHAHRINA CHOWDHURY[1,2,3] and LARISSA SWEDELL[1,2,4,5]

[1]Anthropology, Graduate Center, City University of New York (CUNY), [2]New York Consortium in Evolutionary Primatology (NYCEP), [3]Anthropology, Brooklyn College, CUNY, [4]Anthropology, Queens College, CUNY, [5]Archaeology, University of Cape Town

The multilevel social system, male philopatry, and strong male-female bonds characterizing hamadryas baboons make them arguably one of the best models for human social evolution. Male hamadryas baboons are the most sexually coercive of the non-human primates; males herd females into one-male units (comprising a "leader" male, females, and sometimes "follower" males) that are formed through successive male "takeovers" of females. While male coercion is prevalent in this system, takeovers can occur aggressively or non-aggressively and the adaptive value of male aggression is unclear. Using behavioral and demographic data from Filoha, Ethiopia, we examined the use of aggression and its relationship to various fitness proxies. We did not find a relationship between a male's percentage of takeovers that were aggressive and any of these fitness proxies. However, we did find that a male's intensity of aggression, both toward other males and toward females around the time of a takeover, was negatively related to the collective birth rate of females in his unit. In addition, we found that the intensity of male aggression directed toward females was higher in interband compared to intraband takeovers. These findings suggest that leader males are flexible in their use of aggression: the use of male aggression, particularly toward females, varies based on the context of the takeover, and those who limit their aggression are conferred greater fitness benefits. Overall, these results highlight the evolutionary benefits and costs of intermale tolerance and female suppression in a multilevel society with great applicability to human social evolution.

Funding was provided by The Leakey Foundation, the Wenner-Gren Foundation, the National Geographic Society (6468-99 and 8309-07), the CUNY Graduate Center, the PSC-CUNY Award Program, and NYCEP.

Estimation of the age-at-death of subadults (0-5 years) based on craniofacial dimensions

ANDREJ A. EVTEEV[1], TAISIYA A. SYUTKINA[2] and NIKOLAI E. STAROVEROV[3]

[1]Anuchin Research Institute and Museum of Anthropology, Lomonosov Moscow State University, [2]Institute of Ethnology and Anthropology, Russian Academy of Science, [3]Department of Electronic Instruments and Devices, Saint Petersburg Electrotechnical University "LETI"

The estimation of the age of infant skeletons is typically based on dental development and postcranial metrics. But numerous studies show that both methods display a high level of uncertainty due to inter-individual variability. The assessment of dental age is also largely dependent on the skills and experience of the observer.

The first five years of life is the time of the most rapid growth in all craniofacial dimensions. The growth trajectories of the dimensions are not linear and vary substantially. Thus, the combination of the levels of maturation of different dimensions can potentially provide quite a precise estimation of the age-at-death.

High-resolution clinical CT scans of 501 individuals of both sexes were studied, including 171 infants of the 1st year of life, 261 children from 2nd to 6th years, and 69 adults (reference). The dataset was divided into 4 age cohorts for the 1st year of life, and 5 yearly cohorts for the older subadults. A set of linear measurements describing the main morphological features of the facial skeleton was calculated based on 3d landmark data. An ensemble of random forest and SVM support vector machine algorithms of machine learning was employed. The results were evaluated via 10-fold cross-validation.

In both sex-specific and combined samples, the proportion of fully correct estimations (i.e. exactly matching the actual cohort) was 70-80%, partially correct (to neighboring cohorts) - higher than 90%. Fairly high precision of the estimation could be reached even if use only a few of the dimensions.

MSU, research theme "Heritage of the Society of Naturalists, Anthropologists and Ethnographers (OLEAE) at Moscow University: museum funds and documents"

Social organisation and biological distance: a comparison of Iron Age populations from northeast and southwest England

KATIE E. FAILLACE[1] and MALLORY J. ANCTIL[2]

[1]Department of Archaeology and Conservation, Cardiff University, [2]Department of Anthropology, University of Alaska Anchorage

Recent genetic investigations have suggested a regional patterning in the genetic structure of the British Iron Age (800BCE – 43CE), influenced by migrations during the preceding Bronze Age. However, since this genetic structure seems to have remained stable throughout the Iron Age, the relationship between biological affinity, cultural change, and social organisation at this time is unclear. The present study investigates this question further, taking a population-level approach to compare communities in northeast and southwest England in the Middle-to-Late Iron Age. By using intra- and inter-region comparisons from a limited chronology, this study explores the social organisation of these communities using under-utilised (in Britain) methods of biological distance analysis.

The Arizona State University Dental Anthropology System was used to record 36 crown and root traits from 8 sites in the modern counties of Yorkshire, Hampshire, and Dorset, representing 306 individuals. Population affinity was analysed using the Mean Measure of Divergence (MMD).

The biological affinity results indicate that 1) phenetic heterogeneity is evident among the broad northeast and southwest regional samples (p=0.000), 2) the samples from Yorkshire represent biologically distinct populations (p=0.005), 3) phenetic homogeneity is evident among the southwest samples (Hampshire and Dorset) (p=0.078). These findings support archaeological evidence from Hampshire and Dorset that during the later Iron Age, people were participants in wide-reaching networks rather than members of singular, bounded communities, while the evidence from Yorkshire supports the presence of stricter social boundaries between neighbours and more rigid group identities that influenced reproductive strategies.

Carbon and strontium isotope ratios shed new light on the paleobiology and collapse of *Theropithecus*, a primate experiment in graminivory

LUKE D. FANNIN[1,2], JUSTIN D. YEAKEL[3], VIVEK V. VENKATARAMAN[4,5], CHALACHEW SEYOUM[6], DENIS GERAADS[7], PETER J. FASHING[8,9], NGA NGUYEN[8,9], KENA FOX-DOBBS[10] and NATHANIEL J. DOMINY[1,5]

[1]Anthropology, Dartmouth College, [2]Graduate Program in Ecology, Evolution, Environment, and Society, Dartmouth College, [3]School of Natural Sciences, University of California Merced,

[4]Anthropology and Archaeology, University of Calgary, [5]Biological Sciences, Dartmouth College, [6]Pathology and Anatomical Sciences, University of Missouri, [7]CR2P, Muséum National d'Histoire Naturelle, CNRS, Sorbonne Université, [8]Anthropology, California State University Fullerton, [9]Biosciences, University of Oslo, [10]Geology, University of Puget Sound

The rise and spread of tropical grasslands was a signal event in the Cenozoic, causing many ungulates to evolve adaptations to a diet of graminoid (grass) tissues, or graminivory. In parallel, a lineage of monkeys (*Theropithecus*) is distinguished among primates for its large size and commitment to graminivory, a trait expressed by species throughout the Plio-Pleistocene fossil record and *T. gelada*, the sole surviving species today. An open question concerns the behavioral mechanics of how fossil species of *Theropithecus* handled graminoid tissues. They might have exhibited preference, selecting specific plant tissues within a given tuft of grass, or they might have practiced more indiscriminate bulk- feeding in a manner analogous to larger grazing ungulates. To differentiate between these two handling behaviors, we used time- and graminivore-calibrated carbon stable isotope values to show progressive reliance on high- throughput bulk-feeding graminivory during *Theropithecus* evolution. Variation in this behavior explained a significant amount of variation in fossil *Theropithecus* body mass across the Plio-Pleistocene, and the fracture mechanics of modern representative plant tissues included in this dietary shift suggest an increase in dietary fracture toughness. We describe all these covarying traits, which peaked in the Pleistocene of Africa, as evolutionary traps. To support this characterization, we report evidence of temporal increases in strontium isotope variability among North African theropiths, a result suggesting greater lifetime travel and energetic costs in response to diminishing food resources, a probable factor in the extinction of *Theropithecus oswaldi*, the largest monkey that ever lived.

Funding: David and Lucile Packard Foundation (Fellowship no. 2007-31754), San Diego Zoo, an OTS-STRI Andrew W. Mellon Research Exploration Award, and three National Science Foundation Graduate Research Fellowships.

The internal architecture of the hominoid clavicle and its implications for assessing locomotor behavior

HANNAH N. FARRELL, CALLUM F. ROSS and ZERESENAY ALEMSEGED

Department of Organismal Biology and Anatomy, University of Chicago

Living hominoids can be identified by their orthograde posture and highly mobile shoulder joint, both of which contribute to the extensive locomotor diversity and versatility in this group. Despite its central role as the only bony connection between the upper limb and thorax, the functional morphology of the hominoid clavicle remains poorly understood. As common analogs for the strength of a bone under bending and torsional loads and the magnitude of such loads, cross-sectional geometric traits and trabecular metrics may provide insight into how the clavicle is loaded differently during different locomotor behaviors. Additionally, the combination of these data may prove more biomechanically informative than analyses done on either in isolation. Using micro-CT scans of adult hominoid clavicles (N = 16), the R package 'morphomap', and the software 'medtool 4.5', cross-sectional area, minimum and maximum area moments of inertia, and area moments of inertia in the antero-posterior and cranio-caudal planes were calculated in the diaphysis and trabecular bone density was calculated in the entire clavicle to document variation and investigate its implications for assessing locomotor behavior. Results suggest increased relative trabecular density in regions of prominent muscle attachment, which may indicate increased use during locomotor and postural behaviors. Also, unlike previous studies of the upper limb skeleton of primates, the I_{max}/I_{min} values along the central diaphysis suggest arboreality may not be linked to a more circular cross-sectional shape in the hominoid clavicle.

Social precursors and fitness outcomes of group fission in geladas

JACOB A. FEDER[1], JACINTA C. BEEHNER[2,3], NOAH SNYDER-MACKLER[4,5], AMY LU[1,6] and THORE J. BERGMAN[2,7]

[1]Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, [2]Department of Psychology, University of Michigan, [3]Department of Anthropology, University of Michigan, [4]School of Life Sciences, Arizona State University, [5]Center for Evolution and Medicine, Arizona State University, [6]Department of Anthropology, Stony Brook University, [7]Department of Ecology and Evolutionary Biology, University of Michigan

Across primates, living in large groups can impose severe costs, including increased infanticide risk. To mitigate such costs, oversized groups may permanently fission into two or more smaller groups. However, permanent fissions are rare events in long-lived animals; thus, data across several groups are often necessary to identify both the underlying mechanisms and fitness consequences of fissioning. Here, we leveraged 15 years of longitudinal data to examine the behavioral and demographic precursors and fitness outcomes of nine fission events in a wild population of geladas (*Theropithecus gelada*), where infanticide is most frequent in larger groups. Groups generally became less cohesive and more modular in the year prior to fissioning. Rates of aggression and submission also rose during the pre-fission period (β=0.49±0.07), reflecting increased social conflict and instability. Close relatives and closely-ranked individuals had the strongest grooming relationships during the pre-fission period, which in turn were associated with co-membership in post-fission "daughter" groups (β=0.80±0.25; n=234 female-female dyads). Fissions occurred only in larger groups (8+ adult females), such that daughter groups often contained 5-7 adult females — a size range that corresponded with the lowest infant mortality rates. Indeed, infants born within the first three years after fission exhibited lower mortality than the population average (10.9% vs. 26.3%). Altogether, these data highlight the potential role of fissions in ameliorating the costs of group-living, fostering demographic flexibility, and allowing for tolerant relationships between daughter groups that may facilitate the formation of multilevel societies.

Funding: The National Science Foundation (BCS-0715179, BCS-0824592, BCS-1723228, IOS-1255974, IOS-1854359), The Leakey Foundation (multiple awards), National Geographic Society (Gr. #8100-06, #8989-11, #NGS-50409R-18), Fulbright, University of Michigan, Stony Brook University

Twist and chew: three dimensional tongue kinematics during chewing in macaque primates

KARA L. FEILICH[1], JD LAURENCE-CHASEN[1], COURTNEY ORSBON[2], NICHOLAS J. GIDMARK[3] and CALLUM F. ROSS[1]

[1]Department of Organismal Biology and Anatomy, University of Chicago, [2]Department of Radiology, University of Vermont Medical Center, [3]Biology Department, Knox College

Three-dimensional (3D) tongue movements are vital for feeding but are undocumented in primates. Abd-el-Malek suggested that during chewing by humans the middle of the tongue twists to the biting side to position the food bolus between the teeth as they come together. This model of tongue kinematics, although influential, is purely qualitative, and his descriptions of tongue kinematics are difficult to relate to simultaneous mandible kinematics. Tongue kinematics were recorded during grape chewing by macaques using biplanar videoradiography and the XROMM workflow. Our results reveal that shape changes in the tongue during chewing are dominated by flexion in the tongue's sagittal planes and roll about its long axis. During tongue retraction the middle (molar region) of the tongue rolls to the chewing (working) side simultaneous with sagittal flexion, while the tongue tip flexes to the other (balancing) side. Twisting and flexion reach their maxima early in the fast close phase of chewing gape cycles, positioning the food bolus between the approaching teeth prior to the power stroke. Although 3D tongue kinematics undoubtedly vary with food type, the mechanical role of this movement—placing the food bolus on the post-canine teeth for breakdown—is likely to be a powerful constraint on tongue kinematics during

the fast close phase of the chewing cycle. The muscular drivers of these movements remain to be determined, but are likely to include a combination of intrinsic and extrinsic tongue muscles. These results suggest that Abd-el-Malek's hypothesis regarding tongue kinematics in humans also applies to macaques.

Grant sponsor: NIH (NIDCR and NICHD); NSF (MRI and BCS-DDRIG); Grant numbers: R01-DE023816 and T32-HD009007 (NIH); DBI-1338066 and BCS-1732175 (NSF)

Ethnographic accounts of charcoal consumption in Philippine tarsiers: Comparison across islands

LORI L. FIELDS[1] and NANDA B. GROW[2]

[1]Department of Anthropology and Geography, Coastal Carolina University, [2]Department of Anthropology, Washington State University

Philippine tarsiers (*Carlito syrichta*), endemic to the islands of Mindanao, Samar, Leyte, and Bohol, are a central part of an established ecotourism industry in the Philippines. Differences between islands in economic strategies and the frequency of human-primate interactions may relate to differences in local beliefs about tarsiers. One pervasive Filipino belief is that exclusively carnivorous tarsiers in fact consume charcoal, despite no documented evidence of this behavior. The earliest account of this belief can be traced to Cook (1939), and throughout the decades, several more accounts of local beliefs concerning consumption of charcoal by tarsiers have been published. In this study, semi-structured interviews (N=210) with local Filipinos were conducted in August 2014 through March 2015 in the provinces of Bohol and Leyte. Of these interviews, 10% (N=20) of respondents independently expressed this belief, without prompting from the interviewer. Of these respondents, the majority (19/20) lived in Leyte. Compared to Leyte, Bohol has an established ecotourism industry that centers around tarsiers. These results indicate that differences in accurate knowledge about primates relates to the economic integration of those primates; residents in Bohol are more familiar with tarsier diet and habitat due to their husbandry in the tourism industry. Community connections to local fauna are integral for the transmission of correct information about tarsiers, which can translate to conservation benefits for the species. Further, the persistence of ideas about tarsier diet warrants further investigation into the origin of the belief.

This project was supported by the Fulbright U.S. Student Program, L.T. Jordan Institute for International Awareness, and the Department of Anthropology and College of Liberal Arts at Texas A&M University.

Three-dimensional functional capacity of the intrinsic hand musculature in humans and chimpanzees

MARA G. FIELDS[1], EDEN M. MACKERETH[1], SPIRO P. SULLIVAN[1], KEVIN M. MIDDLETON[1], CASEY M. HOLLIDAY[1], FAYE R. MCGECHIE[2] and CAROL V. WARD[1]

[1]Department of Pathology and Anatomical Science, University of Missouri, [2]Department of Organismal and Evolutionary Biology, University of Chicago

Accurately interpreting the functional significance of variation in hand morphology has been central to discussions of the evolution of in hominoids, especially humans. Although there is an extensive literature on bony morphology, muscle size, muscle strength, kinematics, and use of the hand, to date it has not been possible to visualize and quantify the mechanics of the of the hand *in situ.*

This study compared the intrinsic hand muscles of *Homo sapiens* and *Pan troglodytes* in 3D. Each specimen was fixed, stained with Lugol's iodine, and microCT scanned [<61 µm resolution]. Bones, muscles and the flexor retinaculum were segmented using Avizo. Avizo Xfiber was used to visualize and quantify fascicle orientation within muscles, which permits quantification of both whole muscle and within muscle fascicle orientations. Fascicle length, pennation angles and muscle volume were used to calculate PCSA and estimate force output of each muscle. Together, these data are used to compare functional capability of muscles individually and in aggregate.

Data reveal differences in force-generating capacity and force orientations of muscles, and with finer-scale variation of within-muscle fascicle orientations. The most significant differences were found in the adductor pollicis and opponens pollicis, which are larger and more transversely oriented in humans than in chimpanzees. Data also reveal differences in other thenar and hypothenar muscles, affecting the capacity to effect different grips.

Our approach and results highlight the importance of evaluating of the musculoskeletal system of the hand in 3D which can then be used to compare to bone form across hominoids.

University of Missouri Research Council, National Science Foundation (IOS 1457319)

Fake News in the middle of the SARS-CoV-19 SYNDEMIC: Analysis of news broadcast via WhatsApp application, Amazon, Brazil

LIGIA A. FILGUEIRAS[1], RANDERSON JOSÉ DE ARAUJO SOUSA[2], ANA GABRIELA DE SOUSA COSTA[2], ADRIANA VANESSA RIBEIRO MAFRA[2], ILGA MILLA CHAVES SILVA[2] and VIVIAN DE CARVALHO AVELINO[2]

[1]Natural Sciences, Pará State University - UEPA, [2]Medicine Course, Pará State University - UEPA

The virtual environment has become even more active in the daily routine due to the current SARS-CoV-2 syndemic. There has been a strengthening of a culture focused on the virtualization of relationships and the exaggerated dissemination of information, which can often be considered as Fake News. Based on discourse analysis criteria, we analyzed for ten days the content of questionable material submitted by users of a WhatsApp phone number during the Covid-19 syndemic. We randomly selected a video where a man claimed the virus did not exist in Brazil because there were unoccupied beds in hospitals in Rio de Janeiro; a video about the burrial of empty coffins used possibly to increase the number of deaths from the virus in Minas Gerais and, finally, a text message regarding alternative treatments for COVID-19. All were classified as Fake News, considering: alarmist tone, unverified or non-existent sources of information, quotes from supposedly false or non-existent authorities, spelling errors, exaggerated requests for massive sharing causing despair and chaos, self-medication, disbelief in science. The motivations that lead to the manufacture of fake news are economic interests and an ideological bias with the intention of dominating and frightening social reality. The belief in conspiration theories, sensationalist rumors and antivaccine movements difficult adhere to preventive measures, even Brazil reaching more than 602 thousand deaths nowadays. However, the best instrument to fight Fake News is critical sense, trust in education and especially trust in science, which, unfortunately, in Brazil, is being severely penalized by the current government.

Ungulate hypsodonty and mesowear indicate environmental change associated with hominin species turnover at Laetoli, Tanzania

ELIZABETH N. FILLION

Center for the Study of Human Origins, Department of Anthropology, New York University, New York Consortium in Evolutionary Primatology

Laetoli, in northern Tanzania, provides important evidence for understanding the environmental drivers of hominin adaptation and evolution, as it spans a period when environmental change in eastern Africa coincides with the regional extinction of *Australopithecus* and the emergence of *Paranthropus* and *Homo*. The paleoenvironment of the Upper Laetolil Beds (ULB) (3.63-3.85 Ma), in which *Australopithecus afarensis* occurs, is well-documented. The paleoenvironment of the Upper Ndolanya Beds (UNB) (2.66 Ma), which includes some of the earliest fossils of *Paranthropus aethiopicus*, is less well understood. Hypsodonty and mesowear show that the dietary composition of the ungulate community changed between these units, suggesting that the paleoenvironment of the UNB differed from the ULB.

Mesowear indicates most species in the UNB consumed more abrasive grazing diets compared to those in the ULB. Hypsodonty results were mixed. Most bovid species were more hypsodont and thus more adapted for abrasive diets in the UNB compared to the ULB, but this was not true for other ungulates. Community analyses combining mesowear and hypsodonty data with taxonomic abundance show that species with hypsodont teeth and moderate to high degrees of mesowear were more common in the UNB than the ULB. The greater preponderance of ungulates consuming an abrasive grazing diet in the UNB suggests there was a shift towards more extensive grass cover. This has implications for the paleoecology of *Paranthropus aethiopicus*, which was one of the novel species that appeared at Laetoli as part of the faunal turnover that coincided with a change in the paleoenvironment.

Funding: National Science Foundation (BCS-2018563), New York University Graduate School of Arts and Science, American Philosophical Association

Portion size matters: carrion ecology lessons for medicolegal death investigations - a pilot study in Cape Town, South Africa

DEVIN A. FINAUGHTY[1,2], CLAIRE L. DU TOIT[1], MAXIMILIAN J. SPIES[1] and VICTORIA E. GIBBON[1]

[1]Department of Human Biology, University of Cape Town, [2]School of Anthropology and Conservation, University of Kent

A principal goal of forensic taphonomic research is improvement in estimates of post-mortem interval. Key to this process is quantitatively accounting for the myriad of factors that influence the decompositional ecosystem. In this, vertebrate scavengers remain understudied role-players due to the limited incorporation of carrion ecology theory in taphonomic investigations. Variation in carrion biomass is well known to affect the inter- and intra-specific interactions of vertebrate scavengers at carrion. Yet, the extent remains unclear for many biogeographic circumstances, compounded by the fact that most taphonomic studies utilise multiple carcasses – often closely spaced – representing the minority of forensic cases. The aim was to assess the impact of sample size on vertebrate scavenging and decay rate. Baseline decomposition data for a single ~60kg clothed porcine carcass were compared to those of a multiple carcass deployment in a forensically significant habitat of Cape Town, South Africa. Results showed that the single carcass reached 75% weight loss in 83 days, while carcasses in the multi-carcass deployment reached 67% weight loss in 113 days on average, after which stasis was noted. The single carcass also experienced more scavenger visits, longer scavenger hours, longer multi-scavenger visit durations and a shorter decomposition cycle. The difference in results between these studies clearly demonstrates the poorly explored impact of multiple carcass deployments on decomposition rate and pattern in forensic taphonomic studies. These findings need further corroboration; however, forensic realism needs consideration in taphonomic study design to ensure the obtained results are forensically accurate, locally appropriate, and usable.

The University of Cape Town's Research Contracts & IP Office and Faculty of Health Sciences; The South African National Research Foundation (Grant 115357).

Foraging proficiency decreases with age in old male chimpanzees at Ngogo, Kibale National Park, Uganda

BENJAMIN J. FINKEL[1], SHARIFAH NAMAGANDA[2], MARCUS CLAUSS[3], MELISSA EMERY THOMPSON[4], JOHN C. MITANI[1] and ANDREW J. MARSHALL[1]

[1]Department of Anthropology, University of Michigan, [2]College of Natural Sciences, Makerere University, [3]Clinic of Zoo Animals, Exotic Pets and Wildlife, Vetsuisse Faculty, University of Zurich, [4]Department of Anthropology, University of New Mexico

Waning fitness in old age shapes the evolution of longevity, a hallmark of primate life history. While research on fitness decline has focused on changes to sociality with age, changes in foraging have received less attention. Foraging can link aging and fitness because body condition corresponds to feeding performance, which in turn determines energy available for fitness-related activities. Here, we investigate whether foraging proficiency decreases with age in a cross-sectional study of chimpanzees at Ngogo in Kibale National Park, Uganda. We present data from adult males (n=20, 21-53 years) over 11 months of observation. We built generalized linear models to examine the effect of age in models of ingestion rates (n=21 hours), fecal particle size (n=189 samples), foraging budget (n=1385 observation hours), and urinary C-peptide insulin (n=722). Among our findings, older chimpanzees ate leaves, but not fruits or figs, more slowly than younger adults (>95% ω). Fecal particles were larger with age, suggesting that older chimpanzees chewed less efficiently (>99% ω). Age, however, did not influence total foraging time nor energy balance as measured by C-peptide insulin. These results suggest that aging male chimpanzees become less proficient at consuming particular foods. Dental senescence may explain some of this decline. The absence of accompanying food stress indicates either that these chimpanzees were not food limited or that older chimpanzees may compensate by investing less in expensive behaviors like reproduction. The latter offers a mechanism for how certain physical deteriorations of senescence could precipitate a decline in fitness

The Leakey Foundation, National Science Foundation (BCS-1927384), American Philosophical Society, International Primatological Society, University of Michigan.

Exploring medical care through dental calculus analysis: St Leonard's medieval leprosy hospital, Peterborough, England

ELENA FIORIN[1], ROBERT LAYFIELD[2], CHRISTOPHE SNOECK[3], MARIA LUISA ASTOLFI[4], CHRISTINA LEE[5], CHARLOTTE ROBERTS[6] and EMANUELA CRISTIANI[1]

[1]Department of Oral and Maxillo Facial Sciences, Sapienza University of Rome, [2]School of Life Sciences, University of Nottingham, [3]Research Unit: Analytical, Environmental & Geo-Chemistry, Department of Chemistry, Vrije Universiteit Brussel, [4]Department of Chemistry, Sapienza University of Rome, [5]School of English, University of Nottingham, [6]Department of Archaeology, Durham University

Medieval European people with leprosy had a special place in society. Historical sources indicate attitudes towards this disease could be contentious. Among other measures, leprosy hospitals were founded to segregate people (11th C onwards, England). Unfortunately, workings of leprosy hospitals are not well documented. While historical sources provide narratives about people lives, they rarely mention specifics of treatments. Bioarchaeology may hold some answers, and human dental calculus has been proven to preserve a range of information. For the first time here, data are generated from entrapped organic and inorganic micro-remains preserved in calculus from teeth of people diagnosed with leprosy from a medieval English leprosarium. These data help to characterize not only medical treatments and diets these people consumed, but also levels of hygiene within which they lived. This study analyses calculus samples from 41 adult individuals (24 males and 17 females) recovered from St Leonard leprosy hospital cemetery (Peterborough, England, founded 1125 AD). Samples were examined using different techniques: optical polarized microscopy was employed to identify micro-remains embedded within the matrix; proteomic analysis was applied to reveal dairy product consumption; AMA and CV-AFS were employed to measure mercury concentration whereas ICP-MS was used to investigate other chemical elements that could have been the result of treatment. Initial results provide information about possible medical treatments and dietary constituents. In particular, fish,

milk, cereals, and legumes were consumed, and evidence of toxic heavy metals (mercury) points towards specific medical practices that are only cursorily attested by written sources.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under the Marie Sklodowska-Curie grant agreement No 844364

A Tooth Size Apportionment Investigation of Bodo Origins

BROOKE A. FISHER and BRIAN E. HEMPHILL

Department of Anthropology, University of Alaska Fairbanks

The Bodo are a Tibeto-Burman-speaking ethnic group that resides in the hill country north of the Brahmaputra River valley of Assam, India. Most linguists classify the Bodo language with Naga-Kuki languages spoken south of the valley suggesting origins in northern Myanmar and Yunnan in southern China. However, others classify Bodo language with Tibeto-Burman languages spoken in Nepal, Tibet, and Sikkim, which suggests origins north of the Himalayas in Tibet. Mesiodistal and buccolingual diameters of the permanent tooth crown among 119 Bodos (52 males, 67 females) were scaled against the geometric mean by sex to remove the effects of gross size reflective of the duration of food production and ceramic technology. The scaled data was compared to three comparative groups located north of the Brahmaputra valley (n= 347) and three comparative groups located south of this valley (n= 402). Northeast Indian groups, including the Bodo, were placed in subcontinental perspective through comparison with three ethnic groups from Southeast peninsular India (n= 557), west-central peninsular India (n= 562), and northern Pakistan (n= 644), respectively. Tooth size allocation analysis was undertaken with four multivariate data reduction techniques: neighbor-joining cluster analysis, multidimensional scaling, Mantel matrix correlation analysis, and principal component analysis. The results not only confirm the uniqueness of northeast Indians relative to other South Asians, but confirm a north-south division of northeast Indians with Bodos showing closer affinities to ethnic groups residing north of the Brahmaputra River than to those residing south of the river, thereby supporting a Tibetan origin for Bodo populations.

This research is supported by URSA Award for Undergraduate Research to BAF and a Fulbright Senior Research Fellowship to BEH.

An Analysis of Lethal Anti-Transgender Violence and Forensic Disempowerment using the Transgender Day of Remembrance Database

TAYLOR FLAHERTY[1], ADRIANNE DIZON[2], JENNIFER BYRNES[1], SAMANTHA BLATT[3], MARIYAM I. ISA[4] and AMY MICHAEL[5]

[1]Department of Anthropology, University of Nevada, Las Vegas, [2]School of Life Sciences, College of Sciences, University of Nevada, Las Vegas, [3]Department of Anthropology, Idaho State University, [4]Department of Sociology, Anthropology, and Social Work, Texas Tech University, [5]Department of Anthropology, University of New Hampshire

Transgender and gender expansive (TGE) individuals disproportionately experience structural vulnerability and lethal violence due to systemic marginalization. Deprecation of TGE individuals permeates forensic investigations as methodologies and biases inflict harm in a gender-insensitive medicolegal system. The Transgender Day of Remembrance database (TDOR) is open to the public for reporting and accessing global cases, offering unique insight into antemortem and postmortem treatment of TGE individuals. Currently, TDOR lists 4,284 decedents, of which 84.3% (n=3,611) died violently, most often involving shootings (33.4%, n=1,431), stabbings (18.1%, n=771), and/or beatings (10.6%, n=450). Many are simply categorized as "murder" (5.8%, n=247) or "not reported" (11.9%, n=507) due to neglectful practices of forensic analysts and investigators. Further, TDOR suggests that TGE residents in Brazil (38.3%, n=1,648), the U.S. (15.8%, n=678), and Mexico (12.9%, n=552) are the most at-risk for lethal violence. Of those with known ages (64.6%, n=2,767), 95.8% (n=2,652) were younger than 50, signifying a decreased life expectancy for the TGE population. To avoid misidentifying decedents, TDOR does not list gender, assigned sex, race or ethnicity. It does, however, indicate that external factors such as intimate partner violence, sex work, language usage, and employment, housing and incarceration status greatly affect antemortem and postmortem vulnerabilities. TDOR likely underestimates the true proportions of lethal violence; however, it is the most expansive database to date. Thus, this presentation will introduce TDOR as a source for continued research that centers TGE individuals, whilst also raising awareness of the structural vulnerabilities and lethal violence faced by this population.

Assessing the Relationship Between Biomechanical Stress and Double-Zonal Osteons

AILEEN FLANERY and DAWN MULHERN

Department of Anthropology, Fort Lewis College

Within the field of bone histology and histomorphometry, double-zonal osteons, a type of secondary osteon, are something of a mystery. Characterized by a hyper-mineralized arrest line, double-zonal (DZ) osteons have been hypothesized to be caused by a disruption during the formation of a Type I osteon, but what might trigger this disruption remains unknown. Possible explanations posited over the years include age, disease, nutrition, change in mineral density, and mechanical stress. This research explored the latter hypothesis by analyzing the number and size of double-zonal osteons found in 23 diaphyseal adult femur samples from the Kulubnarti cemetery in Sudanese Nubia (A.D. 1250-1450). In order to assess the effects of tension and compression on the frequency of DZ osteons, the ratio of double-zonal osteons to Type I osteons was compared in defined lateral and medial sections. If compression and tension forces differentially affect DZ osteon frequency, the medial and lateral quadrants of femoral cross-sections should demonstrate a difference in DZ osteon frequency relative to intact osteon frequency. An independent t-test (SPSS version 28.0) showed no statistically significant difference between compression and tension cortices, so the null hypothesis was retained. This research does not support the idea that differential mechanical stress affects DZ osteon frequency.

Living on the Edge: Osteobiographies of Five Children in the Roman Borderland

ELIJAH C. FLEMING[1], KATHERINE L. REINBERGER[2] and ADAM RABINOWITZ[1]

[1]Classics, University of Texas at Austin, [2]Anthropology, University of Georgia

In this study we present osteobiographies of five children buried in a late Roman necropolis outside the city of Histria at the edge of the Danube delta on the Black Sea. The osteobiographic method involves a life history assembled from all skeletal information available for an individual and seeks to reconstruct the complex layers of human life, both social and biological. Ancient children are less visible in material and literary culture, so benefit from the focused use of osteobiographies to explore the lived experience of individuals. We use this method to explore life at a time of upheaval in the region. Under the early Roman Empire, Histria was a bustling port city on the Danube frontier, but the silting up of the harbor created economic issues leading to the decline of the city into the 5th-6th centuries. We hypothesize the economic decline to have negatively impacted the health and wellbeing of the inhabitants.

All five of the children, whose ages range from birth to 5 years old, were buried with no grave goods and minimal grave markings. The osteobiographies report the presence of pathological markers on two of the youngest children, including periostitis and lesions from nutritional deficiencies. We also present carbon and nitrogen isotope values to explore their diet (δ13C=-17.99±1.29‰, δ15N=12.43±1.65‰), finding evidence of

inconsistent weaning practices. These osteobiographies allow us to contextualize the childhood experience of these individuals within the socioeconomic forces of the Roman borderland during a period of turmoil.

This study is funded in part by Planet Texas 2050 from the University of Texas at Austin.

Critical Translation and Transparency in Community Centered Ancient DNA Research: Insights from the Anson Street African Burial Ground Project

RAQUEL E. FLESKES

Department of Anthropology, University of Connecticut

The enduring legacies of colonialism and white supremacy are manifested in the unequal representation of marginalized populations in the archival record, especially for African or African-descended individuals in colonial period North America. Ancient DNA analysis provides one means of investigating these subaltern histories through estimations of genomic relatedness, biological sex and ancestral origins. However, genomics—and science more broadly—are intertwined with histories of abuse and scientific racism. As researchers who have inherited and are working within these forms of knowledge-making, it is critical to confront how we work to decolonize science so that it does not perpetuate these systems of harm. Rather, it is imperative to focus on how science can responsibly work for communities through critical translation and transparency of research methods and outcomes.

The Anson Street African Burial Ground Project team worked to incorporate these principles in a community centered DNA project that focused on understanding the unrecorded histories of 36 African or African-descended people whose burials were unearthed during construction in Charleston, South Carolina. Between 2017 and 2019, we worked closely with the Gullah Society to hold a series of 'Community Conversation' meetings with the Charleston African-American community. At these meetings, we identified the needs and questions of the community, discussed the benefits and drawbacks of the proposed DNA research, and presented real-time updates on research progress and results. Prioritizing community perspectives allowed the ancient DNA findings to embody meaning beyond the scope of Western science, as demonstrated in the Naming and Reinternment Ceremonies.

This research was funded by the National Geographic Society (#NGS-52378R-18, #NGS-54324E-18); The City of Charleston; The Gullah Society, Inc.; University of Pennsylvania; University of Tennessee.

Livestock grazing in lemur habitats: Using passive acoustic monitoring to characterize grazing intensity

NINA FLOWERS[1], LYNDSAY L. RANKIN[2], NAYUTA YAMASHITA[1,3] and ANNE C. AXEL[2]

[1]Institute of Population Genetics, University of Veterinary Medicine, Vienna, [2]Department of Biological Sciences, Marshall University, [3]Austrian Academy of Sciences

In southern Madagascar, critically-endangered Verreaux's sifaka (*Propithecus verreauxi*) and the endangered ring-tailed lemur (*Lemur catta*) are found in remnant tropical dry forest patches embedded in human-dominated landscapes. The predominant economic opportunities in the region are agriculture and pastoralism, activities that pose threats to tropical dry forests. Forest grazing can impact lemur populations directly through the loss of herbivorous ground cover and reduction of leaf biomass. Monitoring livestock activity and intensity is an important component of protected area management for lemurs, however, it can be labor-intensive and costly. This project aims to assess livestock grazing intensity using passive acoustic monitoring (PAM) in Beza Mahafaly Special Reserve (BMSR), which supports large populations of the two lemur species.

We hypothesized that more livestock vocalizations would be detected on PAM recordings in areas having greater signs of grazing impacts. For 1 year, 12 SM2+ Song Meters were deployed at BMSR in forest areas experiencing different grazing intensities (high, moderate, low). The devices recorded for 1 minute, at 15-minute intervals, continuously. Using the acoustic software Kaleidoscope Pro, livestock vocalizations in recordings were detected and quantified. Preliminary results show that vocalizations detected by PAM accurately reflect the level of observed grazing impacts. In a subset of data, 14.15% of recordings in heavily disturbed regions contained evidence of livestock; in moderately disturbed areas, 13.73%; and in little to no disturbance areas, 7.89%. We conclude that PAM is an efficient, cost-effective means of monitoring livestock activity in tropical dry forests.

This study was supported by a Scientific Product Grant from Wildlife Acoustics, a NASA WV Space Grant Consortium Graduate Fellowship, and Marshall University.

Experimental Assessment of $\delta^{15}N$ Shifts in Prey Meat and Bone in Response to Ambient Temperature Curing and Storage – Implications for Paleodietary Reconstruction

KIMBERLY K. FOECKE and ALISON S. BROOKS

Anthropology, George Washington University

Paleodietary reconstruction using the nitrogen isotope system is commonly applied to human skeletal remains in order to discern trophic position. There is increasing interest in expanding the limited information that exists assessing the impact of cultural food modification behaviors on food item $\delta^{15}N$ baselines and how these shifts may be passed into humans or other hominins. Previously-presented experimental approaches have assisted in illuminating these impacts across heat treatments, but curing and preservation methods that do not include the application of heat have yet to be considered. This study experimentally assessed the impact of a set of simple curing and preservation techniques on $\delta^{15}N$ shifts in four species of prey meat. Techniques were selected for their prevalence across archaeological and historical populations, and their use by hunter-gatherer groups. The methods tested include simple salt curing, brining, fermentation, and fat storage. Prey species tested encompass main variants in animal physiology, and include both wild and domestic species. Results from this study have generated a sizeable reference dataset for the impacts of these methods on $\delta^{15}N$ baselines for food items, and have the potential to assist in more complex bioarchaeological dietary analyses. The inclusion of bone-in meat sections in this study also shows potential for identifying a skeletal chemistry signal for the use of these methods in preserved faunal collections, which could have implications for assessing diet in earlier periods.

Funding provided by the National Science Foundation (1940816), Wenner-Gren Foundation, and Leakey Foundation.

Testing adaptive explanations for same-sex sociosexual behavior in bonobos (*Pan pansiscus*)

LILLIAN J. FORNOF[1], LIRAN SAMUNI[1,2] and MARTIN SURBECK[1,2]

[1]Department of Human Evolutionary Biology, Harvard University, [2]Interim Group Primatology, Max Planck Institute for Evolutionary Anthropology

The evolution of same-sex sociosexual behavior is puzzling given its non-reproductive nature. Adaptive explanations of same-sex sociosexual behavior emphasize its relevance in the establishment and maintenance of important social relationships (*the social bond hypothesis*), in the mediation of social dominance status (*the social status hypothesis*) or in the reduction of tension (*tension reduction hypothesis*). In one of our closest living relatives, bonobos (*Pan paniscus*), we observe a high prevalence of sociosexual behavior between females (GG rubbing). In this study we test predictions of the social bond hypothesis, which predicts frequency is higher among bonded individuals, the social status hypothesis, which predicts GG rubbing positioning is biased by dominance, and the tension reduction hypothesis, which predicts that GG rubbing may occur between individuals farther in rank or less bonded individuals. We investigated two groups of habituated wild bonobos at the Kokolopori

Bonobo Reserve in DRC and collected 1,618 observations of GG rubbing between 104 dyads with 912 observations of spatial positioning. We found no support for the social status or the social bond hypotheses. Differences in dominance rank of individuals in a dyad did not predict GG rubbing positioning. Dyads that GG rubbed more groomed less frequently, supporting the tension reduction hypothesis. However, a dyad's difference in dominance rank did not predict the frequency of GG rubbing. This study corroborates previous findings on the role of GG rubbing in tension reduction, indicating it may mediate more tense interactions between less closely bonded individuals.

Funding: This study was funded by Harvard University.

A non-destructive method for determining season of death in extant African Bovidae using dental microwear: Implications for seasonal variation in hominin resource availability and site occupation.

FRANCES L. FORREST

Education, American Museum of Natural History

The current study presents preliminary data on a new, non-destructive method for investigating seasonality at early human occupations. Seasonality would have played a significant role in the lives of early hominins. Nonetheless, we know little about the effects of seasonal resource availability on hominin evolution. For example, was meat primarily eaten as a seasonal fallback food or year-round resource at Early Stone Age sites? Few methods can reliably infer seasonal site occupation and degree of seasonal variability. One method is serially sampling isotopes from dental enamel using laser ablation. Enamel isotopes can provide a record of seasonal variation during tooth development but cannot determine the season of death. Dental cementum analysis can infer the season of death but is too destructive to be widely applicable to fossil assemblages. We looked at 26 species of extant African bovids across four broad feeding categories (Grazer, Mixed feeding grazer, Browser, and Mixed feeding browser) to explore how dental microwear patterns are influenced by seasonal rainfall. Bovids are often used as paleoenvironmental proxies at early hominin sites because they are among the most commonly recovered large mammals and occupy a wide range of environmental niches. Microwear features were examined using the semi-automated MicroweaR package in R. Results demonstrate that the number and percentage of pits and scratches are highly correlated with average rainfall at the time of death (p-value <.01 for all feeding categories). This method is extremely promising and will help answer questions relating to hominin mobility patterns, dietary flexibility, and behavioral variability.

Mechanical Properties and Enamel Chemistry in Primate Teeth

FREDERICK R. FOSTER and ROBERT S. SCOTT

Anthropology, Rutgers, the State University of New Jersey

Tooth enamel is a durable tissue possessing mechanical properties, including stiffness and hardness, that vary throughout primate teeth with implications for dietary adaptation. High stiffness and hardness at the occlusal surface resists crumbling and wear, and low stiffness at the EDJ resists fracture. Gradients in mechanical properties through enamel are hypothesized to form during tooth mineralization when enzymes moving from the surface to the EDJ convert protein to mineral. A general association between mineralization and mechanical properties has been observed in primate enamel, but the relationship has not been investigated. Here, we test the hypothesis that variation in enamel mechanical properties is related to mineralization in a sample of 22 lower molars from 10 primate species, sectioned buccolingually through the distal cusps. Electron microprobe analysis was used to measure enamel chemistry and infer mineralization, and nanoindentation was used to measure mechanical properties. Measurements were made along parallel transects spaced roughly 50 µm apart; one transect for each instrument in seven regions of the tooth. Chemistry and mechanical property data were paired by averaging over 40 µm increments. Generalized linear models were used to test for significant relationships between chemistry and mechanical properties. Our results show that mechanical properties are significantly correlated with mineralization in 15 samples, but with small effect sizes. The results support the hypothesis that mineralization phase of tooth formation causes variation in mechanical properties suggesting that it may be a target of selection in dietary adaptation, but small effect sizes indicate that other factors play a role.

This project was funded by the National Science Foundation Doctoral Dissertation Research Improvement Grant (NSF BSC-1847941) and the Rutgers University, Center for Human Evolutionary Studies Albert Fellows Award.

Social relationship quality predicts coalition formation among adult female chimpanzees at Kanyawara, Kibale National Park, Uganda

STEPHANIE A. FOX[1], DREW K. ENIGK[1], ZARIN P. MACHANDA[2], MARTIN N. MULLER[1], EMILY OTALI[3], NICOLE THOMPSON GONZÁLEZ[4], RICHARD W. WRANGHAM[5] and MELISSA EMERY THOMPSON[1]

[1]Anthropology, University of New Mexico, [2]Anthropology, Tufts University, [3]Kibale Chimpanzee Project, Fort Portal, Uganda, [4]Anthropology, University of California Santa Barbara, [5]Human Evolutionary Biology, Harvard University

Females of many primate species build strong, affiliative social relationships, which can be utilized to form coalitions to compete for resources and status. Among chimpanzees, females express infrequent affiliation and rarely cooperate to form coalitions (joint aggressive attacks or threats, including aggressive displays). However, even weakly affiliative relationships may still influence coalition formation. We investigate whether female chimpanzees tend to form coalitions with partners that they affiliate with more often.

We examined eight years (2010-2017) of party-level and focal-level data (N=4241 unique observer days, N=60284 15-minute scans) from 22 adult female chimpanzees (Pan troglodytes schweinfurthii) in Kibale National Park, Uganda. We observed 153 coalitions across 205 unique dyads (0-10 coalitions per dyad per biennial period). Over biennial periods, three commonly used measures of dyadic relationship quality – party association, five-meter proximity, and grooming – each significantly predicted coalition formation when contained in a model together (negative binomial generalized linear mixed effect regression, B=1.79 , B=5.26, B=0.56 , respectively, p<0.05 for all measures). Similarly, when comparing all available partners at the time of each coalition, a model containing all three measures of relationship quality demonstrated that party association and grooming, but not five-meter proximity, predicted partner choice (logistic mixed effect regression, B=2.66, B=0.62, respectively, p<0.001 for both measures).

These results suggest that even non-female bonded species can leverage existing social ties for cooperation. Additionally, our results highlight a divergence between chimpanzees and bonobos, as patterns of affiliation fail to predict coalitionary support among female bonobos despite frequent affiliation and coalition formation.

Phylogeny and association with locomotory context of posterolateral knee sesamoids in primates

NELLY A. FRAGOSO[1], SARAH ELTON[2] and MICHAEL A. BERTHAUME[1]

[1]Division of Mechanical Engineering and Design, London South Bank University, [2]Department of Anthropology, Durham University

Sesamoids (skeletal elements found in tendons and ligaments) have been proposed as a source of anatomical innovation, providing skeletal flexibility in the relatively conservative tetrapod bauplan. Four sesamoids can be found in the primate knee (the patella, medial and lateral fabellae, and cyamella) and, except for the patella, the sesamoids are variably present. As sesamoids can redirect muscle forces, increase muscle mechanical advantage, and strengthen the muscle-tendon connection, hypotheses concerning sesamoid presence/absence include

improving grip strength in arboreal primates (e.g., the enlarged cyamella increasing the force production of the popliteus) and reducing energy consumption in quadrupeds (e.g., the fabella, being more laterally located in these primates, may function like a patella). Here, we examine the relationship between knee sesamoid presence and phylogenetic history, and test for evolutionary associations between habitat use and locomotory style and sesamoid presence/absence. A systematic review identified 89 species with knee sesamoid presence/absence data. Phylogenetic signal (Pagel's lambda; fitDiscrete function in Geiger) was high (lambda = 0.57, 0.74, 0.61) for the medial fabella, lateral fabella, and cyamella, respectively, implying a large percentage of the variation in the presence/absence data can be explained by evolutionary history. The evolutionary correlations between each sesamoid and habitat use (arboreal vs terrestrial) and locomotory style (quadrupedal vs non-quadrupedal) were low (threshBayes function in phytools), ranging from -0.076 to 0.192. These results imply habitat use and locomotory style are uncorrelated to knee sesamoid presence/absence in primates, and the variably present sesamoids in the knees of primates may have undergone neutral selection.

The London South Bank University doctoral programme

Secular trends in the Cayo Santiago rhesus macaque population

GEORGE N. FRANCIS and QIAN WANG

Department of Biomedical Sciences, Texas A&M University College of Dentistry

The Cayo Santiago rhesus macaque population represents one of the most important non-human primate resources after its introduction to the Caribbean area (Latitude: 18.1564˚N; Yearly sunlight hours: 2964) from Lucknow, India (Latitude: 26.8470˚N; Yearly sunlight hours: 2708) in 1938. The derived skeletal collection from the colony spans 10 generations with known pedigrees, providing an unprecedented opportunity for investigating secular trends in terms of adaptation to the island's climate, landscape and management strategies, especially the impact of major events including nutritional provisioning and hurricane devastations. In this study, body weight, bone size and bone density of skeletally mature males and females were collected and compared in a temporal framework. Results demonstrate that overall, body weight, bone density, and a majority of craniofacial and long bone sizes have decreased over time. This decline may delineate acclimation effects in compliance with Bergmann's rule as a thermoregulatory response to a tropical environment which, along with locomotion adaptation to the island substrate, and reduced levels of physical activity due to lack of predators and food provisioning, override the effects of better nutrition in recent decades. Moreover, the trend is more prominent in males with remarkable declines in male long bone lengths coupled with a stasis in females leading to decreasing sexual dimorphism, indicative of a relaxation of selection pressures in males. No apparent link is found in association with major climate disasters, nor trend in fluctuating asymmetry in this investigation. More studies with inclusion of non-adult individuals, reproduction strategy, and population dynamics are warranted.

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.

Differential tissue shrinkage in diceCT

KATHERYN P. FRANKLIN[1], TIMOTHY D. SMITH[2,3] and VALERIE B. DELEON[1]

[1]Department of Anthropology, University of Florida, [2]School of Physical Therapy, Slippery Rock University, [3]Department of Anthropology, University of Pittsburgh

Lugol's iodine solution (I_2KI) is used for diffusible iodine contrast-enhanced computed tomography (diceCT) imaging. This contrasting agent can introduce error in size and spatial position of tissues due to osmotic imbalances triggering significant tissue shrinkage in specimens. The aim of this study was to quantify differential shrinkage of tissues in newborn primates.

We compared tissue shrinkage in bony elements, brain, and muscle tissue under two conditions, a high (5%) and low (1%) concentration Lugol's solution. Imaging data from conventional CT prior to staining and periodic diceCT allowed us to collect longitudinal data for the same tissues at multiple timepoints. Tissue volumes were segmented in 3DSlicer, and volumes and surface areas were recorded. In 5% Lugol's solution significant shrinkage was apparent, with brain showing the greatest reduction in volume and bone showing the least. In one specimen of *Otolemur*, the entire volume of the specimen was reduced by 60% in 34 days of 5% Lugol's staining. In contrast, the 1% Lugol's solution produced minimal shrinkage. For example, in one specimen of *Aotus*, cranial length remained the same and the outer volume of the brain after 69 days in 1% Lugol's was 86% of endocast volume determined prior to staining. These results illustrate the differential shrinkage of certain tissues in diceCT and confirm that a 1% concentration of Lugol's iodine produces minimal shrinkage in newborn primate specimens. We also report our results from more recent experiments with a B-Lugol's solution to reduce shrinkage through the deacidification and pH stabilization of the solution."

Funded by the National Science Foundation (BCS-1830894 and BCS-1830919)

How the external environment shapes cartilage development, fate and evolution: insights from teleosts

TAMARA A. FRANZ-ODENDAAL

Department of Biology, Mount Saint Vincent University, Canada

This abstract is part of the symposium *Cartilage and Craniofacial Growth.* Teleost cartilages are a diverse tissue unlike in mammals. This presentation will discuss various environmental influences that can affect cartilage development and thus impact its final morphology and ultimate evolution.

Teleosts are superb models to study craniofacial development and growth because their entire life history can be studied in a laboratory setting. While chemical manipulations (e.g. addition of BMP inhibitors) are easy to conduct and enable us to observe the effects of modulating particular signaling pathways, experimental manipulation opens doors to understanding the more complex interactions between the environment and the development of an organism, and vice versa. By experimentally manipulating behaviour, we are able to observe the impacts of mechanosensation and musculoskeletal interactions on cartilage induction, development and growth.

In this presentation, I present data from my team to demonstrate the plasticity of cartilage development and the remarkable ability of a developing organism to respond to environmental influences quickly. These responses often have lasting impacts on the resulting phenotype and provides a hint at how development influences evolution.

This research was funded by the Natural Sciences and Engineering Research Council of Canada.

Linear regression analysis of patellar measurements for stature estimation is not suitable for forensic casework

ERIC FRAUENHOFER

College of Medicine, University of Florida

Stature is an important component used to identify unknown human skeletal remains. Although it is best estimated using a complete set of remains, complete skeletons are rarely recovered in forensic settings, requiring forensic anthropologists to rely on methods utilizing partial skeletal remains. Common methods for estimating stature include linear regression analysis of a single bone or a combination of elements, particularly complete or partial long bones. In the absence of long bones, anthropologists must have methods for assessing the elements that are available. The patella, for instance, has been shown to be a robust element that survives taphonomic change and is often recovered. However, it has not been reported whether it can be used for estimating stature. Therefore, this study examined stature estimation using linear regression analysis of

patellar measurements. The sample consisted of 360 female and male African Americans and European Americans of known stature from the Hamann-Todd Osteological Collection. Seven measurements were taken of each individual's left patella. SPSS was used to derive linear regression functions for each sex of each ancestral group. R-squared values ranged from 0.0001 to 0.34, indicating the measurements do not exhibit a strong linear correlation with stature. An independent sample indicated the accuracy of the functions ranged from 40% to 80%, with a mean accuracy of 57.5%, demonstrating the functions are not suitable for forensic casework. This study will impact the forensic anthropology community by demonstrating that linear regression analysis of patellar measurements is not accurate for estimating stature.

This research was partially funded by the Office of Undergraduate Research at SUNY Buffalo State.

Combating frailty: Application of a modified skeletal frailty index to forensic anthropology contexts

EMILY M. FRAZIER[1], DOUGLAS E. CREWS[2,3] and KATHRYN E. MARKLEIN[1,4]

[1]Department of Anthropology, University of Louisville, [2]Department of Anthropology, The Ohio State University, [3]School of Public Health, The Ohio State University, [4]Center for Archaeology and Cultural Heritage, University of Louisville

Conceptualizing, quantifying, and evaluating frailty in human skeletal remains is critical to understanding and interpreting physiological health and stress among past populations. While many researchers focus on frailty in bioarchaeological samples, developing models for mortality risk and individual- and population-specific indices of stress, no current methods directly address frailty in forensic contexts. This study considers the applicability of a modified index for assessing frailty in forensic anthropology by comparing distributions of 8 biomarkers of stress (linear enamel hypoplasia; periodontal disease; caries; osteoarthritis; intervertebral disc disease; rotator cuff disorder; antemortem fracture; and surgical procedure) using the original skeletal frailty index (SFI) to a modified skeletal frailty index (SFI+) between self-identified military veterans (n=10) and civilians (n=9) from the Bass Donated Skeletal Collection. Mann-Whitney U tests showed statistically significant differences between SFI and SFI+ distributions overall (p<0.001), with SFI (4.10±1.29) yielding higher average distributions than SFI+ (2.03±0.98). This variation in SFI and SFI+ distributions affected subsequent differences in results comparing military and civilian subsamples, SFI+ (p=0.04) and SFI (p=0.35). In this forensic context, the SFI+ reflects both increased levels of skeletal preservation within modern samples and medical interventive care that may mitigate frailty. Further, it implements severity scales, rather than relying on presence/absence binaries, for evaluating frailty biomarkers as low or high. These modifications present an effective way of quantifying frailty that highlight complexities of modern embodied experiences, and results support the applicability of SFI+ to forensic anthropology contexts.

Reanalysis of Disarticulate and Commingled Human Remains: Burning as Complex Mortuary Ritual

J. CRISTINA FREIBERGER and DEBRA L. MARTIN

Anthropology, University of Nevada, Las Vegas

In the American Southwest, there have been over a hundred commingled and disarticulated human remain deposits identified from Ancestral Pueblo groups (circa AD 800-1700). In 1991, Christy and Jacqueline Turner examined 76 of these deposits and reported on the presence and frequency of burning. Fifty-six percent of those deposits showed signs of burning. In a re-analysis of the published data, the amount of burning found in these deposits varied from 0.5% to 98.6%. Anthropophagy was used as an explanation since previous reports have found (2.6% to 79.4%) burn rates on faunal bones from middens. However, more recent criticisms of the interpretation of anthropophagy have proposed that bone burning could be part of a complex mortuary ritual. In a detailed review of Puebloan ethnographic accounts, fire is viewed as a tool of transformation and purification. There are accounts of fire being used to ritualistically destroy villages as well as to annihilate the bodies of those accused of witchcraft. These ethnographic accounts demonstrate that the burning of the bodies may be due to factors other than anthropophagy. Compared with other known cases of anthropophagy, large mammal consumption cooking patterns, and non-anthropophagy post-mortem treatment of bodies, the more plausible explanation for Ancestral Pueblo disarticulated, commingled, and burned bone includes purification rites for some considered collections and the massacre and annihilation of bodies in other cases.

Impact of Covid-19 on the Accessibility of Digital Osteological Resources

MEGAN H. FRY[1], SAMANTHA M. MCCRANE[1] and S. CONNER WELTY[2]

[1]Anthropology, University of Florida, [2]Archaeology, University College London

The onset of the Covid-19 pandemic has undoubtedly created many struggles for educators, students, and researchers. Among them, the switch to distance learning and research necessitated available online, digital resources for teaching and research purposes, which many institutions lacked. To remedy this, numerous faculty, students, and labs volunteered their time to digitize their institutional collections. Most were created using high-resolution photography, 3D modelling (via photogrammetry or laser scanning), radiographs, or computed tomography (CT) scans, depending on the availability of resources at hand. However, since these digitized datasets were compiled by individual persons or labs for their institutions they were not necessarily made widely available. This study analyzed learning forums, online teaching/research communities, social media and blogs centered on promoting research and education, and relevant institutional websites, to compile a list of digitized osteological collections. These repositories were assessed qualitatively and catalogued according to type, content, and access (public vs. requiring verification). We rank these repositories by accessibility, and discuss recommended practices for aggregating and sharing osteological data. Additionally, we provide all this information within a single open-access resource. Digital collections allow students and early career researchers the ability to engage with collections that may have been unattainable due to a lack of financial support previously. By removing the burden of long-distance travel they also promote accessibility as well as interinstitutional and interdisciplinary collaborations. Thus digitization efforts should continue and expand in a post-pandemic world, but in ways that optimize accessibility.

Using ecological niche modeling to assess how frugivorous non-primate mammals impact frugivorous primate distributions on a global scale.

AMANDA J. FUCHS[1], RACHEL B. BELL[2], ARYA KUNAPARAJU[1], JOHN ROWAN[3], LYDIA BEAUDROT[4], KAYE E. REED[5] and JASON M. KAMILAR[1,2]

[1]Department of Anthropology, University of Massachusetts, Amherst, [2]Graduate Program in Organismic and Evolutionary Biology Graduate Program, University of Massachusetts, Amherst, [3]Department of Anthropology, University at Albany, State University of New York, [4]Department of Biosciences, Rice University, [5]Institute of Human Origins, School of Human Evolution and Social Change

Research suggests that climatic variables influence the distribution of primate species. However, few studies have investigated the impact of community structure and interspecific competition on primate distributions. In this study, we examine how non-primate mammalian frugivores affect the distribution of frugivorous primates in the Neotropics, Asia, Africa, and Madagascar. We hypothesize that potential competitors limit the distribution of primates through competitive exclusion, and that these effects will differ between study regions due to variation in community structure and biogeographic history. To test this, we constructed ecological niche models (ENMs) for each primate species (n=100), one containing abiotic variables and a second including abiotic and biotic predictors. Abiotic models included BioClim variables, NDVI values,

soil pH, and elevation. Biotic models included the previous abiotic variables along with the geographic ranges of potential competitors as predictors. Our ENMs indicate that abiotic models produce a larger and less accurate area of suitability for the primate species compared to models that included biotic variables. In fact, in most cases we found that the non-primate competitors were among the most important predictors of frugivorous primate distributions. Interestingly, competitor species had less of an impact on Malagasy lemur distributions, which may be due to the relatively low level of non-primate mammal biodiversity. In the Neotropics, abiotic and biotic ENMs had the largest differences between them, suggesting competitor species are more important for determining primate distribution here. These results emphasize the importance of community structure and interspecific competition when assessing the distribution of primates and their conservation.

This research was funded by the National Science Foundation (NSF SBE Awards 1551799 and 1551810).

Burned house, (un)burnt bodies. Bioarchaeological insights in the life and death of Tripolye Culture mega site inhabitants (3800–3600 BCE)

KATHARINA FUCHS[1], LIUDMYLA SHATILO[2], ROBERT HOFMANN[2], SUSANNE STORCH[3], VLADISLAV CHABANYUK[4] and JOHANNES MÜLLER[2]

[1]Institute of Clinical Molecular Biology, Kiel University, [2]Institute of Prehistoric and Protohistoric Archaeology, Kiel University, [3]Anthropologist, Freelance, [4]Trypillia Culture State Historical and Cultural Reserve

In this paper, we present the unique case of human remains associated with the Tripolye Culture (ca. 4800–3000 BCE), which is famous for inhabiting the largest settlements of Neolithic Europe. Rich archaeological information of these Tripolye communities draw a picture of fully agricultural economies and complex social systems, but primary data from the inhabitants themselves are extremely rare. Main objective of this bioarchaeological study are human remains found in the context of a burnt domestic scenery within the Eneolithic site Kosenovka (ca. 80 ha), located in the today's Uman region of the Ukraine.

Results of archaeological analysis, radiocarbon dating, and osteological analysis conclude that (i) the demographic composition of seven individuals indicates a family structure, (ii) cremated human bones were located inside the house structures, while non-cremated were found in its periphery, and (iii) that the depositional event(s) took place between ca. 3600–3800 BCE. In addition, CN stable isotopes signatures and microscopic analysis of three preserved teeth provided information regarding the dietary behaviors of these individuals, such as consuming both plant-based and animal-based foodstuffs as well as using toothpicks to clean out interdental spaces. This offers exceptional insights into the life of the Tripolye mega site inhabitants.

Moreover, the results allow for various scenarios as to how this archaeological situation came about, for instance a specific burial practice, or a fire event. We discuss these possibilities by including analogue findings.

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).

A survey of microaggression, discrimination and harassment within the Faculty of Science at the University of Cape Town

TARRYN SASHA FULLERTON, KERRYN WARREN and REBECCA R. ACKERMANN

Archaeology, University of Cape Town

Discrimination ranges from overt, aggressive forms, such as harassment, to more passive or subversive discrimination, such as microaggressions and exclusions. The University of Cape Town (UCT) has taken a zero-tolerance approach to any form of behaviour that demeans others, including but not limited to discrimination and harassment, but have these approaches been effectively adopted by all departments? The purpose of this research is to assess the prevalence of microaggression, exclusion and/or harassment occurring within all departments for those enrolled in the Faculty of Science at UCT. The study consisted of two phases of a mixed method modality: (1) Phase 1, a 5-point Likert based instrument modelled after previously standardised, reliable and validated scales; (2) Phase 2, a qualitative interview for participants who opt in. The survey was distributed to all students from undergraduate to post-doctoral level; a total of 87 participants completed phase one, and four completed phase two. Phase one data were collected by means of the survey system LimeSurvey and analysed in SPSS using Chi-squared non-parametric tests. Phase two data were analysed by thematic coding and NVivo. Results indicate that a significant number of students have experienced harassment (9%), exclusion (26%), and microaggression (41%) while enrolled within the faculty, with gender and racial discrimination most prevalent. These results indicate an alarmingly high frequency of both subvert and passive forms of discrimination, highlighting that there is a considerable way to go in terms of transformation and inclusivity in the sciences. Qualitative data further support these conclusions.

Funding was obtained from the National Science Foundation of South Africa

Modeling dietary adaptation in the paraconid cusp using power law parameters

ETHAN L. FULWOOD[1], TONY HARPER[1], MADISON BRADLEY-CRONKWRIGHT[2], ALISHA ANAYA[2], BLAKE DICKSON[2] and DOUG M. BOYER[2]

[1]Department of Anatomy, Lincoln Memorial University, [2]Department of Evolutionary Anthropology, Duke University

Occlusal morphology and diet appear strongly related in primates. The shapes of tooth cusps are likely responsive to the same adaptive forces, but this has been difficult to quantify. To examine this question, we combine mesh segmentation methods implemented in the 'Hecate' package of algorithms with parameters describing the shape of conical tooth components derived from a power law relationship between radius and depth. 266 m2 meshes from 74 species spanning Euarchonta were segmented into 10 meshes of regionally consistent shape. Paraconid segments were "sliced" in Blender into five bands running longitudinally along the cusp and total area and centroid location calculated along each cross-section. The slope of the relationship between log distance (measured longitudinally from the apex of the protoconid) and log radius (approximated from cross-sectional area) was estimated using RMA regression and the aspect ratio of each cusp calculated as height divided by maximum diameter. Finally, the dental topography metric DNE was calculated on each paraconid. Radius and depth appear to be linearly related as expected by the power law. Spatial ANOVA supports a high correlation between DNE and the morphospace, suggesting that power law parameters relate to sharpness. DFA using slope and aspect reclassified members of the sample to one of three dietary ecologies with relatively high success rates, particularly within suborders (Euarchonta = 49%, haplorrhines = 56%, strepsirrhines = 64%). The shape of the isolated protoconid appears to reflect dietary adaptation at a surprisingly high resolution, suggesting that molar cusp shape is responsive to diet.

NSF BCS 1552848 (to DMB)

How Human Admixture Impacts the Genomic Landscape

ALYSSA FUNK[1,2] and EMILIA HUERTA-SÁNCHEZ[1,3]

[1]Center for Computational and Molecular Biology, Brown University, [2]Molecular and Cellular Biology, Brown University, [3]Ecology and Evolutionary Biology, Brown University

Admixture between previously isolated populations is an important force in shaping patterns of genetic variation and facilitating human adaptations. Despite growing evidence of repeated and ongoing admixture events, we understand little about how admixture alters patterns of genetic variation, thereby changing standard expectations for genome heterozygosity, linkage disequilibrium,

haplotype structure, and number of segregating sites. Without knowing how these genomic patterns change, choosing an appropriate positive selection statistic for an admixed population is difficult. We calculate the number of segregating sites and heterozygosity in a simulated population that resembles admixed populations in the Americas. We find that both segregating sites and heterozygosity differ from the expectation of an unadmixed population. Given these results, admixture is also likely to change other expected genomic patterns and could affect the power of selection statistics to detect positive or negative selection. We also evaluate the best comparison populations to use for the Population Branch Statistic (PBS), which can detect positive selection in a chosen population if proper comparison and outgroup populations are selected.

Alyssa Funk is supported by National Institute of Health grant [R35GM128946] to Emilia Huerta-Sánchez.

Comparing Close-Range Photogrammetry to microCT Scanning Using Hominin Molars: Regional and Sensitivity Analyses

MARGARET J. FURTNER[1] and JULIET K. BROPHY[1,2]

[1]Department of Geography & Anthropology, Louisiana State University, [2]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand

This study expands on a prior comparison between close-range photogrammetry and microCT surface scanning that suggests comparability between the two methods. In this study, a regional analysis was conducted to determine the surface location upon which deviation is greatest between corresponding photogrammetric and microCT models of teeth. Surface models of fossil (*Homo naledi*), archaeological, and contemporary human molars displaying either the occlusal or non-occlusal (side) surfaces were compared using point-to-point surface deviation analysis (SDA). For teeth possessing qualities allowing for greater photogrammetric accuracy, such as staining, the occlusal surfaces had greater deviations than the side surfaces. Contrastingly, for teeth lacking these qualities, greater deviation occurred on the side surfaces. A one-tailed t-test shows a significantly higher severity of surface difference on models where side surfaces possess the greater deviation ($p = 0.0093$).

A sensitivity analysis was also conducted on complete photogrammetric models of three *H. naledi* molars to assess the minimum quality of camera necessary for accurate photogrammetric results. Photogrammetric surfaces were downsampled by increments of 1000 triangles and compared to their corresponding microCT model at each increment using SDA. The results show the accuracy of the models decreasing minimally at each lower resolution until a threshold is passed (~5000-6000 triangles) upon which accuracy decreases sharply. This tradeoff between accuracy and resolution indicates that inexpensive and lower-resolution cameras may be suitable for photogrammetric scanning depending upon subject and budget. The results of these two analyses will aid researchers in further refining photogrammetric protocols and analyzing their results.

This research was funded by the R.J. Russell Graduate Student Research Award and the G&A Graduate Research Materials Award through the Department of Geography & Anthropology at Louisiana State University.

Depression and suicidality as credible signals of need in the face of adversity

MICHAEL R. GAFFNEY[1], KAI H. ADAMS[2], KRISTEN L. SYME[3] and EDWARD H. HAGEN[1]

[1]Department of Anthropology, Washington State Univeristy, [2]Haas School of Business, UC Berkeley, [3]Department of Experimental and Applied Psychology, Vrije Universiteit Amsterdam

Mental health professionals generally view major depression and suicidality as pathological responses to stress that elicit aversive responses from others. An alternative hypothesis grounded in evolutionary theory contends that depression and suicidality are credible signals of need in response to adversity that can increase support from reluctant others when there are conflicts of interest. To test this hypothesis, we examined responses to emotional signals in a preregistered experimental vignette study involving claims of substantial need in the presence of conflicts of interest and private information about the signaler's true level of need. In a sample of 1,240 participants recruited from Amazon Mechanical Turk, costlier signals like depression and suicidality resulted in greater perceptions of need, reduced perceptions of manipulativeness, and increased likelihood of support compared to simple verbal requests and crying without further symptoms. Additionally, as predicted, the effect of signaling on likelihood of support was largely mediated by the effect of signaling on participants' belief that the signaler was genuinely in need. Our results support the hypothesis that the costlier symptoms of depression and suicidality, are credible signals of need that elicit more support than verbal requests, sad expressions, and crying when there are conflicts of interest.

This study was funded by a WSU Vancouver research mini grant.

Taxonomic assignments based on worn crown outlines are not affected by observer error

JULIA GALWAY-WITHAM[1,2] and SHARA E. BAILEY[1,2]

[1]Center for the Study of Human Origins, Department of Anthropology, New York University, [2]New York Consortium in Evolutionary Primatology, (NYCEP)

Moderately worn crown outlines have proven to be effective in taxonomic assessment of fossil and recent human teeth. Before analysis, interproximal wear is often corrected by qualitatively reconstructing the missing portion of the outline. However, the potential for error in these estimations is understudied. Here, researchers of different levels of familiarity with dental anatomy independently reconstructed the missing portion of crown outlines for a comparative sample of hominin permanent lower first molars (*Homo erectus* [*n*=2]; Middle-Pleistocene *Homo* [*n*=5]; *H. neanderthalensis* [*n*=8]; early *H. sapiens* [*n*=3]; Upper Palaeolithic *H. sapiens* [*n*=5]; recent *H. sapiens* [*n*=3]). The outlines were defined by 25 sliding semilandmarks and one fixed landmark at the buccal groove, which were oriented and scaled via a generalized Procrustes analysis. The outlines were included in Procrustes regressions, where 'taxon', 'observer' and 'size' were included as variables, and then compared via Procrustes ANOVA. The Procrustes coordinates were also subjected to a principal components analysis. We conclude that there is a moderate degree of bias introduced by observers. The disparity between observers in the crown outline reconstructions was amplified in specimens with relatively high degrees of wear. Additionally, our analysis of intraobserver error found a moderate amount of error introduced during repeated observations. Importantly, however, taxonomic assignment explained considerably more variation than the observer (34% versus 2.5%, respectively, in our Procrustes regression and ANOVA). Therefore, we conclude that taxonomic assignment is unaffected by these disparities, and we support the continued use of this method for assigning moderately worn postcanine teeth to taxa.

JGW is supported by the NSF GRFP and the NYU MacCracken Fellowship. SEB was financially supported by the Max Planck Institute and NYU during data collection used in this study.

Enamel dentine junction in population dynamics: A case study of ancient northern Iberian populations

BEATRIZ GAMARRA[1,2], MARINA LOZANO[1,2], ANTONIETTA DEL BOVE[1,2], EULÀLIA SUBIRÀ[3], MANUEL EDO[4,5], CONCEPCIÓ CASTELLANA[4], JOSEP MARIA. VERGÈS[1,2], JUAN IGNACIO MORALES[6], ARTUR CEBRIÀ[6], FRANCESC X. OMS[6], CARLOS TORNERO[1,2] and ANNA GÓMEZ-BACH[7]

[1]Department of Paleoanthropology, Institut Català de Paleoecologia Humana i Evolució Social (IPHES-CERCA), [2]Departament d'Història i Història de l'Art, Universitat Rovira i Virgili (URV), [3]Unitat d'Antropologia Biològica, Departament BABVE, Universitat Autònoma de Barcelona, [4]CIPAG, Col¬∑lectiu per a la Investigació de la Prehistòria I l'Arqueologia de Garraf-Ordal, [5]Institut d'Arqueologia, Universitat de Barcelona, [6]SERP, Departament Història i Arqueologia, Universitat de Barcelona, [7]Departament de Prehistòria, Universitat Autònoma de Barcelona

Neolithisation process arrived at the Iberian Peninsula (IP) around 5,500 calBC, having diverse impacts on genomic and cultural diversity. During the Late Neolithic–Chalcolithic, changes occurred at funerary and cultural material level, with also evidence of narrower exchange networks. Genomic diversity decrease at this period suggests human mobility and genetic flow among Iberian populations from different areas. Dental morphology studies have contributed to our understanding of biological and genetic affinities among ancient human groups. Surprisingly, phenotypic variability in dental inner tissues has scarcely been examined in prehistoric European populations and its use in establishing historical and biological relationships between them. Here we analyzed the enamel-dentine junction (EDJ) and cervical outline morphology of first upper molars by means of 3D geometric morphometric methods to explore biological affinities of northern IP populations and the decrease in genetic variability detected during the Late Neolithic–Chalcolithic period. Shape and form space PCA show that the EDJ and cervical morphologies of the northern IP populations were generally homogeneous, indicative of genetic admixture as a result of human mobility and exchange networks. However, differences in the inner tissues' traits of some sites analyzed here indicate distant biological affinities, suggesting a particular biological history. Additionally, the hypocone associated dentine area and the position of the trigon dentine horns relative to each other on the occlusal surface best describe the variability found among the samples studied. This study highlights the utility of EDJ morphology as a genetic proxy in Holocene population dynamic studies when paleogenomic studies are absent.

This study is part of the Beatriu de Pinós Post-doctoral fellowship (2017 BP 00210; AGAUR, Government of Catalonia). Data was obtained through StEP (2017SGR1040) and MICINN/FEDER - PGC2018-093925-B-C32 projects.

Conjuring the dead: Using ancient DNA analysis to understand human artistic endeavors

DANALAXSHMI S. GANAPATHEE

Program II, Duke University

Early modern humans of the African Middle Stone Age began to increasingly engage in symbolic behavior and technological innovation after about 100 kya, and these behaviors accelerated after 50 kya, giving rise to the Later Stone Age (Africa) and Upper Paleolithic (Eurasia). Neandertals of Europe and western Asia, in contrast, engaged in either symbolic expression or technological innovation, including art-making, to a lesser extent. Some paleoanthropologists attribute the behavioral difference between these species to differences in cognitive abilities, while others point to extrinsic factors such as population density. This study explored, through the lens of genomics, the neurobiological and cognitive bases for the possible behavioral differences between Neandertals and modern humans. A list of genetic changes occurring post-split between Neandertals and modern humans was used as a pool of candidate genes and the expression of these genes was verified in brain regions that are believed to be implicated in art-making. Two genes– KRTAP24-1, HOXD4 were filtered out because they did not show any expression in the brain regions of interest. The remaining genes showed broad expression across most brain regions, making it difficult to spot areas of specialized activity. Thus, it was impossible to eliminate any other gene from consideration and narrow down the list of candidates further from the large list of 172 genes. However, the compiled information can be used to pinpoint genes that are implicated in traits of interest. One could find out genes showing enhanced activation for brain regions underlying joint attention or imagination for instance.

Health and dietary drivers of human oral microbiome composition in ancient Britain

ABIGAIL S. GANCZ[1], ANDREW G. FARRER[2], KEITH DOBNEY[3], STERLING L. WRIGHT[1] and LAURA S. WEYRICH[1,2]

[1]Anthropology, The Pennsylvania State University, [2]Australian Centre for Ancient DNA, University of Adelaide, [3]Department of Archaeology, Classics and Egyptology, University of Liverpool

Assessing health and disease patterns in past populations provides important insights into causal pathways associated with social, environmental, and dietary factors. These findings are critical for establishing the origins of modern diseases and can be used to inform modern health interventions. Here, we demonstrate previously untraceable connections between health, oral microbiomes, and diets in ancient London. We reconstructed and analyzed the ancient oral microbiomes composition of 127 ancient individuals from Medieval and Post-Medieval London (1066 to 1853 CE) who were associated with extensive demographic and pathological metadata in the context of health and diet. Using novel analytical strategies that controlled for previously unaccounted biases, such as oral geographies, we found significant links between oral microbiome composition and skeletal markers associated with chronic inflammatory conditions including nonspecific periostitis, osteophytic lipping, and joint porosity. In addition to these findings, our functional dietary analysis in this study indicated that oral microbiome composition was linked with dietary indicators associated with lactose and carbohydrates. While links between the oral microbiome and systemic health have been observed in modern populations, this is the first time they have been demonstrated in an ancient society. Examining how these relationships have changed over time can inform health interventions today.

Research support provided by: NSF GRFP #DGE1255832

Genetic insights into local adaptation of lipid metabolism in fishing-based populations in southern East Asia

YUTI GAO[1] and ZI-YANG XIA[2]

[1]Department of Anthropology, University of Colorado Boulder, [2]Department of Genetics, Evolution and Environment, University College London

The genetic history of the southern East Asian (SEA) populations is unclear, given limited sampling of ancient genomes. However, a recently published ancient DNA data set of SEA populations enables modelling genetic histories of these populations. Here, we relate natural selection to the genetic history of SEA populations, scanning for signatures of polygenic adaptation and archaic introgression. We used newly published modern and ancient genomes, analyzing these data through tests of selection. Analyses included population branch statistics (PBS, divergence-based), graph-aware retrieval of selective sweeps (GRoSS, allele frequency-based) and other methods. Our pilot study identifies many local adaptive signals in SEA populations. In ancient and modern Austronesian-speaking Taiwanese, we identified > 15 high selection signals. Among these signals, MIR1297 is significantly related to oily fish intake. In addition, we found that allele frequencies of the FADS gene family in ancient island Taiwanese, Japanese, and Southern Chinese may be higher than other Asian populations. The FADS gene family has proven to be associated with fatty acid metabolism. Thus, results of MIR1297 and FADS may correspond to adaptations changes in lipid metabolism away from a fish-based diet in SEA populations (especially ancient Austronesian populations). Selection of genes related to lipid metabolism in rice-cultivating agriculture areas may indicate a transition of diets and lifestyle from fishing and gathering to agriculture, where metabolizing carbohydrates into lipids would be advantageous.

It's not you, it's…just random: mate change in pair-living, genetically monogamous primates (*Aotus azarae*)

ALBA GARCIA DE LA CHICA[1], CAROLA BORRIES[2] and EDUARDO FERNANDEZ-DUQUE[3]

[1]Biological Anthropology, Owl Monkey Project, [2]Department of Anthropology, Stony Brook, [3]Department of Anthropology, Yale University

Factors promoting mate change and its consequences have been largely explored in pair-living, monogamous birds. In mammals the topic remains less understood. We analyzed 68 mate

changes in owl monkeys (*Aotus azarae*), a pair-living, monogamous primate. Mate change is always initiated by incoming floaters, young adults dispersed from their natal groups that replace resident adults. We predicted that replacements would be more frequent when conception is possible and for groups without infants, since this may signal breeding failure; and that the loss of either parent would have negative consequences on infant survival given biparental care in the species. Replacements were not more frequent during the conception than the non-conception season (obs [exp], 22 [21.3] vs. 29 [29.8]). Neither was the number of groups without infants that had mate changes different from the number of groups without infants that did not have changes: 44% (57/129 pairs-years) vs. 50% (34/68 pairs-years). Survival was lower for infants without a parent than for those with both parents (infants 0-6 months: 50% (4/4) vs 82% (63/77); infants 6-12 months: 75 % (6/8) vs 90% (57/63); juveniles 12-24 months: 89% (16/18) vs 89% (51/57). Mate change does not appear clearly related to reproductive periods or previous reproductive success but has negative consequences for the current breeding status of resident adults. We propose that in habitats with very few available territories and high intruder pressure, mate change does not function as an adaptive strategy, but as a series of opportunistic chances.

Leakey Foundation, National Geographic Society (EC-54383R-18), Wenner-Gren Foundation, NSF-BCS-0621020; RAPID-1219368, 1232349, 1503753; DDIG-1540255, 1743395, 1848954; NSF-REU-0837921, 0924352, 1026991, National Institute Aging (P30-AG012836-19, NICHD-R24-HD-044964-11), University Pennsylvania Research Foundation, Zoological Society San Diego

Hypotheses of dental integration and their impact on hominin cladistic analysis

JACQUELINE M. GARNETT and DAVID S. STRAIT

Department of Anthropology, Washington University in St. Louis

Morphological integration refers to the covariation between traits due to shared function, genetic architecture, developmental pathways, and/or selective pressures. Such integration presents a considerable challenge to cladistic analyses because this method assumes independence between characters. Teeth are likely to be highly integrated because as serially homologous structures, they share many genetic and developmental pathways. Moreover, teeth figure prominently in paleoanthropological cladistic analyses due to the overrepresentation of teeth within the hominin fossil record. As such, the inclusion of many dental traits in cladistic analyses without consideration of their integration may hinder our ability to reliably reconstruct hominin evolutionary relationships. We constructed a character matrix containing dental traits known to vary within hominins which have previously been used in studies of hominin phylogeny. We then conducted two cladistic analyses to analyze the effect of dental integration on tree topology: (1) assuming independence among all traits, and (2) assuming integration between traits grouped by morphogenic field (i.e., tooth type). Compared to the analysis assuming independence, the analysis considering integration resolved a polytomy within a clade containing *Homo*, *Paranthropus*, and *A. africanus* and impacted the position of *A. afarensis* relative to these taxa, suggesting a deeper split between *Paranthropus* and *Homo* within gracile australopiths prior to the divergence between *A. afarensis* and *A. africanus*. Our results demonstrate the importance of accounting for integration in cladistic analyses.

A test of subadult stature estimation equations on modern samples

HEATHER M. GARVIN[1] and TANNER PULSIPHER[2]

[1]Department of Anatomy, Des Moines University, [2]College of Osteopathic Medicine, Des Moines University

Stature estimation from skeletal remains is important to various subfields of biological anthropology, including paleoanthropology, bioarchaeology, and forensic anthropology. Nonetheless, there are only a handful of studies that present methods for subadult stature estimation and those methods lack thorough validation.

This study uses a cross-sectional sample of 419 modern subadult postmortem CT and Lodox scans (1-12 years of age) from U.S. and South African samples to test two published methods of subadult stature estimation: Ruff (2007) and Smith (2007). Diaphyseal long bone lengths were collected from the scans and stature estimated from the published equations. Method accuracy and bias were assessed using absolute and relative differences between documented and estimated statures and the percentage of individuals within the estimate confidence intervals.

Both methods resulted in an overall average absolute difference between documented and estimated statures of ~3cm; despite the fact that the Smith equation pools ages 3-10 years and the Ruff equations are presented by 1-year cohorts. Seventy-eight percent of the equations tested resulted in less than 80% of the cases falling within the 95% confidence intervals; ~10% of the equations tested resulted in less than 50% of the cases falling within the 95% confidence intervals. Results also confirm that stature estimation is better in the younger age groups (years 1-6). Factors that may be contributing to estimate discrepancies include differences in modality and sample compositions. Utility of the methods depends on the application, as potential implications of erroneous estimates need to be considered in individual case analyses.

Project supported by grant award: NIJ 2015-DN-BX-K409. Opinions and findings expressed in this presentation are those of the author(s) and do not necessarily reflect those of the Department of Justice.

Signal conflict in hominin phylogenetic reconstruction

JOANNA R. GAUTNEY

Department of Sociology and Anthropology, Weber State University

The validity of phylogenetic reconstructions is a contentious debate in paleoanthropology. The analytical tools used in most analyses have limitations that make exploring evolutionary relationships between paleospecies all the more difficult. Previous examinations of the issue have assessed the relative reliability of characters by cranial region and have indicated that certain regions of the cranium may be more reliable than others in reconstructing phylogenies. This study consists of an exploratory data analysis of fossil hominin morphological data using the network-based analytical method NeighborNet. NeighborNet produces graphs that give a clear indication of the degree of conflict present in a dataset. 198 craniodental characters are divided by cranial region (dental characters, masticatory characters, the vault, basicranium, face, and temporal bone), then each cranial region is analyzed using the NeighborNet algorithm. Levels of character conflict present in each region are then compared to one another. Results strongly indicate that of the six regions analyzed, the highest levels of signal conflict are present in the masticatory and facial characters. By contrast, the lowest levels of conflict are present in the dentition, basicranial and temporal regions. This suggests that because of their relative plasticity, masticatory and facial characters may be unreliable indicators of phylogeny and that future attempts at phylogenetic reconstruction could benefit by their omission.

Isotopic Analysis of modern human tooth enamel

LILY M. GEORGIEVSKI[1], AMANDA N. FRIEND[2], GEORGE D. KAMENOV[3], GARY I. ALTSCHULER[4] and JOHN S. KRIGBAUM[1]

[1]Department of Anthropology, University of Florida, [2]SNA International in support of DPAA Hawaii, [3]Department of Geological Sciences, University of Florida, [4]Altschuler Periodontic and Implant Center

The Bone Chemistry Lab Tissue Bank at the University of Florida (IRB #201900952) was established to provide baseline tooth enamel isotope data from modern patients with known life history and provenance. These data can help

with georeferencing human remains that ultimately may aid in forensic investigation. This research provides the unique opportunity to look at modern humans of known age and origin to test for congruency amongst published regional isoscapes in the continental United States. In this paper, we present bulk carbon and oxygen isotope ratios for prepared tooth enamel samples from 25 individuals who participated in this pilot study. With respect to the total sample (N=33), $\delta^{13}C$ averaged -9.3±0.97‰ (-7.7 to -12.3‰) and $\delta^{18}O$ averaged -3.7±0.92‰ (-6.0 to -2.5‰). Age cohort was established for different teeth assayed, and four individuals have data for more than one cohort (0-3 yrs, 3-6 yrs, etc.). Carbon values are consistent with a North American supermarket diet, although one individual from the UK was a true outlier, significantly depleted in ^{13}C. Oxygen values were converted to compare tooth data with interpolated oxygen maps of observed meteoric and tap water $\delta^{18}O$ from the published literature. For those individuals (N=20) born in the continental United States, calculated $\delta^{18}O$ for drinking water values ranged from -9.3 to -3.6‰ and are congruent with published isoscapes. This work contributes to the growing body of data to better understand the efficacy of geospatially distributed isotopes for provenancing human remains.

Impact of the COVID-19 on the Health and Wellbeing of 2SLGBTQ+ Peoples Living in Toronto: A Biocultural Analysis

JAMES K. GIBB[1,2], SARAH WILLIAMS[3], KASPARS MIKELSTIENS[2], LEELA MCKINNON[4], LAURA BEACH[4], JADA CHARLES[2,6], ZARIN TASNIM[4], PAM TSUI[5], LUSEADRA MCKERRACHER[7] and JESSICA FIELDS[2,5]

[1]Department of Anthropology, Northwestern University, [2]Department of Health & Society, University of Toronto Scarborough, [3]Department of Anthropology, Brown University, [4]Department of Anthropology, University of Toronto, [5]Department of Sociology, University of Toronto, [6]Department of Sociology, University of British Columbia, [7]Aarhus Institute for Advanced Studies, Aarhus University

The impact of the coronavirus disease 2019 (COVID-19) pandemic and the public health measures put in place to control COVID-19 transmissions (e.g., social distancing, self-isolation) is heterogenous, with greater consequences among populations experiencing social, economic, and political marginalization, including members of the 2-Spirit, Lesbian, Gay, Bisexual, Trans, Queer, (2SLGBTQ+) community. Using a biocultural approach, we examine the mental health impacts of the COVID-19 pandemic using data from a mixed methods study of 455 self-identified 2SLGBTQ+ adults living in Toronto, Ontario, Canada, collected from March 2021 to July 2021. Participants were recruited using respondent-driven sampling to complete an internet-based survey including measures of psychological distress and minority stress. A subset of participants (n =44) completed a semi-structured qualitative interview to contextualize their mental health experiences during the COVID-19 pandemic. Bivariate analysis revealed that self-reported anxiety (P= 0.029), depression (P = 0.001), perceived stress (P = 0.002), and somatic symptom scores (P = 0.014) were elevated among participants who reported living with family during the pandemic. These differences persisted in regression analysis adjusting for sexual identity, gender expression, race/ethnicity, age, citizenship, education, household size, and income. Our findings offer important insights that will enable Toronto and other Canadian public health agencies to better respond to the needs of 2SLGBTQ+ and other vulnerable communities during ongoing COVID-19 pandemic and future health crises.

Funded by the Toronto COVID-19 Action Initiative (Grant #508850), the University of Toronto Scarborough, and the University of Toronto.

External auditory exostoses as an aquatic activity marker in South Africa: were Later Stone Age coastal foragers diving for resources?

VICTORIA GIBBON[1], TASHNEEM HARRIS[2], BRONTE DAVIES[1], ELIZABETH DINKELE[1] and JUDITH SEALY[3]

[1]Division of Clinical Anatomy and Biological Anthropology, Department of Human Biology, University of Cape Town, [2]Department of Otolaryngology Groote Schuur Hospital, University of Cape Town, [3]Department of Archaeology, University of Cape Town

External auditory exostoses (EAE) are caused by repetitive aquatic activities, especially in cold water, exacerbated by exposure to cold winds. Building on a single published observation of EAE in a South African coastal forager dated to ca 2300 BP, we analysed the external auditory meati of 152 Late Holocene individuals to assess the frequency and distribution of EAE. Compared with contemporary populations in Cape Town, in coastal foragers the tympanic rings of the external auditory meati were observed to be short and wide. This finding requires further quantification and morphometric analysis. 74% (112/152) individuals studied were from the coast. EAE, prominent tympanomastoid and tympanosquamous sutures were identified in 4% (5/112) of the young to middle-aged adults in the coastal sample, specifically one female from the south coast and four males from the west coast. EAE were found in 3% (3/112) of coastal individuals. This is likely due to exposure to the cold waters of the south Atlantic, and strong winds. All five individuals were radiocarbon dated to 3220-900 BP. Since the species of shellfish, fish, crayfish, etc. found in coastal archaeological sites can be obtained from the intertidal or fringes of the subtidal zone, most archaeologists assumed coastal foragers were land-based, perhaps wading into shallow water and rock pools. The implication of our findings is that these people were also diving to obtain marine resources, with significantly increased opportunities for human impact on coastal ecosystems. This shifts our understanding of Holocene coastal adaptations in southernmost Africa.

National Research Foundation, the South African Research Chairs Initiative, and the Biogeochemistry Research Infrastructure Platform, supported by the Department of Science and Innovation of South Africa.

Mechanical properties of embryonic mouse cartilage and bone

JULIAN A. GIFFORD-MAHANY[1], SARAH N. KIEMLE[2], MIZUHO KAWASAKI[1], TIMOTHY B. TIGHE[2], KAZUHIKO KAWASAKI[1] and JOAN T. RICHTSMEIER[1]

[1]Department of Anthropology, Pennsylvania State University, [2]Materials Characterization Laboratory, Pennsylvania State University

Differences in material characteristics of cartilage and bone are primarily known through investigation of postnatal specimens but the mechanical properties of these tissue during embryogenesis are less well studied. Importantly, embryonic cartilage and bone have not been tested extensively in aqueous environments, limiting the validity of previous investigations. Our goal is to characterize the stiffness and strength of embryonic cranial bone and cartilage using atomic force microscopy. We test the hypothesis that embryonic cartilage is stronger than embryonic bone against the null hypothesis that embryonic tissue response is comparable to adult tissue in which bone is the stronger of the two tissues. *In vivo* conditions are simulated by immersing tissues in room-temperature phosphate-buffered saline before and during testing. Data are acquired using calibrated AFM probes that yield quantitative and qualitative data. Force-distance curves include data on topography, adhesion, and DMTModulus, and the latter can be transformed into Young's Modulus through models which approximate the shape of the AFM probe, including the Sneddon model. Calcified tissue intended for testing is verified on the micro scale using AFM topography and on the macro scale using calcein dye. Each 2 square micron topographical image is accompanied by 16,384 force versus distance curves which yield a value for modulus of elasticity. Data show DMTModulus values ranging from approximately 200 kPa to 7.7 MPa for cartilage and 120 kPa to 3.0 MPa for bone providing preliminary data indicating that cartilage varies more than bone and may be significantly stronger than bone in mouse embryos.

This work is supported in part by NICHD/NIH grant P01HD078233 and NIDCR/NIH grant R01DE027677.

Ground reaction force and contact time improve energetic expenditure prediction

CRISTINA M. GILDEE[1], ALEXANDRA G. HAMMERBERG[3] and PATRICIA A. KRAMER[1,2]

[1]Department of Anthropology, University of Washington, [2]Department of Orthopaedics and Sports Medicine, University of Washington, [3]R&D Engineering, Hy5

Energy devoted to movement cannot be used for maintenance or reproduction; therefore, understanding the evolution of bipedal walking requires the estimation of the energetic expenditure (EE) of locomotion. Because measuring EE directly is invasive, expensive, and difficult for subjects, the development of predictive formulae is critical. Mass and velocity can be used to predict 60-80% of the variation in EE within and between species, but the predictiveness of other variables (e.g. limb morphology) has proven ephemeral. Biomechanical proxies of EE, such as contact time and ground reaction forces (GRFs), are promising because the duration and intensity of muscle activation during stance have a direct metabolic cost. The value of contact time and GRF for predicting EE in human walking, however, remains untested. Here we explore whether contact time and/or GRFs improve EE prediction in level walking over models that utilize mass and velocity alone.

EE and GRFs were gathered from 15 healthy female participants during level treadmill and overground walking trials conducted at multiple self-selected velocities. Using clustered, multiple regression analysis, we found that contact time ($p<0.001$) and the anteroposterior component of the GRF ($p=0.003$) are significant predictors of EE in a model that includes mass and velocity ($r^2=0.80$).

Contact time and anteroposterior GRFs improve the predictions of EE in level walking, but hominins undoubtedly moved in other conditions (e.g. over uneven terrain, on gradients, with burdens). Future work will investigate the efficacy of biomechanical variables to predict EE.

The impacts of exercise routine disruptions on postpartum depression risk during the COVID-19 pandemic among individuals living in the United States

THERESA E. GILDNER[1] and ZANETA M. THAYER[2,3]

[1]Department of Anthropology, Washington University in St. Louis, [2]Department of Anthropology, Dartmouth College, [3]Ecology, Evolution, Environment & Society Program, Dartmouth College

The COVID-19 pandemic has negatively affected physical and mental health worldwide. New parents exhibit an elevated risk for depression compared to the general public, a pattern expected to have been exacerbated by the pandemic. Certain lifestyle factors, including moderate exercise, may support postpartum mental health, but it is unclear how the prolonged pandemic has impacted these associations. Here, we test whether pandemic-related exercise routine disruptions and reduced physical activity in the previous three months are associated with higher postpartum depression scores. This study used data from the COVID-19 And Reproductive Effects (CARE) study, an online convenience survey of U.S. participants. Third wave data collected from participants at least five months postpartum were used (n = 233). Linear regression analyses assessed whether reported COVID-19-related exercise disruptions or reductions were associated with depression score, measured using the Edinburgh Postnatal Depression Survey. Participants who reported exercise disruptions exhibited significantly higher depression scores compared to those reporting no changes (B = 1.3, p = 0.024). However, reduced physical activity in the past three months was not significantly related to depression score. These results suggest that the ability to maintain an exercise routine during the pandemic may support postpartum mental health. Interestingly, it appears that control over routine – rather than decreased physical activity – was an especially important factor. Moreover, high postpartum depression scores are biologically relevant, potentially impairing parental wellbeing, while also influencing infant growth and development. Additional work is needed to test how pandemic-associated disruptions, including to exercise, may have intergenerational effects.

Support: Claire Garber Goodman Fund in the Department of Anthropology at Dartmouth College

The modernity that wasn't: The archaic state of contemporary human origins

MICHELLE M. GLANTZ[1], SHEELA ATHREYA[2] and ADAM VAN ARSDALE[3]

[1]Anthropology, Colorado State University, [2]Anthropology, Texas A & M University, [3]Anthropology, Wellesley College

Identifying biological and behavioral modernity has been the animating force driving late Pleistocene paleoanthropological research for the past four decades. It is invoked to explain and model the appearance of *Homo sapiens*, and is the gold standard for identifying our species in the fossil, archaeological, and even ancient genomic record. Yet, "modernity" is not an evolutionary concept, nor is it commonly shared among organismal biologists and others who study evolution. The notion of "anatomically modern humans" privileges specific geographic and historical definitions of "modernity", and discussions of our "origins" are largely atheoretical and discovery-driven, rendered without regard to the contextual specificity of the evolutionary landscapes of the late Pleistocene. These biases are vestiges of the discipline's colonial past, difficult to escape because of deference to existing frameworks and an arcane, often unconscious reliance on typological methods of analysis. Here we provide an alternative framework that deconstructs the dominant model of human origins, highlighting evidence drawn largely from areas viewed as peripheral to the evolutionary events that currently describe the origins of bio-behavioral modernity. These datasets make clear that the bio-behavioral changes occurring among late Pleistocene humans are profound but not spatiotemporally uniform in character or process. The alternative empirical approach we describe abandons searching for a type, and instead emphasizes processes that can account for the known variability and complexity of human evolution during the late Pleistocene. "Becoming modern" is an insufficient universal guide for understanding, or standard for studying, the evolutionary record of humans.

Exploring Interrelationships at the Qinifab School Site, Sudan

KANYA GODDE[1], BRENDA J. BAKER[2] and JAIME ULLINGER[3]

[1]Anthropology Program, University of La Verne, [2]Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona State University, [3]Anthropology Program, Quinnipiac University

Sixty-eight cranial and 17 dental nonmetric traits from 67 adults were analyzed to explore intracemetery relationships at the Qinifab School Site (UCSB 03-01 and 03-02) in northern Sudan, used from the late Meroitic through Christian periods (ca. 250-1440 CE). Fifteen cranial and seven dental nonmetric traits had adequate sample sizes for inclusion. Missing data were imputed with the MissForest algorithm, a random forest machine-learning multiple imputation method. A *k*-modes clustering algorithm (k=3) was applied to the categorical skeletal and dental data to ascertain membership for three potential clusters. A time period variable was included to help classify individuals due to the large timespan represented. The resulting three clusters roughly sorted by time period. Older late Meroitic to Post-Meroitic individuals dominated Cluster 3, while Clusters 1 and 2 were a mix of mostly Post-Meroitic and Christian period individuals. Plotting on site maps shows that Clusters 1 and 3 spread from southwest to northeast. Cluster 3 occupies nearly all the west end (UCSB 03-02), extending minimally into the eastern portion (UCSB 03-01) of the cemetery. Cluster 2 includes the largest Post-Meroitic tumuli, which encircle the more centrally located individuals in Cluster 1. Cluster 1 burials, in contrast, were in smaller tumuli or unmarked subsurface graves. By the early Christian period, rock cairn graves of both Cluster 1 and 2 individuals predominate. The

patterning suggests a founding group (Cluster 3) that was largely supplanted by Cluster 2 individuals anchoring the eastern portion of the cemetery in the most prominent tumuli.

This research was supported by an Arizona State University Center for Bioarchaeological Research Pilot Study grant to the authors.

Quantifying Variation in Palate Shape among Three Modern Populations using Elliptical Fourier Analysis

CHRISTOPHER M. GODEN[1] and ALICE F. GOODING[2]

[1]Skeletal Biology Research Laboratory, Injury Biomechanics Research Center, The Ohio State University, [2]Bone Biomechanics Laboratory, Department of Geography and Anthropology, Kennesaw State University

Methodologies for the estimation of population affinity involve the use of macroscopic trait observation. While methods exist that identify the frequency of expression of character states consistent with specific population groups, research investigating quantifying the amount of variation that exists in macroscopic traits is still needed. This study investigates the variation of maxillary palate shape of the human craniofacial complex among three modern population groups utilizing Elliptical Fourier Analysis (EFA). Computed tomography scans of 180 individuals of Black, White, and Hispanic population affinities were obtained from the New Mexico Decedent Imaging Database and were used to construct 3D volume renderings of the cranium. Following construction of a volume rendering, images of each palate were taken and were then outlined using a landmark-based approach. Resulting outlines were quantified using EFA to obtain shape quantification and then analyzed using Principal Component Analysis (PCA). EFA and PCA data were then further subjected to statistical analyses to assess for variation within and among population groups. Results of ANOVA testing failed to identify significant variation across the three population groups in this study ($p>0.05$). PCA results and subsequent reconstructed contours demonstrate that variation expressed within and between groups are visually similar exemplifying that the variation in expression of the palate shape is more complex than previously understood. Moreover, findings of the PCA analysis suggest that palate shape of modern individuals may be more informative the individual level rather than at the population level.

Geospatial distribution in age at menarche

CLAIRE L. GOLD[1], CATHERINE KITRINOS[1], LYNNETTE L. SIEVERT[1] and JASON KAMILAR[1,2]

[1]Department of Anthropology, University of Massachusetts, Amherst, [2]Department of Organismic and Evolutionary Biology, University of Massachusetts

Menarche, a key life history event that shapes the female reproductive trajectory, is important to the study of human evolutionary biology because of the associated epidemiological and social outcomes. Using secondary analysis of data collected from Saffa et al. (2019), we examined the effects of geospatial distribution and climate variables in relation to age at menarche for modern human populations. We applied linear modelling and the sum of AICc weights to determine which factors (demographic and climatic) were the strongest predictors of age at menarche. We found that the strongest predictor of a later age at menarche was fertility, followed by mean age at death (mortality), then precipitation seasonality, and then annual rainfall. Climatic factors, such as precipitation variability and amount, may provide an important role in explaining variation in age at menarche. Populations living in areas with high precipitation variability—as well as tropical geographic locations with heavy seasonal rainfall—may be more likely to suffer from intermittent food or water scarcity, water-borne diseases such as malaria and cholera, undernutrition, and tropical storms. We propose that later age at menarche in populations with high annual seasonal rainfall is a life-history strategy developed in response to climatic conditions that result in high allostatic load and the prioritization of growth and maintenance by females rather than reproduction.

Molecular signatures of aging in the rhesus macaque liver

ELISABETH A. GOLDMAN[1], KELLI L. VAUGHAN[2], MAILI SMITH[1], SAM WARD[3], KIMBERLY A. NEVONEN[3], BRETT A. DAVIS[3], NOAH SNYDER-MACKLER[4,5], JULIE A. MATTISON[2], STEVEN G. KOHAMA[6], LUCIA CARBONE[3,7] and KIRSTIN N. STERNER[1]

[1]Department of Anthropology, University of Oregon, [2]National Institute on Aging, National Institutes of Health, [3]Department of Medicine, KCVI, Oregon Health and Science University, [4]Center for Evolution and Medicine, Arizona State University, [5]School of Life Sciences, Arizona State University, [6]Division of Neurobiology, Oregon National Primate Research Center, [7]Division of Primate Genetics, Oregon National Primate Research Center

Environmental variables such as diet can alter how we age, but the mechanisms through which these changes are accomplished remain largely unknown. Because the rate of aging is not uniform across organs and tissues, tissue-specific analyses are necessary to elucidate variation in rates of age-related decline in organs with distinct physiological roles. Here we focused on the liver, which plays a central role in metabolic regulation, to construct a liver-specific epigenetic clock and characterize age-related DNA methylation changes. We generated methylation data from 96 banked rhesus macaque liver samples (ages 3-33 years, roughly equivalent to ages 9-99 years in humans) using reduced representation bisulfite sequencing (RRBS). We built a liver-specific clock model that predicted age with high accuracy ($r = 0.94$, median absolute deviation [MAD] = 1.74 years) and are currently examining how dietary restriction influences the course of molecular aging. Our preliminary analyses identified 455 genomic regions (FDR<0.1) exhibiting significant differences in methylation status between the youngest (3-5 years) and oldest (20 years and older) age groups. Of 103 differentially methylated promoter regions, 72% were hypermethylated with age. Hypermethylated promoter regions were enriched for genes involved in the arginine and proline metabolism KEGG pathway (GO term and KEGG pathway enrichment analysis, FDR<0.1). Our study provides a useful biomarker of biological aging and will help characterize how diet affects the aging process as well as the ways in which aging-related epigenetic change manifests uniquely in the liver.

Funding provided by the National Science Foundation (Award # BCS-1920350), the Intramural Research Program of the National Institute on Aging, the ONPRC (P51 OD 011092), and the University of Oregon.

Preliminary Investigation of Relationships between Sex, Body Size, and Inorganic Content of Human Tibiae

CARLA L. GOLDSMITH, ANGELA L. HARDEN and MANDY AGNEW

Injury Biomechanics Research Center, The Ohio State University

Bone ashing, a method that treats bone at 600˚C for 18 hours, has been used to quantify inorganic bone content ex-vivo. Previous studies identified relationships between mechanical properties and inorganic bone content utilizing this technique. However, relationships between sex and body size with inorganic bone content, specifically percent mineralization, have not been investigated. Percent mineralization (ash weight/dry weight) quantifies mineral content (i.e., calcium, magnesium, and other minerals) in relationship to the sample. The objective of this research is to identify if relationships exist between sex and body size in comparison to percent mineralization of ashed human tibiae. Ashing samples (N=16) were acquired from the distal 15% site of each tibia, which was determined from the total length excluding the medial malleolus. All samples were ashed following methods developed from previous studies, and percent mineralization was calculated for each sample (Min=61.1%, Max=68.2%, M=65.5%, SD=0.0269). Graphical trends displayed the highest average percent mineralization for 75th percentile females (M=66.6%) and the lowest for 5th percentile females (M=64.9%), leaving 50th percentile males in the middle (M=65.1%). Two-sample t-tests revealed no significant differences in percent mineralization between sexes (N=8 male, N=8 female; $p=0.363$) nor between body sizes ($p=0.318$; 50th percentile males, N=8;

75th percentile females, N=5; and 5th percentile females, N=3). These preliminary findings suggest that sex and body size do not have a relationship with percent mineralization. Future research will explore relationships between inorganic content and histomorphometric variables (i.e., porosity, cross-sectional geometry) to evaluate which intrinsic variables influence variation in mineralization.

Severity measures of dental lesions

JESSICA C. GOMEZ[1], CLAIRE A. KIRCHHOFF[1], SIOBHÁN B. COOKE[2,3] and CLAIRE E. TERHUNE[4]

[1]Department of 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

Like humans, nonhuman primates suffer from dental diseases, analysis of which helps place public health concerns in a broader context. Previous studies have documented craniodental lesion rates in some primates, but how disease progress/severity affects overall health is more difficult to assess. We evaluated lesion severity measures in *Macaca fascicularis* (n=110) and *Papio anubis* (n=76) to determine whether this provides information beyond presence/absence data. We evaluated skulls for evidence of TMJ osteoarthritis (OA), antemortem tooth loss, dental abscesses, pulp cavity exposure, caries, and alveolar recession according to standard criteria. Severity measures include the percentage of teeth lost antemortem (%AMTL), percentage of remaining teeth with pulp cavity exposure, the percentage of alveoli with evidence for abscesses (%abscess), the combined maximum diameter of carious lesions per individual in macaques, and the maximum diameter of the largest abscess fistula in baboons. Using nonparametric tests in SPSS, we evaluated covariation in lesion presence/absence and severity measures. In both species, there were significant associations between presence/absence of several lesion types ($p<0.05$). Severity measures also demonstrated additional associations not detected by presence/absence data. In *Macaca*, TMJ OA was associated with %AMTL ($p=0.028$) and %abscess ($p=0.024$). The relationship between presence of pulp cavity exposure and caries area was also significant ($p=0.042$). In *Papio* males, abscesses and %AMTL were associated ($p=0.013$), as were %abscess and AMTL ($p=0.029$). Severity measurements for craniodental lesions may provide additional information on dental disease in primates.

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

Variation in jaw and tongue kinematics with dietary grit in tufted capuchins

KATYA GONZALEZ[1], MICHAEL C. GRANATOSKY[2], JOSE IRIARTE-DIAZ[3], CALLUM F. ROSS[4] and MYRA F. LAIRD[5]

[1]Department of Human Biology, University of Southern California, [2]Department of Anatomy, New York Institute of Technology, [3]Department of Biology, University of the South, [4]Department of Organismal Biology and Anatomy, University of Chicago, [5]Department of Integrative Anatomical Sciences, University of Southern California

Dietary grit features prominently in discussions of dental microwear formation but the effect of grit on tongue movement has not been investigated. The tongue plays a key role in detecting and moving grit particles around the mouth, mitigating damage to occlusal surfaces, but the extent to which tongue and jaw movements are differentially impacted by the presence of grit is unknown. We examined the effect of dietary grit on jaw and tongue kinematics of three female tufted capuchins (*Sapajus apella*). We hypothesized that the tongue undergoes greater kinematic variation compared to the jaw in both gritty and clean foods. Additionally, we hypothesized that foods containing grit of larger particle sizes would elicit greater kinematic variation at the apex and anterior tongue compared to the posterior tongue.

We tested these hypotheses in 116 gape cycles recorded using bi-planar videoradiography and the X-ray Reconstruction of Moving Morphology (XROMM) workflow. Subjects were fed cubes of Jell-O containing no grit or 10 ml of silt-like (75 microns), sand-like (180 microns), or granular (1400 microns) grit. Kinematics of the jaw and tongue were measured relative to the fixed cranium. Our results suggest the tongue undergoes greater displacement compared to the jaw, and that dietary grit influences both jaw and tongue kinematics. Additionally, the anterior tongue exhibits greater variation compared to the posterior. These results suggest the tongue, particularly the anterior section, may play a key role in food and grit movement within the mouth influencing dental microwear formation.

This research was supported through the National Science Foundation (NSF-BCS-1440516, NSF-BCS-1440541, NSF-BCS-1440542, NSF-BCS-1440545, NSF-BCS-1627206) and the AAPA Cobb Award.

DNA Survival in Water Immersion for Forensic Identification Applications

ASHE L. GOODEN-HERMAN and HANNAH E. MARSH

Department of Anthropology, University of Central Missouri

DNA recovery is crucial to forensic anthropology and is frequently the basis for a positive identification of skeletonized remains. However, DNA survival in exposed remains is highly impacted by the depositional environment. Whereas DNA does degrade over time, water, and other harsh environments, can lead to a greater decrease in DNA survival. This research seeks to document DNA survival from a Central Missouri lake to compare not only the concentration of DNA but also the efficiency of a DNA extraction strategy that is available and cost-effective for investigators. Two pig hemimandibles were immersed in a lake for two months, and two hemimandibles were preserved in a freezer for the same timeframe. After the exposure period, the mandibles were sampled for DNA using the DNEasy Blood and Tissue kit. The goal was to assess whether the post-exposure DNA concentration in bone met thresholds for positive identification sequencing. DNA survival levels in both the immersed and frozen samples were lower than a fresh specimen, although there was no statistically significant difference between the immersed and frozen samples. Importantly, in the majority of samples, enough DNA survived after the two-month exposure to hypothetically be sequenced for a positive identification. In cases of longer immersion, we hypothesize that there could be a dramatic decrease in DNA survival. Pertaining to short-term immersion, this research shows that bone can retain an adequate amount of DNA, which could be sequenced and result in a positive identification in forensic work.

3D Genomic Strategies to Understand Complex Trait Genetic Architecture

STRUAN F.A. GRANT

Department of Pediatrics, University of Pennsylvania

We are employing cutting-edge 3D genomic approaches to facilitate understanding of genetic loci for common complex disease, including for bone-related traits. We are leveraging genome wide association study (GWAS) signals to discover effector genes involved in regulating bone formation and resorption. While numerous GWAS efforts have been successful in discovering key genetic variants associated with bone mineral density (BMD) and fracture, including our own efforts in children, GWAS only reports genomic signals associated with a given phenotypic trait and not necessarily the precise localization of culprit effector genes. Approaches are now emerging to make these determinations.

We recently published our high-resolution genome-wide 'variant to gene mapping' efforts, where we integrated RNA-seq, ATAC-seq and promoter-focused Capture C in primary human osteoblasts to implicate culprit effector genes for osteoporosis, including validating two novel effector genes, *EPDR1* and *ING3*. However, many GWAS loci remain to be resolved, so in order to uncover additional aspects of the genetic architecture of bone density determination we are now studying temporally specific roles that are dependent on the stage of differentiation

In the absence of robust public domain genomic datasets for bone, our goal is to comprehensively functionalize GWAS by discovering and validating osteoblast and osteoclast genes that physically interact with key enhancers harboring putatively causal SNPs involved in regulating BMD and fracture risk, thus representing the genomic basis for osteoporosis. The ultimate aim is to provide the bone community with new, high value targets to aid in understanding mechanism, and eventually therapies, for osteoporosis.

R01 HD100406 R56 AG072705

Inclusive fitness, age differences, and the dynamics of sibling relationships in mountain gorillas

NICHOLAS M. GREBE[1], JEAN PAUL HIRWA[2], TARA S. STOINSKI[2] and STACY ROSENBAUM[1]

[1]Department of Anthropology, University of Michigan, [2]Karisoke Research Center, Dian Fossey Gorilla Fund International

Sibling relationships vary greatly in form and function across animals. Among long-lived organisms, siblings may reside with each other for many years and differ considerably in age, providing the foundation for dynamics of affiliation and agonism that vary across temporal dimensions. Additionally, social systems can influence the sex composition and relatedness of sibling dyads, introducing additional axes of variation with potential relevance for dyadic interactions. We examine these factors in a population of wild mountain gorillas (*Gorilla beringei beringei*) monitored by the Dian Fossey Gorilla Fund's Karisoke Research Center. We present results from a preliminary dataset recording annual rates of affiliative and agonistic behavior in 83 maternal sibling pairs, and 71 age- and sex-matched non-sibling dyads that reside in the same social group. We find that full siblings spend more time affiliating with each other than half siblings, who themselves spend more time affiliating than non-siblings. Among siblings, we find only weak evidence that individuals closer in age spend more time together on average; rather, certain gregarious individuals appear to strongly drive proximity patterns, regardless of age differences. Brothers and mixed-sex siblings play with each other more frequently than do sisters, and to a lesser extent, sisters groom each other more frequently than brothers. We find little evidence that patterns of aggression differ across sibling types, likely due to the extreme rarity of these behaviors in our dataset. Our results suggest that a complex mix of sex composition, expected inclusive fitness benefits, and idiosyncratic individual differences influence gorilla sibling relationships.

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 Intersections of Sex and Inequality in a Mixed-Status Industrial London Sample

ANNA L. GREEN and CHERYL P. ANDERSON

Department of Anthropology, Boise State University

Saint Pancras Burial Ground and its inhumated priests, paupers, aristocrats, and migrants provide a unique perspective into the interactions between sex and inequality in 18th and 19th century industrial London. Frequencies of caries, dental calculus, periodontal disease, linear enamel hypoplasia, periapical lesions, tuberculosis, treponematosis, rickets, and trauma among 224 females from St. Pancras were compared to 27 low-status females from Crossbones Burial Ground and 74 primarily high-status females from Chelsea Old Church Cemetery. Based on the information known about those buried at St. Pancras, it was hypothesized that the frequencies of health indicators in St. Pancras should fall between the high and low status cemeteries.

For this research, Pearson Chi-square was used to test if differences in frequencies were statistically significant. The results show that for St. Pancras the frequencies were significantly lower ($p<0.005$) than Crossbones for caries (SP=61%, CB=88%), periodontal disease (SP=42.2%, CB=96%), periapical lesions (SP=8.7%, CB=40%), and trauma (SP=11.6%, CB=37%). Frequencies of dental calculus (SP=81%, CC=95.1%), periodontal disease (SP=42.2%, CC=67.5%), and periapical lesions (SP=8.7%, CC=31.1%) were also significantly lower ($p<0.05$) in St. Pancras compared to Chelsea Old Church. However, St. Pancras's prevalence of LEH (80.8%) was significantly higher ($p<0.05$) than Chelsea Old Church (56.1%). Overall, the individuals from St. Pancras had better dental health compared to the other two samples and lower frequencies of trauma compared to Crossbones. This suggests that circumstances, such as migration, may have uniquely affected the lived experiences of women from the St. Pancras sample when compared to other local samples.

Diverse monsoon seasonality in eastern Africa recorded by papionin tooth enamel $\delta^{18}O$

DANIEL R. GREEN[1,2], JANAÍNA N. ÁVILA[3,4], WENDY DIRKS[5], IAN S. WILLIAMS[4] and TANYA M. SMITH[3,6]

[1]Lamont-Doherty Earth Observatory, the Earth Institute, Columbia University, [2]Human Evolutionary Biology, Harvard University, [3]Griffith Centre for Social and Cultural Research, Griffith University, [4]Research School of Earth Sciences, Australian National University, [5]Department of Anthropology, Durham University, [6]Australian Research Centre for Human Evolution, Griffith University

We report seasonal tooth enamel $\delta^{18}O$ profiles from six contemporaneous papionins spanning a gradient of aridity in eastern Africa from the Ethiopian rift (n = 5 teeth), to the Ethiopian highlands (n = 2), to Ugandan forests (n = 2). Using the Sensitive High-Resolution Ion Microprobe (SHRIMP SI), serial samples from the innermost enamel demonstrate that these 17 years of c. weekly $\delta^{18}O$ measurements (n = 901) reflect the amounts and oxygen isotope composition of regional rainfall. Mean $\delta^{18}O$ values are highest in *Papio hamadryas* from the arid scrubland of the Awash rift (25.9 ‰, VSMOW), slightly lower in *Theropithecus gelada* from highlands near Derdre (24.8 ‰), and lowest in *Papio anubis* from mixed grassland and gallery forest near Rubirizi (21.6 ‰). $\delta^{18}O$ ranges are particularly useful in differentiating these hydrological regimes, with $\delta^{18}O$ values in highland papionins 2-3 ‰ lower than those in the rift. Lomb-Scargle frequency analysis of spatial $\delta^{18}O$ values transformed onto temporal scales using daily incremental features reveals dominant temporal $\delta^{18}O$ periods. Strong annual cycles are detected in all Ethiopian rift and highland teeth, but only weak cyclicity is found in Ugandan teeth, reflecting higher annual Ugandan rainfall with reduced seasonality. Particularly strong 6-month cycles are also detected in highland *Theropithecus*, a likely consequence of monsoon intensity and selective feeding by geladas on plants with $\delta^{18}O$ enrichment responsive to seasonal aridity. These data demonstrate that high resolution $\delta^{18}O$ data from primate enamel recover diverse monsoon and feeding patterns, aiding paleoenvironmental and behavioral reconstructions.

Australian Academy of Science, Australian National University, Australian Research Council (DP210101913), Griffith University, Lamont-Doherty Earth Observatory and Earth Institute at Columbia University, Harvard University, National Science Foundation (Award # 2021666).

Reassessing Clustering Parameters of Biological Affinities: Utilization of k-means to Understand Eurasian Population Variation

MADELYN K. GREEN[1], DANIEL FIDALGO[2] and MARK HUBBE[1,3]

[1]Department of Anthropology, The Ohio State University, [2]Museu de Arqueologia e Etnografia, Universidade de São Paulo, [3]Instituto de Arqueología y Antropología, Universidad Católica del Norte

Cluster analyses are useful for assessing the biological affinities and evolutionary relationships of past and present human groups. Biological clusters are commonly defined through the analysis of different types of phenotypic and genotypic data at various scales of analysis (local, regional, and global). However, the determination of the number of clusters that reflect meaningful partitions of the observed variance (i.e., the number of natural groups in the data) can be subjective. Indeed, few studies of the morphological variance of modern humans have evaluated ways in which to best identify the underlying structure of affinities among populations. To contribute to this

discussion, in this study we use the association of k-means clusters of cranial morphological data to geographic and climatic data and to evaluate the structure of biological affinity among Eurasian populations. Morphological distances among 58 Eurasian populations (3935 individuals) were calculated using Mahalanobis distances, and populations were classified in a progressive number of clusters (k=2 to 10) using k-means algorithms. The validity of cluster membership was evaluated through the ratio of geographic and average temperature distances within cluster to distances between clusters. The results show ratios declining until the populations are separated into six groups, suggesting that this is the maximum number of populations that are defined by natural geo-climatic parameters. Moreover, the ratio for geographic distances (0.302) is smaller than the ratios observed for distances (0.499), supporting previous studies which found geographic isolation as a more relevant force in the partitioning of variance in the region.

Musculoskeletal markers: A comparison of the influence of three biological factors on robusticity

MEGAN M. GREENE

Department of Geography and Anthropology, Louisiana State University

Research suggests that musculoskeletal markers (MSMs) can provide information about the lives of deceased individuals. The majority of studies focus on single factors that influence the morphology of MSMs in pre-modern societies (i.e., medieval, hunter-gatherers, pre-industrial, etc.). This study analyzes MSMs of skeletons of 72 females and 83 males from the United States whose ages at death range from 30 to 89 to understand the relationship between various biological factors and MSM morphology. Eight MSMs (attachments of pectoralis major, deltoid, brachialis, supinator, iliopsoas, gluteus maximus, quadriceps, and soleus) were analyzed and categorized as phases 0, 1, 2, or 3 depending on the degree of robusticity, with phase 0 showing no robusticity and phase 3 being the most robust. Correlational and chi square tests were used to assess the relationship of the MSMs with age, sex, and estimated body mass. Results show a positive correlation in both females and males and in both left and right bones between age and entheseal robusticity for attachments of brachialis and quadriceps muscles. Interestingly, MSMs were not significantly associated in their robusticity within individuals. No generalization can be made for the few differences between sexes and among body masses for MSM robusticity. As the robusticity of a MSM is interpreted as reflective of muscular force imposed on bone, this study suggests that females and males of "advanced" age in the United States do not differ in these forces.

Age and Inclusivity in Umm an-Nar Communal Tombs from Southeastern Arabia

LESLEY A. GREGORICKA[1], JAIME M. ULLINGER[2], CHRISTIAN BERENDS[3], ALYSSA BOLSTER[4], BRITTANY CLARK[5], HANNAH JEANLOUIS[6], URVI KAUL[7] and RACHAEL ORKIN[8]

[1]Department of Sociology, Anthropology, & Social Work, University of South Alabama, [2]Department of Sociology, Criminal Justice, and Anthropology, Quinnipiac University, [3]Department of Anthropology, University of Michigan, [4]Department of Anthropology, Vanderbilt University, [5]Department of Sociology and Anthropology, Georgia Southern University, Savannah, [6]Department of Anthropology, University of Central Florida, [7]Department of Anthropology, University of Connecticut, [8]Department of Life Sciences, Los Angeles Pierce College

Umm an-Nar (2700-2000 BCE) tombs in the United Arab Emirates contained the commingled remains of hundreds of individuals interred across multiple generations. Archaeologists commonly reference tomb demographics as being inclusive of all ages, but this assumption is based on a handful of studies that rarely distinguish age categories beyond "subadult" or "adult." An undergraduate research training program sought to examine age distributions – and thus inclusivity in tomb membership – in greater detail, focusing on fetal and older adult age categories.

A combination of traditional and novel aging techniques were applied to bones from tombs Unar 1 (U1; MNI = 194) and 2 (U2; MNI = 410) at Shimal. Transition Analysis 3 scores for the femur, humerus, and pubic symphysis revealed older age categories not previously recognized in the region, with means ranging from 40.4-47.8 years, contrasting with an average of 31 years produced by Suchey-Brooks. Measurements identified fetuses and perinates in both tombs using the basilar (U1: 5; U2: 10), petrous (U1 left: 29; U2 right: 33), and distal femur (U1 left: 5; U2 left: 11), some as young as 20-22 fetal weeks. MicroCT scans of suspected fetal humeri (U1: 10; U2: 14) revealed a lack of bioerosion, confirming that stillborn infants were permitted access to tombs. These data substantiate the presence of very young and older adults in both tombs, and demonstrate that despite subsistence and environmental changes tied to increasing social stratification during this period, no age group was separated from the larger community in death.

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

Bulk Isotopic Paleodietary Reconstructions of the Mammalian Communities of the Ngorora Formation (Tugen Hills Succession, Baringo Basin, Kenya)

ELLIOT GREINER[1], JOHN KINGSTON[1] and WILLIAM J. SANDERS[1,2]

[1]Department of Anthropology, University of Michigan, [2]Museum of Paleontology, University of Michigan

The Ngorora Formation of the Tugen Hills Succession (Baringo Basin, Kenya) spans 13.0-8.5 Ma, and has yielded fossil mammalian assemblages, including primates, from an interval poorly documented in Africa. Based on isotopic analyses of fossil tooth enamel collected over the past fifty years by the Baringo Paleontological Research Project (BPRP), paleoenvironmental and dietary reconstructions were generated for the terrestrial, large-bodied mammalian herbivore guilds. Bulk enamel isotope profiles indicate the presence of widespread C_4 dietary ecology at 9.5 Ma, providing provisional support for a hypothesized expansion of C_4 grasslands in East Africa at ~10 Ma, based on n-alkane data. Equid dental enamel records the most enriched $d_{13}C$ values in the Ngorora Fm. (ranging from -8.3 to -0.5 ‰), starting after 10 Ma, while hippopotamids (-11.1 to -2.7‰), rhinocerotids (-10.0 to -7.2‰), and bovids (-11.2 to -6.3‰) maintain less $d_{13}C$ enriched, but variably mixed C_3/C_4 feeding signatures. Suids (-10.8 to -8.9‰) and proboscideans (-11.2 to -8.8‰) exhibit even less enriched $d_{13}C$ values than other guilds, consistent with interpretations of browsing-adapted molar morphologies. Compared with previously published $d_{13}C$ enamel isotopic data from the Tugen Hills Succession's Lukeino Fm. (6.0-5.6 Ma), the Ngorora Fm. reveals a greater proportion of C_3 plants in mammalian diets, indicating that ecosystems in the Baringo Basin experienced increased exploitation of C_4 biomass during the Middle to Late Miocene, preceding the more generalized patterns of C_4 mammalian dietary ecology that coincided with the diversification hominins in the Plio-Pleistocene.

The head remains stable when locomoting on unstable suprastrates in *Hylobates lar*

NEYSA GRIDER-POTTER[1], RYOSUKE GOTO[2], TETSUYA SHITARA[3], KENJI OKA[4] and YOSHIHIKO NAKANO[3]

[1]Department of Cell Systems and Anatomy, University of Texas Health San Antonio, [2]Faculty of Health Sciences, Gunma Paz University, [3]Graduate School of Human Sciences, Osaka University, [4]School of Rehabilitation, Osaka Kawasaki Rehabilitation University

Visual and vestibulocochlear organ functions require head stability in order to facilitate safe, efficient locomotion through complex, arboreal environments. Compliant tree branches are a component of that complexity. Previous work

has demonstrated how primates use postcranial behavioral strategies, like increasing elbow flexion, to increase whole-body stability on unstable substrates. However, the head also has an important locomotor function. Because compliant substrates are riskier, they should require greater visual information and, therefore, smaller head ranges of motion to navigate them. If the angular motion is facilitating gaze fixation on the substrate, there should be a directional correlation between linear and angular movement (when the head moves up in space it angles downward).

We tested these predictions in *Hylobates lar* (n=1) during brachiation on compliant, PVC and stiff, metal poles. Cranial landmarks lateral canthus, tragion, and external occipital protuberance were marked. Gait cycles were filmed with five cameras at 120fps and markers digitized using DLTdataviewer and angular motion calculated in MatLab. Linear mixed models demonstrate neither linear or angular head motion changes significantly with suprastrate. Normalized cross-correlation analysis showed a strong correlation between superior-inferior linear motion and head pitch during locomotion. Both the stability of the head, regardless of suprastrate, and the strong correlation between linear and angular motion highlight the importance of head stability and visual feedback while locomoting and also suggests that forelimb kinematics and neck muscle activity may differ between suprastrates in order to stabilize the head.

This study was supported by the Japan Society for the Promotion of Science (PE18761).

The Relationship Between Alzheimer's Disease Memory Symptoms and Caregiver Burden Differs in Mexico and the United States

ERIC E. GRIFFITH

Samuel DuBois Cook Center on Social Equity, Duke University

Past research, including some biocultural anthropology, has documented ways in which the relationship between a person living with Alzheimer's disease (PLwAD) and a familial caregiver has a bi-directional effect on both AD symptoms and caregiver burden. This project investigates whether caregiver perception of memory impairment aligns with the symptoms experienced by the PLwAD, and how that relationship affects perceived burden.

Methods: Sixty-two caregivers of PLwAD were interviewed across field sites in Springfield, Massachusetts and Puebla, Mexico over a span of 24 months. The caregivers lived with a family member who had a diagnosis. The PLwAD was also interviewed and a battery of neuropsychological questionnaires were used to catalog symptoms. Interviews were open-ended, lasting 2-4 hours, and included questions aimed at identifying the impact that memory loss in diagnosed individuals had on caregivers.

Results: Level of memory impairment, as measured by both neuropsychological testing and subjective reporting, did not differ between the United States and Mexico but perceived caregiver burden attributed to memory symptoms (i.e., "forgetting") did differ between the two field sites. Additionally, caregiver descriptions of what individuals diagnosed with Alzheimer's "forgot" and "did not forget" differed between the U.S. and Mexico.

Caregiver experiences, especially perceived burden, play a crucial role in both the creation and management of AD symptoms. Differences in the effect that "forgetting" has on familial caregivers has important implications for both how the public health effect of AD may vary cross-culturally, and also on what interventions will be most effective at a given location.

Partially funded by a Wenner Gren Dissertation Fieldwork Grant (#9279).

'What big teeth you have!': Cervicometric Approaches to Sex Estimation of Juveniles

MAURA K. GRIFFITH

Institute of Archaeology, University College London

Effective methods for juvenile sex estimation continue to evade bioarchaeologists. Biomolecular methods, such as aDNA and peptide analysis, are promising for individual cases. However, these methods are difficult to conduct at scale due to cost, expertise, and need for specialized laboratories. Osteological sex estimation of juveniles is challenging due to confounding factors of growth and development. In this presentation for the invited symposium *'Advances and Challenges in the Identification of Sex and Gender in Human Osteological Contexts,'* I will outline how cervical measurements of teeth (Hillson *et al*. 2005; Pilloud and Hillson 2012) could provide a comparatively inexpensive and replicable method for estimating the sex of juvenile remains.

Dental elements, unlike skeletal elements, undergo little change after their development has finished. Their static nature combined with taphonomic resilience creates conditions where sex estimation methods have high potential for success. Utilizing cervicometrics from six different documented skeletal collections, both permanent and deciduous teeth are used to generate discriminant functions to estimate sex of juvenile skeletal remains. Teeth were entered into analysis based on tooth type (deciduous and permanent), arcade (both, maxilla only, and mandible only) and dimension (mesiodistal and buccolingual), leading to a maximum of twelve different discriminant functions. Using permanent teeth, classification functions reach a positive predictive value of 0.696 – 0.810. Classification functions using deciduous teeth reach a positive predictive value of 0.636 – 0.649. This work suggests that cervicometrics are a promising avenue for further research in juvenile sex estimation.

Learning through movement: tactile methods for interpreting muscle movement in osteology

ALICIA R. GROSSO[1], SHARON A. TOTH[2,3] and ALYSHA J. LIEURANCE[2]

[1]Department of Physical Therapy, Clarkson University, [2]Department of Anthropology, University of Pittsburgh, [3]Virginia Cooperative Extension, Virginia Tech

Undergraduate osteology coursework often focuses on students identifying, siding, and recognizing features of bones. Muscles are generally incorporated into the discussion, with focus on origin, insertion, and action. Biological anthropology students often choose to take both osteology and anatomy courses, but when it comes to muscular anatomy, the content is too repetitive. I argue here that further repeating isolated muscle actions in anatomical position without reference to realistic movements is problematic. This repetition encourages rote memorization of a muscle's basic action but leaves students struggling to extrapolate to larger body movements,. Similarly, presenting muscle attachments as origin and insertion inhibits understanding that muscle involvement differs given body positioning. This academic year (2021-2022) while teaching anatomy, I removed the terms origin and insertion, replacing them instead with attachment sites to emphasize that mobile and stable muscle ends can change. Students used kinesthetic learning by taping elastic bands between muscle attachments on articulated skeletons to interpret a muscle's role when its line of action changed and analyzed larger movements on themselves by interpreting concentric and eccentric contraction of muscle groups, while considering how body positioning affected muscle recruitment. Students were more analytical about muscle roles than previous years students, which was reflected in their overall understanding and test scores. Teaching movement, rather than isolated action, encouraged critical thinking and active learning. This deeper understanding of overall movement can better help students evaluate how movement affects skeletal features and variability, increasing and advancing interpretations for bioarcheological, paleopathological, non-human primate, and modern human studies.

Exploring angles: A new method for sex estimation using the obturator foramen

MELANIE J. GRUENSTERN

Department of Anthropology, University of Wisconsin - Milwaukee

This project sought to develop and test a new method for sex estimation using the obturator foramen of the os coxa. My sample comprised the left os coxa of 223 individuals, 112 females and 111 males, from the Hamann-Todd Osteological Collection at the Cleveland Museum of Natural History. In assessing the interior pubic angle of the obturator foramen, I was able to detect sexually dimorphic variability in angle size (measured in degrees), and then design a method to consistently find and measure the angle in question. In order to find the point of intersection, a line is first drawn from the base portion of the pubic symphysis to the obturator foramen. Utilizing a digital protractor, the specified interior pubic angle of the foramen is then measured using the point indicated as the angle vertex. Females were found to have a mean angle size of 91.9˚, with a range of 82.4˚ – 97.8˚ as the most frequent. Males meanwhile were determined to have a 121.7˚ mean angle size, and a common range of 117.5˚ – 129.6˚. Based on the sexually dimorphic ranges observed, this method and angle can be used to accurately estimate an individual's sex, and therefore further aid in sex determination in both bioarchaeological and forensic contexts where the anteromedial portion of the os coxa is recovered.

Travel funding provided by the University of Wisconsin - Milwaukee Anthropology Department.

Early-Life Dietary Experience and Frailty after Colonization and Conversion in Medieval Prussia

ARIEL GRUENTHAL-RANKIN[1,2], MARISSA RAMSIER[1], KATHERINE GADDIS[3] and ARKADIUSZ KOPERKIEWICZ[4]

[1]Anthropology, Humboldt State University, [2]Anthropology, Binghamton University, [3]Anthropology, University of Nevada, Las Vegas, [4]Archaeology and Ethnology, University of Gdańsk

Frailty is defined as the differential risk of disease and death across the lifecourse. In bioarchaeological contexts, frailty is often investigated via skeletal indicators of physiological stress. Drawing from an interdisciplinary framework, we explore the utility of incorporating early-life dietary data into traditional evaluations of archaeological frailty.

This study included 30 individuals (midpoint age-at-death: 9-65 years) from the medieval (14th-15th c.) cemetery at Bezławki, Poland. During this period, the region was inhabited by Indigenous Prussians battling prolonged colonization and conversion by the Teutonic Order during the Baltic Crusades. We assessed whether the early-life diet of Prussian individuals was related to morbidity and mortality patterns. We analyzed serial samples of collagen derived from first molars (M1) for stable nitrogen and carbon values, and compared the results with cumulative skeletal frailty scores and age-at-death.

There was a significant negative correlation between δ15N and δ13C values before the age of 5.5 and age-at-death. These results were highly significant for dietary values prior to the age of approximately 3.5 (δ15N: n=28, r2=-0.571, p=0.002; δ13C: n=28, r2=-0.503, p=0.006). No significant associations were found between early-life diet and morbidity.

These results suggest that infant and early childhood dietary experience was associated with decreased survival into adulthood but not physiological stress in the skeleton. We discuss these results with respect to the impact of dietary stress on stable isotopic values, biocultural experiences of colonization in Prussia, and the explanatory power of skeletal frailty indices.

Secondarily derived altriciality in humans: the conceptual contributions of Portmann to the Obstetrical Dilemma

NICOLE D.S. GRUNSTRA[1,2,3], NICOLE M. WEBB[4,5], ROBERT D. MARTIN[5,6] and MARTIN HAEUSLER[5]

[1]KLI, Konrad Lorenz Institute for Evolution and Cognition Research, [2]Department of Evolutionary Biology, University of Vienna, [3]Mammal Collection, Natural History Museum Vienna, [4]Department of Paleoanthropology, Institute of Archaeological Sciences, Senckenberg Centre for Human Evolution and Palaeoenvironment, Eberhard Karls University of Tübingen, [5]Institute of Evolutionary Medicine, University of Zurich, [6]Science & Education, The Field Museum

Despite being mostly precocial – the typical condition for primates – human neonates display an atypical degree of neurological immaturity and helplessness. Portmann proposed the term *secondary altriciality* for this unique condition, implying a reversal from the ancestral precocial primate condition toward the putatively ancestral mammalian condition of altriciality. The applicability of this label to humans, along with the implication that humans are born "early", has been questioned based on the lack of resemblance of human neonates to classically altricial species (e.g. most insectivores), and the fact that precociality is not a monolithic life history strategy by which human neonates can be judged. We argue, on conceptual grounds, that altriciality similarly cannot be considered a monolithic package of traits, and that the *secondarily* derived nature of human neonatal helplessness is an important distinction, which predicts an incomplete reversal to an ancestral condition. We draw on other examples, such as bats, to illustrate that mammals can show a mosaic of precocial and altricial traits. Although a broad distinction between precocial and altricial mammals can be recognized, the dichotomy is not without exceptions. We propose that the discussion around secondary altriciality as applied to humans is largely semantic, given the broad consensus that human neonates are sensomotorically underdeveloped, or, relatively "helpless." Furthermore, we demonstrate a negative relationship between percentage adult brain size at birth and absolute adult brain size in haplorrhine primates and cetaceans, suggesting that the associated degree of sensomotoric helplessness at birth is best characterized as a continuum within groups.

Molar features linked to durophagy in habitual (*Cercocebus*) and fallback (*Lophocebus*) hard-object feeders

DEBBIE GUATELLI-STEINBERG[1], GARY T. SCHWARTZ[2], MACKIE C. O'HARA[1], KAITA GURIAN[1], JESS RYCHEL[1] and W. SCOTT MCGRAW[1]

[1]Department of Anthropology, The Ohio State University, [2]Department of Human Evolution and Social Change and Institute of Human Origins, Arizona State University

How feeding and food material properties influence tooth form remain productive areas of study. For example, although all mangabeys have thickly enameled molars, *Cercocebus atys* practices durophagy year-round while members of *Lophocebus* consume hard foods only when less mechanically challenging foods are unavailable. We investigate if the demands of habitual vs. intermittent (i.e., fallback) hard-object feeding can be discerned in cercopithecid dentitions by comparing absolute enamel thickness (AET), relative enamel thickness (RET), and absolute crown strength (ACS) in microCT slices of 34 *C. atys* and 8 *Lophocebus* (*L. albigena* and *L. aterrimus*) upper molars. AET and ACS were significantly greater in *Cercocebus*, while RET was greater in *Lophocebus,* differences due, in part, to the larger size of *Cercocebus* molars relative to those of *Lophocebus*. We also created an index to quantify crown features argued to be more specifically related to durophagy than RET. The index included ACS, the ratio of linear occlusal enamel basin thickness to AET, and the ratio of linear functional cusp thickness to AET, analyzed using a bootstrapped t-test on a subsample (4 *Lophocebus* and 16 *C. atys* molars). Compared to *Lophocebus*, *C. atys* had significantly greater Z-scores for this index, primarily driven by its greater ACS and ratio of occlusal basin thickness to AET. These results tentatively support the notion that ACS and elements of enamel thickness distribution are better predictors of durophagy than RET. Our analysis further suggests that it may be possible to distinguish fallback from habitual hard-object feeders based on molar crown features.

Supported by NSF Award 1945008 to D.G.S., W.S.M., and G.S.

ABSTRACTS

Lower thoracic vertebra morphology reveals adaptations to bipedal posture and locomotion in fossil hominins

JORDAN S. GUERRA[1,2], DANIEL GARCÍA-MARTÍNEZ[3], MARC R. MEYER[4] and SCOTT A. WILLIAMS[1,2]

[1]Center for the Study of Human Origins, Department of Anthropology, New York University, New York, NY 10003, [2]New York Consortium in Evolutionary Primatology, New York, NY 10024, [3]Physical Anthropology Unit, Department of Biodiversity, Ecology, and Evolution, Faculty of Biological Sciences, Complutense University of Madrid, Madrid, Spain, [4]Department of Anthropology, Chaffey College, Rancho Cucamonga, CA 91737

The hominin thorax is adapted to efficient respiration and bipedal locomotion. How the transition from an ape-like thorax to a human-like thorax took place is not well understood. Here, we carry out three-dimensional geometric morphometric (3DGM) analyses on great ape (*Pongo*, *Gorilla*, *Pan*), modern human, and fossil hominin (*Australopithecus afarensis*, *A. africanus*, *A. sediba*, *P. robustus*/early *Homo*, *H. naledi*) lower thoracic vertebrae. A set of 36 Procrustes-transformed 3D landmarks on antepenultimate thoracic vertebrae (i.e., T10 in hominins and *Pongo*, T11 in African apes) were submitted to principal components analysis (PCA). The first principal component (PC1) is largely driven by spinous process orientation (*Pan* has a more cranially oriented spinous process than other taxa), whereas PC2 is dominated by vertebral body shape (where *Gorilla* has craniocaudally shorter, dorsoventrally deeper vertebral bodies than other taxa). We run a second PCA excluding great apes to focus on differences between modern humans and fossil hominins, which reveals that most of the variance along PC1 is explained by vertebral wedging, where *A. africanus* (Sts 14) is ventrally wedged like modern humans and the other fossil hominins demonstrate more neutral wedging. Along PC2, fossil hominins demonstrate more variation in transverse process orientation than modern humans. Whereas the australopiths fall within the distribution of modern humans, *H. naledi* (U.W. 102-036) and a fossil from Swartkrans attributable to either *P. robustus* or early *Homo* (SKX 41692) exhibit strong dorsal transverse process orientation, suggesting hyper-invagination of the vertebral column into the thorax in these specimens. Functional implications are discussed.

Differences in epigenetic aging of the prefrontal cortex and cerebellum in humans and chimpanzees

ELAINE E. GUEVARA[1,2], WILLIAM D. HOPKINS[3], PATRICK R. HOF[4,5], JOHN J. ELY[6], BRENDA J. BRADLEY[2] and CHET C. SHERWOOD[2]

[1]Department of Anthropology, University of North Carolina Wilmington, [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

The neural specializations of human-specific cognitive and behavioral adaptations may have left humans more vulnerable to age-related brain degenerative pathologies. To examine molecular aspects of human brain aging, we investigated human-specific patterns of methylation in two brain regions, the dorsolateral prefrontal cortex and cerebellum. We generated genome-wide CpG methylation data for humans, chimpanzees, and rhesus macaques. We identified human-specific methylation overlapping likely regulatory elements in both brain structures and calculated epigenetic age for humans and chimpanzees. We found human-specific methylation at genes involved in neuroinflammation and degeneration in both brain structures. These genes include *ADAM30*, which plays a role in processing amyloid precursor protein and has been previously found to be downregulated in Alzheimer's disease, and *ANKS1B*, which binds amyloid precursor protein, influencing amyloid beta protein production. We also found that both the dorsolateral prefrontal cortex and the cerebellum age epigenetically more slowly than blood in both humans and chimpanzees. However, humans appear to show faster epigenetic aging in the dorsolateral prefrontal cortex compared to the cerebellum, which is consistent with previous findings. Chimpanzees, in contrast, show comparable rates of epigenetic aging in the two brain structures. Greater epigenetic change in the human dorsolateral prefrontal cortex may reflect the protracted development of this structure in humans, as well as its greater age-related vulnerability to neurodegenerative pathology. These results highlight the plasticity of epigenetic processes across tissues and species and their potential relevance to human brain aging and etiologies of age-related brain disorders.

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).

Assessing Facets of Error in µCT Scans of Enamel to Facilitate Scan Sharing

KAITA N. GURIAN[1], MACKIE C. O'HARA[1], JESS RYCHEL[1], GARY T. SCHWARTZ[2], W. SCOTT. MCGRAW[1] and DEBBIE GUATELLI-STEINBERG[1]

[1]Department of Anthropology, The Ohio State University, [2]School of Human Evolution and Social Change and Institute of Human Origins, Arizona State University

The recent practice of sharing micro-computed tomographic (µCT) scans increases data accessibility and reduces the need for repeated scans of any given specimen. However, the use of the same TIFF stacks or DICOMs by multiple individuals for a single purpose (e.g., enamel thickness measurements) has the potential to introduce new sources of error. Here, we record sources of inter-observer error for molar enamel thickness measurements derived from the specimen, 2D slice positioning, cusp reconstruction, and measurement. Five *Cercocebus atys* UM1s were µCT scanned and TIFF stacks were produced. Two observers created mesial 2D slices, reconstructed any worn cuspal enamel, and measured 9 aspects of enamel thickness on each rendered 2D slice. Average absolute interobserver error ranged from 0.39-2.68%. EDJ length, enamel cap area, mid-crown diameter, average and relative enamel thickness (AET and RET, respectively) measurement errors were unaffected by any of the sources of error evaluated here. The specimen significantly increased BCD error. Slice maker affected BCD and dentine area measurements. Reconstruction maker affected BCD, occlusal basin diameter, and crown area measurements. While BCD error is affected by several factors, it represents the most reliable measure in our study with an absolute average error of only 0.39% (range, 0.0-0.92%). Cross-lab training, discipline-wide standards, and published descriptions of slice placement and reconstruction protocols may increase precision for the generation of comparable datasets, but we find very little error overall and feel confident that molar scans can be reliably shared and used by multiple groups, even those performing the same measurements.

Funding: Supported by NSF Award 1945008 to D.G.S., W.S.M., and G.T.S.

Differental Patterns in Burned Remains

ELIANA B. GUTIERREZ and DANIEL WESCOTT

Department of Anthropology, Texas State University

The charred body score (CBS) was developed to quantify decomposition after burning. The original study examined charred pig remains at a Crow-Glassman Stage 1 (CGS1) and tested over a relatively short period. The CBS is the sum of scores for three anatomical regions and range from 3-32, where 3 is freshly burned and 32 is dry bone. The purpose of this study was to examine decomposition rates in human remains burned in a typical indoor scene. The bodies were exposed to thermal heat for 14 minutes past smoke alarm signal. The CBS was observed on 30 occasions throughout the study period. Two of the bodies were at CGS 2 and one at stage 3. A running accumulated degree day (ADD) total was recorded throughout the study period. All three bodies decomposed rapidly during the first month but the two CGS2 bodies remained at CBS 22 throughout the second month (ADD 326-940). The body in CGS3 decomposed at a more rapid rate than the two bodies in CGS2 and reached CBS 30 (>50%

skeletonization) by 1386 ADD. The other two bodies did not reach CBS 30 until 1956 and 2493 ADD, respectively. By the end of the study period all bodies were at a CBS 32. In the original study a greater than 50% skeletonization was reached by approximately 500 ADD in the CGS1 pigs. These results suggest differential rates of decomposition based on degree of burning and that caution should be used when using CBS to estimate the postmortem interval.

This research received a grant from Texas State University: Undergraduate Research Fellowship (URF).

Human gestation length: is it truncated?

MARTIN HAEUSLER[1], NICOLE D.S. GRUNSTRA[2,3,4], ROBERT D. MARTIN[1,5] and NICOLE M. WEBB[1,6]

[1]Institut of Evolutionary Medicine, University of Zurich, Winterthurerstrasse 190, 8057 Zürich, Switzerland, [2]Konrad Lorenz Institute (KLI) for Evolution and Cognition Research, Martinstrasse 12, 3400 Klosterneuburg, Austria, [3]Department of Evolutionary Biology, University of Vienna, Djerassi-Platz 1, 1030 Vienna, Austria, [4]Mammal Collection, Natural History Museum Vienna, Burgring 7, 1010 Vienna, Austria, [5]Science & Education, The Field Museum, 1400 S Lake Shore Drive, Chicago, IL 60605, United States, [6]Department of Paleoanthropology, Institute of Archaeological Sciences, Senckenberg Centre for Human Evolution and Palaeoenvironment, Eberhard Karls University of Tübingen, Germany

Adolf Portmann (1897-1982) proposed that human gestational length would need to be more than twice the current 9 months to equip neonates with the same degree of physical, neurological and cognitive development as in non-human primates. One explanation for the delivery of the human fetus at a relatively more immature, secondary altricial stage of development is provided by the obstetrical dilemma hypothesis, as it mitigates the evolutionary conflict originating from the trade-off between the need for a capacious birth canal and selection pressures for a shortened sacroiliac-to-hip joint distance as an adaptation to bipedal locomotion.

However, human gestation length approximates that which is expected for a primate with our body size, an observation used to contest the validity of the obstetrical dilemma hypothesis. Here we show that this assumption is based on a misunderstanding of Portmann's 1941 paper, in which he did not consider human gestation length as truncated, but instead contemplated why it is not *even longer* than in great apes, given the relationship of longer gestation length with higher 'organisational complexity' among mammals. This may elucidate why genetic studies have yielded inconclusive evidence of positive selection for preterm birth in humans. Consequently, we revisit Portmann's concept that human infants continue to grow in length and body mass at the same rate as *in utero* for about a year postpartum, which he accordingly called the 'extrauterine Frühzeit', or extrauterine fetal time, whereas in non-human primates growth velocity slows down near birth.

This abstract is part of the Portmann symposium.

This project was financially supported by the Swiss National Science Foundation (grant 31003A_176319).

The Core Human Fecal Metabolome

JACOB J. HAFFNER[1,2], MITCHELLE KATEMAUSWA[2,3], THÉRÈSE S. KAGONE[4,5], EKRAM HOSSAIN[2,3], DAVID JACOBSON[1,2], KARINA FLORES[2,6], ADWAITA R. PARAB[2,7], ALEXANDRA J. OBREGON-TITO[1,2], RAUL Y. TITO[1,2], LUIS MARIN REYES[8], LUZMILA TRONCOSO-CORZO[9], EMILIO GUIJA-POMA[10,11], NICOLAS MEDA[4], HÉLÈNE CARABIN[12,13,14,15], TANVI P. HONAP[1,2], KRITHIVASAN SANKARANARAYANAN[2,7], CECIL M. LEWIS, JR[1,2] and LAURA-ISOBEL MCCALL[2,3,7]

[1]Department of Anthropology, University of Oklahoma, [2]Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, [3]Department of Chemistry and Biochemistry, University of Oklahoma, [4]Burkina Faso Ministry of Health, Burkina Faso Ministry of Health, [5]Centre MURAZ Research Institute, Centre MURAZ Research Institute, [6]Department of Biology, University of Oklahoma, [7]Department of Microbiology and Plant Biology, University of Oklahoma, [8]Instituto Nacional de Salud, Instituto Nacional de Salud, Lima, Peru, [9]Facultad de Medicina, Universidad Nacional Mayor de San Marcos, [10]Facultad de Medicina Humana, Universidad de San Martín de Porres, [11]Centro de Investigación de Bioquímica y Nutrición, Facultad de Medicina Humana, Universidad de San Martín de Porres, [12]Department of Biostatistics and Epidemiology, College of Public Health, University of Oklahoma Health Sciences Center, [13]Département de Pathologie et Microbiologie, Faculté de médecine vétérinaire, Université de Montréal, [14]Département de médecine sociale et préventive, École de santé publique de l'université de Montréal, [15]Centre de Recherche en Santé Publique (CReSP), l'université de Montréal et du CIUSS du Centre Sud de Montréal

The metabolome (the biological system of small molecules) defines the human phenotype, reflecting molecular pathways associated with human genetics, health, behavior, and environment. The range of human variation of the metabolome, and the consequences of human lifestyle on the metabolome, have only begun to be explored. Here, we used untargeted liquid chromatography-tandem mass spectrometry to analyze the fecal metabolomes of 90 human individuals from Africa and the Americas – the birthplace and last continental expansion of our species. These samples represent six distinct populations categorized into four groups based on diet, demography, behavior, and industrial influence. A total of 36,324 metabolite features were detected with 28,288 features shared by all our populations, despite geographic, dietary, or behavioral differences, thus representing a core human fecal metabolome shared by human populations. These shared metabolites were maintained across multiple filtering criteria and were all detected in a co-analysis containing 1,286 samples from 10 fecal metabolome datasets, highlighting the ubiquity of this core metabolome. We also report chemical differences along an industrialization gradient, where industrialization influence correlates with metabolomic changes. Metabolite features like leucyl-leucine and urobilin were identified as major metabolomic differences associated with these lifestyle shifts. Our results illustrate that, while there is a core metabolome maintained across human populations, a diverse range of lifestyles, behaviors, and industrialization strongly influence metabolite presence and abundance. This study represents the first characterization of the core human fecal metabolome through untargeted mass spectrometry analyses of distinct human populations and lifestyles.

Understanding women's support for patriarchal gender norms in Taiwan and China

RENÉE V. HAGEN and H. CLARK BARRETT

Department of Anthropology, University of California, Los Angeles

Many studies have found that not only men, but also women sometimes endorse norms that may be considered as patriarchal or sexist, and against women's interests. Such observations have been explained as resulting from women's socialization into a patriarchal gender ideology, resulting in their 'false consciousness'. Patriarchy likely has its roots in an evolutionary history of sexual conflict (Smuts 1995), but potential variation among women's interests in norms is often overlooked. This study attempts to critically evaluate the gendered costs and benefits of specific norms. We consider whether women themselves can sometimes benefit from supporting patriarchal norms, such as through gains from alliances with high-status men or benefits to male relatives. Also, younger women likely experience higher costs from patriarchy than older women. We tested whether these hypothesized interests are reflected in women's stated attitudes in the Chinese General Social Survey (n = 4126) and Taiwanese Social Change Survey (n = 2024). Findings show that women's views grow more patriarchal with age, and this happens faster than for men (Taiwan: β = -.07, P(β < 0) = .87, China: β = -.06, P(β < 0) = .99), suggesting this is not due to generational norm changes alone. As predicted, higher social status is associated with more patriarchal views among Taiwanese women (β = -.28, P(β < 0) = .93), although not among Chinese women. A gender-bias in children affects attitudes in Chinese (β = -.11, P(β < 0) = .94) but not Taiwanese women.

Potential association between pterion suture pattern and incidence of craniodental lesions in platyrrhines

LAUREN B. HALENAR-PRICE[1,2], CLAIRE A. KIRCHHOFF[3], CLAIRE E. TERHUNE[4] and SIOBHÁN B. COOKE[2,5]

[1]Department of Biology, Farmingdale State College (SUNY), [2]New York Consortium in Evolutionary Primatology Morphometrics Group, NYCEP, [3]Department of Biomedical Sciences, Marquette University, [4]Department of Anthropology, University of Arkansas, [5]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

It has long been recognized that there is substantial variation across primates in the pattern with which the bones articulate at pterion. Several hypotheses for why this variation exists have been proposed, but few have been systematically tested. In *Alouatta* specifically, it has also been noted that cranial sutures fuse particularly early in ontogeny. This premature suture fusion has been suggested to be pathological in nature, raising questions as to whether other variation in pterion suture pattern is also related to pathology.

Here, we investigate the association between pterion suture pattern and craniodental lesions in *Alouatta, Ateles, Cebus, Sapajus*, and *Saimiri*. While both the incidence of suture pattern (except asymmetrical individuals) and of craniodental lesions varied significantly from one taxon to the next ($p=0.005$ to <0.0001), neither rates of specific lesion types nor the general presence of lesions was associated with pterion category ($p>0.05$). Also, while there are sex differences for some lesion rates in *Alouatta*, there are no sex differences in any taxon with regards to pterion ($p>0.05$), an interesting result given that several of these taxa are sexually dimorphic in other aspects of morphology.

The lack of association seen here between variation in pterion suture pattern and incidence of craniodental lesions suggests that a pathological explanation for this variation may be less relevant. Future work should instead focus on other hypotheses such as brain size and growth, functional consequences for dissipating force during mastication, or nonfunctional explanations like genetic drift.

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

Cartilage development and the structure of craniofacial variation

BENEDIKT HALLGRIMSSON[1], JOSE D. APONTE[1,3], MARTA VIDAL GARCIA[1], DANIELA M. ROTH[2], DAVID C. KATZ[1], DANIEL GRAF[2] and RALPH S. MARCUCIO[3]

[1]Cell Biology and Anatomy, University of Calgary, [2]Dentistry, University of Alberta, [3]Orthopaedic Surgery, University of California San Franscisco

Vertebrate skulls are composed of bones that form via endochondral ossification on the one hand and intramembranous ossification on the other. The former group, the chondrocranium, forms the cranial base as well as capsules around the sensory organs of the head. It has long been recognized that the processes by which these bones form and grow are key developmental determinants of craniofacial form both within and among species. Here, we demonstrate the central importance of these processes for craniofacial shape via analyses of mutations in mice that affect growth and differentiation of cartilage. Geometric morphometric analyses of 3D microCT scan images of these mutants demonstrate the existence of an axis of covariation for craniofacial shape that is associated with modulation of cartilage growth. This axis combines variation in cranial base angle, facial length, neurocranial height and globularity as well as the orientation of the petrous temporal. These changes are largely consistent with the predictions of the spatial packing model. Interestingly, this same axis of covariation is recovered from a multivariate genotype-phenotype mapping approach to a sample of 1200 mice from the Diversity Outbred mouse panel. This work confirms earlier work by DeBeer and others that position the chondrocranium as a central determinant of vertebrate cranial form. More importantly, it illustrates how a focus on development-process determinants of craniofacial variation can provide insights into the structuring of variation by development which is central question of evolutionary developmental biology.

NIH 2R01DE019638 and CIHR Foundation grant 159920 to BH and RM; NSERC Discovery grant 238992-17 to BH

Utilizing Empirical Behavioral Indicators to Create Individualized Care Plans for Special Needs Chimpanzees (*Pan troglodytes*) at a Sanctuary

ANDREW R. HALLORAN

Chimpanzee Behavior & Care, Save the Chimps

Save the Chimps, Inc. is home to over 220 chimpanzees retired from biomedical research, the pet trade, and the entertainment industry. Due to the disparate histories of each chimpanzee (past traumas, limited or no social interactions with other chimpanzees, lack of space, etc.), there are individual behavioral challenges to some of the key factors of what we would define as thriving for a chimpanzee: a rich social environment, freedom of choice / self-determination, and an enriching and spacious environment that promotes freedom of movement. As such, the sanctuary attempts to mitigate these challenges by creating individualized care plans that identify present needs and mandate care protocols based on these needs. In order to arrive at these care plans, every chimpanzee receives an annual 60 day assessment period where staff perform daily observations with regard to empirical indicators on a Likert Scale. These indicators fall into such categories as social behaviors, self directed behaviors, diet and feeding, movement, indications of pain or discomfort, and a subjective overall assessment. By compiling these indicators, sanctuary staff are able to identify individual needs and challenges while coming up with individual care plans to meet these needs. In the two years since implementing this methodology in creating individual care plans, 80% of chimpanzees who, due to behavioral challenges, previously had lived with limited space and social interactions at the sanctuary, have mitigated these challenges to the point of having full access to social groups and large spacious habitats.

How inter-species variation in strontium-calcium ratios of leaves and fruit informs dietary reconstructions

MARIAN I. HAMILTON[1], B. LEE. DRAKE[2], ALEX GALLOWAY[1], EMILY DZHINENKO[1] and SHERRY V. NELSON[2]

[1]Department of Anthropology, University of Northern Colorado, [2]Department of Anthropology, University of New Mexico

Previous research demonstrates that strontium-to-calcium ratios (Sr/Ca) can differentiate between major dietary groups, including herbivores and carnivores or within primate communities, frugivores and folivores. While both leaves and fruits take up calcium in similar quantities, leaves take up higher concentrations of strontium; this offset leads to a higher Sr/Ca in leaves and a lower Sr/Ca in fruit. This distinction is mirrored in tissues of primarily frugivorous species, who have lower Sr/Ca, versus primarily folivorous species, with higher Sr/Ca. However, variation in the *magnitude* of the concentration differences between tree species has not yet been explored. Data presented here, gathered through non-destructive X-ray florescence (XRF) measurements, demonstrate a significant difference in the Sr/Ca ratio offset between fruits and leaves collected from different tree species in Kibale National Park, Uganda. Trees group into "low-offset" species (ex: *Ficus natalensis*) and "high-offset" species (ex: *Ficus brachylepis* and *Ficus capensis*) ($P < 0.05$). These differences do not appear to be driven by canopy height or maximum tree height, but they may help explain patterns observed in faunal tooth enamel that do not follow expectations based on diet alone; for example, while both red colobus and black-and-white colobus monkeys are folivorous, red colobus monkeys incorporate more fruit into their diets than black-and-white colobus monkeys do. Nonetheless, red colobus monkeys have the highest measured enamel Sr/Ca. This more nuanced understanding of

inter- and intra- species variation in fruit-leaf Sr/Ca offsets is necessary before applying this promising, non-destructive method to fossil contexts for dietary reconstructions.

Funded in part by the University of Northern Colorado and the University of New Mexico

Dying of Pestilence: Gender, Stature and Mortality Risk during a Plague Epidemic in 13th Century Kyrgyzstan

DAVID W. HANSEN[1], SHARON DEWITTE[1] and PHILIP SLAVIN[2]

[1]Department of Anthropology, University of South Carolina, [2]Division of History and Politics, University of Stirling

Bioarchaeological studies have provided important information about mortality patterns during the Second Pandemic of Plague, including the Black Death, but to date have focused exclusively on European contexts. This study represents a temporal and spatial expansion of plague bioarchaeology, importantly focusing on Central Asia, the likely origin of the Second Pandemic. We examine the relationship between stature, gender, and mortality risks during an outbreak of plague at two fortified settlements in northern Kyrgyzstan in 1338-39, the earliest archaeological sites known to contain victims of the Black Death in Eurasia.

Stature has frequently been used as a proxy for health in bioarchaeological literature, and previous research in England examining the association between stature and risk during plague outbreaks found higher risks of mortality during the Black Death for relatively short individuals. These prior studies used sex estimated from the skeleton as a proxy for gender; however, in this study, epigraphic data provides culturally specific data on gender within the population. Epigraphic data and in situ measurements from Syriac Christian cemeteries at these sites, obtained from field notes from excavations conducted by Russian archaeologists in the 1880s (n=119 individuals), provides detailed information about the interred individuals, including occupations, year of death, and gender.

This study finds that shorter males are disproportionately affected by plague when compared to non-plague years. Conversely, there is no association between stature and mortality during plague and non-plague years for women. These results might reflect variation by gender/sex with respect to physiological or cultural buffering.

This material is based upon work supported by the National Science Foundation Graduate Research Fellowship Program under Grant No. DGE – 2034711.

Effect of age-related changes on facial asymmetry of Czech adults: 3D landmarks-based method

KATARÍNA HARNÁDKOVÁ, KAROLINA KOČANDRLOVÁ, LENKA KOŽEJOVÁ JAKLOVÁ and JANA VELEMÍNSKÁ

Department of Anthropology and Human Genetics, Charles University, Prague

Facial morphology, including age-related changes and asymmetry, is widely studied nowadays. This research is crucial for the evaluation of aesthetics, attractiveness, treatment of craniofacial malformations and trauma, forensic identification, and more. We followed studies of age-related changes of skulls or soft tissue thickness where asymmetry was usually related to the neonatal positioning, mastication laterality or developmental and involution changes of these tissues. According to our hypothesis, facial asymmetry (1) does not depend on sex and (2) increases with age.

The sample of our cross-sectional study consisted of 3D facial models of 300 Czech adults without craniofacial trauma or anomalies in the age range from 20 to 80 years. Shape asymmetry analysis was based on 28 landmarks and assessed by geometric morphometry and multivariate statistics.

Our results showed that the manifestation of asymmetry was similar in each age category and in both sexes. In contrast to ideal symmetrical average face, the right upper face was located higher, nasal and mandibular region led to the left. In frontal view, the upper face was rotated slightly clockwise and the lower face counterclockwise. After 60th year of age the manifestation of facial asymmetry began to differ significantly from young subjects. Sex differences in facial asymmetry were significant before the age of 60.

In conclusion, the general pattern of asymmetry is not fundamentally related to age, but after 60th year, asymmetry begins to vary significantly from younger subjects. These findings are consistent with our previous results of skull asymmetry assessments using computer tomography.

This study was supported by Charles University Grant Agency – GAUK 372221.

Calcaneal trabecular variation among gorilla taxa

CHRISTINE M. HARPER[1], BIREN A. PATEL[2,3] and ADAM D. SYLVESTER[4]

[1]Department of Biomedical Sciences, Cooper Medical School of Rowan University, [2]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [3]Human and Evolutionary Biology, Department of Biological Sciences, University of Southern California, [4]Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine

The external morphology of the calcaneus differs significantly with degree of arboreality among gorillas. Whether gorilla internal structure displays similar functional correlations, however, is unknown. Here we analyze whole-bone and regional calcaneal trabecular structure of *Gorilla gorilla* (n=10), *Gorilla beringei graueri* (n=2), and *Gorilla beringei beringei* (n=5).

Calcanei were micro-CT scanned (voxel size 38-50µm). A three-dimensional geometric morphometric sliding semilandmark analysis was carried out and final landmark configurations were used to position 163 spherical volumes of interest (VOIs) within each calcaneus. Trabecular properties were calculated using the BoneJ plugin for ImageJ and MATLAB. Non-parametric MANOVA tests were performed on all VOI results for each parameter to compare taxa. In addition, ANOVAs on each VOI were used to determine regional differences in trabecular structure among taxa. Parameter distribution was summarized using principal components analysis and visualized using color maps.

G. b. graueri and *G. gorilla* differ significantly from *G. b. beringei* (p=0.01 and 0.004, respectively) in having more anisotropic bone throughout the calcaneus. Greater anisotropy likely reflects the more variable foot positioning and non-stereotypical mechanical loading patterns through the foot associated with greater habitual arboreality. *G. b. beringei* and *G. b. graueri* also differ significantly in trabecular thickness (p=0.024), particularly between the posterior talar facet and the cuboid facet. The relatively thicker trabeculae in the distal calcaneus of *G. b. beringei* suggests a relatively higher magnitude of mechanical loads through both the calcaneocuboid and subtalar joints as a consequence of terrestrially.

This project was supported by the National Science Foundation (BCS - 1824630 and BCS - 1317047).

Simulating the effects of a highly pathogenic virus across rural, peri-urban, and urban Bangladesh poultry worker's social networks

IAN HARRYMAN[1], ASHLEY HAZEL[2] and JAMES H. JONES[1]

[1]Department of Earth System Science, Stanford University, [2]Proctor Foundation, University of California, San Francisco

Zoonoses account for most emerging viruses and pose a serious threat to global public health. Assessing the socio-ecological drivers of these infections across cultural landscapes is particularly important at the human-animal behavioral interface where spillover opportunities are abundant. We used ethnographically derived social network data of Bangladesh poultry workers to model the effect of a hypothetical highly pathogenic respiratory virus across social and occupational environments. In 2014, we collected

social network data from ~300 poultry workers in rural, peri-urban, and urban settings (N=903), representing highly gendered environments, with work ranging from subsistence backyard flocks, small-scale family-run operations, and wholesale and commercial markets. Using H5N1 and H7N9 avian influenza strains as reference parameters, we simulated an epidemic over each network to test whether the highly assortative interactions of women in rural social networks would produce a more severe epidemic than the other contexts. We found that rural networks, which are characterized by high density, gender homophily, and kin ties, produce faster and larger epidemics than the urban and peri-urban contexts. On average, rural outbreaks occur 11 days earlier and have a peak prevalence of ~20% of the population, compared to ~12% and ~13% in urban and peri-urban epidemic simulations. Our results show that the more cohesive social structure found among rural poultry workers produce an increased risk of an outbreak. Occupational norms surrounding support networks, gendered social ties, and geographic constraints can have large impacts on epidemic dynamics, and social scientists can offer valuable contributions to our understanding of these dynamics.

Fieldwork for this paper was supported by R01TW009502 to Peter Daszak and EHA AI-3287-FY13-ICDDRB from EcoHealth Alliance, as well as The Freeman Spogli Institute for International Studies.

Seasonal variation in Verreaux's Sifaka ranging patterns based on resource availability

BRYNN M. HARSHBARGER[1], REBECCA J. LEWIS[2] and ANNE AXEL[3]

[1]Department of Biology, Utah State University, [2]Department of Anthropology, University of Texas at Austin, [3]Department of Biology, Marshall University

Primates inhabiting seasonal forests must adapt to fluctuations in resource availability. Verreaux's sifaka (*Propithecus verreauxi*) live in Madagascar's highly-seasonal tropical dry forests and experience extremes in resource availability. While studies suggest Verreaux's sifaka adopt an energy-minimizing strategy to cope with resource scarcity, none have examined seasonal ranging behavior over long periods. We address the question, does home-range pattern vary by resource availability? We used the vegetation index, EVI, as a proxy for food availability to test whether sifaka home-range and core-area size contracts when food is limited. We hypothesized that 1) sifaka groups would contract their home range/core area during periods of resource scarcity, and 2) there would be a positive relationship between home-range/core-area size and EVI values. To address this question, we 1) mapped the spatial arrangement of group home ranges by season over 9 years , 2) compared home-range and core-area size by season and quantified areas of seasonal overlap, and 3) tested for relationship between home-range area and EVI using linear mixed models to EVI values. Sifaka groups generally had smaller home-range/core-areas in the resource scarce season. The resource availability (as measured by EVI) was a significant, positive predictor of home-range/core-area size ($p<0.001$). Additionally, there were clear shifts in a group's core-areas between seasons. This study supports the hypothesis that sifaka adopt an energy-minimizing strategy during periods of resource scarcity and suggests how sifaka may respond to changes in forest vegetation under a warming climate.

Three-dimensional functional correlates of digitally dissected strepsirrhine masticatory muscle fiber architecture visualized through DiceCT

ADAM HARTSTONE-ROSE[1], EDWIN DICKINSON[1,2], CASSIDY E. DAVIS[1], MADISON A. MANZO[1], ASHLEY S. CARTER[1], SHRUTI KOLLI[1,3], ALYSA SCHWENK[1], CINDY LIU[1] and NAIMISHA L. VASIPALLI[1]

[1]Department of Biological Sciences, North Carolina State University, [2]Department of Anatomy, New York Institute of Techology College of Osteopathic Medicine, [3]Department of Biological Sciences, University of Denver

While masticatory muscle architecture has been described in numerous primates using traditional, destructive gross dissection techniques, this fascicular anatomy has only previously been described for four species using diffusible iodine-based contrast-enhanced computed tomography (DiceCT), in which specimens are stained with Lugol's iodine that binds to muscle fibers to increase their radio-opacity to the point of discrimination with x-ray-based imagery. In the current study, we apply this technique to nine strepsirrhine species (across four genera of lemurid, *Propithecus*, *Daubentonia* and *Otolemur*), reporting data on muscle volume, fascicle length (FL), physiological cross-sectional area (PCSA), fascicular curvature and 3D orientation. Our findings confirm that gross and digital dissection techniques yield similar results for FL and PCSA for most of these taxa (though data on some muscles/specimens suggests that acid digestion may impact some fascicle lengths, an observation that requires closer investigation). Fascicle angularity seems to be clearly related to gouging in *Daubentonia* (with highly angular fascicles that relate to its anteroposterior jaw motions). Meanwhile, fascicular compression may relate to diet, with the most frugivorous taxon in our sample, *Varecia*, having the most compressed fascicles at near occlusion (1.16 arc:chord ratio) and that ratio being more than 7% lower in *Propithecus*, our most folivorous taxon. While these digital methods cost more time and money than do gross dissections, these expenses are reducing with technological advancement, and these techniques not only yield data non-destructively (allowing the study of specimens too precious to physically dissect), but also preserve important three-dimensional spatial relationships previously unavailable.

Funding was provided by the National Sciences Foundation IOS-15-57125

Facial Widths in the Three Adult Morphs of Orangutans

FAYE S. HARWELL[1], ZOE E. ALBERT[1] and CHERYL D. KNOTT[1,2]

[1]Anthropology, Boston University, [2]Biology, Boston University

Orangutans challenge our dichotomous perception of phenotypic sex seeing as they have three sexually-mature adult morphs: females, unflanged males, and flanged males. In males, a significant increase in androgen levels is associated with numerous changes in physical characteristics and behavior that develop during the flanging process. While unflanged males lack these obvious secondary sexual characteristics, they still have higher testosterone levels compared to females. Here, we test whether captive unflanged males and females have similar facial ratios (facial width/bi-orbital distance), since flanges form from a facial compartment that contains androgen receptors and is present prior to flanging. When flanging, males deposit fat to these compartments. In the field, unflanged males can be hard to distinguish from female orangutans, without a clear view of the genitalia. Flanged males (3.9 ± 0.5, range=2.7-5.1, N=20) have significantly wider facial ratios compared to unflanged males (2.4 ± 0.3, range=2.1-3.0, N=9) and females (2.3 ± 0.3, range=1.9-2.7, N=22; $F(2,48)= 98.18$, p-value >0.0001), who are similar in their facial ratios. Inter-observer reliability between measurements (N=74) of the bi-orbital distance (V=1171, p=0.3251), facial width (V=1711, p=0.04779), and facial ratio (V=496.5, p=0.2434) are low. While there are other morphological differences between them, unflanged males and females do not differ in their facial ratios. The lack of significant differences in facial ratios between unflanged males and females, despite the higher testosterone levels in unflanged males, is consistent with them having an alternative 'sneaker' male reproductive strategy that includes mimicking female size and appearance.

National Science Foundation BCS-2118082, Boston University's Women's Guild

Arched footprints reveal bipedal kinematics, not arched foot anatomy, of fossil hominins

KEVIN G. HATALA[1], PETER L. FALKINGHAM[2] and STEPHEN M. GATESY[3]

[1]Department of Biology, Chatham University, [2]School of Biological and Environmental Sciences,

Liverpool John Moores University, [3]Department of Ecology, Evolution, and Organismal Biology, Brown University

The longitudinal arch of the human foot is viewed as a pivotal adaptation that makes us proficient bipedal walkers and runners. Arched foot morphology is difficult to interpret from skeletal fossils, but most agree that fossil footprints record evidence of arched hominin feet as far back as the Pliocene. However, the extent to which footprints faithfully record the shapes of the feet that created them has never been determined. Here, we use biplanar X-ray experiments, 3-D animation, and particle simulation to directly study the mechanistic origins of arched footprints. We developed a new tool to measure arches of tracks and feet in 3-D, and we used this to study the conformation between foot anatomy and footprint morphology. We found that anatomical fidelity in this region is poor; even the most flat-footed experimental subjects produced substantially arched tracks in soft muds. Excitingly, our mechanistic study shows that arched footprints are actually the direct product of the heel-sole-toe rollover kinematics that are integral to our inverted pendular walking gait. We applied our new 3-D measurement tool to evaluate arch morphologies in Pliocene footprints from Laetoli, Tanzania, Pleistocene footprints from Ileret, Kenya, and Holocene footprints from Walvis Bay, Namibia. We found that the Laetoli footprints preserve evidence of a heel-sole-toe rollover, and presumably inverted pendular mechanics, yet they record propulsive kinematics different than observed in modern humans. The Ileret footprints offer the earliest known evidence for fully human-like foot kinematics, suggesting that important changes to hominin bipedalism occurred between 3.66 and 1.5 Ma.

This work was supported by the National Science Foundation (BCS-1825403 to KGH and PLF; BCS-1824821 to SMG).

DHEAS and nutritional status among Sidama, Ngandu, and Aka children

COURTNEY HELFRECHT[1], COURTNEY L. MEEHAN[2], HUI WANG[3] and SAMUEL J. DIRA[4]

[1]Anthropology, University of Alabama, [2]Anthropology, Washington State University, [3]Applied Statistics, University of Alabama, [4]Anthropology, Hawassa University

Adrenarche, the biological event marked by rising production of dehydroepiandrosterone and its sulfate (DHEA/S), may represent a sensitive period in postnatal child development, with important implications for adolescence and beyond. Yet, the triggers for adrenarche remain unclear. Nutritional status, particularly adiposity, has long been hypothesized as a factor in onset of DHEAS production, but findings are inconsistent. We here evaluate the association of height, weight, and BMI with DHEAS concentrations among children from three sub-Saharan populations - Sidama agropastoralists (Ethiopia), Ngandu horticulturalists (CAR), and Aka hunter-gatherers (CAR). Height, weight, and BMI were collected from 206 children (Sidama=155, Ngandu=28, Aka=23) aged 2.75 to 18 years old. Height- (HAZ), weight- (WAZ), and BMI-for-age (BMIZ) were calculated using CDC standards. Hair hormone analysis was conducted to evaluate DHEAS and cortisol concentrations. There are significant differences in height/HAZ and weight/WAZ between Aka and both Ngandu and Sidama, but no differences in BMI/BMIZ across cultures; the majority of children in all three populations had BMI z-scores > -2.0 SD. Results for HAZ and WAZ were much more varied. None of the measures of nutritional status except BMI had any significant effect on DHEAS concentrations, controlling for age, age-squared, sex, cortisol, population, and population-sex interactions (adj. R-sq.= 0.38; $p < 0.000$). Holding all other variables constant, Sidama children have significantly lower DHEAS concentrations than Aka or Ngandu children. Although consistent with the idea that adiposity may play a role in adrenarche, these findings suggest an additional role for stress and ecology in patterns of DHEAS production.

This research was funded by the National Science Foundation, Grant Numbers: BCS-1260428 and BCS-0955213.

HARVEST: A multidisciplinary approach to understanding ancient hominin use of plants

AMANDA G. HENRY, SANDRINE GALLOIS, BJØRN PEARE BARTHOLDY and EMMA J. DEVEREUX

Faculty of Archaeology, Leiden University

The evolutionary history of the modern human dietary repertoire is a major research challenge. However, for various reasons, existing information about ancient diets is heavily biased towards the consumption of animal foods. Plants are known to be important components of modern hunter-gather diets, and the inclusion of plant foods and the development of processing technologies have been implicated in grade shifts within the hominin lineage. Using a behavioral ecology framework, the ERC-funded HARVEST project has asked: What types of plants did hominins eat, and why did they choose the ones they did? Analyses of microremains and residues preserved in dental calculus has provided a snapshot of the kinds of foods consumed. We have furthermore developed a model dental calculus system that allows us to develop new analytical methods and address hidden biases associated with the extraction and analysis of microremains. Our studies of food preferences and energetic costs of various subsistence-related behaviors among the Baka have highlighted the interactions between cultural mores, individual preferences, and energetic constraints. Our analysis of variation in plant properties among microhabitats in African environments similar to those used by hominins has allowed us better model what nutritional qualities drive their food choices. Finally, we have assessed how the energetic costs of fire might influence food processing choices. Results from these studies have indicated that plants were an essential part of the hominin dietary repertoire throughout our evolutionary history, and that the consumption of plants is determined by environmental, caloric, cultural, and personal influences.

This research has received funding from the European Research Council under the European Union's Horizon 2020 research and innovation program, grant agreement number STG–677576 ("HARVEST").

Cartilage of the nasal septum: growth, mechanics or both?

SUSAN W. HERRING[1], AYMAN A. AL DAYEH[2], MICHAEL C. BALDWIN[3] and KATHERINE L. RAFFERTY[1]

[1]Department of Orthodontics, University of Washington, [2]Department of Orthodontics, University of Tennessee, [3]Department of Oral Health Sciences, University of Washington

The septum is a unique part of the chondrocranium in that cartilage persists into maturity. The controversy addressed here is whether the septum, a primary cartilage, is the determinant of midfacial growth, a view popularized by Scott decades ago. Alternatively, Moss proposed that the septum was a vertical strut, bracing the snout against masticatory forces. We tested these theories using pigs, which have rapid, prolonged midfacial growth. Using in vivo recording, we disproved the vertical strut hypothesis by showing that the septum was under anteroposterior compression during mastication, whereas tension was predicted. Mechanical testing showed the septum was much less stiff and strong than bone, thus better suited for dampening than transmitting stress. We have not been able to discredit the cartilage theory. Morphologically, the septum is firmly attached to bone dorsally and anteriorly but free to slide ventrally, consistent with the notion that septal elongation could pull bones forward. A breed of pigs with short midfaces had patent sutures but early ossification of the posterior septum. At slow strain rates, residual stiffness appeared sufficient to separate facial sutures. Cell proliferation was high throughout the septum of juvenile pigs, especially ventrally. Continuous telemetric measurement over several days demonstrated that the septum grew episodically at a faster rate than the overlying suture. Growth spurts in the two structures were correlated in time (r=0.7-0.8) but with a tendency for the suture to lag the septum. Collectively, these results constitute evidence that the cartilaginous septum is a driver of midfacial growth.

These studies were supported by the National Institute for Dental and Craniofacial Research, grants R01DE018142, R21DE024814, and T90DE021984.

Diverse femoral biomechanical properties are interrelated among Later Stone Age Southern Africans

MADELYN HERTZ[1], JESSICA WOLLMANN[2] and MICHELLE E. CAMERON[2]

[1]Department of Anthropology, University of Western Ontario, [2]Department of Anthropology, University of Toronto

Long bone cross-sectional geometric properties (CSGPs) are frequently used to infer lower limb loading patterns. Femoral curvature and femoral anteversion have also been used to infer loading patterns. The relationship between these variables and CSGPs has not been explored in Later Stone Age (LSA) Southern Africans, who have lower limb CSGP values indicative of high terrestrial mobility alongside small body sizes and unique body proportions.

Here, we examine intra-individual relationships between CSGP variables (including total subperiosteal area, second moments of area, and polar second moment of area), femoral curvature, and femoral anteversion among LSA Southern Africans from the Namib Desert (n= 17) and the central interior of contemporary South Africa (n= 47). Femoral curvature is predicted to positively correlate with CSGPs. Femoral anteversion is predicted to negatively correlate with CSGPs based on observed ontogenetic decreases in anteversion with the onset of bipedal locomotion. Femoral CSGPs, curvature, and anteversion were assessed using whole-bone 3D models. Intra-individual relationships between these variables were assessed using linear regression at 5% intervals along the femoral diaphysis.

Femoral curvature has a significant positive relationship with most femoral CSGPs at 50%, weakening at sections proximal and distal to midshaft. Femoral anteversion has a significant negative relationship with CSGPs, but only between 70 and 45 % of the shaft. Overall, femoral curvature and femoral anteversion likely reflect the loading environment of the lower limb and may be used in biomechanical investigations of physical activity patterns.

This research was funded by the Social Sciences and Humanities Research Council of Canada; the University of Edinburgh Tweedie Exploration Fellowship; and the Palaeontological Scientific Trust of South Africa.

Patterns of physical aging in *Propithecus coquereli*, a long-lived strepsirrhine primate

NICHOLAS R. HESLEP[1], ELAINE E. GUEVARA[2] and ROSHNA E. WUNDERLICH[1]

[1]Department of Biology, James Madison University, [2]Department of Anthropology, University of North Carolina Wilmington

Primates are characterized by slow life histories, including protracted development and long lifespans. Humans exhibit physical senescence, including decreased strength and physical activity, later in life. Little is known about the degree to which this pattern of physical aging is conserved across primates or specific to humans. *Propithecus* are particularly slow-developing strepsirrhine primates with long lifespans for their body size. *Propithecus* are highly arboreal, and vertical clinging and leaping comprise a large portion of their locomotor repertoire. Previous laboratory studies have suggested that sifakas exhibit few signs of physical senescence. In order to investigate further potential evidence for physical aging in *Propithecus*, we measured percent time active/resting, energy expenditure due to movement (as overall dynamic body acceleration, ODBA), and peak accelerations in 18 free-ranging captive *Propithecus coquereli,* aged 1–25 years, using lightweight inertial sensors. When free-ranging in natural habitat enclosures, the oldest age category (20+) *Propithecus* exhibited significantly lower active/rest time, lower ODBA, lower average peak acceleration and lower number of peak accelerations per hour than adults. Contrary to previous studies finding only subtle gait changes during aging in *Propithecus*, these results indicate a pattern of age-related physical senescence in captive sifakas, especially in natural habitat environments, that may parallel some human physical aging characteristics. Variation in these parameters due to captivity and enclosure type requires further investigation. These data will inform comparative analyses of aging in strepsirrhines exhibiting different life history strategies and environmental adaptations and ultimately inform our understanding of the evolution of human lifespan.

This work was supported by the Duke Pepper Center (NIA P30AG028716), the Duke Center for Population Health and Aging (NIA P30AG034424 to Lynch), and the Duke Lemur Center Director's Fund.

Two Measures of Fecal Glucocorticoids and Their Relationship to Social Group Size and Composition in Bonobos

ALEXANA J. HICKMOTT[1,2], KLAREE J. BOOSE[1], MONICA L. WAKEFIELD[3], COLIN M. BRAND[4,5], FRANCES J. WHITE[1] and J.JOSH SNODGRASS[1,6]

[1]Anthropology, University of Oregon, [2]Public Health, Texas Biomedical Research Institute, [3]Sociology, Anthropology, and Philosophy, Northern Kentucky University, [4]Epidemiology and Biostatistics, University of California, San Francisco, [5]Bakar Computational Health and Sciences Institute, University of California, San Francisco, [6]Global Health Biomarker Lab, University of Oregon

Stress is an important part of everyday life, and can mediate sociality. In primates, stress has been found to differ by sex and has been linked to social group size. We aimed to test the relationship between stress and social group size with two fecal glucocorticoids, corticosterone and cortisol in bonobos (*Pan paniscus*). We collected 32 fecal samples, 27 samples from the Iyema field camp, Lomako forest, Democratic Republic of Congo and five from the Cincinnati Zoo for assay and collection protocol validation. We ran ELISA assays to analyze all 32 dried fecal samples for corticosterone and cortisol. We performed ANOVAs on sex, age, social group size, and if a female had an infant. Social group size significantly explained variation in corticosterone [$F(7,28) = 6.176$, $p = 0.000199$] and cortisol [$F(8,28) = 4.343$, $p = 0.00169$]. Females with infants had significantly higher levels of cortisol [$F(1,24) = 6.443$, $p = 0.018$]. Breaking down the composition of the social group, the number of males in a social group [$F(1,27) = 5.212$, $p = 0.0305$] and the total group size [$F(1,29) = 4.247$, $p = 0.0484$] significantly explained corticosterone values. Our results suggest that the size of a social group and the number of males in a social group may influence bonobo stress levels. From an evolutionary perspective, there appears to be an optimality point where the size and composition of a social group influences stress in social group living primates.

Funded by grants and fellowships from Northern Kentucky University to MLW, UO Gary Smith Summer Development grant to AJH, and a UO Faculty Research Award to FJW.

History of the Vienna Protocol –Guidelines on How to Deal with Holocaust Era Human Remains

SABINE HILDEBRANDT

Department of Pediatrics, Boston Children's Hospital/Harvard Medical School

The Vienna Protocol is a new guideline that prescribes steps for properly dealing with Holocaust-era human remains, and includes not only considerations of medical ethics, but also a Jewish medical ethics perspective for its advice. It is part of a more general set of recommendations for dealing with Holocaust-era human remains that came out of a 2017 symposium at Yad Vashem, the World Holocaust Remembrance Center in Jerusalem. This conference represented a scholarly deliberation by an interdisciplinary international group of experts in response to the discovery human remains from the Nazi period in different places between 2014 and 2017. One of the locations was on the Dahlem campus of the Free University (Freie Universität - FU) of Berlin of human skeletal remains from possible victims of experiments carried out at the concentration camp of Auschwitz by Dr. Josef Mengele; another discovery concerned one of the Max-Planck-Institutes and its collections of neuroanatomical specimens, which included tissues from "euthanasia" victims.

The Vienna Protocol will be discussed as unique among similar recommendations on Nazi era human remains in its representation of the voice of those having suffered violence and being targeted as victims. It will be argued that the

Vienna Protocol is formulated in such a general and practical manner that it can be adapted to specific other contexts of human rights abuses and crimes against humanity.

The effects of food shape on maximum ingested bite size in lemurs

GABRIELLE A. HIRSCHKORN[1], GIULIA R. LAGOMARSINO[1], ASHLEY R. DEUTSCH[1], MADISON G. DOCABO[1], PETER MCGRATH[2] and ADAM HARTSTONE-ROSE[1]

[1]Department of Biological Sciences, North Carolina State University, [2]Department of Mathematics, North Carolina State University

Previous primate research has shown relationships between dietary specialization, food mechanical properties, and Maximum Ingested Bite Size (V_b) – the largest piece of food an animal will ingest whole without first biting. While previous studies have used precisely cut cubes of food (the easiest shape to cut consistently and accurately) to measure an individual's V_b, cubes are not a realistic proxy shape for naturally occurring food and may not truly reflect feeding behaviors. The current study addresses this in nine lemur species by comparing V_b based on cubed food with foods cut to a more naturalistic, spheroidal shape: a tricylinder (i.e., foods cut in the three orthogonal planes using a cylindrical punch). Tricylinders have ~59% the volume of a cube of equivalent side length to the tricylinder diameter – thus allowing us to assess whether V_b is more closely related to linear gape during ingestion (i.e., cubes and tricylinders consumed of equivalent length and diameter respectively with the latter having substantially smaller volumes) or oral volume (i.e., cubes and tricylinders consumed of equivalent volumes with the latter having substantially larger diameters). Surprisingly, we found that lemurs eat tricylinders of food that are both more voluminous and of greater diameter than consumed cubes of the same foods. Thus, shape has a significant impact on V_b beyond the relationship between maximum linear and voluminous measures. While lemurs consumed significantly larger pieces of more naturalistically shaped foods, further inquiry could determine which geometrical aspect of food shape most closely influences feeding behaviors.

Tied Together: Pleiotropic Effects Across the Integument

LESLEA J. HLUSKO

Dept. of Paleobiology, CENIEH, Dept. of Integrative Biology, University of California Berkeley

This abstract is part of the symposium *Integumentary Anthropology: Examining the Exterior*. This presentation introduces two gene signaling pathways that influence the adhesion between epithelial cells: the ectodysplasin pathway and the non-canonical Wnt10A pathway. Numerous studies demonstrate that genetic variation in these pathways leads to variation across a wide range of integumentary structures through the phenomenon of pleiotropy (when one genetic variant simultaneously effects multiple anatomical structures), such as mammary glands, sweat glands, skin, and teeth.

Most integumentary structures decay quickly after death and are only occasionally preserved beyond a few thousand years. Teeth are 96% inorganic and therefore, more resistant to decay and the hazards of deposition and fossilization than any other part of the body. This durability is why teeth dominate the vertebrate fossil record, including that of the human lineage. Because of the pleiotropic effects of the ectodysplasin pathway and Wnt10A signaling, variation in the shape of teeth and the evolution of that variation can provide a window into the evolutionary history of other integumentary structures.

These pleiotropic effects offer a new set of opportunities for the study of the dentition. I present data from my published research collaborations and a few others to demonstrate that we can use knowledge of pleiotropy and the incredible propensity of the dentition to be preserved in the fossil and archaeological records to open a window to the evolution of the integumentary structures that are tied to teeth through pleiotropic effects.

Research presented herein was supported in part by National Science Foundation grants DBI 2128146, BCS 1720128, BCS 1025263, BCS 0130277, BCS 0500179, and BCS 0616308.

Masculine voice is associated with better mucosal immune defense in adolescent and adult males

CAROLYN R. HODGES-SIMEON[1], GRAHAM ALBERT[1], TIMOTHY MCHALE[1], STEVEN J.C. GAULIN[2], MICHAEL GURVEN[2], JESSICA K. HLAY[1] and STEVEN A. ARNOCKY[3]

[1]Anthropology, Boston University, [2]Anthropology, University of California, Santa Barbara, [3]Psychology, Nipissing University

The immunocompetence handicap hypothesis (ICHH) contends that testosterone-dependent, masculine traits are honest signals of the bearers' ability to withstand immunosuppression, yet empirical studies testing the ICHH have produced mixed results. The present research addressed the relationship between masculine vocal parameters and immunity in two samples: young adult men from the US and Canada (N = 267) and adolescent males from Bolivia (N = 44). All participants provided saliva samples, assayed for a biomarker of mucosal immunity associated with respiratory disease resistance: secretory immunoglobuilin-A (sIgA). Participants also contributed speech samples, analyzed for two sexually dimorphic aspects of the human voice: 1) fundamental frequency (i.e., perceived pitch; f_o) and vocal tract length (VTL; estimated using formant frequencies). Multiple regression models were used to assess the association between masculine vocal parameters and sIgA. Results indicated that lower voice pitch (i.e., f_o) and longer VTL were associated with higher sIgA levels. That is, both adult and adolescent males with more masculine voices showed better mucosal immunity (and therefore disease resistance) than those with less masculine voices. Although this accords with several previous studies on voice and sIgA, it stands in contrast with standard ICHH-derived predictions. We suggest that life-history theory provides a more parsimonious conceptual framework than the ICHH for understanding the association between testosterone-dependent secondary sexual characteristics and immunity.

Biological affordances: A framework for acknowledging the non-deterministic possibilities of biology

MORGAN K. HOKE

Anthropology, University of Pennsylvania

Biological anthropologists and likeminded scholars have long struggled against the trap of deterministic thinking when it comes to the biology in shaping human health. Biocultural and critical approaches like those championed by the late Lewontin, as well as Goodman & Leatherman, and others have stressed the contingent, dialectical interplay between biological and sociocultural forces in the unfolding of human health. Despite these efforts, we still seem to lack frameworks that allow us to effectively acknowledge the role that biology has in shaping our world without falling into overly simplistic and deterministic language. One potentially fruitful concept in addressing this issue is that of affordances or the possibilities that are provided or furnished by an environment, substance, surface, agent, etc. Anthropologists of different stripes have used affordances to avoid reductionistic thinking in examining naturalistic explanations in psychological and linguistic processes alongside more the normative observations of ethnography. In this paper, I draw on affordances to interrogate biological processes within their broader ethnographic context. As a case study, I explore the ways in which the study of genetics in human populations must mediate between naturalistic phenomena and processes such as DNA, gene expression, transcription, etc., and the complex, socially constructed milieu in which genes interact with the environment and other biological processes to influence, but not necessarily determine, human health and wellbeing.

ABSTRACTS

Breastfeeding frequency is associated with differential abundance of bacteria in human milk

ELIZABETH A. HOLDSWORTH[1], JANET E. WILLIAMS[2], RYAN M. PACE[3], EDWARD H. HAGEN[1], AVERY A. LANE[1], MARIA GARTSTEIN[4], MARK A. MCGUIRE[2], MICHELLE K. MCGUIRE[3] and COURTNEY L. MEEHAN[1]

[1]Department of Anthropology, Washington State University, [2]Department of Animal, Veterinary and Food Sciences, University of Idaho, [3]Margaret Ritchie School of Family and Consumer Sciences, University of Idaho, [4]Department of Psychology, Washington State University

The human milk microbiome (HMM) is thought to be responsive to variation in the maternal-infant ecology, calibrating the HMM to infant needs. However, little data exist on how infant-mother communication via breastfeeding patterns shapes the HMM. We hypothesized that number of breastfeeding bouts (breastfeeding sessions separated by ≥30 seconds) throughout the day would be associated with HMM alpha diversity (richness, Shannon diversity/evenness) and abundance of individual taxa. We conducted infant observations during 12-hours over 3 days to document breastfeeding frequency and analyzed milk samples collected after observation for microbial diversity and composition from 45 mother-infant pairs living in the US Pacific Northwest. DNA was extracted from milk samples, and the V1-V3 region of the 16S rRNA gene amplified and sequenced. Sequencing reads were processed and analyzed in R. Sample read counts were rarefied to an equal depth for alpha diversity analyses, and raw read counts were used for differential abundance analysis using ANCOM-BC. In linear regression models controlling for maternal age, infant age, parity, and number of people who held the baby during observations, number of breastfeeding bouts trended inversely with HMM richness (β=-0.31, p=0.07), but was not associated with Shannon diversity or evenness. Forty-one of 83 taxa were differentially abundant (q<0.05) among breastfeeding bout tertiles, including *Cutibacterium*, *Micromonospora*, *Polaromonas*, and *Turibacter*. These results indicate breastfeeding patterns may modulate the abundance of specific human milk bacteria. This has implications for understanding how shifts in breastfeeding practices throughout our evolutionary history may have impacted milk and infant development.

Funding provided by the Washington State University Health Equity Research Center

Encephalization in fossil *Homo*

TRENTON W. HOLLIDAY

Anthropology, Tulane University, Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand

In 1997, Ruff and colleagues examined encephalization in Pleistocene *Homo* using a largely ataxonomic approach. Specifically, the encephalization quotient (EQ) for Pleistocene *Homo* was calculated using a formula from Martin (1981). Here, similar analyses are performed using a large dataset of 630 mammalian species (Boddy et al., 2012). This analysis also includes fossil species of *Homo* identified in the last 25 years. Given evidence for late-surviving small-brained members of our genus, a taxonomic approach is used.

EQ is calculated as brain mass in grams / (0.056 x body mass in grams$^{0.746}$). Of the extant mammals, humans are by far the most encephalized (6.48). The second-most encephalized mammal is the white-fronted capuchin (*Cebus albifrons*; 4.53), third is the red-faced spider monkey (*Ateles paniscus*; 4.48), and fourth is the harbor porpoise (*Phocoena phocoena*; 4.43). None of the extant apes makes the top ten.

The most encephalized fossil hominins are the "Cro-Magnons" (6.64 LUP; 6.57 EUP), followed by Skhūl-Qafzeh (6.50). Neandertals and *H. heidelbergensis* (*sensu lato*) are somewhat less encephalized (5.89 and 5.20). *Homo naledi* and *H. floresiensis* show much lower EQs (3.24 and 3.26), lower than those of early Pleistocene *H. erectus* from Africa (4.25) and Dmanisi (3.83). In fact, neither *H. naledi* nor *H. floresiensis* would make the top ten mammalian EQ list. African *H. erectus* would hold fifth place, while the Dmanisi hominins would come in ninth, between two species of macaques.

While these data should not be overinterpreted, they are consistent with cognitive differences among species of fossil *Homo*.

Supported by NSF (#SBR-9321339), the L.S.B. Leakey Foundation, the University of the Witwatersrand, and Tulane University.

Ontogenetic changes in jaw leverage in tufted and untufted capuchins

MEGAN A. HOLMES[1], PARKER M. TAYLOR[2], ROCIO RAMIREZ[3], MARIANA DUTRA FOGAÇA[4,5], JANINE CHALK-WILAYTO[6], CLAIRE E. TERHUNE[2] and MYRA F. LAIRD[3]

[1]Department of Family Medicine and Community Health, Duke University School of Medicine, [2]Department of Anthropology, University of Arkansas, [3]Department of Integrative Anatomical Sciences, University of Southern California, [4]Department of Biomedical Sciences, Institute of Population Genetics, University of Veterinary Medicine Vienna, [5]Neotropical Primates Research Group, NeoPReGo, [6]Department of Biomedical Sciences, Mercer University School of Medicine

Changes in jaw leverage are well-documented across the toothrow, but leverage variation during ontogeny in primates has rarely been investigated. Here we examine changes in jaw leverage with age and skull size and shape between tufted (*Sapajus*) and untufted (*Cebus*) capuchins. Unlike *Cebus*, *Sapajus* have a mechanically challenging diet resulting in a suite of morphological adaptations to high bite force, and field data indicate these foods are exploited early in their development. We hypothesize that i) *Sapajus* will exhibit greater jaw leverage across ontogeny, reflecting their mechanically challenging diet relative to *Cebus*, and; ii) intergeneric variation in skull shape will appear early in ontogeny.

Fifty-three capuchin skulls with ages spanning from early infancy to adulthood were MicroCT scanned; age for each specimen was estimated based on dental eruption/wear. Three-dimensional landmarks were placed on surface models of the skull and dentition. These landmarks were used to capture shape variation in the cranium and mandible using 3D geometric morphometrics and to calculate jaw leverage for the masticatory muscles relative to the center of the erupted tooth. Results indicate jaw leverage varies with age across species and that mechanical advantage is consistently greater in tufted compared to untufted capuchins at each bite point throughout development ($p < 0.01$). Additionally, shape analyses display cranial shape differences between genera being compounded with age. These results suggest tufted capuchins have elevated jaw leverage across ontogeny relating to their early exploitation of mechanically challenging foods and that differences between genera increase during maturation.

Funding statement: This research was supported by grants from the National Science Foundation's Biological Anthropology directorate (NSF-BCS-1945771, NSF-BCS-1944915, NSF-BCS-1945283, NSF-BCS-1945767).

Forest terrains influence walking kinematics among indigenous Tsimane of the Bolivian Amazon

NICHOLAS B. HOLOWKA[1], THOMAS S. KRAFT[2,3], IAN J. WALLACE[4], MICHAEL D. GURVEN[3] and VIVEK V. VENKATARAMAN[5]

[1]Department of Anthropology, University at Buffalo, [2]Department of Anthropology, University of Utah, [3]Department of Anthropology, University of California Santa Barbara, [4]Department of Anthropology, University of New Mexico, [5]Department of Anthropology and Archaeology, University of Calgary

Metabolic studies suggest that one major evolutionary advantage of bipedalism is enabling humans to walk with relatively low energy expenditure. However, such studies typically record subjects walking on even surfaces or treadmills that are not representative of the irregular terrains our species encounters in natural environments. Lab-based studies that simulate irregular terrains find that such surfaces cause people to deviate from the kinematic strategies that make human bipedalism so energetically economical, such as walking with fully extended legs. However, few

studies have quantified walking kinematics in real natural environments. Here we measured marker-based walking kinematics on natural terrains in 21 individuals from a Tsimane forager-horticulturalist community in the Bolivian Amazon. We recorded high-speed videos of participants walking on three different terrain types: a dirt field, a forest trail, and a transect through unbroken forest. Compared to walking in the field, when walking in the unbroken forest participants contacted the ground with more protracted legs and flatter foot postures, had more inclined trunks and flexed hips and knees at midstance, and raised their feet higher during leg swing. In contrast, kinematics were generally similar between forest trail and field walking. These results indicate that irregular natural surfaces like those in unbroken forests cause humans to use different walking kinematics from those used on even surfaces, such that traveling through such environments could be considerably more expensive than typically assumed from lab-based gait studies. These results have important implications for the evolutionary energetics of human foraging in environments with challenging terrains.

Funding provided by the American School of Prehistoric Research (Harvard University) and the National Institute of Aging within the National Institute of Health (RF1AG054442).

Righting tibial retroversion: A functional and ontogenetic analysis

CHRISTINA L. HOLZHAUSER and LIBBY W. COWGILL

Department of Anthropology, University of Missouri

Tibial retroversion, or the posterior angulation of the tibial plateau relative to the diaphysis, has been tentatively linked to several behaviors in the anthropological literature. A large body of work, dating as far back as the late 1800's, associated this morphology to squatting postures, while Boule's (1910) seminal but discredited description of La Chapelle-aux-Saints suggested this morphology in Neanderthals resulted in a bent-knee gait. Ultimately, Trinkaus and Rhodes (1999) suggested that retroversion is related to extensor muscle moment arm development.

This research attempts to clarify the underlying etiology of tibial retroversion by analyzing it in an explicitly ontogenetic and functional perspective. First, this analysis explored age and population-level variation in tibial retroversion. Second, the relationship between tibial retroversion and long bone strength via cross-sectional geometric properties was evaluated.

This study used a large cross-sectional sample of immature modern human remains from seven historical and archaeological osteology collections that vary in location of origin and activity patterns (n=422). Results of this analysis indicate that while there is no relationship between tibial retroversion and age, populations do differ in their magnitude of retroversion. Furthermore, these population-level differences emerge at early ages, suggesting that at least some of the variation in this feature may be genetic. Finally, there is no relationship between tibial retroversion and size-standardized, cross-sectional geometric properties, implying that variation in this feature is not purely a function of loading and activity levels.

Oral microbial ecologies reconstructed from pre-colonial era Wichita ancestors from North America provide insights into the global "silent epidemic" of oral disease

TANVI P. HONAP[1,2], CARA R. MONROE[1,2], SARAH J. JOHNSON[1,2], KRITHIVASAN SANKARANARAYANAN[2,3], MARC LEVINE[1,4] and CECIL M. LEWIS[1,2]

[1]Department of Anthropology, University of Oklahoma, [2]Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, [3]Department of Microbiology and Plant Biology, University of Oklahoma, [4]Sam Noble Oklahoma Museum of Natural History, University of Oklahoma

Tooth decay is the most common chronic condition in the world today. While this "silent epidemic" is a byproduct of acid-producing oral bacteria, oral disease progression is a complex, multi-factorial, biocultural process. In partnership with The Wichita and Affiliated Tribes, a federally recognized tribe in Oklahoma, we studied the oral microbial ecology and prevalence of oral disease in pre-colonial era Wichita ancestors. Skeletal remains of Wichita ancestors from 24 archaeological sites, dating 500-700 years before present, were paleopathologically assessed for presence of oral disease. DNA was extracted from dental calculus samples, built into partial uracil deglycosylase-treated, double-stranded libraries, and shotgun-sequenced using Illumina technology. Bioinformatic tools and custom scripts were used for microbial community profiling, contamination assessment, genome reconstruction, phylogenetic analyses, and estimates of ecological resilience. Altogether, dental calculus samples from 27 Wichita ancestors yielded well-preserved oral microbiome profiles. Paleopathological analysis revealed signs of oral diseases such as caries and periodontitis in this population. Reconstructed partial genomes of opportunistic oral pathogen species implicated in periodontitis, such as *Tannerella forsythia* and *Treponema denticola*, provided information regarding strain diversity and biogeographical patterns. Ecological approaches were used to determine keystone taxa and assess functional response diversity metrics. To the best of our knowledge, this study presents the largest collection of ancient oral metagenomes from a pre-colonial era American population and allowed us to characterize a human oral ecology prior to globalization, industrialization, and European colonialism.

This work was funded by a grant from the National Science Foundation (NSF BCS-2045308).

Morphological variance of human joint articular surfaces

HALEY HORBALY[1], MARK HUBBE[2,4], ADAM D. SYLVESTER[3] and BENJAMIN M. AUERBACH[1]

[1]Department of Anthropology, University of Tennessee, [2]Department of Anthropology, The Ohio State University, [3]Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine, [4]Instituto de Arqueología y Antropología, Universidad Católica del Norte, Chile

As points of interface between neighboring limb bones, joint articulations must accommodate a range of movements while maintaining stability in those actions. This tension between mobility and stability is presumably reflected in the morphology of articular surfaces, yet few studies have analyzed joint variance with respect to articular shape. This study uses geometric morphometric analysis on 200 modern human skeletons to analyze shape variance of the articular surfaces constituting the left shoulder, elbow, hip, and knee. Articular shape was approximated by placing landmarks on 3D surface models. Variance was measured as the trace of variance-covariance matrices of Procrustes-transformed landmarks and was used in non-parametric permutation tests to evaluate differences between the sexes. Results show that only the glenoid fossa and femoral head exhibit significantly greater variance among females than males ($p < 0.03$). To compare variances of different articulations, the average distance between homologous landmarks (RMSD) between pairs of individuals was calculated. Resulting RMSD distributions were compared using pairwise Kolmogorov-Smirnov tests, which show that all surfaces are significantly different from one another ($p < 0.01$), with the largest variances observed in the acetabulum, glenoid fossa, proximal ulna, and proximal tibia. Interestingly, articulating surface pairs from each joint show one extremely invariant convex surface and one highly variant concave surface. These results suggest that variance-producing processes prioritize constraint on the convex articulation of the joint. Establishing this observed hierarchy of articular variance in relation to joint function will assist in future studies of joint development and evolution.

Unusual Lives, Unusual Deaths: Integrating Osteology and Orientation in the Study of Early Medieval Deviant Burials

LAUREN HOSEK[1] and AUSTIN MASON[2]

[1]Department of Anthropology, University of Colorado, Boulder, [2]Department of History, Carleton College

In medieval Europe, normative burials were generally extended, supine inhumations with the head to the west. Atypical forms included prone, flexed, crouched, disarticulated, decapitated, multiple interment, etc. Different burial orientation is often noted as a type of unusual mortuary treatment but is rarely explored in depth. Visualizations of burial orientations plotted on a compass rose in R, initially developed for topographical analysis of Anglo-Saxon cemeteries, are employed to integrate orientation into a study of deviant burials. We then examine osteological signatures of pathology and trauma to determine how particular life circumstances may have contributed to these variations in mortuary treatment.

A total of 260 burials were analyzed from two contemporaneous cemeteries (Akropole and Kanin) from the early medieval site of Libice in Czechia. Most of the 117 burials at Akropole were normative, extended inhumations and only three (2.5%), had unusual body positions. Two of these skeletons exhibited osteological evidence of severe pathology. However, of the 143 individuals from Kanin, 32 individuals (22%) were buried in unusual positions. Of these, 20 burials (62.5%) also had atypical orientations, a finding significantly higher than that found among normative burials (9%). Furthermore, nine of the deviant individuals at Kanin exhibit skeletal trauma. The frequency of deviant burials with traumatic injury (28%) is significantly higher than among the normative interments (7%, n=8) indicating that trauma may have been a factor in mortuary treatment. Together, these data suggest that different circumstances contributed to variation in early medieval mortuary ritual, even on an intrasite scale.

This research was funded by a National Science Foundation GRFP, DGE-1247399.

The inclusion of biocultural and biohistorical data of a modern american population in population affinity research

ABIGAIL E. HOUKES

Department of Geography and Anthropology, Louisiana State University

Forensic anthropologists traditionally evaluate skeletal elements to assess ancestry within a biological profile. Though researchers today understand race's harmful origins and impacts on marginalized populations, ancestry classification inevitably mirrors racial categorizations. Alternatively, population affinity research appraises population formation through a biohistorical and biocultural approach. The current study includes such data in assessing the maxillary sinuses to discern whether population affinity differences are present and why. The left and right maxillary sinuses' volume and dimensions (maximum height, length, width, and surface area) were examined using 3D modeling of computerized tomography (CT) scans. The sample was selected from a modern New Mexico population and included 90 individuals who identify socially or culturally as Black (n=30), White (n=30), and Hispanic (n=30).

Results of ANOVA reveal no significant differences ($p > 0.05$) among prescribed ancestry groups when sexes are combined in any of the five variables. When each sex was analyzed separately, no significant differences were found for females; however, for males, there were significant differences among ancestry groups in the left volume ($p = 0.0336$), left surface area ($p = 0.0309$), and right length ($p = 0.0496$).

The study results indicate that quantifiable data alone do not contribute to a straightforward classification of proposed ancestry. Moreover, reporting ancestry as immutable is inaccurate and fails to consider biohistorical and biocultural processes that shape populations. By incorporating population affinity into research, the disconnection between researchers and the studied populations is illuminated and, thus, opportunities for equitable representation and growth in the field can occur.

This study was supported (in part) by an award from the G&A Materials Graduate Student Research Award from the Department of Geography and Anthropology, Louisiana State University.

Characterizing gene regulation responses to mechanical stress using in vitro skeletal cell culture models at population- and evolutionary-scales

GENEVIEVE HOUSMAN[1], ANTHONY HUNG[2] and YOAV GILAD[1,3]

[1]Section of Genetic Medicine, University of Chicago, [2]Medical Scientist Training Program, University of Chicago, [3]Department of Human Genetics, University of Chicago

Skeletal cells are highly responsive to environmental signals, especially mechanical stress. It is reasonable to assume that these responses may be mediated through gene regulation changes which may be partially genetically controlled. However, studying such gene-by-environment interactions in primate skeletal cells is particularly challenging. To begin characterizing how primate skeletal gene regulation patterns dynamically change in response to environmental perturbations, we have developed a primate skeletal cell culture model and optimized in vitro mechanical stress treatments. In our model, we differentiate induced pluripotent stem cells (iPSCs) into chondrogenic cells (cartilage) or osteogenic cells (bone). Following differentiation, we expose iPSC-derived skeletal cells to a cyclic tensile strain regimen using the Flexcell® FX-6000™ Tension System to induce a matrix-degrading phenotype. We then compare bulk- and single-cell RNA-seq data collected from control cells and treated cells to evaluate gene-by-environment interactions. In a sample set of three human iPSC-derived chondrogenic cell lines, we detected over 1000 differentially expressed (DE) genes between control and treatment conditions. Fittingly, these DE genes are enriched for osteoarthritis and joint health related gene sets. Further, we identified a subset of genes that display inter-individual changes in expression following in vitro mechanical stress treatments – potential examples of gene-by-environment interactions. Expanding this sample set to include iPSC-derived skeletal cells from additional humans and other nonhuman primates, such as chimpanzees, will allow us to detect interspecific differences in regulatory responses to mechanical stress that may contribute to evolutionary differences in skeletal development, maintenance, and disease susceptibility.

Funding was provided by the National Institutes of Health (F32AR075397 to G.H., F30AG071412 to A.H., and R35GM131726 to Y.G.).

Giving Back the Past - the role of biological anthropology in recovering histories of the marginalized.

ROBYN A. HUMPHREYS[1,2,4], JUNE BAM HUTCHISON[4], WENDY BLACK[2,3] and REBECCA ROGERS ACKERMANN[1,2]

[1]Archaeology, University of Cape Town, [2]Human Evolutionary Research Institute, University of Cape Town, [3]Archaeology, Iziko Museums of South Africa, [4]San And Khoi Centre, University of Cape Town

One of the primary arguments for access to human remains from archaeological sites is that they provide insights into pasts that were not recorded in the historical record. These arguments erase the work of black and indigenous scholars who have found creative ways to recover histories outside of bio-archaeological approaches. Here, I will compare two historical burial grounds from the same site discovered at different times. Both dated to the 18th century include the bodies of indigenous people and the enslaved, discovered in Green Point, Cape Town.

The first, Cobern Street Burial Ground discovered in 1994 during development/construction resulted in the exhumation of human remains. The human remains exhumed from this site have been subject to biological anthropological research. However, this research has not translated into tangible memorialization of the site.

The second, Prestwich Street Burial Ground discovered in 2003, during development/construction was the subject of contestation

which prevented research on the human remains exhumed. The remains have been reinterred in a memorial in Green Point to honour the dead. Communities advocated for a social-historical approach to learning about the history of the site and for producing the memorial. The intervention at the Prestwich Street Burial Ground exhumation resulted in a memorial that makes visible the presence of the enslaved and their descendants in Green Point, where their contributions to building the city have been erased. I will explore if biological anthropology has the capacity to give back the past, given the history of the discipline.

This research was funded by the National Research Foundation South Africa, DST/NRF Centre of Excellence in Palaeosciences South Africa and the National Institute of Humanities and Social Sciences South Africa

Dmanisi, Malapa, and the Evolution of Broca's Language Area

SHAWN D. HURST[1], RALPH L. HOLLOWAY[2], ALANNAH PEARSON[3], GRACE BOCKO[1], HEATHER M. GARVIN[4], LEE R. BERGER[5] and JOHN HAWKS[6]

[1]Biology, University of Indianapolis, [2]Anthropology, Columbia University, [3]Archaeology & Anthropology, The Australian National University, [4]Anatomy, Des Moines University, [5]Palaeoanthropology, University of the Witwatersrand, [6]Anthropology, University of Wisconsin-Madison

In their recent description of the Dmanisi endocrania, Ponce de Leon *et al*. suggested the Dmanisi hominins (attributed to *Homo cf. erectus*) were primitive in terms of the morphology of their inferior prefrontal cortex (IPF). This assertion was based on a proxy condition relating the brain's superior precentral sulcus (PCS) relative to the position of the skull's coronal suture (CO). Since their proxy condition for IPF morphology looks chimpanzee-like or "ancestral" in the Dmanisi endocasts, these authors suggest that higher cognitive abilities such as language, associated with Broca's language area in the IPF, evolved after 1.7 MYA in the genus *Homo*.

Here we show their proxy condition is a poor predictor of IPF morphology, with better measures being the prefrontal sulci themselves. We use geometric morphometrics to compare the prefrontal sulci in a large sample of chimpanzee and human brains, which confirms earlier work showing IPF morphology in humans is distinct from that of chimpanzees. Using this and the published identifications of the prefrontal sulci from Ponce de Leon *et al*., we find that these fossils present a range of IPF morphology, including primitive, transitional, and derived specimens rather than a single form. Combined with the transitional morphology of the MH1 endocast, the holotype specimen of *Australopithecus sediba*, similar in ways to the endocast of D4500, these findings suggest the period between 1.7 to 1.9 MYA was a dynamic and variable one in the evolutionary development of the IPF and Broca's language area.

Orangutan conservation on YouTube: The importance of storytelling in productive messaging

MARY C. HYDE[1], CATHRYN A. FREUND[2], JAMES K. ADAMS[3] and ANDREA L. DIGIORGIO[4]

[1]Department of Ecology & Evolutionary Biology, Princeton University, [2]Department of Biology, Wake Forest University, [3]Department of Molecular Biology, Princeton University, [4]Writing Program, Princeton University

Orangutan rescue and rehabilitation (ORR) organizations increasingly use social media to engage with the public and bolster support for their critical work towards orangutan conservation. However, the presentation of orangutans in visual social media outlets such as YouTube can lead to unintended negative consequences. Previous research has shown that the amount of human-orangutan interaction shown, ages of orangutans featured, and mention of threats to wild orangutans in ORR YouTube videos correlates to number of views, likes, and whether viewer comments are helpful or unhelpful for conservation priorities. Building off of this research, we investigate the use of elements of storytelling in ORR YouTube videos, as storytelling is a common and effective technique used in outreach content to connect to an audience on an emotional level. We analyze how the presence of five core aspects of storytelling (story topic, number of moments of change in the storyline, overall emotional intensity, emotional tone at the end of the video, and use of music) affect the views, likes, and sentiment of viewer comments (n= 21,621) in 98 test videos posted by ORR organizations. We found that videos featuring music had higher like and comment ratios than those that did not, videos with a negative-ending story trajectory had a lower proportion of action-taking comments than those with neutral endings, and videos with higher scores of emotional content had a lower proportion of comments negative for orangutans. These results will be useful in the design of more effective orangutan conservation outreach media going forward.

This project was graciously funded by the Princeton University Committee on Research in the Humanities and Social Sciences (A. L. DiGiorgio).

Scaling of articular surface areas in the hominid tarsals

ALEXANDRA C. IDSO[1,2] and WILLIAM E.H. HARCOURT-SMITH[1,2,3,4,5]

[1]Department of Anthropology, The Graduate Center, City University of New York, [2]New York Consortium in Evolutionary Primatology, [3]Department of Anthropology, Lehman College, City University of New York, [4]Division of Paleontology, American Museum of Natural History, [5]Evolutionary Studies Institute, University of the Witswatersrand, South Africa

The relative size of several hindlimb joint surfaces in *Homo sapiens* have long been found to be larger than expected for their body size, presumably as a consequence of bipedal locomotion. However, articular facet size variation and scaling relationships across fossil hominins is poorly understood, particularly for pedal elements. This study evaluates variation in the articular surface areas of the talus, calcaneus, navicular, and cuboid within extant hominids and fossil hominins. The sample includes adult tarsal elements of *H. sapiens*, *Pan*, *Gorilla*, *Pongo*, and a wide range of fossil hominins, including Skhul IV, La Ferrassie 1, Hadar material, Stw 573 ("Little Foot"), MH2, LB1, and selected specimens attributed to *H. naledi*. Using three-dimensional surface scans and Geomagic Wrap software, articular surface facet areas were quantified and the data analyzed using regressions against femoral head diameter as a proxy for body mass. Our results, contrary to predictions, suggest that articular scaling within the tarsals of plantigrade hominids is moderately conserved, and *H. sapiens* does not have relatively large tarsal articular surfaces. In fact, *Pan* is the only extant taxon to have joint surface areas that are larger than expected. Within fossil hominins there is considerable variation in relative joint surface size, with Stw 573 having particularly small talar articular surfaces. These findings are discussed within the broader context of fossil hominin locomotor variation and extant hominid activity patterns.

Riverine diet yesterday and today: selfperception of dietary transition at Caxiuanã region, Pará, Brazil

MARIANA INGLEZ[1], MARK HUBBE[2], MARINA DALE[1], ANDRÉ STRAUSS[3], RUI MURRIETA[1] and BÁRBARA PIPERATA[2]

[1]Department of Biosciences, Universidade de São Paulo, [2]Department of Anthropology, Ohio State University, [3]Museu de Arqueologia e Etnologia, Universidade de São Paulo

Nutrition transition is characterized by a rapid shift from traditional diets rich in cereals, fiber, and micronutrients, to energy-dense, nutrient-poor diets high in sugar, animal-source fats, and processed foods. This process is also associated with reductions in physical activity and increased risk of diet-related chronic disease. While extensively documented in urban settings, these changes also affect rural communities. Research from 2009 found evidence of the nutritional transition in riverine communities in the Caxiuanã National Forest, Pará, Brazil, which was partially explained by enrollment in cash-transfer programs. To continue to track changes in food consumption over the past 10 years, this study

used free-listing interviews to record community members' perceptions of food items in their current and childhood diets. The composition of past and present diets was compared using Wilcoxon tests, chi-square tests, multivariate correspondence analysis, and qualitative comparisons of the most relevant foods consumed in each period and by meal. The results indicate that the overall dietary pattern has not changed significantly, but that the number of purchased food items consumed at each meal increased over time. Moreover, we observed a shift in food availability as some participants reported a greater sense of food insecurity in the past. These results suggest that dietary changes associated with the nutrition transition among rural communities are more complex than often characterized in the literature and highlight the importance of documenting sub-national and sub-regional variation in the pace and pattern of the transition, especially when considering its potential effects on health and food security.

The health of enslaved Africans through the lens of bioarchaeology

KENDRA B. ISABLE

Department of Anthropology, University of Nevada, Reno

Slavery has played a vital role in the economic success of countries across the globe. However, the acquisition of accurate historical information on the lives of the enslaved have largely gone neglected. With the introduction of archaeological studies of burial sites containing enslaved African and African Americans beginning in the late 1960's, scholars began making significant strides in developing a body of literature that appropriately addresses the lived experience of these individuals. This research is a review of the existing bioarchaeological literature of enslaved populations from which a database was created to explore the biological impacts of slavery.

Within this newly created database, a total of 44 sites were identified throughout eastern North America, the Caribbean, northern South America, Portugal, South Africa, and St. Helena. These sites accounted for 1,956 enslaved individuals. Pathological conditions of the oral cavity were most commonly discussed and included dental caries, periodontal disease, antemortem tooth loss, and hypercementosis. Pathological conditions include cribra orbitalia, porotic hyperostosis, subperiosteal new bone formation, osteomyelitis, osteoarthritis, and malformed lower limbs. Evidence of growth disruption includes linear enamel hypoplasia and Harris lines. Degenerative joint disease and entheses were also discussed. There was also evidence of antemortem and perimortem blunt force trauma throughout the skeletons. Overall, this meta-analysis can speak to the difficult living conditions of enslaved Africans across the trans-Atlantic slave route and serve to identify areas of future research to more fully understand the devastating impacts of slavery.

Hominin skin as a versatile, biocultural interface

NINA G. JABLONSKI

Anthropology, The Pennsylvania State University

The evolution of functionally naked, potentially sweaty, and pigmented skin was a key innovation in the hominin lineage. Comparative and functional genomics and evolutionary developmental biology have provided important insights into the nature and timing of events in hominin skin evolution, but they haven't told the whole story. For early hominins, including earliest representatives of the genus *Homo*, skin was the primary interface between the physical environment and the interior of the body. Later hominins, especially those of the last 500,000 years, have created increasingly sophisticated and effective means of buffering the effects of the environment on the body through modifications of diet and activity patterns, development of body coverings, and use of shelters and fire. These cultural and behavioral changes, in turn, modified the nature of selective pressures acting on the skin. In the course of modern human dispersals, the evolution of skin pigmentation has been influenced by the combined action of population bottlenecks and diverse cultural practices, which together have modified the nature and actions of skin pigmentation genes.

The appearance of skin also has affected the nature and course of genetic admixture over time, with skin color and cultural modifications of skin appearance affecting mate choice. Hominin skin has been profoundly affected by biological evolution and the appearance of the skin – including added decoration – has, in turn, affected mating patterns, population genetic processes, and biological evolution.

Assessing the long-term impacts of covid-19 on primate field research

KATHARINE M. JACK and NELLE K. KULICK

Anthropology, Tulane University

The SARS-CoV-2 pandemic brought most primate field research to a halt in early 2020. Ethical concerns of transmitting the virus from researchers to primates and surrounding human communities strongly motivated the pausing of projects, and continue to inform decisions regarding the resumption of research. Between June and September 2020, we surveyed field primatologists regarding the impacts of the pandemic on their research. We received 91 responses from respondents residing in 21 countries, though most were from the United States (53%) and Canada (12%). Of the respondents, 62 were Project Directors/Co-directors, 23 were Graduate Student Researchers, 3 Post-Doctoral Researchers, 2 Research Assistants, and 1 was unspecified. Only 2% reported continuing research as usual, 35% reported continuing research with some decrease in productivity, 42% reported postponing research projects, and 21% reported cancelling projects or postponing research indefinitely. Only projects that were run by or employed source-country primatologists and assistants were able to continue research in some capacity during the early months of the pandemic and all implemented COVID-19 safety measures. Increased poaching, losing or being unable to pay local assistants, frozen research funds, declining habituation, and disruptions to data collection were the top concerns of primatologists. Field researchers most severely impacted by the pandemic were those establishing new field sites (usually new PhDs) and graduate students whose projects were postponed or cancelled due to the closure of field sites. Using these data we outline a "best practices approach" to guide the resumption of primate field research and plan for future disruptions.

Landscape composition and configuration differentially impact lemur occupancy within a fragmented landscape in eastern Madagascar

ZACHARY S. JACOBSON[1], PAMELA NARVÁEZ-TORRES[1], DEVIN M. CHEN[2], OLIVIA TIAFINJAKA[3], TYPHENN A. BRICHIERI-COLOMBI[4], NICOLA K. GUTHRIE[1], EDWARD E. LOUIS JR.[5] and STEIG E. JOHNSON[1]

[1]Department of Anthropology and Archaeology, University of Calgary, [2]Department of Wildlife, Fisheries, and Aquaculture, Mississippi State University, [3]Faculté des Sciences, de Technologies et de l'Environnement, Université de Mahajanga, [4]Centre for Conservation Research, Calgary Zoo, [5]Conservation Genetics Department, Omaha's Henry Doorly Zoo and Aquarium

Land-use change shapes the composition and configuration of forests within a landscape, ultimately affecting species distributions. Landscape disturbances are especially prevalent in Madagascar, where nearly all lemur species are facing extinction due to extensive forest loss. In this study, we used camera traps and satellite imagery to determine the multi-scale landscape drivers of occupancy in five threatened lemur species in Kianjavato, Madagascar. We hypothesized that occupancy probability would be influenced by forest cover, edge density, and landscape division index (LDI), and that species with small home ranges would respond at smaller scales than species with larger home ranges. From May-August 2019, we used camera traps to sample 30 sites within five forest fragments. Next, we generated a land-use/land-cover map to quantify landscape variables at 15 scales ranging from 0.5-80 hectares. We found forest cover was an

important predictor of occupancy for four species: the greater dwarf lemur (*Cheirogaleus major*; occupancy=0.40±0.11), red-bellied lemur *(Eulemur rubriventer*; occ.=0.15±0.11*)*, red-fronted lemur *(E. rufifrons*; occ.=0.52±0.15) and Jolly's mouse lemur (*Microcebus jollyae*; occ.=0.11±0.09). Edge density was an important predictor of occupancy for *C. major*, *E. rubriventer*, *M. jollyae*, and the black-and-white ruffed lemur (*Varecia variegata*; occ.=0.15±0.07). LDI was an important predictor of occupancy for all species. We also found species responded to landscape variables at differing scales, though home range size did not significantly predict scale of response. Our results suggest that forest composition and configuration strongly predict occupancy across lemur species. Further, our findings highlight the importance of measuring species-habitat associations at the appropriate scale.

This study was supported by Alberta Innovates, the Natural Sciences and Engineering Research Council of Canada, Re:wild, American Society of Primatologists, Primate Conservation Inc., and the Animal Behavior Society.

Facial growth and development in subadult hominoids and fossil hominins

AMBER C. JAEGER[1], JULIE LAWRENCE[1,2] and GARY T. SCHWARTZ[1]

[1]School of Human Evolution and Social Change and Institute of Human Origins, Arizona State University, [2]Department of Human Evolutionary Biology, Harvard University

Stw 183, a partial subadult face attributed to *Australopithecus africanus*, is pivotal in assessing early hominin taxonomic variation since it has morphological attributes of both *A. africanus* and *Paranthropus robustus*. The number of species within Sterkfontein Member (SM) 4, from which Stw 183 derives, is a highly contentious issue. Our project assesses the likelihood that four features of the zygomaticomaxillary region, relevant to Stw 183's taxonomic attribution, express the adult phenotype. Previous research demonstrates that some facial features in *A. africanus* undergo age-related changes during the latter stages of ontogeny, i.e., the growth interval spanning M2-M3 emergence, calling into question whether subadults should be included alongside adults in comparative analyses. We evaluate the ontogenetic stability of facial anatomy in a comparative sample of extant hominoids (n=71) using coordinate data derived from 3D surface scans. Chimpanzee and human subadults experience age-related changes in the zygomaticomaxillary region, including a significant increase in anterior-posterior thickness of the zygomatic root (t-test; p<0.001), while gorillas do not. Morphology that distinguishes *A. africanus* from *P. robustus* – relative position of the infraorbital foramen and degree of zygomaticoalveolar crest curvature – remains constant throughout later ontogeny, suggesting that these two features can be utilized with confidence in analyses that include both subadults and adults. On the whole, aspects of hominoid zygomaticomaxillary form in subadults are sufficiently similar to adults and warrant their inclusion in comparative analyses. Caution should be taken, however, when including positional and metric data on zygomatic roots as these features exhibit measurable ontogenetic changes.

Supported by an IHO fellowship to A.C.J.

Gut microbial diversity predicts brain immune gene regulation in a model nonhuman primate

MAREIKE C. JANIAK[1,2], ALEX R. DECASIEN[1,3,4], KENNETH L. CHIOU[5,6], CATALINA I. VILLAMIL[7], MICHALA K. STOCK[8], AMBER E. TRUJILLO[1,3], ALLEGRA N. DEPASQUALE[2], JOSEPH D. ORKIN[9], ANGELINA V. RUIZ-LAMBIDES[10], JOSUÉ E. NEGRÓN-DEL VALLE[6], CAMILLE TESTARD[11], SAMUEL E. BAUMAN SURRATT[12], OLGA GONZALEZ[13], CAYO BIOBANK RESEARCH UNIT[11], MELWEEN I. MARTÍNEZ[12], CHRISTOPHER S. WALKER[14], JÉRÔME SALLET[15,16], MARIA GLORIA DOMINGUEZ-BELLO[17], MICHAEL J. MONTAGUE[11], SUSAN C. ANTÓN[1], AMANDA D. MELIN[18,2], LAUREN JN. BRENT[19], MICHAEL L. PLATT[11], NOAH SNYDER-MACKLER[5,6] and JAMES P. HIGHAM[1,3]

[1]Department of Anthropology, New York University, [2]Department of Anthropology & Archaeology, University of Calgary, [3]New York Consortium in Evolutionary Anthropology, [4]Section on Developmental Neurogenomics, National Institutes of Mental Health, [5]Center for Evolution and Medicine, Arizona State University, [6]School of Life Sciences, Arizona State University, [7]School of Chiropractic, Universidad Central del Caribe, [8]Department of Sociology and Anthropology, Metropolitan State University of Denver, [9]Institut de Biologia Evolutiva, Universitat Pompeu Fabra-CSIC, [10]Department of Human Behavior, Ecology and Culture, Max Planck Institute for Evolutionary Anthropology, [11]Department of Neuroscience, University of Pennsylvania, [12]Caribbean Primate Research Center, University of Puerto Rico, [13]Disease Intervention & Prevention, Southwest National Primate Research Center, [14]Department of Molecular Biomedical Sciences, College of Veterinary Medicine, North Carolina State University, [15]Department of Experimental Psychology, Wellcome Integrative Neuroimaging Centre, University of Oxford, [16]Stem Cell and Brain Research Institute, Université Lyon, [17]Department of Biochemistry and Microbiology, Department of Anthropology, Rutgers University, [18]Alberta Children's Hospital Research Institute & Department of Medical Genetics, University of Calgary, [19]Center for Research in Animal Behaviour, University of Exeter

Gut microbiota can modulate host physiology, metabolism, and immune function via the gut-brain axis (GBA), and potentially influence social behaviors. Yet much of what we know about this link comes from studies of lab-reared rodents, and we have limited knowledge of how this translates to humans and other primates – key data for assessing the evolutionary importance of the GBA as well as identifying its role in the etiology of human health and disease. Here, we probed associations between gut microbial diversity and brain gene expression in 35 free-ranging rhesus macaques (*Macaca mulatta*) from Cayo Santiago. We sequenced 16S amplicons from rectal swabs and quantified microbial alpha diversity. For the same individuals (19 females, 16 males), we generated RNA-seq data for 15 brain regions. To investigate the relationship between gut microbial diversity and brain gene expression, we modeled gene expression within each brain region as a function of sex, age, number of social partners, and microbiome alpha diversity, controlling for genetic relatedness and technical covariates. We then applied multivariate adaptive shrinkage to increase the precision of our effect estimates, and identified 1213 (9.6%) genes whose expression was significantly correlated with (lfsr<0.05) microbial diversity. These genes were associated with multiple pathways involved in response to or production of type I interferon, suggesting that the gut microbiome may modulate immune responses in the brain. These findings provide the first evidence of GBA links in a nonhuman primate and thus have important implications for understanding human health and disease.

AAPA Cobb Award (MCJ), Leakey Foundation (SCA, JPH), NSERC and CRC (ADM), NIH: R01MH096875, #8-P40-OD012217-25, T32AG000057, R01MH118203, U01MH121260, R01AG060931, R00AG051764; NSF: BCS-1800558, BCS-1752393, NYU MacCracken (ARD)

Substrate-related variation in limb joint kinematics in wild primates

JUDITH JANISCH[1], ALLISON MCNAMARA[2], NOAH T. DUNHAM[3], TAYLOR PHELPS[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

Arboreal locomotion is precarious and places multiple challenges upon stability 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). We tested if these strategies are also adopted by wild howler monkeys (*Alouatta palliata*) freely ranging over a variety of supports in their natural habitat at La Suerte Biological Field Station, Costa Rica. 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.

Spearman rank order correlations were used to test for associations between joint posture and support diameter/inclination (measured using a forestry-grade rangefinder). Our results partially confirmed previous kinematic studies of captive primates. Wild howlers increased knee flexion, elbow yield and shoulder/hip excursion as supports became increasingly steeper but did not significantly adjust joint kinematics to variation in support diameter. These results suggest that variation in support orientation, rather than diameter per se, may exert a stronger influence on quadrupedal gait kinematics in primates moving in natural environments.

Supported by NSF BCS-1921135, BCS-1921314, BCS-1640552 and BCS-1640453.

Evolved to be special: Portmann's concept of human uniqueness

FILIP JAROŠ

Department of Philosophy and Social Science, University of Hradec Králové

From a philosophical perspective, the problem of anthropological difference is focused on the following question: Is there any fundamental difference between humans and animals that is prior to all other differences? In his attempt to solve this problem, Portmann (1941, 1942) famously classified human species as "secondarily altricial" and provided a metaphor of a "social womb": human children are born premature in comparison with other primates, and they find a second womb in a social environment nurturing their healthy development.

Though Portmann's findings have a solid empirical basis, they are also significantly framed by the general program of philosophical anthropology (Scheler, Plessner): to find a qualitative difference between humans and non-human animals. In this tradition, the cognitive faculties of non-human species are seen as intrinsically linked to their species-specific life-world (*Umwelt*). In contrast, humans, due to their faculty of language, are able to detach from their immediate life-world through cultural representations.

Although one has to agree that cultural processes form the human species to an unmatched extent, it remains an open question if the conceptual distinction between organic inheritance and cultural evolution is unique to our species. The last decades boast numerous studies on animal cultures, mainly in the case of apes (cf. Laland and Galef 2009). I suggest that the idea of the social womb might be extended to non-human species linking the existence and transfer of group traditions to a sensitive period of early postnatal development.

Czech Science Foundation (GAČR), project "Adolf Portmann - a pioneer of the eidetic and semiotic approach in the philosophy of the life sciences" (grant number 19-11571S)

Imaging soft biological structures using micro computed microtomography (µCT)

TEA JASHASHVILI[1,2], TAUTIS SKORKA[3] and PETER S. CONTI[3,4]

[1]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, Los Angeles, CA 90033, USA, [2]Department of Geology and Paleontology, Georgian National Museum, Tbilisi 0105, Georgia, [3]Department of Radiology, Molecular Imaging Center, Keck School of Medicine, University of Southern California, Los Angeles, CA 90033, USA, [4]Department of Biomedical Engineering, and Pharmaceutical Sciences, Keck School of Medicine, University of Southern California, Los Angeles, CA 90033, USA

Visualizing myological variation in different primates facilitates evaluation of adaptive features in their musculoskeletal systems. High resolution computed tomography (µCT) is advantageous for visualizing structural details of low-density soft tissue structures, such as muscles, in a non-destructive manner, but it requires the application of contrast to be successful. Improving existing staining methods and/or developing new ones can greatly aid investigations of muscle structure with µCT imaging. Binding high-atomic number elements to the components of these soft tissue structures of interest takes advantage of osmotic differences that attract high electron density material. Here, we present novel results using a ratio of Phosphate-buffered saline (PBS) and Phosphotungstic acid (PTA) (PBS/PTA) in a staining solution applied in contrast-enhanced CT of soft tissue. Each specimen was placed in a size-matched tube to permit freedom of movement of the sample. The tube was filled with 3% PBS/PTA solution and placed on a rocking table for a minimum of 3 days to ensure the staining solution was absorbed by the sample. Afterwards, specimens were checked for stain progression with a quality control µCT scans. Solution concentration was gradually increased until suitable enhancement in X-ray images was achieved. Final scans were performed once a well-defined peak was available in the gray scale histogram corresponding to the soft tissue structure of interest. This approach has the potential to improve visualization of soft tissue structure through augmented image definition based on gray scale histogram values.

Sleeping less is related to higher levels of estradiol in women of reproductive age

GRAZYNA JASIENSKA, MAGDALENA MIJAS, ANDRZEJ GALBARCZYK, MAGDALENA KLIMEK, KAROLINA MIŁKOWSKA, KINGA SŁOJEWSKA and ANNA TUBEK

Department of Environmental Health, Jagiellonian University

Sleep duration and pattern are related to many aspects of human physiology and health. In many non-human species, circadian rhythms strongly influence reproductive function, but it is not clear if similar relations are present in human females. The link between the physiology of menstrual cycles and the hormone melatonin, levels of which change in relation to sleep, is well established. Thus, we hypothesized that women who differed in sleep patterns would show a corresponding variation in their reproductive physiology.

Forty seven Polish, healthy, regularly menstruating women, aged 22 to 37 provided daily saliva samples for estradiol (E2) and progesterone (P) analyses. Data on their physical activity and sleep were recorded continuously using Fitbit Alta HR activity tracker for one entire menstrual cycle. Women who, on the average, slept less than 7 hours per day had 24% higher levels of E2 than women who slept longer ($\beta = .44$, $p = .001$), when controlling for age and BMI. The length of sleep did not predict mean P levels or E2/P.

These results provide new insights about relations between sleep, reproductive physiology, and women's health. While results from our study do not point to the direction of the observed relationship between sleep and E2 levels they do support the current understanding of bi-directional cross-talk between melatonin and sex hormones. The evolutionary and health significance of higher levels of E2 of women with shorter sleep should be discussed in the areas of human reproductive ecology and disease prevention.

Ministry of Education and Science (Poland) grant nr. N43/DBS/000171

A moonlit dinner: Comparative gum feeding ecology of two sympatric galagos (*Otolemur crassicaudatus and the Galago moholi*) living in an afromontane temperate environment

RAVEN W. JAYNE[1], MICHELLE L. SAUTHER[1], JAMES B. MILLETTE[1], BENTLEY SCHOLZ[1] and FRANK P. CUOZZO[2,3]

[1]Department of Anthropology, University of Colorado, [2]Mammal Research Institute, University of Pretoria, [3]Lajuma Research Centre

Temperate environments are rarely inhabited by primates, are challenging, and are especially difficult for smaller-bodied nocturnal species. Due to cold temperatures, high humidity, often higher altitude, and seasonal changes in food availability feeding can be complicated. We explored gum feeding behavior in two sympatric nocturnal, strepsirrhine primates, *Otolemur crassicaudatus* (1090g), and *Galago moholi* (150g), living in a temperate high-altitude (>1200 meters) habitat at the Lajuma Research Centre in northern South Africa. Using camera trap analyses, data was collected from January 2017-June 2018. Results from 13,161 camera trap images document the two species utilize acacia gum as a monthly valuable food resource. *O. crassicaudatus* used gums more during the hot season than the cold season

(DF= 1, X^2 = 93.30, p < 0.0001) and more during the hot season than *G. moholi* (DF= 1, X^2 = 93.30, p < 0.0001), while *G. moholi* used gums more in the cold season compared to the hot season (DF= 1, X^2 = 204.80, p < 0.0001). The two species' feeding behaviors are affected by moon phase. *O. crassicaudatus* is lunarphobic, with greater gum use during the new moon compared to the full moon, (DF = 1, X^2 = 108.06, p-value < 0.0001). *G. moholi* is lunarphilic, using gum more during the full moon (DF = 1, X^2 = 190.82, p-value < 0.0001). In this challenging, Afromontane environment, two bushbaby species of notably differing size use the same resource in different ways, likely reflecting their different metabolic, predator defense, and other needs.

Funding: The National Science Foundation, USA (BCS 1638833), The University of Colorado-Boulder.

Use of Thermogravimetric Analysis to Estimate Collagen and Hydroxyapatite Contents in Archaeological Bone

NATALIA JIMENEZ[1], RICKY DURGA[1], SIVAKUMAR RAMANTHAN[3], PRANNOY SURANENI[2] and WILLIAM J. PESTLE[1]

[1]Department of Anthropology, University of Miami, [2]Department of Civil and Architectural Engineering, University of Miami, [3]Civil and Construction Engineering, Oregon State University

The present study evaluates the effectiveness and accuracy of thermogravimetric analysis (TGA) in estimating the amounts of collagen and hydroxyapatite in archeological human bone specimens. As a minimally destructive and relatively inexpensive method --compared to more popular chemical/molecular focused methodologies-- TGA offers the opportunity for quick, preliminary testing that avoids the superficiality of other collagen quantification methods such as vibrational spectroscopy.

Our assessment of TGA centers around twenty-four previously analyzed archeological bone samples and their respective mass losses in the approximate temperature ranges of 300–500˚C, 220–600˚C, and 600–900˚C, corresponding to collagen mass loss, organic mass loss, and hydroxyapatite mass loss, respectively. Our findings show strong correlations between independently determined collagen content and the ranges of 300–50˚C (r=0.90, df=22, p<0.01) and 220–600˚C (r=0.99, df=22, p<0.01), but no strong correlations between the range of 600–900˚C and hydroxyapatite (r=0.08, df=22, p=0.722) suggesting that TGA, while effective in indicating the collagen content/preservation of archeological bone specimens, still requires further study to explore its potential in assessing hydroxyapatite. For the purposes of this study, however, these findings sufficiently support TGA as another tool in the toolkit of archeologists and forensic scientists alike. TGA provides another modality for quality control of archeological materials and offers great promise as a technique for archaeological exploration.

A Global Examination of microRNA Genes in Modern and Ancient Human Genomes

HUNTER R. JOHNSON[1], JOSÉ A. GALVÁN[2], WILLIAM J. HIGGINS[2], SAMY GADI[1] and NATHAN H. LENTS[2]

[1]Mathematics and Computer Science, John Jay College, The City University of New York, [2]Sciences, John Jay College, The City University of New York

Compared to that of proteins, the evolution of gene expression control remains an underexplored area of research in human evolution. Our laboratory recently reported the evolution of new microRNA genes in the human lineage, which are shared with Neanderthals and Denisovans but not with extant apes. A single miRNA can affect gene expression of hundreds or just a few genes and in either a global or highly tissue-specific manner. Further, the genes targeted by a given miRNA can be altered by point mutations with far-reaching effects throughout the organism. Thus, miRNAs could be a powerful and underappreciated force in the evolution of gene expression. In this project, we analyze the entire pool of known miRNA genes in Neanderthals, Denisovans, and modern humans. Taking into account polymorphisms, we have determined which miRNAs are conserved across the genomes and which have evolved uniquely, roughly 200 in each lineage. We have characterized the precise nature and effect of the sequence changes, particularly in the seed region where target specificity is encoded. We also explore the relative rates of evolution of these genes compared to protein-coding and noncoding DNA in each genome. And finally, we explore how the shared and unique networks of miRNA target genes have evolved in each lineage. This work shows how slight tweaks to miRNA genes can alter gene expression networks involved in development of the nervous system, immune system, energy metabolism, etc., driving major physiological changes with little or no alterations to protein-coding genes.

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.

Untangling Louisiana's unmissed: How forensic anthropologists can use population demographics to aid in identifications

LIAM J. JOHNSON[1], TERESA V. WILSON[2] and GINESSE A. LISTI[2]

[1]Department of Anthropology, University of Nevada, Las Vegas, [2]Department of Geography and Anthropology, Louisiana State University

To work with unidentified remains is to engage with those who are missing; however, not all individuals who are missing are reported as such. These "unmissed persons" are those individuals whose absence is not reported but who nevertheless are missing. By engaging more closely with missing persons databases, forensic anthropologists may better understand unmissed persons as well as gain a more nuanced understanding of the unidentified. As such, the current study examines demographic representations between a state-level missing person database and census data. Case files of 557 missing persons reported between 1974-2020 were analyzed from the Louisiana Repository for Unidentified and Missing Persons Information Program ("Repository"); these data then were compared to the 2018 state census. While some data patterned similar to the census (e.g., age), some demographic traits of the Repository's missing population, like social race and sex, are more divergent. Specifically, when compared to census data, males are represented 14.1% more in the Repository. Additionally, cases that recorded a non-white social race were 8.2% over-represented in the Repository. These data demonstrate that disparities exist between the demographics of missing persons databases and the parent population, and that such disparities may illuminate structural and sociological inequities involving one's vulnerability of going missing, the likelihood of officially being reported as missing, and differential rates of case closure. Such information can be used by forensic anthropologists, sociologists, law enforcement, and others to more effectively communicate with under-represented communities and, ultimately, may help to resolve long-term unidentified remains cases.

Investigating the changes in oral microbial ecologies of ancestral Maya individuals from Belize accompanying shifts in subsistence patterns

SARAH J. JOHNSON[1,2], TANVI P. HONAP[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, 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

While humans have undergone dietary shifts during our evolutionary histories, it remains unclear to what extent these transitions impacted the human oral microbiome and subsequently, oral health. To investigate changing microbial ecologies, we analyzed dental calculus samples and reconstructed oral metagenomes from directly dated ancient humans recovered from two rock-shelters in the Maya Mountains of Belize. Based on previously quantified stable isotopic

ratios, these individuals are categorized as having pre-maize (9600-4700 cal BP, n=9), transitional maize (4700-4000 cal BP, n=1), and staple maize (4000-1000 cal BP, n=14) diets. Total DNA was extracted from dental calculus and partially uracil deglycosylase-treated, double-stranded libraries were prepared and shotgun-sequenced with Illumina technology. A largely unexplored endodontic pathogen (*Pseudoramibacter alactolyticus*) was found in high abundance in the pre-maize individuals, but not after maize incorporation. We reconstructed partial genomes of *P. alactolyticus* (at least 50% of the reference covered at greater than five-fold depth) from six ancestral Maya individuals and four partial genomes from previously published oral metagenome datasets from Europe and Africa. Both SNP-based and multi-gene phylogenetic analyses showed that strains from ancestral Maya individuals clustered with a modern American strain, and those from Europe and Africa formed a separate cluster. Clear geographic structuring within the species demonstrates long-term host-microbial association despite variations in abundance accompanying shifting maize utilization patterns. Further investigations of keystone taxa and functional networks will reveal the impact of changing dietary patterns on the oral microbiomes of the ancestral Maya population and the implications for oral health.

This work was funded by a grant from the National Science Foundation (NSF BCS-2045308).

The effects of treatment methods on human teeth dissolved in HCL: Indications for forensic anthropological studies on acid disposal

CHRISTINE A. JONES and TAMMY BRACEWELL

Social Sciences, Texas A&M University Central Texas

In forensic anthropology, researchers have explored the use of acid in the disposal of human remains through experimental research studies. The current scant literature exposes a lack of consistency and shows methodological variations including different sample sizes, lack of control samples, use of different tooth types, and variation in sample treatment. We hypothesized that the treatment methods, repeated rinsing and drying, applied to tooth samples during the experimental process increased dissolution rates. For this study, a sample of five intact permanent human molars were completely immersed in hydrochloric acid (HCL, 38%). Two samples were left undisturbed as controls, and three treatment methods were applied for the remaining samples: (1)rinse only, (2)rinse and dry, and (3)rinse, dry, and replace acid. Our results demonstrated that the control samples dissolved completely at 70 and 89 hours. The treated samples took significantly less time to dissolve and by 28-29 hours were between 94.95% and 99.04% dissolved. The addition of treatments increased dissolution rates by over 50%. Our results suggest that treatment methods such as rinsing and drying, often used to allow researchers to weigh or photograph specimens during experimentation, have a significant effect on the timing of dissolution and results from previous studies. The continued use of acid as a means of body disposal necessitates accurate and repeatable forensic studies which apply experimental methodologies using acid and human remains. Validation studies with larger sample sizes are needed to further characterize the effects of treatment methodologies.

The Emergent Structure of Subsistence Risk-Management Networks

JAMES HOLLAND JONES[1] and ELSPETH READY[2]

[1]Earth System Science, Stanford University, [2]Department of Human Behavior, Ecology and Culture, Max Planck Institute for Evolutionary Anthropology

As with all subsistence populations, hunter-gatherers are exposed to substantial livelihood risk because of the inherently variable nature of their resource base. The primary mechanism of risk management among hunter-gatherers is food-sharing and extensive sharing creates networks. We test the hypothesis that the structure of these networks contains design features that manage the substantial livelihood risks faced by subsistence populations. We suggest that generalized exchange is the foundation for subsistence risk-management networks. Not surprisingly, the micro-foundations of generalized exchange have historically been couched in terms cyclical tie-formation. However, we show that networks formed by a preponderance of cyclical relations would not satisfy the fundamental risk-management objective, and suggest instead that transitive closure, a process typically associated with hierarchical social relations, should be the primary mechanism of sharing-network formation. Networks formed by strong transitive closure are characterized by high tie density that produces many paths over which generalized exchange can be realized. We expect that resulting networks to be characterized by a strong core-periphery structure. We test the hypothesis with data on country-food sharing among Inuit hunters in Nunavik and find that our predictions are strongly supported. The food-sharing network has very high transitivity and is characterized by a striking core-periphery structure. We conclude with a discussion of network structure under different modes of livelihood risk management and what these networks tell us about cultural transmission and adaptation to contemporary climate change.

The evolutionary history of infectious disease in the ancient Americas and the pathogenic consequences of European contact

SOPHIE K. JOSEPH and JOHN LINDO

Anthropology, Emory University

The increasing availability of next generation sequencing techniques in recent decades has led to new discoveries, and sometimes the redefinition of conventional hypotheses, regarding many complex human-pathogen evolutionary relationships. These new discoveries are particularly poignant in studies of the Americas, where research into Indigenous ancestry and migration has historically been largely ignored. As a result, conventional hypotheses regarding the origin of global pathogens like tuberculosis, syphilis, and malaria in the Americas and their spread within the continents have been mischaracterized. Fortunately, recent studies using molecular techniques have now superseded these missteps, which were often based in anecdotal accounts from colonial missionary reports rather than rigorous scientific study. It is now clear that there was not a unidirectional pipeline of pathogen introduction that began with European contact; instead, a rich and varied microbiological landscape already existed in the Americas. This synthesis of research regarding the origin and spread of pathogens in the Americas examines the scope of this changing perception within the fields of paleogenomics and paleomicrobiology.

The current status of methods usage in forensic anthropology casework using the Forensic Anthropology Database for Assessing Methods Accuracy (FADAMA).

CHELSEY A. JUAREZ[1], CRIS E. HUGHES[2] and AN-DI YIM[3]

[1]Anthropology, Fresno State University, [2]Anthropology, University of Illinois at Urbana-Champaign, [3]Health and Exercise Science, Truman State University

The use of specific methods for estimating the biological profile in forensic anthropology casework is tied to factors including available elements, methods validation, and practitioner training. This study investigates cases uploaded to the Forensic Anthropology Database for Assessing Methods Accuracy, FADAMA for which data on 101 different methods was available. The goals of this study are to understand methods usage across time, assess methods adoption, and discuss potential limitations. The case sample is dated from 1978- 2021 (N=361). For sex, age, ancestry, and stature estimation there were N=342; N= 948, N= 290, and N=132 instances of methods used recorded by practitioners in the database. Results indicate a focus on a small group of methods for each category of the biological profile over time and limited adoption of newer methods. Five

sex estimation methods represented 92% of the methods used with a median methods date of 2008. Four age estimation methods represented 65% of the methods used, with a median methods date of 1987. Four ancestry estimation methods represent 97% of the methods used with a median methods date of 2005. Two stature estimation methods represent 90% of the methods used with a median methods date of 1996. Interestingly, the use of some older methods significantly increases over time, while the vast majority of recent methods gain little traction. These trends suggest the need to investigate how factors like method validation (or lack of), pedagogical traditions, and systematic access to methods training impact the selection of methods used in casework.

This project was supported by Award No. 2018-DU-BX-0213 awarded by the National Institute of Justice, Office of Justice Programs, U.S. Department of Justice.

Examination of degrees of modularity in the anthropoid axial skeleton

HYUNWOO JUNG[1,2] and NOREEN VON CRAMON-TAUBADEL[2]

[1]Department of Anatomy, Midwestern University (AZ), [2]Department of Anthropology, University at Buffalo

This study examines the degrees of modularity in the anthropoid axial skeleton. It is hypothesized that hominoids will show relatively stronger degrees of modularity than other anthropoids, and that there may have been reduced constraint for the evolution of novel axial skeletal morphology in hominoids.

For this, 3D scans of the cranium, mandible, vertebrae (13 elements), and sacrum of five hominoid genera and seven Old and New World Monkey genera were used. Intrageneric variation (e.g., sex, species) was controlled by mean-standardization. Degrees of modularity were calculated as the covariance ratio coefficient (CR) using variance/covariance matrix of inter-landmark distances. CR was calculated in all possible pairs of axial skeletal elements. Spatial arrangement of taxa in low dimensional space was visualized using 2D non-metric multidimensional scaling (MDS) of Euclidean distance matrices representing the pairwise differences between the CR results among taxa.

The results supported the hypothesis as there was generally stronger degrees of modularity (i.e., lower CR) in the axial skeletal elements in hominoids than other anthropoids except *Alouatta*. In the 2D MDS results, hominoids and *Alouatta* were generally separated from other anthropoids. Thus, the results suggest that there may have been less constraint on the evolution of axial skeletal morphology in hominoids and less constraint may have pre-existed in hominoid ancestors for the evolution of novel axial skeletal morphology in hominins. In addition, *Alouatta* may show convergent degrees of modularity to hominoids in terms of similar locomotor behaviors (e.g., climbing, bridging, and suspensory behaviors).

This work is supported by the National Science Foundation under grant number BCS-1830745 and the Mark Diamond Research Fund of the Graduate Student Association at the University at buffalo (SUNY).

The influence of locomotion and body mass on the primate ulna: new insights into behavioral postures in fossil taxa

JASON P. JUNG[1], MARC R. MEYER[2], JEFFREY K. SPEAR[3,4], ISABELLA FX. ARAIZA[3,4] and SCOTT A. WILLIAMS[3,4]

[1]Biology, California State University, San Bernardino, [2]Anthropology, Chaffey College, [3]Anthropology, Center for the Study of Human Origins, New York University, [4]New York Consortium in Evolutionary Primatology, NYCEP

Despite exhibiting a range of specializations in locomotion most primates have a relatively generalized postcranial skeleton, enabling extensive locomotor flexibility. However, a small number of forelimb traits, including in the morphology of the ulna, exhibit strong functional signals that may provide a link between skeletal morphology and locomotor behavior. Here we evaluate ulnar shaft and proximal complex shape using elliptical Fourier analysis against locomotor pattern, body mass, and taxonomic group in a sample of 418 ulnae across 88 extant primate species. We also examine six fossil ulnae from genus *Plesiadapis*, *Theropithecus*, *Nannodectes*, *Notharctus*, and *Daubentonia*.

Principal component and factor analyses indicate that locomotion contributes to proximal complex shape across primates, but increasing body mass exerts a stronger influence on proximal complex contours. With increasing allometry the olecranon becomes progressively reduced until it is fully situated beneath the anconeal process. By contrast, locomotion has the strongest influence on ulna shaft shape across the full primate sample, particularly in primates over 6 kg.

Discriminant function analysis of Fourier descriptors place *Theropithecus* securely among the terrestrial quadruped locomotor group, although with a greater degree of arboreal adaptation than in extant *Papio*. The *Plesiadapis* fossil ulna falls close to the arboreal quadruped group, but like the remainder of the fossil sample classifies most strongly with the vertical clinger and leaper locomotor group. These results instantiate the efficacy of Elliptical Fourier analysis in mathematically modeling ulnar morphology, and its utility in helping to understand allometric, locomotor, and taxonomic variability in both extant and fossil contexts.

Colonial Logics and Captive Bodies: Radical reckonings with question of ethics in the collection of human remains

DELANDE JUSTINVIL

Department of Anthropology, National Museum of Natural History, Smithsonian Institution

Founded in 1999, the core mission of the Indigenous Peoples Council on Biocolonialism (IPCB) is "to assist indigenous peoples in the protection of their genetic resources, indigenous knowledge, cultural and human rights from the negative effects of biotechnology." Biocolonialist tactics mobilize the promise of science for the welfare of humankind as a facade for practices that expand legal, political, and economic domination over already forcibly marginalized communities. While this domination pertains to organic, biological matter such as land and people, many scholars advocate for it also includes the onto-epistemological sphere as well. Biocolonialism commodifies and capitalizes on the different modes of knowing and feeling undergird the foundation of multicultural life-worlds. However, while the majority of research on its destructive capacities specifically focus on Indigenous life, I argue that many similar - if not the same - practices are coerced upon the biologies of Black bodies across the African diaspora. With renewed attention to the treatment of Black people, both living and dead, as scientific matter amid calls for an African American Graves and Repatriation Act (AAGPRA), I argue for a shift in the ideological landscape of the fight against biocolonialism so that it becomes an extension of Afro-Indigenous solidarity against capitalist, colonialist, imperialist violence.

Why ancestors haven't mattered: Received epistemic values in American Physical/Biological Anthropology impeding discipline-wide conversations around ethics

ANN M. KAKALIOURAS

Anthropology, Whittier College

This abstract is part of the symposium *Ethics in the Curation and Use of Human Skeletal Remains* and represents a paper that is the result of original historical research, not the testing of a research hypothesis. This presentation focuses on the recent history of biological anthropology, specifically the epistemic effects of the fluorescence of paleopathology in the 1960s and the consolidation of bioarchaeology as a discipline in the 1970s.

There are recent historical connections between the adoption of a processual approach in physical anthropology and the concretization of the idea that human remains are uniquely invaluable to, and exclusively for, scientific study. That is, when researchers began to seek out ever larger skeletal samples to answer their questions, they also began to construct every single bone as necessary--the irreplaceable remain of a unique

individual. This is in contrast to previous disciplinary conceptions, where either crania took precedence, or specific bones showing pathological changes were more valued than those that did not.

Implicit and explicit racism, as well as colonial practices, are clearly the most crucial historical and contemporary realities we have to face in American biological anthropology. I argue, though, that the above confluence of valuing both volume and uniqueness also left us wholly unprepared to face Indigenous repatriation, and, for that matter, any intersections between our science and politics. Additionally, these epistemic values continue to imperil discipline-wide examinations of the emerging crises over the ethical treatment of African-American ancestors and those of other historically marginalized peoples.

This research was funded, in part, by a 2015-16 fellowship from the Whitney Humanities Center at Yale University

The Ecology and Evolution of Primate Hair

JASON M. KAMILAR[1,2] and BRENDA J. BRADLEY[3,4]

[1]Department of Anthropology, University of Massachusetts, Amherst, [2]Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts, Amherst, [3]Center for the Advanced Study of Human Paleobiology, The George Washington University, [4]Department of Anthropology, The George Washington University

This abstract is part of the symposium *Integumentary Anthropology: Examining the Exterior*. Hair is an ideal system for studying the role of ecology and evolution on trait diversity from molecular to macro scales. Hair is an anatomical trait that is shaped by both natural selection (e.g. providing camouflage against predators, protection from parasites, maintaining body temperature in cold environments) and sexual selection (e.g. signaling sex, age, status). It is a universal characteristic of mammals, yet across species there is striking variation in the color, pattern, growth, and texture of hair. Moreover, many hair traits, such as tail stripes, or thick woolly coats, seem to have evolved repeatedly in different mammal lineages. Hair is also a trait for which small genetic differences can have major phenotypic effects (e.g. red hair in humans is often due to variation at a single gene) and many hair-related loci show signatures of local adaptation across human populations. Importantly, the hair/skin often serve as the first line of defense for an individual, acting as both a physical and chemical barrier to the environment, as well as source of sensory perception. From an explicitly anthropological perspective, the hair/skin patterns of humans are unique and distinguish us from other primates. In this presentation, we discuss the current state of knowledge about the ecology and evolution of primate hair and its implications for understanding human uniqueness and primate biology and health. In addition, we will outline future research avenues that should yield interesting insights into biological anthropology.

Leakey Foundation, NSF (BCS #1546730, BCS #1606360), Wenner-Gren Foundation, The George Washington University, University of Massachusetts, Amherst, Yale University, and the Natural Environment Research Council, UK.

Craniofacial variation in early *Homo sapiens*

TANIA KAPOOR and SUZANNA WHITE

Department of Anthropology, University College London

The evolutionary process for the origin of *Homo sapiens* in Africa (at least ~300 ka) remains debated, with models ranging from 'Out of Africa'/Single African Origin to Pan-African Multiregionalism. A recent alternative to the latter polycentric model is the structured African Metapopulation model which also recognises a pan-African origin of our species but in a more complex, dynamic and reticulate context. The debate is further muddled by the corresponding fossil evidence displaying much craniofacial mosaicism, with the full suite of modern human (MH) features only appearing from ~100–40 ka, and unusually vast morphological variation lumped under the *H. sapiens* species umbrella.

The present study explored craniofacial variation and mosaicism in the relevant fossil record by assessing whether there was any temporal and geographical patterning in variability of different craniofacial aspects, with a view to test different models of MH origins in Africa. This study used a combination of traditional morphometrics and qualitative trait-based morphological assessment on craniofacial fossils of Middle–Late Pleistocene *Homo* specimens, including putative archaic and early *H. sapiens*, across four geographical regions: the Levant, North Africa, East Africa, and South Africa. Here, we report on morphological trends detected in the available hominin fossil record, including temporospatial patterns of key diagnostic MH craniofacial traits, such as neurocranial globularity and the presence of a chin. Preliminary results indicate potential geographical substructure in specific anatomical attributes of the craniofacial anatomy associated with a derived versus archaic state among the Middle–Late Pleistocene *Homo* population across Africa and the Levant.

New insights into the evolution of hominin thumb dexterity

FOTIOS ALEXANDROS KARAKOSTIS[1,2], DANIEL HAEUFLE[3,4], IOANNA ANASTOPOULOU[5], KONSTANTINOS MORAITIS[5], GERHARD HOTZ[6], VANGELIS TOURLOUKIS[1] and KATERINA HARVATI[1,2]

[1]Paleoanthropology, University of Tübingen, [2]DFG Centre of Advanced Studies "Words, Bones, Genes, Tool," University of Tübingen, [3]Hertie Institute for Clinical Brain Research and Werner Reichardt Centre for Integrative Neuroscience, University of Tübingen, [4]Institute for Modelling and Simulation of Biomechanical Systems, University of Tübingen, [5]Department of Forensic Medicine and Toxicology, National and Kapodistrian University of Athens, [6]Anthropological Collection, Natural History Museum of Basel

Efficient tool use constitutes a major component of bio-cultural evolution. Traditionally, the emergence of increased manual dexterity and habitual tool using behaviors had been associated with the genus *Homo*. Recently, however, this notion has been questioned due to the discovery of potential stone tool industries predating the genus *Homo* (>3 million years ago) and the identification of early hominin hand skeletons (*Australopithecus*) presenting anatomical indications of heightened manual dexterity. Nevertheless, most previous research on early hominin dexterity did not directly assess biomechanical efficiency, but instead relied on morphological comparisons across species, assuming that each species' dexterity is equivalent to the degree of its similarity with the modern human form. Here, we address this major research gap through a novel approach that for the first time integrates virtual muscle modeling with a three-dimensional (3D) geometric morphometric analysis of bone shape. We focus on muscle *opponens pollicis* and the act of thumb opposition, a fundamental component of human-like precision grasping and tool use. Our results highlighted the presence of increased, human-like, levels of thumb opposition dexterity in two fossil hominin thumb specimens from South Africa (Swartkans), dated to about 2 million years ago. In contrast, the earliest proposed tool-using species, the Australopithecines (including *Australopithecus sediba*), consistently exhibited lower biomechanical efficiencies. Importantly, all later species of *Homo* (including *Homo sapiens*, Neanderthals, and the small-brained *Homo naledi*) showed similarly heightened thumb opposition dexterities, highlighting the value of this evolutionary advantage for later human bio-cultural evolution.

This research was supported by the European Research Council (ERC CoG-724703), the German Research Foundation (DFG FOR 2237), and the Ministry of Science, Research, and Arts Baden-Württemberg (Az: 33-7533.-30-20/7/2).

Mixed-species and same-species siamang pairs exhibit similar activity and proximity patterns

FRANCESCA V.E. KASER[1], GARRETT REBARCHEK[1], ANNEKE MORESCO[2,3] and AMY L. SCHREIER[1,2]

[1]Department of Biology, Regis University, [2]Animal Wellness and Research, Denver Zoo, [3]Reproductive Health Surveillance Program

Siamangs and gibbons have monogamous mating systems, living in long-term male-female pairs. When a female siamang (*Symphalangus syndactylus*) was left without a partner, in 2018 Denver Zoo paired her with a male gibbon (*Nomascus gabrielle*; mixed-species pair) so that these social primates would not be alone. In 2021, however, a male siamang joined the female (same-species pair). To investigate whether housing mixed-species pairs benefits welfare, we compared behavioral patterns across pairs. We conducted scan sampling of focal individuals in each pair, recording data on activity and proximity every minute over 30-minute samples (mixed-species pair=31 hours; same-species pair=33.5 hours). While there were no significant differences across pairs in time spent resting, locomoting, and feeding, the same-species pair spent significantly more time grooming (1.5%) than the mixed-species pair (0.95%). With respect to proximity, both pairs spent equal amounts of time in physical contact, although the mixed-species pair spent significantly more time farther than 2m apart (mixed-species pair=71%; same-species pair=53%). Given the overall similarity in activity budgets and close proximity, our findings suggest that housing pair-bonded species in mixed-species pairs likely maintains animal welfare when a same-species partner is unavailable. While the mixed-species pair did spend more time farther apart than the same-species pair, it is unclear whether this can be attributed to species affiliation, the length of time the animals had been housed together, or individual personalities. To tease these possibilities apart, it will be important to reassess the same-species pair's activity budget once they have been living together for longer.

Reassessment of the Human Mandible from Bañolas (Girona, Spain)

BRIAN A. KEELING

Anthropology, Binghamton University

The Bañolas mandible was discovered in 1887 during quarrying activities near the present-day city of Girona, Spain, in the northeast of the Iberian Peninsula. Since its discovery, researchers have generally emphasized its archaic features, including the lack of chin structures, and suggested affinities with the Neandertals or European Middle Pleistocene specimens. U-Series and ESR dating suggest the mandible dates to the Late Pleistocene, approximately c.45-66 kya. This study reassessed the taxonomic affinities of the Bañolas mandible compared to samples of Pleistocene and recent human specimens, relying on both the expression of morphological features as well as 3D geometric morphometrics. The results of the comparative morphological analysis revealed no derived Neandertal features, while the 3D geometric morphometric analysis clearly grouped Bañolas with fossil and recent *H. sapiens* individuals. The contemporaneous age range with Neandertals but lack of Neandertal features in Bañolas is surprising. A consideration of the Middle Pleistocene fossil record in Europe and southwest Asia suggests that Bañolas is unlikely to represent a late-surviving Middle Pleistocene population. The lack of chin structures also complicates an assignment as *H. sapiens*, although early *H. sapiens* fossils do show variable development of the chin structures. Possible admixture with a non-Neandertal archaic *Homo* population might explain the lack of Neandertal features and chin structures in Bañolas, however no such population has been identified in the European Late Pleistocene fossil record. Thus, Bañolas represents a non-Neandertal Late Pleistocene European individual and highlights the continuing signal of diversity in the hominin fossil record.

Causal pathways between social determinants of maternal health, biomarkers of allostatic load, and hypertensive disorders of pregnancy vary among US racial/ethnic groups

MONICA H. KEITH and MELANIE A. MARTIN

Anthropology, University of Washington

Hypertensive disorders of pregnancy are increasing in the US and disproportionately impact racial and ethnic minorities. Allostatic load refers to the cumulative psychological and physiological effects of stress experienced across the life course and conceptually links social determinants of health with biomarkers. We hypothesize that higher cumulative stressors act directly and indirectly via health behaviors to increase maternal allostatic load across gestation, which in turn increases risk of developing hypertensive disorders of pregnancy. We developed a structural equation model (SEM) that integrates social determinants of health with individual-level changes in allostatic load measures across pregnancy to assess causal pathways that lead to maternal hypertensive disorders among a US dataset of nulliparous women (n=7658).

We ran our SEM for five hypertensive outcomes (superimposed, severe, and mild preeclampsia; new onset ante- and intra/postpartum hypertension) among three racial/ethnic groups (non-Hispanic Black, non-Hispanic white, and other identification) to account for the racialized processes by which stressors become embodied as disparate maternal morbidity risks in the US. Black mothers in this data experienced more severe hypertensive outcomes than other groups, and our model identified several pathways and risk factors that vary in magnitude and significance across racial/ethnic groups. For example, gestational weight gain predicts superimposed preeclampsia among Black mothers only, and socioeconomic factors have a stronger impact on weight among this group than others. Path coefficients estimate linear effects of specific risk factors and identify causal pathways that warrant further research and attention to address racial/ethnic disparities in maternal health outcomes.

Partial support for this research came from NICHD research infrastructure grant P2C HD042828, to the Center for Studies in Demography & Ecology at the University of Washington.

Benefiting from new interaction spheres during the Middle Horizon in ancient Peru at Tenahaha (AD 850-1050): merging strontium isotope and archaeological data

CORINA M. KELLNER[1], JUSTIN JENNINGS[2], WILLY Y. ALVAREZ[2] and FRANK C. RAMOS[3]

[1]Anthropology, Northern Arizona University, [2]Department of Art and Culture, Royal Ontario Museum, [3]Department of Geological Sciences, New Mexico State University

The Middle Horizon (MH, AD 500-1000) in the ancient Andes saw the rise of new social, political, and ideological networks, spurred in part by the rise of two powerful states: Wari and Tiwanaku. While analyses have centered state power in these MH interactions, societies emerged that benefited from these networks outside of direct state control. The population at Tenahaha, a Wari-influenced ritual center in the Cotahuasi Valley of south-central Peru (AD 850-1050), experienced a population surge, social stratification, and increasing foreign influence during the MH. New strontium data from human tooth enamel (n=16) of juveniles and adults buried in various tombs across the site suggests that Wari people did not migrate to Tenahaha (range of 0.706895-0.707097). These new analyses dovetail with previously analyzed archaeological data showing that Tenahaha was relatively peaceful during this tumultuous time and copied Wari ceramic iconography and architecture to profit from Wari's ideological cachet. Tenahaha may have succeeded in aligning themselves with new, popular ideologies and interaction networks without sacrificing local control. Past patterns of migration and the ability to opt out of direct state control is likely more variable as modern-day societies can successfully negotiate these interactions.

Funding from NSF#0630081.

Sex-biased evolutionary constraints: how cross-sex genetic correlations and evolvability affect the evolution of canine size dimorphism

CHRISTA D. KELLY[1], CHARLES C. ROSEMAN[2], KATHLEEN S. PAUL[1], J. MICHAEL PLAVCAN[1] and LUCAS K. DELEZENE[1]

[1]Anthropology, University of Arkansas, [2]Animal Biology, University of Illinois

Sexual dimorphism evolves due to differing selective pressures acting upon males and females. One target of sexual selection in primates is the maxillary canine, for which among-species differences in absolute and relative canine size and magnitudes of dimorphism are well documented. Less well understood is the impact of sexual selection on the genetic architecture (e.g., intralocus sexual conflict) that constrains the independent evolution of males and females. Using a pedigreed sample of *Papio hamadryas* (females, n = 321; males, n = 138), seventeen measurements were collected from casts of the permanent maxillary dentition (mesiodistal length and bucco/labio-lingual breadth for all teeth, as well as canine height). Using these measurements, two parameters, evolvability and cross-sex genetic correlation, were quantified. Evolvability measures microevolutionary potential, with sexually dimorphic traits predicted to have high evolvability. Cross-sex genetic correlation is a measure of the potential for male and female traits to evolve independently. Highly dimorphic traits are expected to have low cross-sex genetic correlations compared to sexually monomorphic traits. In line with these predictions, we find that for both sexes canine size has relatively high evolvability, with male canine measurements having the highest evolvability of all measurements. The cross-sex genetic correlations for canine measurements were the lowest. This suggest that intralocus sexual conflict resulted in the evolution of sex specific alleles or allele regulation of canine size in *Papio*. If other primates follow this pattern, this conflict, in conjunction with different selective pressures on each sex, is essential in the evolution of canine size dimorphism.

Age filtration in paleoepidemeological research: a cautionary tale and ways forward

SAIGE KELMELIS[1] and MICHAEL H. PRICE[2]

[1]Anthropology and Sociology, University of South Dakota, [2]Anthropology, Santa Fe Institute

Issues of equifinality and hidden heterogeneity plague paleodemographic and paleoepidemeological research. In their 1992 paper ("The Osteological Paradox: Problems of Inferring Prehistoric Health from Skeletal Samples") Wood and colleagues highlight three core challenges that afflict paleoepidemeological inference: demographic non-stationarity, selective mortality, and hidden heterogeneity. We believe at least one additional phenomenon must be added to the list: age filtration bias. By age filtration bias, we mean that the scientific sample available for study has been selectively and systematically filtered so that certain ages are overrepresented while others are underrepresented. Failure to account for this effect will lead to incorrect reconstructions of mortality hazard, a vital measure in paleoepidemiology. Worse, it can lead to incorrect estimates of parameters that are assumed not to depend on age. We simulated skeletal data that showed evidence of a nominal disease (n=100) both with and without age filtration using a three-state illness-death model, where the transition hazard from the 'well' (nonlesioned) to 'ill' (lesioned) state was constant and the level of age filtration was large but not implausible. Across 100 simulations, the reconstructed value for the transition hazard was systematically biased by -16% for the filtered case but was not biased for the unfiltered case. This suggests that caution be used in interpreting datasets for which age filtration may exist and will inhibit our ability to accurately interpret past epidemics. We close by offering ways forward, notably the use of Bayesian priors to model age filtration when it may exist but cannot be directly measured.

Differential use of arboreal substrates during leaping in free-ranging primates and squirrels

ADDISON D. KEMP[1], HANA HENDI[2], ALLISON MCNAMARA[3], NOAH T. DUNHAM[4], TOBIN L. HIERONYMUS[5], TAYLOR PHELPS[5], LIZA J. SHAPIRO[3] and JESSE W. YOUNG[5]

[1]Integrative Anatomical Sciences, University of Southern California Keck School of Medicine, [2]Biology, Duke University, [3]Anthropology, University of Texas at Austin, [4]Conservation and Science, Cleveland Metroparks Zoo, [5]Anatomy and Neurobiology, Northeast Ohio Medical University

Primates and squirrels are both highly adept at navigating complex arboreal environments despite their disparate locomotor and visual adaptations. Experimental data suggest that primates' wide binocular field enables them to engage in leaps landed accurately on relatively narrow substrates. Here, we evaluate whether wild primates navigating a natural environment leap to relatively narrower substrates than wild squirrels, which have a significantly narrower field of binocular vision. Videos of leaping in free-ranging *Sciurus carolinensis* (n=98) and *Cebus capucinus* (n=46) were filmed at Hiram College and La Suerte Biological Field Station, respectively. For leaps with trajectories roughly perpendicular to camera orientation, the diameter of landing and launch substrates as well as leap length were measured in DLTdv8 and scaled to animal trunk width. Wild primates both launched from and landed on branches that were relatively narrower than those used by squirrels ($p < 0.005$). In 21% of leaps to branches narrower than the animal's trunk, squirrels landed on clusters of branches. Primates used exclusively single-branch landings even at very small relative substrate sizes. Additionally, we found no significant relationship between leap length and launch substrate diameter in the wild squirrels, mirroring experimental findings that launch substrate diameter does not impact force production during leaping in squirrels. The significant difference in landing branch size and single- vs multi-branch landing at small substrate size between wild squirrels and primates supports the suggestion that primates' visual adaptations may facilitate precise arboreal leaping.

Research supported by NSF BCS-1640552 and BCS-1640453.

Identifying candidate SNPs shaping dental morphological trait expression

DORI E. KENESSEY, LEAH AUCHTER and MARIN A. PILLOUD

Department of Anthropology, University of Nevada, Reno

Dental morphological data are utilized as proxies for genetic variation to address various hypotheses within biological anthropology. However, the exact biological and genetic mechanisms responsible for the regulation of these traits remain mostly unknown. Recent work has sought to determine if genetic variants responsible for guiding the regulation of various ectodermal traits may also direct dental morphological trait expression due to a shared developmental origin. Through this approach, researchers successfully identified single nucleotide polymorphisms (SNPs) of the EDAR and WNT10A pathways that influence the morphological expression of both teeth and hair (Kimura et al. 2009, 2015). Here, we expand on these efforts by comparing the prevalence of SNPs influencing hair morphological variation with population-specific cusp 7 frequencies.

Data on cusp 7 trait frequency and genetic variants associated with hair morphology were collected from the literature focusing on ten populations (China, Japan, Vietnam, Colombia, Mexico, England, Finland, Nigeria, Kenya, and Gambia). Pearson's correlation with Holm's correction was performed to explore associations between the population frequencies of hair morphology SNPs and cusp 7 expression. Out of the 45 SNPs examined, 12 demonstrated a significant correlation ($p \leq 0.05$) to cusp 7 frequency, four were positive (rs6658216, rs310644, rs6841926, rs6912993) and eight were negative (rs7349332, rs12896399, rs499697, rs12116609, rs345542, rs12030667, rs10173381, rs10903929). These results highlight

candidate SNPs that may shape both hair and dental morphological variation. Future studies will explore the validity of the current findings in the context of a genome-wide association study.

The correlation between geographic distance and macaque skeletal morphology

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

Aside from humans, macaques are the most geographically widespread primate genus, living throughout Eurasia and northern Africa. However, the extent to which geographic distance correlates with macaque morphology is relatively unknown. Here we tested how well different aspects of the macaque skeleton reflect geography.

Data included 3D surface scans from nine species (*M. arctoides, M. fascicularis, M. fuscata, M. mulatta, M. nemestrina, M. nigra, M. radiata, M. sylvanus,* and outgroup *Trachypithecus cristatus*) representing different geographic locations for 297 individuals. Fixed and semilandmarks (*n*=293) were applied to eight skeletal elements for each individual (crania=45; mandible=31; scapula=66; humerus=38; radius=33; os coxa=28; femur=40; tibia=40), a regression analysis minimized the effects of sexual dimorphism, and the residuals were transformed into pairwise Euclidean distance matrices. A geographic distance matrix was calculated as the pairwise great circle distances between average latitude and longitude coordinates for each species. The two matrices were used as primary input variables for Mantel tests, assessing the significance between geographic and morphological distance. Least-squares Procrustes rotation based on 2D MDS plots were used to visualize how well geographic and morphological centroids tracked each other.

Results suggest that macaque morphology is correlated with geography, where some species like African *M. sylvanus* and Japanese *M. fuscata* more closely track their relative geographic position than southern-dwelling macaques. The innominate correlated the best with geography while the scapula correlated the worst. Thus, as primates continue to move and evolve in new locations due to changing climates, it is worth remembering the effect of geography on morphology.

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).

Early life adversity during the post-apartheid transition and COVID-19 stress independently predict adult post-traumatic stress disorder risk in urban South Africa

ANDREW W. KIM

Department of Anthropology, University of California, Berkeley, SAMRC Developmental Pathways for Health Research Unit, Faculty of Health Sciences, University of the Witwatersrand

The coronavirus disease 2019 (COVID-19) pandemic in South Africa introduced new societal adversities and mental health threats in a country where one in three individuals are expected to develop a psychiatric condition sometime in their life. Growing evidence has highlighted the role of early life adversity in exacerbating future adult mental illness, yet the pathways underlying this association are not well known. Scientists have suggested that psychosocial stress and trauma exposure during early childhood development may increase one's vulnerability to the mental health impacts of future stressors later in life – a process known as stress sensitisation. While this mechanism has been well evaluated in high-income, Western contexts, a small handful of studies have examined the stress sensitisation hypothesis in low- and middle-income settings and have largely relied on retrospective data. This analysis assesses the role of early life adversity experienced among South African children at age 5 (c. 1995) during the post-apartheid transition in exacerbating the mental health impacts of stress and trauma experienced during the COVID-19 pandemic in Soweto, South Africa (c. 2020-2021). Participants come from a longitudinal birth cohort study based in Soweto, South Africa. We find that greater childhood adversity and higher stress exposure during COVID-19 independently predict worse post-traumatic stress disorder (PTSD) symptoms risk in adults. Our results, however, show that early adversity at age 5 does not potentiate the mental health effects of greater COVID-19 stress in adulthood at age 30-31, suggesting null evidence for the stress sensitization hypothesis.

National Science Foundation, Wenner-Gren Foundation, National Institutes of Health, Social Science Research Council, Andrew W. Mellon Foundation, Woodrow Wilson National Fellowship Foundation, Northwestern University

Allometric scaling of maxillary sinus volume in modern humans

SUHHYUN KIM[1,2], LAUREN N. BUTARIC[3] and SCOTT D. MADDUX[1]

[1]Center for Anatomical Sciences, University of North Texas Health Science Center, [2]Texas College of Osteopathic Medicine, University of North Texas Health Science Center, [3]Department of Anatomy, College of Osteopathic Medicine, Des Moines University

Previous studies have questioned whether maxillary sinus (MS) volume scales isometrically, with some researchers hypothesizing that differences in MS volume may be associated with predictable alterations in MS shape. However, this allometric hypothesis has not been directly tested. Accordingly, this study assessed MS volume scaling patterns employing CT scans of crania ancestrally derived from three geographic regions: Europe (n = 54), Equatorial Africa (n = 58), and East Asia (n = 50). Using 3DSlicer, six 3D coordinate landmarks were collected from the left MS, from which linear measurements of MS height, width, and length were calculated. MS volume was then obtained by semi-automated segmentation of the sinus. Across-group and pooled within-group multivariate regression analyses were conducted to test for volume-associated 3D shape transformations. Results indicate that individuals with larger MS volumes exhibit relatively wider, taller, and anteroposteriorly shorter sinuses than those with smaller MS volumes, in both across-group ($r = 0.57$, $p < 0.0001$) and within-group analyses ($r = 0.49$, $p < 0.0001$). Further, a multiple regression analysis employing linear measurements indicates that differences in MS width ($\beta = 0.43$, $p < 0.0001$) contribute considerably more to variation in MS volume than MS height ($\beta = 0.32$, $p < 0.0001$) or length ($\beta = 0.31$, $p < 0.0001$). These results support previous suggestions that MS volume scales allometrically. As such, future studies of MS morphology should account for differential patterns of volumetric distribution (i.e., shape) rather than exclusively focusing on volume alone.

This work is partially supported by a grant funded to Dr. Jamboor Vishwanatha by the Cancer Prevention and Research Institute of Texas (Award #: RP170301).

Growth of the eyes and nasal airways in *Aotus nancymaae*

SCOT EE. KING[1], VALERIE B. DELEON[2] and TIMOTHY D. SMITH[1]

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

Within the integrated tissues of the head, the pace of growth of soft tissue organs has a transformative effect on skeletal anatomy of the skull. Individual organs can act as modular drivers that influence characteristics such as basicranial angulation and facial orientation. Here, we measured the volume of the eyes, nasal airways, and paranasal spaces in a newborn and adult owl monkey (*Aotus nancymaae*) using diceCT scans of one adult and one newborn. Through segmentation via Amira software, we reconstructed the eyes and nasal airways, and then obtained volume using the Material Statistics function. The preliminary data suggest the nasal airway increases 11x from newborn to adult; in contrast, the maxillary sinuses present with 25x growth and pneumatized spaces overall (maxillary, frontal, and cupular sinuses) increase 100x. In comparison, the eyes of *Aotus* increase 9x from birth to

adulthood. Based on previous work, some distortion is expected due to iodine staining in diceCT, but the newborn Aotus specimen was exposed to only low concentrations of Lugol's iodine and displays minimal shrinkage. Still, results indicate *Aotus* defers much growth of the eye and airways until postnatal development. The airways and eyes expand at a nearly similar pace. However, the process of secondary pneumatization of cranial bones postnatally is revealed to vastly outpace expansion of the main nasal airways.

Funded by NSF grant #s BCS-1830894 and BCS-1830919.

Asymmetry in context: Examining heterogeneity in femoral cross-sectional geometry at Medieval Pieve di Pava (Tuscany, Italy)

KATHERINE M. KINKOPF[1], SABRINA C. AGARWAL[2,3], GIULIA RICCOMI[4], SIMONA MINOZZI[4], STEFANO CAMPANA[5], DAVIDE CARAMELLA[6] and VALENTINA GIUFFRA[4]

[1]Department of Geography and Anthropology, California State Polytechnic University, Pomona, [2]Department of Anthropology, University of California, Berkeley, [3]Archaeological Research Facility, University of California, Berkeley, [4]Division of Paleopathology, University of Pisa, [5]Department of History and Cultural Heritage, University of Siena, [6]Department of Radiology, University of Pisa

Cross-sectional geometry studies yield important insights into past people's behavior, labor practices, limb use, and mobility. We present results from our study, where we aimed to identify the relationship between biocultural factors, such as sex-gender and age, with cross-sectional geometry in the femur and historical evidence about labor and activity at the rural Medieval site of Pieve di Pava in Tuscany (central Italy). Cross-sectional geometric analysis of femoral midshafts from 111 individuals (male n=67, female n=54) was used to examine trends in bone quantity, shape, and bending strength and rigidity between and among age and sex groups, as well as in emergent clusters identified through Hierarchical Cluster Analysis (HCA). We found that population-level analyses of cross-sectional geometry data obscured within-group differences, especially regarding directional and absolute asymmetry. Overall, our study sample showed remarkable heterogeneity amongst males, and our HCA revealed that males can be more precisely described in terms of three distinctive groups possibly indicating that males had more specialized behavior or differential participation in physical activities. Females had less heterogeneity and were more similar to each other, suggesting females were "generalists" in their physical activities. We emphasize the importance of carefully considering asymmetry within individuals, as well as at the population-level for studies attempting to understand physical activity and labor divisions in the Medieval period. Gender roles and norms for men in Medieval Europe, particularly Medieval Italy, were more heterogeneous and these differences likely influence the divergent trends we see in their cross-sectional geometry.

University of Pisa School of Medicine and Surgery Visiting Fellows Programme; Stahl Graduate Research Grant and Stahl Faculty Grant, Archaeological Research Facility University of California Berkeley

New Uintan primates from the Uinta Basin of Utah and the Tornillo Basin of Texas

E. CHRISTOPHER KIRK[1,2], RACHEL H. DUNN[3], BENJAMIN RODWELL[1] and K. E. BETH TOWNSEND[4]

[1]Anthropology, University of Texas, [2]Geological Sciences, University of Texas, [3]Anatomy, Des Moines University, [4]Anatomy, Midwestern University

Primate faunas from the Uintan North American Land Mammal Age (NALMA) are often characterized as demonstrating greater regional endemism than those of the preceding Bridgerian NALMA. However, between-basin comparisons of Uintan primates are often complicated by a dearth of described specimens, which in turn may contribute to uncertainty regarding the taxonomic identity of individual fossils. Collecting over the last two decades has greatly expanded the sample of Uintan primates from both the Uinta and Tornillo Basins. Here we present the findings of an analysis of expanded hypodigms of three Uintan taxa: *Ourayia*, *Mytonius*, and *Diablomomys*. Although the generic distinctiveness of *Ourayia* and *Mytonius* has been questioned, new fossils strongly favor recognition of the two genera. In addition to size differences, *Ourayia* and *Mytonius* differ in numerous details of dental morphology, particularly in the morphology of the maxillary cheek teeth and mandibular 4th premolar. Both genera further differ from *Macrotarsius* in having less molariform mandibular 4th premolars and in lacking maxillary molar pericones. *Diablomomys* likewise differs from the similar-sized taxa *Omomys* and *Gunnelltarsius* in many dental features, including having maxillary molars with a miniscule or absent hypocone, no pericones, and an absent or discontinuous lingual cingulum. At present, *Ourayia*, *Mytonius*, and *Omomys* appear to be relatively cosmopolitan taxa known from multiple basins, whereas *Diablomomys* and *Gunnelltarsius* are regional endemics known only from Texas and Southern California (respectively). Phylogenetic analyses favor the conclusion that *Ourayia*, *Mytonius*, and *Diablomomys* are united within a clade of mainly Uintan omomyids from North America.

Is there a core primate hair microbiome?

CATHERINE E. KITRINOS[1], RACHEL B. BELL[2], BRENDA J. BRADLEY[3,4] 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]Center for the Advanced Study of Human Paleobiology, The George Washington University, [4]Department of Anthropology, The George Washington University

Examining the core microbiome (i.e., microorganisms that are widespread within a set of host samples) across species can provide a baseline from which to compare evolutionarily divergent hosts, assist in understanding host biology, and provide insight into host health status. Hair and skin operate as the outermost barrier between a host and the external environment and are the first physical line of defense against external pathogens. Yet, the nonhuman primate core hair and skin microbiome––to the extent there is one––has not been well characterized. In this study, we examined the core microbiome of plucked hair tufts (n=159) from eight body sites across 12 primate species to identify genus-level microbial taxa based on 16S sequencing. Based on a threshold of shared similarity across 75% of our samples, we found that the core microbiome of primate plucked hair consists predominantly of microbes that have been previously associated with the gut, skin, and abiotic environment, including *Prevotella*, *Staphylococcus*, *Kocuria*, and *Methylobacterium*. The ubiquity of these microbial taxa across various types of host samples suggests that the transmission and retention of specific microbes from other microhabitats to the hair is common across captive primate species. Because *Staphylococcus* in human skin includes both pathogenic (*S. aureus*) and symbiotic, immunologically significant (*S. epidermis* and *S. hominis*) variants, further study into the function and classification of nonhuman primate hair-associated *Staphylococcus* is warranted.

This study was funded by Umass Amherst, the Leakey Foundation, and The George Washington University

The earlier the better: age at first reproduction mediates the association between facial fluctuating asymmetry and reproductive success in women

MAGDALENA KLIMEK, URSZULA M. MARCINKOWSKA, ANDRZEJ GALBARCZYK, ILONA NENKO and GRAZYNA JASIENSKA

Department of Environmental Health, Jagiellonian University Medical College

The level of fluctuating asymmetry is a signal of developmental stability and genetic quality, thus more symmetric individuals should be in better biological condition. Therefore, we hypothesize that facial asymmetry should be negatively related to reproductive success, as a better biological condition contributes to greater reproductive

potential. Data were collected among 164 post-reproductive women aged 46-92 (mean 64.3; SD 9.93), living at the Mogielica Human Ecology Study Site in Poland. The population was characterized by high parity for many decades. Demographic and reproductive data (age at marriage, age at first and last reproduction, number of children), were collected via questionnaire. Facial photographs were taken in order to calculate the level of overall facial asymmetry (OFA) according to standard procedures. The two-step analyses included multiple regression modeling and analysis of mediation. There was a statistically significant relationship between the OFA and the number of children born, which was mediated by the age at first reproduction. Women with more symmetric faces had an earlier age at first reproduction and, in consequence, a greater number of children, when controlled for year of birth of a woman, education, and age at marriage (p=0.031). Because fluctuating asymmetry is established in utero, our results suggest that higher reproductive success, mediated by an earlier age at first reproduction, may partly result from women's better biological condition, originating prenatally. These findings shed light on the possible life-long importance of developmental conditions in shaping women's reproductive potential and performance.

This work was supported by the National Science Centre [NN404 273440, 2013/11/N/NZ7/00364]; the Ministry of Science and Higher Education [IdP2011000161, N43/DBS/000068, N43/DBS/000069], and Salus Publica Foundation.

Understanding the dietary behavior of a 7th–9th century Avar community from Jagodnjak, Croatia using stable isotope of bone collagen

MARLON KOCI[1], DINKO T. PAVIČIĆ[2], ANITA DUGONJIĆ[3], MARIO NOVAK[4] and J. MARLA. TOYNE[1]

[1]Department of Anthropology, University of Central Florida, [2]Kaducej Ltd., Split, Croatia, [3]Archaeological Museum in Zagreb, Croatia, [4]Center for Applied Bioanthropology, Institute for Anthropological Research, Zagreb, Croatia

The dietary behavior of past communities is influenced by several factors such as environmental sources, socioeconomic organization, individual preferences, and physiological needs. Every society has its characteristics and understanding the dietary choices of its individuals expands the knowledge about lifestyle continuities and changes. Applying biochemical tracers, we can explore the food choices of an Early Medieval Avar community. The Jagodnjak cemetery (n=35) in Croatia is dated to the 7th–9th century. Historical and archaeological records are currently limited for Avar populations. Jagodnjak is a transitory community from a period where different historical events shaped the community's way of life. This research evaluates the dietary variation of carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotopes in bone collagen. Results produce an average $\delta^{13}C$ of −16.28 ±1.72‰ and an average $\delta^{15}N$ of +10.94 ±1.5‰. We test the hypotheses that there are dietary differences between males and females, adults and juveniles, and between the Jagodnjak sample and nearby communities. The stable isotope analyses suggest that adult males and females had similar food choices for plants and different for terrestrial animals/freshwater fish, and that adults and juveniles had similar choices for dietary protein. However, the adults' and juveniles' dietary behavior indicates different proportions of C_3 food resources. Stable isotopic comparisons suggest that Jagodnjak and some contemporaneous communities did not have similar dietary behaviors. This study of Jagodnjak provides insight into an Avar community during this time of residential and lifestyle transition as well as expanding bioarchaeological research in Croatia.

This research was supported by the Trevor Colbourn Endowment in Anthropology Fund at the University of Central Florida, and the Center for Applied Bioanthropology, Institute for Anthropological Research, Zagreb, Croatia.

Sex-specific relationships between 17β-estradiol and depression in an aging adult population of forager horticulturalists

STEPHANIE V. KOEBELE[1], THOMAS KRAFT[2], ANGELA R. GARCIA[1], DANIEL K. CUMMINGS[3], HILLARD KAPLAN[3], MICHAEL GURVEN[4], JONATHAN STEIGLITZ[5] and BENJAMIN C. TRUMBLE[1,6]

[1]Center for Evolution and Medicine, Arizona State University, [2]Department of Anthropology, University of Utah, [3]Department of Health and Economics and Anthropology, Economic Science Institute, Argyros School of Business and Economics, Chapman University, [4]Department of Anthropology, University of California, Santa Barbara, [5]Institute for Advanced Study in Toulouse, Université Toulouse I Capitole, [6]School of Human Evolution and Social Change, Arizona State University

Age-related changes in reproductive hormones frequently co-occur with depression and other aspects of physiological senescence (e.g., metabolic dysfunction, memory deficits). Depression is hypothesized to serve as part of an evolved strategy to regulate energy allocation, which is partially mediated by reproductive hormones. Understanding of age-related metabolic and hormone shifts is derived from industrialized populations; less is known about relationships between hormones and depression in subsistence populations that live in kin-based social networks, experience energetic limitation, and have high fertility, leading to different age-related hormone trajectories (e.g. relatively low testosterone). To test whether relationships between reproductive hormones and depression are similarly expressed across environments, we evaluated whether age, sex, and hormones predict depression using a composite score derived from a 5-item depression inventory among Tsimane forager-horticulturalists of Bolivia. In Tsimane adults (n=667 observations from 556 individuals, aged 38-87, 49% female) older age (β=0.03, CI:0.01−0.04, p<0.001), being female (β=-3.93, CI:-6.56− -1.29, p<0.01), and lower testosterone (logT; β=-0.22, CI:-0.44− -0.01, p<0.05) were associated with greater depression symptoms. A sex by 17β-estradiol interaction was present (logE2; β=0.56, CI:0.16-0.96, p<0.01). Among adults aged 50+, lower logE2 predicted depression in women, while higher logE2 predicted depression in men. Results suggest relationships between reproductive hormones and depression are similar across socioecological environments and are unlikely to be a byproduct of modern energetic or social conditions. Moreover, findings highlight the need to investigate sex-specific mechanisms of depression and its role as a putative adaptive strategy to regulate altered energy expenditures occurring with reproductive hormone changes during aging.

This study was funded in part by NIA (RF1AG054442) and NSF (1748282). JS acknowledges French National Research Agency under the Investments for the Future funding (Investissements d'Avenir) programme (ANR-17-EURE-0010).

Modeling ontogenetic changes in bite force and gape potential in *Microcebus murinus* through the use of multibody dynamics analysis

SHRUTI KOLLI[1,2], EDWIN DICKINSON[1,3] and ADAM HARTSTONE-ROSE[1]

[1]Department of Biological Sciences, North Carolina State University, [2]Department of Biological Sciences, University of Denver, [3]Department of Anatomy, New York Institute of Technology College of Osteopathic Medicine

The masticatory apparatus – consisting of the masticatory muscles, bony skull, mandible, and dentition – defines the forces that an individual can both generate and resist when eating. The masticatory adductor muscles contribute the forces imparted into the system and limit the excursion potential of the jaw, and the skeletal components regulate the efficiency of converting intrinsic force into bite force and linear gape. Through multibody dynamics analysis based on micro-CT scanned skulls and muscle fiber architecture data collected on the same sample, we calculated bite force and gape potential throughout ontogeny in *Microcebus*. Based on our previous architectural analyses, we predicted that a) bite force will increase until adulthood and decline at senescence, b) gape potential will increase during development and remain constant between adulthood and senescence, and c) observed differences in bite force during ontogeny will be a product of changes in both

the muscular and skeletal components of the masticatory apparatus. We found that the senescent model had a slightly lower bite force at each bite point while the adult had the highest forces (the forces of the infant and juvenile models were lower than those of the other two models). Additionally, the adult and senescent models had similar maximum gape potential, with maximal gape in our juvenile closer to the adult/senescent models than to the infant. Finally, both myological intrinsic force potential and osteological mechanical advantage shifted notably during ontogeny. Thus, our predictions were supported, confirming the value of modeling for simulating masticatory functional development.

Funding was provided by the National Sciences Foundation IOS-15-57125

Quantitative genetic analysis of the hominin midfoot: from *Ardipithecus* to *Homo*

KLARA KOMZA[1], BENCE VIOLA[1] and LAUREN SCHROEDER[2,3]

[1]Department of Anthropology, University of Toronto, [2]Department of Anthropology, University of Toronto Mississauga, [3]Human Evolution Research Institute, Department of Archaeology, University of Cape Town

The hominin foot is characterized by morphological diversity, reflecting adaptations to a range of bipedal locomotor behaviors. However, the exact evolutionary processes that influenced the foot's morphological diversification are still unclear. Here, we use a series of tests derived from evolutionary quantitative genetics to investigate the evolutionary processes (genetic drift and natural selection) that have shaped metatarsal (Mt) 1 – 4, intermediate cuneiform, and cuboid evolution. Using extant human and chimpanzee models as proxies for within-population variability in hominins, we compare *Ardipithecus ramidus*, *Australopithecus afarensis*, Australopiths from Sterkfontein, the Burtele foot, OH 8 (putatively assigned to *Homo habilis*), and *Homo sapiens*. We found rejection of drift in the Mt1 from *A. afarensis* to *H. habilis*, but not within *Homo*. We also found rejection of drift in the Mt2 and intermediate cuneiform between *H. habilis* and humans, with directional selection likely influencing this morphological transition. Across Mt3s, we found rejection of drift, and possible directional selection between *Ar. ramidus* and *A. afarensis*, but no rejection of drift among australopiths and *Homo*. Genetic drift could not be rejected in all comparisons of the Mt4 and cuboid, but some proportions of the articular surfaces may have been influenced by stabilizing selection, particularly in the cuboid's Mt4 and Mt5 facet dimensions between *H. habilis* and humans. Overall, our results highlight that the tarsals and metatarsals were subjected to a wide range of evolutionary processes, and that the cuboid and Mt4 are more likely to have been shaped by stabilizing selection than more medial elements.

Leakey Foundation General Grant (KK), Natural Sciences and Engineering Research Council of Canada - Discovery Grant (LS), Social Sciences and Humanities Research Council of Canada, Insight grant (BV)

COVID-19 and Food Insecurity Among Resource Insecure University Students: An Applied Life History Perpective

MIRIAM C. KOPELS and CASEY J. ROULETTE

Department of Anthropology, San Diego State University

Food insecurity is a complex biosocial phenomenon on university campuses, with many correlates, such as diminished academic outcomes and psychological distress. These problems were exacerbated when COVID hit; and continue to impact the daily lives of students. This study adds to the growing body of data on COVID and food security by looking specifically at the impacts on resource-insecure university students. The survey questions were administered during Fall 2020 and measured the following: sociodemographic variables; perceptions of extrinsic mortality; economic wellbeing effort; perceptions of support services; and future orientation. An additional sample opted-in to a semi-structured interview, which measured: psychological distress; housing security; dietary intake; and opinions on support services. Individuals were also asked to compare their current living situations and diets to their lives prior to the pandemic – providing novel data on the impacts of COVID. This study address questions that contribute to evolutionary life history theory and its application to human populations. Briefly, this theoretical perspective posits that individuals with greater subjective mortality risk are expected to exhibit a greater proportion of future discounting, favoring short-term rewards over hypothetical long-term investments. Within this population, life history predicts that students with higher perceptions of extrinsic risk will invest less in their long-term economic wellbeing effort. We test this theory against competing theories in psychology that posit psychological distress as the primary factor influencing future orientation. I also address the practical applications of life history, and how these hypotheses can help support resource insecure students on campus.

This study was funded in part by the Student Economic Vulernabilities Initiative (SEVI) and The Economic Crisis Response Team (ECRT) of San Diego State University.

Relative leg-to-arm strength proportions in Bornean and Sumatran orangutans

ALEXANDRA E. KRALICK[1] and MATTHEW W. TOCHERI[2,3,4]

[1]Anthropology, University of Pennsylvania, [2]Anthropology, Lakehead University, [3]Human Origins Program, National Museum of Natural History, [4]Australian Research Council Centre of Excellence for Australian Biodiversity and Heritage, University of Wollongong

Differences in habitat continuity and predators have been posited as explanations for higher rates of terrestrial locomotion in Bornean compared to Sumatran orangutans. However, it is unclear whether greater terrestriality in Bornean orangutans is due to recent environmental changes to their habitats. Orangutan skeletons collected a century ago may shed new light on this question as habitat continuity on both islands would have been greater in the past. Previous research has demonstrated that skeletal cross-sectional geometry tracks levels of relative terrestriality across gorilla species and ages (Ruff et al., 2013, 2018). In this study, cross-sectional geometry ratios were calculated for 35 orangutans from CT scans using ImageJ. We predicted that the ratios for *Pongo* would show less relative leg-to-arm strength than all gorillas and that relative leg-to-arm strength would be stronger in Bornean than Sumatran orangutans. Our results show that both predictions are supported ($p < .05$) by significant statistical differences for natural log of polar section modulus of femur over humerus, tibia over humerus, and tibia over ulna. For instance, both orangutan taxa show significantly less relative leg-to-arm strength than all gorillas, even those that climb the most (i.e., western lowland gorillas and infant mountain gorillas). Moreover, Bornean orangutans display limb bone strength proportions that are consistent with more terrestriality than their Sumatran counterparts. Thus, recent habitat discontinuity in Borneo does not explain greater terrestriality in Bornean orangutans, as also suggested by camera trap data, and is most likely due to the absence of tigers on Borneo.

This project has received funding from the NSF Graduate Research Internship Program (GRIP).

Adipose development in hunter-gatherer children. Implications for diet and adaptive growth

KAREN L. KRAMER[1], BENJAMIN C. CAMPBELL[2] and JOE V. HACKMAN[1]

[1]Anthropology, University of Utah, [2]Anthropology, University of Wisconsin, Milwaukee

Children's growth is a complex response to energetic conditions, ancestral background, history of domestication and dietary shifts in macronutrients, and most recently exposure to simple carbohydrate-rich market foods. Adiposity in particular is sensitive to the consumption of simple carbohydrates. Although adipose development

has been well-characterized in growth standards, it is unclear what features of adipose development are shared across diverse livelihoods and those that might be specific to a hunting and gathering subsistence base distinguished by its diverse, often high protein diet, variable inputs of fat, few simple carbohydrates and active childhoods. Here we construct best-fit adipose growth curves for the Savanna Pumé and Dobe !Kung using triceps, subscapular, and abdominal skinfolds for children ages 3 to 20. Both groups are savanna foragers, who at the time of data collection consumed no market foods. We find 1) little evidence for a clear *adiposity rebound* at the end of childhood. 2) Rather, fat fluctuates in response to other growth demands, with no appreciable accumulation until pubertal onset. 3) This points to a tradeoff, where skeletal growth is prioritized before committing to fat tissue, especially in boys. 4) Hunter-gatherer children offset the energy demands of growth by staggering skeletal and weight growth spurts and adipose accumulation to a much great extent than reference populations, suggesting that plasticity in timing is a key, but understudied feature mediating energy availability. Growth patterns under nonindustrial energetic conditions provide an important baseline for understanding body fat patterns emerging today under food abundance and simple-carbohydrate diets.

The Savanna Pumé research was funded by the National Science Foundation (0349963 and DBS-9123875), the L.S.B. Leakey Foundation, the Milton Fund and Harvard University.

Boosting the signal: using paired dental microwear textures to augment osteobiographies

KRISTIN L. KRUEGER[1], JOHN C. WILLMAN[2] and JESSICA R. SCOTT[3]

[1]Anthropology, Loyola University Chicago, [2]Life Sciences, Universidad de Coimbra, [3]Anthropology, University of Arkansas at Little Rock

Dental microwear texture analysis (DMTA) is commonly used to reconstruct dietary and behavioral strategies in bioarchaeological groups. While molars are examined for dietary signals, incisors are often used to understand behavior, such as using the teeth as tools. Rarely considered is whether paired molar and incisor textures from the same individual can be used to refine these interpretations. When examining paired textures from the South Tombs Cemetery (STC) at the New Kingdom site of Amarna, Egypt, we found an individual with unique texture signals that warranted further analysis.

This individual, SK319, was estimated to be 30-39 years old and female. Pathological lesions include osteochondritis dessicans on the right proximal radius and lipping on several bones of the right thumb. High-resolution casts of her molar facet 9 and labial incisal surface were scanned using a white-light confocal profiler at 100x. Each enamel area (204x276 µm) was examined for defects and uploaded into scale-sensitive fractal analysis software for texture characterization. Her *Asfc* molar value (1.18) was similar to that of the group mean (1.16), which suggested chewing soft but tough foods. However, the incisor *Asfc* value (13.53) was an extreme outlier to the group mean (3.43), and indicated erosion or erosion-abrasion. These results suggest that using paired anterior and posterior teeth from the same individual, along with other contextual data, can be used to augment an individual's osteobiography, and reveal aspects of social identities that are hidden by current research trends that only focus on one tooth type.

Funding for this project was provided to KLK by Loyola University Chicago Research Support Grant. JCW is funded by a Marie Skłodowska-Curie Actions Individual Fellowship (H2020-MSCA-IF-2018, No. 839822).

Entheseal patterns suggest habitual tool use in early hominins

JANA KUNZE[1], FOTIOS ALEXANDROS KARAKOSTIS[2], STEFAN MERKER[3], MARCO PERESANI[4,5], GERHARD HOTZ[6,7], VANGELIS TOURLOUKIS[1] and KATERINA HARVATI[1,2]

[1]Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoenvironment, University of Tübingen, [2]DFG Centre of Advanced Studies "Words, Bones, Genes, Tools", University of Tübingen, [3]Department of Zoology, State Museum of Natural History Stuttgart, [4]Department of Humanities, Section of Prehistoric and Anthropological Sciences, University of Ferrara, [5]Institute of Environmental Geology and Geoengineering, National Research Council, Italy, [6]Anthropological Collection, Natural History Museum of Basel, [7]Integrative Prehistory and Archaeological Science, University of Basel

When human-like tool production and use first emerged in the human lineage is a central question in human evolutionary studies. However, current archaeological and paleoanthropological evidence is inconclusive. We approach this subject by applying our novel Validated Entheses-based Reconstruction of Activity (V.E.R.A.) method to analyze the manual entheseal proportions in early and recent modern humans, Neanderthals, extant great apes, *Homo naledi*, *Australopithecus* species and an unassigned fossil hominin from Swartkrans, South Africa. Our analysis is focused on the attachment sites of the first metacarpal, including the *opponens pollicis*, *abductor pollicis longus* and the first *dorsal interosseus*, due to its importance in human-like manipulation. Previous electromyographic research has shown that the first *dorsal interosseus* (DI1) reaches high levels of activation during human-like tool use, irrespective of the tool type. Therefore, we expected the proportion of its muscle attachment site to differ between tool-using (later *Homo*) and non-tool-using species (great apes).

Results show that DI1 entheseal proportions indeed differentiate between later *Homo* and great apes, with tool-users exhibiting a proportionally larger attachment site congruent with a frequent activation of this muscle. With the exception of an *Australopithecus africanus* specimen, these proportions are shared with the fossil hominins, suggesting a thumb muscle use consistent with habitual human-like tool use. Considering that recent studies reported a low thumb opposition efficiency for *Australopithecus afarensis* and *Australopithecus sediba,* we propose that habitual tool use preceded the adaptation for manual dexterity and potentially acted as a selective pressure on the development of this fundamental trait.

Aspects of this research were supported by the European Research Council (ERC CoG no. 724703) and the German Research Foundation (DFG FOR 2237).

Applications of a regularized deep network micro-CT image auto-segmentation approach to morphological data

SHARON KUO[1], LILY JD. DEMARS[1], AMIRSAEED YAZDANI[2], VENKATESWARARAO CHERUKURI[2], YUNG-CHEN SUN[2], ANTONY COLOMBO[1,3,4], VISHAL MONGA[2] and TIMOTHY M. RYAN[1]

[1]Anthropology, Pennsylvania State University, [2]Electrical Engineering, Pennsylvania State University, [3]Biological, Geological and Environmental Sciences, University of Bologna, [4]Life Sciences, Manchester Metropolitan University

Image segmentation remains one of the most time-consuming aspects of many studies involving micro-CT, particularly when samples include significant sediment infill, poor preservation, or fossilization. The large time requirement often delays a project or necessitates the reliance on multiple individuals of varying experiences with osteological, archaeological, or paleontological material. These factors often introduce segmentation biases or errors that can affect all subsequent results. Here, we present an open source regularized deep network (RDN) model that uses a U-net image segmentation network and a sample of expert segmentations. The model is retrainable for a variety of analytical needs (e.g., fossil material, archaeological material with significant infill, osteological samples surrounded by soft tissue, etc.) using minimal training material (3-5 hand segmented slices in 3 orthogonal planes), reducing the amount of time spent on hand segmentation for each specimen. RDN segmentation of juvenile specimens and images with sediment infill, which often require time-consuming manual segmentations showed that the RDN machine learning model was successful (0.978 Dice overlap, which is the overlap of the current model with expert segmentations) at isolating the targeted material of interest (in this case, bone) and/or took less time to segment compared with traditional segmentation methods. This RDN segmentation

approach offers a promising avenue for faster, more accurate, repeatable, and less training-intensive segmentation in paleontology, archaeology, and biological anthropology.

NSF BCS 1719187, 1719140, 1847806, NSF GRFP DGE 1255832 European Research Council, Grant/Award Number: 617627; RCUK BBSRC, Grant/Award Number: BB/R01292X/1

Rethinking Portmann's legacy in comparative physiological light: The case of altricial-precocial divergence

ANDRES KURISMAA[1] and FILIP JAROŠ[2]

[1]Scool of Natural Sciences and Health, Tallinn University, [2]Philosophical Faculty, University of Hradec Kralove

We propose that the continued interest in Portmann's legacy for biological anthropology is grounded not only in his pioneering concepts of human evolution, but also in the methodological approach he pursued in theoretical biology and philosophical anthropology. Along these lines, Portmann's concepts could transcend not only certain disciplinary boundaries of his time, but also critically approach questions of evolutionary theory that have only recently become subjects of renewed debate – particularly regarding behavioral and developmental factors in evolution.

However, the morphological descriptive nature of Portmann's research prevented a more complete translation of these insights into an alternative framework – one able to show how phenotypic plasticity could translate developmental/behavioral processes into potential targets of selection. Here, we outline how the early comparative physiological approach to development by I.A. Arshavsky (1903-1996) furnished such complementary experimental models. These models, while almost unknown in the West, detailed how key variations in the altricial-precocial spectrum may depend on organisms' postnatal ecological conditions and activity – to the extent that typically precocial patterns (e.g., higher encephalization, longer life-span, allometric changes) could be induced in normally highly altricial species (such as rabbits and rats), given appropriate early-life physiological and locomotor stressors (specifically musculoskeletal, hypoxic, thermal ones). Along with renewed appreciation of stress-induced variations as possible drivers of life-history evolution, these results appear to suggest new predictions and hypotheses on the mechanisms of developmental divergence in eutherian evolution and their possible connections to active behavioral adaptations. These aspects are discussed as an elaboration of Portmann's research program.

Funding: Estonian Research Council (ETAg) Project MOBJD1046

The pelvis is neither geometrically similar nor allometrically constrained: Evidence from a wide range of human populations

HELEN K. KURKI[1] and CARA M. WALL-SCHEFFLER[2]

[1]Department of Anthropology, University of Victoria, [2]Department of Biology, Seattle Pacific University

Models of human pelvic evolution, especially those modeling tradeoffs between obstetric and locomotory influences, assume that as some dimensions of the pelvis change, so too do others. As biiliac breadth reduced over our evolutionary history, so did biacetabular breadth - key components of bipedal locomotor function models. It might be expected that dimensions of the pelvic canal would be similarly affected, breadths of the canal would decrease with biiliac and biacetabular breadth. Under the Obstetrical Dilemma Hypothesis, we might suppose that anterior-posterior (AP) dimensions of the canal would increase in females to accommodate reduced medio-lateral (ML) breadths and maintain obstetric capacity. But does the pelvis change shape in a geometrically similar way across humans? Dimensions of the pelvis and canal were examined across several human samples, representing a range of body sizes (female n = 106, male n = 119). If locomotory, obstetric, and thermoregulatory selective factors act similarly in all populations, or, if the pelvis is constrained developmentally, pelvic proportions should also remain consistent across the range of body sizes. Canal ML and AP dimensions were calculated relative to biacetabular breadth. As biacetabular breadth increases, relative AP dimensions decrease in both sexes (slopes = 0.690 - 0.829, all $p < 0.001$), but relative ML dimensions decrease only in the inlet (slope: F = -0.790, M = -0.829, all $p < 0.001$), not in the midplane or outlet (slopes = -0.061 - -0.076, all $p > 0.05$). These results suggest proportionality of pelvic shape is not consistent in humans.

Considerations of Sex and Gender in Forensic Anthropology and Archaeology

ANNA F. KUYKENDALL

Department of Anthropology, University of Montana

This abstract is part of the symposium *Advances and Challenges in the Identification of Sex and Gender in Human Osteological Contexts*. I present on two challenges in the anthropological and archaeological communities: the methodological challenge of identifying transsexual individuals in grave contexts, and the potentially severe political and social implications of gender bias in the study of human burials. As science and social change in the 1970s revealed that sex is a complex construction, the category of "indeterminate" individuals in skeletal biological profiles became more common.

No forensic anthropological standards exist for the identification of transsexual individuals from skeletal remains. Current standards produce inaccurate biological profiles for transsexual individuals because the designation of sex from skeletal remains relies on pelvic morphology. Misidentification of gender based on conclusions of sex derived from pelvic morphological analysis may mislead law enforcement in identifying individuals and therefore prevent accurate identifications. Forensic anthropologists and archaeologists must recognize that gender and sex are not binary.

I present data from research on studies of graves in Finland, Birka, and Italy to stress the importance of not imposing personal biases of what an individual's sex or gender is based on grave goods. The incorrect interpretation of gender from artifacts in archaeology may lead to misrepresentations of the culture and demography of past populations being studied.

I conclude that gendering individuals based on analysis of skeletal morphology and associated artifacts must be undertaken with careful consideration of cultural factors that may be overlooked or misinterpreted by the observer.

Morphological distance among *Homo erectus* paleodemes: Implications for population dynamics

RACHEL A. KUZMA[1], DAVID S. STRAIT[1] and KAREN L. BAAB[2]

[1]Department of Anthropology, Washington University in St. Louis, [2]Department of Anatomy, Midwestern University

Prior research has shown that morphological distances between modern human populations calculated using the temporal and parietal bones are significantly correlated with genetic distances, presumably due to genetic drift. An implication is that temporal and parietal morphology may provide insights about population history and relationships in fossil hominins. This research tests the hypothesis that morphological distances between paleodemes of *Homo erectus* are correlated with geographic and/or temporal distances. Morphological distance matrices were computed for *H. erectus* using the R-matrix method. The number of PC scores required to explain at least 95% of the overall morphometric variance, for each bone respectively, were used as shape variables to calculate cranial vault morphological relationship matrices using RMET 5.0. The geographic distance matrices were calculated by measuring the distance between each paleodeme's centroid, measuring the shortest distance between centroids following an overland route. Temporal distance matrices were calculated using the mean age of the specimens within sites within a paleodeme. Off-diagonal matrix values from the morphological distance matrices and

the geographic and temporal distance matrices, respectively, were compared using Mantel tests. Results indicate that in *H. erectus* there is a significant correlation between temporal bone morphological distance and both geographic and temporal distance, but this was not observed in the parietal bone. These results suggest that temporal bone morphology may provide information about population dynamics in *H. erectus*.

This research was funded by the National Science Foundation Doctoral Dissertation Research Improvement Grant (BCS-2051014).

(Wo)man the hunter: The Archaeological Evidence Ignored

SARAH A. LACY[1] and CARA OCOBOCK[2,3]

[1]Department of Anthropology, California State University Dominguez Hills, [2]Department of Anthropology, University of Notre Dame, [3]Eck Institute for Global Health, University of Notre Dame

Paleo-fantasies of the past continue to conjure the sexualized and racialized image of "Man the Hunter" and "Woman the Gatherer", and this informs the null hypothesis used in anatomical and physiological reconstructions of the Paleolithic (see Ocobock and Lacy, this conference). However, Ideas of "Man the Hunter" persist in archaeological and paleogenomic interpretations of the past as well. This spans from a fixation on hunting stone tools associated with masculine hunting over processing stone tools associated with feminine food production to assumptions that depictions of feminine bodily figures and genitalia are obviously pornographic. If the archaeology literature perpetuates these ideas, we cannot blame the anatomy and physiology researchers for citing it. Here we present the actual evidence, or lack thereof, to support women's roles in the past as well as challenge oft-cited interpretations of material culture. Such evidence includes stone tool function, food types, site layout, burials, the artist and artist's subject, population density and group size, and aDNA as well as discussions of invisible evidence such as carrying satchels, non-stone based tools, aspects of childcare, and cooking methodology. By pulling together the current state of the archaeological evidence along with the modern physiological evidence, we hope to propose new lines of inquiry that have not been explored and give more support to the idea that humans of all sexes contributed equally to life and evolution in the past. These critiques cannot stand independently from an analysis of the gender composition of the field itself.

The number of daily load cycles positively influences Haversian remodeling in jaws of New Zealand white rabbits (*Oryctolagus cuniculus*)

SUSAN E. LAD[1,2], HANNAH KOWALKOWSKI[3], DANIEL F. LIGGIO[4], HUI DING[3] and MATTHEW J. RAVOSA[3,5,6]

[1]Department of Exercise Science, High Point University, [2]Department of Physical Therapy, High Point University, [3]Department of Biological Sciences, University of Notre Dame, [4]Department of Medicine, Rutgers New Jersey Medical School, [5]Department of Aerospace and Mechanical Engineering, University of Notre Dame, [6]Department of Anthropology, University of Notre Dame

Haversian bone remodeling occurs, in part, as a response to microdamage formation in more mature bone, serving to repair and maintain the skeleton's mechanical integrity. Correlations between secondary osteons densities (i.e., products of remodeling) and the behaviors that engender loads within limb bones and jaws of wild primates have suggested that the number of daily load cycles, rather than load magnitude, influences the degree to which bone is remodeled. Here we test this hypothesis directly using 30 male New Zealand White rabbits (*Oryctolagus cuniculus*) raised for 48 weeks (from weaning onset). All rabbits were fed pellets but half also ate hay daily (n=15 "control" and n=15 "overuse" rabbits). Hay is tougher and stiffer (E=3336Mpa, R=2760Jm^{-2}) than pellets (E=29Mpa, R=1031Jm^{-2}), requiring greater chewing investment and duration to process. It does not, however, substantially alter peak mandibular bone strain compared to pellet mastication. Thus, the mandibles of rabbits raised on hay endured more daily load cycles, with no difference in load magnitude. To compare mandibular remodeling between groups, osteon population density (OPD) and percent Haversian bone (%HAV) were measured from 100µm coronal sections of the right mandibular corpus. Mann-Whitney U tests revealed significant differences in both OPD (P=0.14) and %HAV (P=0.003), with greater OPD and %HAV in the overuse group. This result supports the hypothesis that Haversian remodeling activity is predominantly determined by the number of daily load cycles, not load magnitude. This finding should be heeded by researchers aiming to infer load history from skeletal material in bioarcheological and paleontological contexts.

Funding: NSF BCS-1749453

Celts up and down the Alps. A multi-isotopic exploration of mobility among the pre-Roman population of Verona (NE Italy, 3rd -1st c. BCE)

ZITA LAFFRANCHI[1], ARSENIO GRANADOS-TORRES[2], SANDRA LÖSCH[1], ALBERT ZINK[3], IRENE DORI[4], ANTONIO DELGADO-HUERTAS[2] and MARCO MILELLA[1]

[1]Department of Physical Anthropology, Institute of Forensic Medicine - University of Bern, [2]Biogeochemistry of Stable Isotopes Laboratory, Andalusian Institute of Earth Sciences, Spanish National Research Council-University of Granada, [3]Institute for Mummy Studies, Eurac Research Bolzano, [4]Soprintendenza Archeologia, Belle Arti e Paesaggio per le province di Verona, Rovigo e Vicenza

During the Late Iron Age (4th-1st centuries BCE) Europe was interested by intense migratory processes across the Alps. In this period, several "Celtic" populations settled in the Italian peninsula. So far, only scarce data are available about mobility in these communities. In this work, we explore mobility patterns among the Cenomani population of Seminario Vescovile (SV-Verona, Italy, 3rd-1st c. BCE) through a multi-isotopic perspective and test the possible correlation between mobility, sex, age and funerary treatment.

We analyzed isotopic ratios of oxygen ($\delta^{18}O$) and carbon ($\delta^{13}C$) from bone phosphate and collagen, respectively, of 49 individuals (23 males, 17 females and 9 nonadults). We also compared collagen $\delta^{13}C$ from bone and dentine of 26 individuals. We assessed nonlocality based on individual deviation of isotopic values from the population mean plus three times the median absolute deviation from the median (±3MAD). We then checked for isotopic differences between sexes and type of funerary treatment using Mann-Whitney tests. A nonlocal origin can be proposed for one individual and cautiously suggested for five more individuals. No statistical difference separates sex nor funerary treatment based on isotopic values. Results highlight a local origin of most of the individuals of SV with few individuals that may point to an Alpine origin. The degree of mobility at SV is lower compared with other contemporaneous sites of Europe, a result that can be attributed to chronological and social factors but also to methodological differences with previous studies.

This research was supported by a Swiss National Science Foundation grant to Marco Milella and Albert Zink (grant number: 10531FL_197103 / 1).

Gastropolitics in Early Fort Ancient: Dietary analysis as a means of examining social status during a period of emerging complexity

EMMA M. LAGAN[1], MARK HUBBBE[1], CHRIS W. SCHMIDT[2], LUCA FIORENZA[3], DEBBIE GUATELLI-STEINBERG[1] and ROBERT A. COOK[1]

[1]Anthropology, The Ohio State University, [2]Anthropology, University of Indianapolis, [3]Anatomy & Developmental Biology, Monash University

Traditional methods of recognizing hierarchy in archaeology are not well suited for detecting nuanced distinctions in social status that may develop in societies with emerging complexity.

To discern such distinctions, this study uses a gastropolitical framework to examine dietary correlates of social relationships at the Early Fort Ancient (c.1000–1250 CE) site of Turpin (33HA19) in the Middle Ohio River Valley, USA. Diet is assessed through stable isotope analysis of Carbon-13 and Nitrogen-15, Dental Microwear Texture Analysis, and caries rates of 69 burials. The Turpin site consists of a central burial mound with a surrounding pattern of interments. This study tests the hypothesis that those buried around the mound ate a less preferred diet (more maize) than those buried in the mound. Moreover, it is expected that diet differentiation also was correlated with other aspects of social status, like age and sex. T-tests revealed significant differences at the $p<0.05$ level between mound and pattern burials, with mound burials exhibiting lower nitrogen, carbon, and caries and higher microwear complexity. These data indicate that individuals in the mound likely consumed less maize than their counterparts in the pattern. Additionally, young adults had significantly higher $^{13}C/^{12}C$ carbon ratio than older adults), and males had significantly higher $^{15}N/^{14}N$ ratio nitrogen and caries prevalence. Males therefore appear to have consumed both more meat and more maize than females. This study demonstrates that there were already important layers of social distinction in these Early Fort Ancient sites, as seen in their diets.

Strepsirrhine muscle density by anatomical region – the first reported broadly collected muscle density data for non-human primates

GIULIA R. LAGOMARSINO, GABRIELLE A. HIRSCHKORN and ADAM HARTSTONE-ROSE

Department of Biological Sciences, North Carolina State University

Density is an important variable for the physiological analysis of muscles, especially in the calculation of physiological cross-sectional area (PCSA) – the anatomical variable used to calculate contractile force. Many studies that calculate PCSA from gross dissections use a density "constant" that is taken from one of a few density studies of either unspecified muscles or limb muscles from guinea pigs, rabbits, dogs or cats. A recent series of studies more comprehensively and systematically evaluated muscle density across anatomical regions and refuted the universality of a density "constant" using a sample of mice and rabbits. While other research has evaluated muscle density in some regions in humans, until now, no study has evaluated the density of muscles comprehensively across anatomical regions in non-human primates. We are presenting the results of muscle densities recorded throughout the body in seven strepsirrhine species. We found muscle densities in strepsirrhines that are higher than those previously found in the other mammals; we also found, in congruence with recent studies, regional differences. While on average, strepsirrhine shoulder muscles are less dense than commonly cited density constants, all other strepsirrhine anatomical regions have slightly denser muscles than those in the literature – greater than 1.06 g/cm^3. We are also reporting densities for three broad regions, eight specific sub-regions and all individual muscles. Although these values are similar to those previously found for non-primate mammals, we suggest that taxonomically and anatomically similarity density proxies should be used when unable to derive sample specific muscle densities.

This work was funded by the National Science Foundation IOS-15-57125

Does the capuchin temporalis maintain functional equivalence during chewing?

MYRA F. LAIRD[1], JOSE IRIARTE-DIAZ[2], CRAIG D. BYRON[3], MICHAEL C. GRANATOSKY[4], ANDREA B. TAYLOR[5] and CALLUM F. ROSS[6]

[1]Department of Integrative Anatomical Sciences, University of Southern California, [2]Department of Biology, University of the South, [3]Department of Biology, Mercer University, [4]Department of Anatomy, New York Institute of Technology, [5]Basic Sciences Department, Touro University, [6]Department of Organismal Biology and Anatomy, University of Chicago

Dynamic changes in jaw movement and bite force depend on a combination of neural and muscle architectural factors that have rarely been compared within a muscle. The fan shaped temporalis varies anteroposteriorly in structure and function, but it is unknown whether these segments operate in functional equivalence—maintaining equal shortening and force generation at any degree of gape (jaw depression and elevation). Here we investigate how architecture dynamics vary across a functionally heterogeneous muscle, whether these dynamics maintain functional equivalence, and whether the timing of this variation relates to muscle activation patterns.

We measured fascicle-level muscle architecture dynamics in the anterior, middle, and posterior regions of the superficial temporalis of three adult tufted capuchins (*Sapajus apella*) using bi-planar videoradiography and the XROMM workflow. Architecture dynamics data were paired with fine wire electromyography data and static muscle architecture measurements from the across the temporalis collected in four adult tufted capuchins. Gape accounted for the majority of architectural changes in all three regions of the temporalis. Despite anteroposterior variation in architectural dynamics, regional fascicle shortening was not proportional to the distance from the joint suggesting a lack of functional equivalence. The timing of most dynamic architectural changes did not vary between muscle regions, in contrast to peak muscle activation. We find that muscle architecture dynamics across the temporalis facilitate force production, and most architectural change is driven by gape. Our results suggest that functional differences in the temporalis are largely driven by muscle activation with limited input from regional muscle architecture dynamics.

This research was supported through the National Science Foundation (NSF-BCS-1440516, NSF-BCS-1440541, NSF-BCS-1440542, NSF-BCS-1440545, NSF-BCS-1627206) and the AAPA Cobb Award.

Using a short primatological field school as a high-impact experiential learning opportunity

CELESTE C. LAM, HEATHER DINKINS and LYDIA E.O. LIGHT

Anthropology, UNC Charlotte

Experiential learning has been credited as a highly effective teaching strategy thought to increase student comprehension and retention; however, it has also been argued that emotional and philosophical capacities create deeper connections to one's environment than experiential ones. In this study, we evaluate the effectiveness of a short primatological field school in relation to both experiential and emotional aspects of place-based learning. Twelve UNC Charlotte undergraduate and graduate students completed an eight-day primatological field school held at the Lemur Conservation Foundation's Myakka City Lemur Reserve in central Florida. We conducted short pre- and post-course interviews and participants journaled throughout the course. We also conducted behavioral observations of participants during fieldwork activities. We then coded interview responses and journal entries to identify themes. Interview responses revealed that while 92% of participants enrolled in the course with an interest in pursuing primatology, only 58% of participants remained interested but 100% of the participants enjoyed the course. Journals revealed strong emotional responses to fieldwork activities but occasionally contradicted interviews. Behavioral observations demonstrated that students were actively engaged in activities and followed instructions. Our results suggest that this field school helped students understand primatology more than classroom instruction alone and that both experiential and emotional learning took place. Students' journal responses suggest that emotional learning discouraged students from pursuing primatology. However, we conclude that while this is concerning for the development of the profession, such experiences can be used to encourage pro-environmental behaviors and should be a primary goal of future primatological field schools.

Deconstructing biological sex by fuzzifying osteological sex: Implications for theoretically-informed practice

KATHERINE M. LANE and DONOVAN M. ADAMS

Anthropology, University of Central Florida

Conceptualizing biological sex as binary and discrete reinforces biological normalcy, whereby statistical analyses reify what is considered "normal." Operating in a two-sex model ignores the variation and overlap in biological sex and contributes to the erasure of transgender and gender nonbinary individuals and individuals who do not conform to the traditional sex binary. Therefore, the present research seeks to address how fuzzy logic may be applied in our assessment of sex-related variation.

Cranial and postcranial osteometric data of females (n=711) and males (n=1,260) from the Forensic Data Bank were used to explore the variation in biological (i.e., osteological) sex. Fuzzy c-means (FCM) is a soft, unsupervised clustering technique, allowing memberships across multiple groups, thereby blurring the traditional crisp lines of biological sex. Principal components for cranial, postcranial, and pooled measurements were extracted from a kNN-imputed (k=5), reduced data set and used for the FCM models.

Cluster validity indices suggested two-cluster models were optimal for all data sets. Although sex as assigned by legal documentation and soft-tissues largely separated into these two clusters, overlap (particularly by those identified as "male") was present. Postcranial and pooled data sets resulted in more separated clusters whereas the cranial data showed more overlap between the clusters and had fuzzier degrees of membership.

Despite the rather crisp clustering of some models, fuzzy logic and unsupervised clustering provide an appealing methodology that better accommodates the continuous nature and complexity of biological systems/data and mitigates some of the assumptions of a priori group classification.

Trends of the Carrying Angle of the Elbow in a Modern Human Population

KATHRYN D. LAURIA and LW COWGILL

Department of Anthropology, University of Missouri, Columbia

Defined as the acute angle formed by the long axis of the humerus and the long axis of the ulna, the carrying angle (CA) has been shown to be influenced by age, sex, and dominant-handedness. Previous research indicates that CA is statistically greater in females than in males, and is significantly greater in the dominant arm than in the non-dominant arm, suggesting a possible functional underlying cause. In addition, the larger CA in females may be driven by relatively wider pelvic breadth. This research investigates the relationship between CA and other sexually dimorphic markers, like clavicle length and bi-iliac breadth, as a way to evaluate if CA might vary with body breadth. Further, given the relationship between handedness and CA, we explored the relationship between CA and self-reported strenuous lifting. Computed tomography scans of 80 individuals, 40 male and 40 female, aged 24-40, from the New Mexico Decedent Image Database were digitally visualized in Avizo and Geomagic software. Results of this analysis indicate that carrying angle differs between males and females and right and left arms. However, clavicle and bi-iliac breadth are not major drivers of variation in carrying angle. Future work will study trends between the CA of the human elbow and cross-sectional geometry of the upper limb and forearm.

University of Missouri Life Sciences Fellowship

Does the foot respond to load based on foot types?

STEVEN G. LAUTZENHEISER[1] and PATRICIA A. KRAMER[2,3]

[1]Department of Anthropology, University of Tennessee Knoxville, [2]Department of Anthropology, University of Washington, [3]Department of Orthopaedics and Sports Medicine, University of Washington

The human foot can be approximated as a segmented hemi-dome with longitudinal (LA) and transverse arches. When muscle activation is minimal (as in standing), the LA is compliant because only bony and ligamentous connections hold it together. While walking, muscle contractions stiffen the LA, pulling the tarsals into a close-packed configuration and increasing LA stiffness. Some foot types, however, are close-packed without muscle activation (i.e. cavus feet), prompting us to hypothesize that categorizing foot type might reveal different responses to muscle activation.

Arch index (AI), a noninvasive way to assess LA stiffness, quantifies the amount of sole-to-substrate contact in the midfoot relative to the entire foot. Higher foot forces should produce predictable increased contact area in the midfoot. To test this, we captured peak vertical GRF and unshod footprints of 57 females and 20 males during quiet double (DS) and single stance (SS) and walking at their comfortable walking velocity. AI for each footprint was calculated using ImageJ and categorized as cavus (lowest quartile AI), planus (highest quartile AI), or normal. We also predicted the AI of the dynamic condition by extrapolating the change in normalized force and AI between the DS and SS conditions.

The difference between predicted and measured AI is sensitive to foot type. In cavus feet, DS AI does not predict the difference ($p=0.06$, $r^2=0.05$) but in normal and planus feet it does ($p<0.001$, $r^2=0.56$). Cavus feet potentially respond less to the muscular activations of walking than do normal and planus feet.

A new method for quantifying 3D anatomy of living subjects using low-dose stereo radiographs

AUSTIN B. LAWRENCE[1], MELANIE E. BOEYER[2] and KEVIN M. MIDDLETON[1]

[1]Department of Pathology and Anatomical Sciences, University of Missouri School of Medicine, [2]Missouri Orthopaedic Institute, Department of Orthopaedic Surgery, University of Missouri School of Medicine

Accurate and repeatable assessments of three-dimensional (3D) skeletal morphology are critical to interpretations of vertebrate functional anatomy. 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) 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 using ultra-low dose biplanar radiographs. Biplanar radiographs were obtained using an EOS Imaging System (EOS Imaging, Inc., Paris, France). A custom-built calibration frame with radiopaque markers was scanned using this system on multiple days in multiple positions inside the scanning space. We quantified the 3D coordinates of markers by placing landmarks at the center of each marker in both anterior-posterior and lateral radiographs. Landmark data for each scan were collected independently by two observers to determine inter-observer error. 3D coordinates of landmarks in each scan differed by <1 mm between observers, suggesting strong repeatability in assessing morphology of living subjects. Using a second calibration device, we identified distortion at the edges of EOS images which could significantly impact measurements on skeletal features near the margins of the scan area (i.e., hips, pelvis, lower limbs) and developed a method to mathematically correct for resulting distortion in landmark data. Finally, we demonstrate this method using measurements of iliac blade and spinous process orientation in a sample of living human participants.

This study received funding support from the Department of Pathology and Anatomical Sciences at the University of Missouri School of Medicine.

ABSTRACTS

The Human Pangenome Reference: Building a Global Resource to Map Genomic Diversity

HEATHER A. LAWSON[1], EIMEAR E. KENNY[2], KAREN H. MIGA[3] and TING WANG[1]

[1]Department of Genetics, Washington University in Saint Louis, [2]Institute for Genomic Health, Mount Sinai, [3]Biomolecular Engineering, University of California, Santa Cruz

The human reference genome is the foundational open-access resource of human genetics and genomics, having set the bar for data-sharing and providing a coordinate system for reporting and comparing results. The current reference (GRCh38) is a mosaic assembly comprised of data from over 20 individuals, with a single individual representing approximately 65% of the sequence. This linear assembly does not represent a real genome, and it inadequately represents global diversity. This creates reference biases, affecting variant discovery, disease association studies, and the accuracy of genetic analyses. The Human Pangenome Reference Consortium aims to sequence 350 diverse human genomes and create a comprehensive telomere-to-telomere map of genome variation. We will integrate these references and construct a unified pangenomic representation. A more diverse human reference promises to ensure that eventual applications of genomic research and precision medicine are effective for all populations. We selected the first 100 target genomes from the 1000 Genomes Project (1KG) in an effort to maximize genetic diversity. Recognizing that the 1KG does not capture the full spectrum of human diversity, we assembled a working group of multidisciplinary experts, including legal and ethics experts, to develop a set of principles to guide community engagement, population sampling, and representation. Ultimately, we hope to achieve an inclusive pangenome reference resource that improves genomics and biomedical research as well as provides training and outreach and the sharing of resources, standards and workflows.

NIH/NHGRI Funding: U01HG010971, U41HG010972, 3U41HG010972-03S1

Molecular underpinnings of lifestyle effects on health in the Turkana

AMANDA J. LEA[1,2,3], CHARLES WAIGWA[4,5], BENJAMIN MUHOYA[2,3,4], FRANCIS LOTUKOI[4], TAWNI VOYLES[7], JULIE PENG[2,3], VARADA ABHYANKAR[2,3], JOSEPH KAMAU[5,6], JENNY TUNG[7,8] and JULIEN F. AYROLES[2,3]

[1]Department of Biological Sciences, Vanderbilt University, [2]Department of Ecology and Evolution, Princeton University, [3]Lewis Sigler Institute for Integrative Genomics, Princeton University, [4]Department of Research, Mpala Research Centre, [5]Department of Biochemistry, School of Medicine, University of Nairobi, [6]Institute of Primate Research, National Museums of Kenya, [7]Department of Evolutionary Anthropology, Duke University, [8]Department of Biology, Duke University

Across the world, people are transitioning from traditional, subsistence-level practices to more urban, market-integrated lifestyles. Such transitions are universally accompanied by dramatic changes in diet, activity, and ecology, as well as an increased risk of noncommunicable diseases. This increased disease risk is thought to arise from mismatches between human physiology—which has been shaped by selection pressures in past environments—and urban lifestyles that no longer reflect these conditions. However, few datasets have addressed the molecular basis of such evolutionary mismatch. To do so, we generated an integrative dataset of interview, health biomarker, DNA methylation (n=320), and gene expression data (n=452) from the Turkana, a traditional pastoralist group that is undergoing a rapid lifestyle transition. While our previous work has shown that urban transitions compromise cardiometabolic health in this population, our molecular data shed light on the mechanistic basis of these effects: 1155 genes are differentially expressed between Turkana living a pastoralist versus an urban lifestyle (10% FDR). Lifestyle-associated genes are enriched for immune and metabolic pathways as well as known non-communicable disease genes. Further, differentially methylated, lifestyle-associated CpG sites are enriched near differentially expressed genes, supporting a role for environmentally-induced epigenetic change in driving transcriptional variation. Our ongoing analyses are using evolutionary genomic data to understand how historical selective events have shaped lifestyle-responsive genes, as well as mediation analyses to understand the causal relationships between lifestyle, gene regulation, and cardiometabolic health biomarkers. Together, our comprehensive analyses shed new light on the molecular underpinnings of evolutionary mismatch, with implications for understanding modern disease.

EvoHom: Developing an Edugame for High School Teachers to Increase Literacy in Human Evolution

ROSE LEACH[1,4], JAZMIN RIOS[3,4] and FANUEL MUINDI[2,4]

[1]Department of Anthropology, Kent State University, [2]Department of Molecular and Cellular Biology, Harvard University, [3]Palos Verdes-South Bay Audubon Society, [4]Science, Technology, Engineering, and Mathematics (STEM) Advocacy Institute

EvoHom is a board game currently in development to address issues high school science teachers face: developing interesting and engaging alternative methods of teaching science, while facing time and budgetary constraints. Development of EvoHom started with interviews and surveys of high school educators to identify barriers to developing alternative teaching methods and interest in incorporating game-based learning into curricula. Using the results, we set out to create a fun, heuristic tool that allows high school students to explore evolution and natural selection within the framework of biological anthropology. Game players begin with a randomly selected environmental scenario, based off paleoclimate research in human evolution. They each play as an individual hominin with a given set of traits who must work to survive and reproduce with other hominins to evolve over generations and best fit the environmental scenario, becoming the most reproductively successful. EvoHom is designed to promote accessibility by providing a technology-free tool that reduces economic barriers to alternative methods of learning developed by scientists. It also comes with an accompanying lesson plan for high school teachers that has been designed to incorporate Ohio Science Standards, with a focus on Common Core Standards. Initial distribution of EvoHom is focused on high school science teachers at underserved urban and rural schools in Northeast Ohio, where budgetary and time restrictions are more exacerbated. EvoHom supports high school educators by providing a low-cost, compelling, method of teaching whose framework can be used to develop more edugames addressing other topics within biological anthropology.

EvoHom is being developed with generous support from the STEM Advocacy Institute

A Systematic Review of Sinusitis in Palaeopathology: Preliminary Results - Methodology

MATTHEW J. LEE[1], THOMAS J. SIEK[1], JENNIFER L.D. AUSTEN[2,3] and CARA S. HIRST[1]

[1]No Affiliation, No Affliation, [2]Department of Archaeology, University of Reading, [3]Department of Archaeology and Centre for Forensic Research, Simon Fraser University

Sinusitis is an upper respiratory tract infection characterised by the inflammation of the muscous membranes lining the sinuses. It is frequently reported in modern populations and has been associated with poor air quality, dental disease, and allergies. In palaeopathology, the reported prevalence of sinusitis within past populations has greatly varied and high prevalence has typically been interpreted as an indicator of environmental pollution. However, the frequent reporting of high sinusitis prevalence may indicate a lack of methodological innovation, testing and clinical integration in palaeopathological research. This poster presents the preliminary results of a systematic review of sinusitis within the palaeopathological literature, with a focus on methodological tendencies. Between 1967 and 2021, 68 reports of sinusitis were identified, representing 132 archaeological sites. Of these reports, 32 had methological information which could be

examined. Preliminary results indiciate that the diagnostic methodology and criteria introduced in the mid-1990s has been the most influential and has been explicitly applied with or without modification in 46.88% of the reports examined. This review also highlighted the need for further discussions regarding the ethical consideratoins of the use of destructive examination methods. From these preliminary results, this poster addresses discrepancies in sinusitis diagnosis and reporting, and invites researchers to give their insight and opinion regarding these palaeopathological methodologies via an online survey.

Nitrogen isotope analysis of 125,000-year-old tooth enamel from the Middle Palaeolithic Neanderthal site of Neumark-Nord 2, Germany

JENNIFER N. LEICHLITER[1,2,3], TINA LÜDECKE[1,2,4], ALAN D. FOREMAN[2,6], LUTZ KINDLER[5], THOMAS TÜTKEN[3], THEO TACAIL[3] and ALFREDO MARTÍNEZ-GARCÍA[2,6]

[1]Emmy Noether Group for Hominin Meat Consumtion, Max Planck Institute for Chemistry, [2]Climate Geochemistry Department, Max Planck Institute for Chemistry, [3]Institute of Geosciences, Johannes Gutenberg University Mainz, [4]Biodiversity and Climate Research Center, Senkenberg Museum Frankfurt, [5]MONREPOS Archaeological Research Centre and Museum for Human Behavioral Evolution, Leibniz-Research-Institute for Archaeology, [6]Organic Isotope Geochemistry, Max Planck Institute for Chemistry

This study represents one of the first applications of a novel oxidation-denitrification method to measure the nitrogen isotope composition of tooth enamel in the archaeological record. Efforts to measure nitrogen isotopes in tooth enamel via traditional methods have not been feasible given the low nitrogen content of enamel (<0.01 % wt.) Here we present nitrogen isotope data of tooth enamel, which significantly expands the existing geochemical dataset at Neumark Nord, a high-resolution Middle Paleolithic (~125 kyr) site in Germany and provides insight into the structure of the paleo-food web at this locality, allowing us to make inferences about the environmental and ecological context of Neanderthals prior to the arrival of anatomically modern humans in Europe. In our study, we measured $\delta^{15}N_{enamel}$ values in the tooth enamel of representative herbivore (n = 5), omnivore (n = 1), and carnivore taxa (n = 2) to reconstruct the paleoecology of the fauna at Neumark Nord 2. Our results show that herbivores have, on average, lower mean $\delta^{15}N_{enamel}$ values (x= 5.3 ± 0.9 ‰) than omnivores (x= 7.7 ± 1.6 ‰) and carnivores (x= 6.6 ± 1.8 ‰). A previous study of herbivore $\delta^{15}N_{collagen}$ at Neumark Nord 2 by Britton et al., 2012 found evidence for differences in dietary behavior between bovids and equids. We found similar patterning in $\delta^{15}N_{enamel}$ values for the same taxa although the magnitude of the difference between taxa is somewhat smaller in enamel (1.2 vs. 2.0 ‰) compared to collagen.

Funded by the Max Planck Society (MPG), the European Research Council (ERC 681450 to Thomas Tütken); and the Deutsche Forschungsgemeinschaft Grant (DFG) LU 2199/1-2 to Tina Lüdecke.

Patterns of postcranial sexual size dimorphism in non-captive thick-tailed bushbabies (*Otolemur crassicaudatus*) from northern South Africa

STEVEN R. LEIGH[1], MICHELLE L. SAUTHER[1], FRANK P. CUOZZO[2,3] and ADRIAN SW. TORDIFFE[4]

[1]Anthropology, University of Colorado Boulder, [2]Mammal Research Institute, University of Pretoria, [3]Lajuma Research Centre, [4]Department of Paraclinical Sciences, Faculty of Veterinary Science, University of Pretoria

Patterns of sexual size dimorphism in primates support inferences about behavior, with paleoanthropological applications. However, few data exist concerning how body size dimorphism relates to anatomical elements such as body dimensions.

We compare patterns of postcranial sexual dimorphism in a sample of four primate species, focusing on thick-tailed bushbabies (*Otolemur crassicaudatus*). We predict that overall patterns of postcranial dimorphism will characterize the three dimorphic species (including bushbabies), regardless of degree of dimorphism. We hypothesize that similarities in patterns of sexual dimorphism reflect sexual selection through intermale competition.

Morphometric comparisons include large samples of noncaptive lemurs (*Lemur catta*), bushbabies, captive sooty mangabeys (*Cercocebus atys*), and captive *Papio* baboons. We analyze estimates of sexual size dimorphism (SSD) in mass and 11 linear measurements, including fore- and hindlimb lengths, body length, and circumferences.

Strepsirrhine SSD is uniformly lower than in the cercopithecines (lemurs lack SSD entirely). Body masses are the most dimorphic measures (SSD=1.2 in thick-tailed bushbabies, and approximately 1.7 in both cercopithecines). Despite lower magnitudes of bushbaby SSD, the overall pattern of dimorphism among the dimorphic species is very similar (correlations for bushbabies vs. mangabeys and baboons are 0.89 and 0.75, respectively).

Despite substantial differences in overall levels of SSD, the pattern of SSD is similar across the dimorphic species. This may reflect the consequences of intermale competition, possibly reflecting lower overall levels of competition in bushbabies. Similarities in patterns of SSD in limb dimensions may reflect similar allometric effects of mass growth across the dimorphic species.

Feeding Our Young: The Evolutionary Origins of Mammary Glands from Integumentary Structures

TAORMINA LEPORE

Department of Integrative Biology, University of California Berkeley

This abstract is part of the symposium *Integumentary Anthropology: Examining the Exterior* and aims to provide a deep evolutionary perspective on the key innovation of the Mammalia: milk production. Milk organs signaled a dramatic shift in how vertebrate parents procured food for their young. While a selection of extant vertebrates are known to produce a protective or nutritive liquid for neonates, mammalian milk provides a high energy food source with unique milk sugars, water, and immunoglobulin components, excellent for the survival of fast growing babies, as well as the development of a strong parent-infant social bond. While the metabolic cost to the maternal parent is extensive, the benefits of milk production enabled the diversification and success of the mammalian clade.

But where did milk come from, evolutionarily? I present a comprehensive review of the research literature on the early evolution of milk. I highlight gaps in knowledge that underscore the utility of genomic analysis alongside the histology of stem mammal, mammaliaform, and synapsid dental fossils. Anatomical and genetic evidence suggest a connection between eccrine sweat glands, hair, and mammary glands. Paleontologists attempt to constrain the evolution of milk based on fossil hair, dental features, and putative examples of parental care for altricial young. However, conclusions on the evolutionary origins of mammary glands using fossil evidence often remain in the realm of conjecture. I present evidence demonstrating how an integration of anatomical and genetic data might be able to pinpoint milk's origins more clearly than the current literature reflects.

Metabolic diseases in Non-adults from Neolithic Chuwan (ca. 6000-4400 BP), Henan Province, China

ZIYI LI[1], REBECCA GOWLAND[1], TINA JAKOB[1] and TAO WANG[2]

[1]Archaeology, Durham University, [2]Archaeology, Capital Normal University

The study presents a palaeopathological analysis of non-adults from Chuwan, a Yangshao cultural prehistoric settlement in Henan province, to investigate the life and health of non-adults in central China during the middle-late Neolithic period (6000-4000 BP). Excavations in 2021, by the Department of Archaeology, Capital Normal University and the Institute of Relic and Archaeology of Zhengzhou, revealed one house foundation, 20 urned burials, and 40 graves. Non-adults younger than ca. 3.5 years of age were buried separately in a cluster of urn burials, while the graves of older children

were interspersed with adult graves. A total of 50 individuals were excavated, including 11 non-adults. Analysis revealed a range of pathological indicators indicative of metabolic and other non-specific diseases. These included periosteal new bone formation, ectocranial and endocranial lesions, and severe porotic hyperostosis and other lesions indicative of Vitamin C or Vitamin D deficiency. Comparisons between these findings and non-adult remains from contemporaneous sites in Henan was undertaken. Chuwan shows the most severe lesions linked to metabolic diseases. The diagnosis of pathological lesions in infants is challenging due to similarities with normal growth processes, in conjunction with taphonomic factors. Nevertheless, clear indicators of physiological stress in infants and children at this site suggest sub-optimal maternal health and early childhood adversity. The life-long consequences of this poor start in life for the inhabitants of Neolithic Chuwan are considered.

Intergroup competition and home range geometry

JOYCE LIAO[1], SEAN CROMMELIN[1] and MICHELLE BROWN[1,2]

[1]Department of Anthropology, University of California, Santa Barbara, [2]Department for the Ecology of Animal Societies, Max Planck Institute of Animal Behavior

Space use by animal groups is influenced by a variety of factors, including food availability and competition for these resources. Repeated patterns of attraction to or avoidance of specific areas result in a home range, with a core area being the region of most intense use. Though the size, shape, and placement of core areas varies widely across groups and populations, there is little understanding of the forces driving this variation. We test whether the intensity of intra- and inter-group competition affect the size of home range core areas for 28 groups from three monkey species at four sites in Uganda. We calculated home range peripheries (95% or 99% isopleth) and core areas (50% isopleth or the inflection point of the area: volume exponential curve) as autocorrelated kernel density estimates. We find that the relative size of core areas does not vary with group size (Spearman rank correlations, $P > 0.100$ for all tests) or as a function of whether the group is incompletely surrounded (Wilcoxon rank-sum tests, $P > 0.050$). Surprisingly, however, between-site comparisons indicate that the relative size of core areas increases with group density. This pattern indicates that when many groups are compressed into a habitat, they expand the size of their core areas as a defensive response to intergroup competition.

Funding was provided by the US National Science Foundation (award #s 0333415, 0742450, 1103444, and 2127253); the Leakey Foundation; the Hellman Family Foundation; Columbia University; and UC Santa Barbara.

Humeral morphology and locomotion: Discerning functional signals using weighted spherical harmonics

CATHERINE J. LLERA MARTÍN and ZANA R. SIMS

Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

The relationship between humeral form and function is essential for understanding primate evolution, especially early primate transition to arboreality. Humeral shape in strepsirrhines has been linked to degree of support and grasping ability, however, studies on the relationship between humeral shape and other primate behaviors (e.g., brachiation, leaping, and climbing) are more limited. This study aims to examine the shape of proximal and distal humeral articulations to determine if there is a functional signal that can be attributed to locomotor behavior across primates.

A sample of 18 surface meshes was downloaded from MorphoSource. The proximal and distal articulations for each humerus were isolated by cropping each surface twice at 30% of total length, from either end. Weighted spherical harmonics were used to perform a shape analysis for each articulation. Spherical harmonic analysis is a landmark-free method that represents a surface as coefficients associated with a set of spherical harmonic functions. The coefficients describing each surface were used in a principal component (PC) analysis. Average models for each locomotor group and PC plots were created to analyze differences in humeral shape that could be attributed to locomotor behavior.

Combined, the first three PCs explain 57.87% and 60.37 % of shape variation in proximal and distal humeri, respectively. Though a phylogenetic signal is present at both the proximal and distal articulations, a functional signal was also detected. In this sample, the functional signal is stronger for the proximal articulation. These results have potential implications for contextualizing the locomotor behaviors of fossil primates.

Supported by NSF DGE-1746891

Dental topography and diet of non-cercopithecoid catarrhines from the early Miocene of Kenya

ELLIS M. LOCKE

Department of Anatomy, Idaho College of Osteopathic Medicine

The early Miocene of East Africa documents a rich fossil record of 'non-cercopithecoid catarrhines' (NCCs) – taxa distinct from Cercopithecoidea, but whose phylogenetic position relative to crown Hominoidea is debated. Prior studies of lower second molar (m2) shearing quotients and microwear have yielded conflicting results about the range of dietary adaptations among these taxa. Dental topography provides a toolkit for using 3D tooth shape to infer the dietary ecology of fossil primates. Here, these methods are used to characterize multivariate occlusal topography from m2s of five NCC genera from the early Miocene of Kenya (n=36) and a comparative sample of 18 extant catarrhine genera (n=333).

Principal component analyses show extant catarrhine clades are largely separated by differences in occlusal relief and complexity. Among Miocene catarrhines, small-bodied taxa *Dendropithecus* and *Limnopithecus* plot with extant cercopithecids while the more derived, larger-bodied *Proconsul, Ekembo,* and *Rangwapithecus* overlap primarily with African apes. These differences are consistent in separate analyses of lightly worn and moderately worn molars. Linear discriminant function analyses indicate that m2 occlusal topography correctly classifies extant catarrhines by dietary category at higher rates in hominoid-only models (>90%) than pooled catarrhine models (69-71%) regardless of wear stage. Using the pooled catarrhine model, all fossil taxa are reconstructed as frugivores or hard-object feeders. With a hominoid-only model, *Rangwapithecus* and *Limnopithecus* are classified as folivores based on moderately worn m2s. These results support previous reconstructions of dietary diversity among early Miocene catarrhines and document differences in molar topography that likely reflect both diet and phylogeny.

Support for this research was provided by the National Science Foundation (NSF BCS-1846153) and Arizona State University.

Pressure generated by the modern human hand during vertical climbing

VICTORIA A. LOCKWOOD[1,2], SZU-CHING LU[2,3], SAMANTHA WINTER[4,5] and TRACY L. KIVELL[2,6]

[1]Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, [2]Animal Postcranial Evolution (APE) Lab, Skeletal Biology Research Centre, School of Anthropology and Conservation, University of Kent, [3]Laboratory for Innovation in Autism, School of Education, University of Strathclyde, [4]School of Sport, Exercise and Health Sciences, Loughborough University, [5]School of Sport and Exercise Sciences, University of Kent, [6]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Studying the interaction between the modern human hand and arboreal supports can help clarify the relationship between hand morphology and specific arboreal behaviors. It can also help interpret the functional implications of the hand morphology of fossil hominins. We previously examined the pressures generated by the modern human hand during suspension and here we present data on a comparable sample (n = 14 individuals) during vertical climbing. We used a custom-built climbing apparatus to investigate peak pressure experienced by the hand during

static (with adducted and abducted thumb) and dynamic vertical climbing on three different diameter (45mm, 80mm, and 105mm) supports. Pressure data, which were recorded using a Novel Pliance® pressure system, were normalized using hand surface area and body mass. During static climbing on the 45mm diameter support hand pressures were more variable and significantly higher when the thumb was abducted, but thumb position had no effect on the hand pressures generated on the larger diameter supports. The static thumb abducted and dynamic vertical climbing activities on the 45mm diameter support had the largest coefficients of variation compared to the respective activities on the 80mm and 105mm diameters. Our results indicate that diameter size may act to mediate pressure differences and that the thumb plays an important role in vertical climbing on smaller diameter supports. These results have implications for how we interpret morphology, particularly that of the thumb, in fossil hominins with hand proportions similar to those of modern humans.

Funded by ERC Starting Grant 336301 (TLK, S-CL). Lewis N. Cotlow Fund and Sigma Xi, The Scientific Research Society, Grant-In-Aid of Research, Grant G201903158539371 (VL).

Pictures?! Comparing observer error for dental morphology from direct observations and photographs using ASUDAS

TISA N. LOEWEN[1] and G. RICHARD SCOTT[2]

[1]School of Human Evolution and Social Change, Arizona State University, [2]Department of Anthropology, University of Nevada, Reno

Due to the ongoing Covid-19 pandemic beginning in 2020, scholars were challenged to identify research contingency plans that do not require extensive travel or in-person interactions. A strategy proposed by dental anthropologists has been to record morphological data from photographs; however, the efficacy of this approach has not been validated. In this observer error study, we scored 15 morphological dental traits using ASUDAS (Arizona State University Dental Anthropology System) from sets of the same casts and photographs provided by the ASU Dental Anthropology Collection (N=81). Ordinal scores for each trait were compared for percentage of difference and Absolute Mean Grade Difference (AMGD) while dichotomized data were compared using a paired Student's t-test. Results between photos and casts for UI1 SHOV, UM2 HYP, and LP4 MLC are consistently < 10% for two or more differences. Traits with a high percentage of difference included TD and DAR regardless of tooth, and UM1 C5. However, TD and DAR are considered difficult to reproduce, while C5 scoring was hindered by cast and picture quality. AMGD, which accounts for the directionality of ranked scores, indicates that most traits were scored higher when recorded from casts, except for the hypocone which skewed higher from photos. Dichotomized data scored by the same individual had no significant difference between observations (p=0.8 and p=0.051). Results additionally suggest that experience affected intra-observer repeatability for ordinal scores. Recommendations to maximize comparisons from photographs between observers prioritize lighting, different views and quality of photos and casts, and researcher communication.

Ecological and social pressures interfere with homeostatic sleep regulation in wild baboons (*Papio anubis*)

JON C. LOFTUS[1,2,3,4], ROI HAREL[1,2,3], CHASE NUNEZ[1,2,3] and MARGARET C. CROFOOT[1,2,3,4]

[1]Ecology of Animal Societies, Max Planck Institute of Animal Behavior, [2]Biology, University of Konstanz, [3]Center for the Advanced Study of Collective Behavior, University of Konstanz, [4]Animal Behavior Graduate Group, University of California, Davis

Sleep is fundamental to the health and fitness of all animals. The physiological importance of sleep is underscored by the central role of homeostasis in determining sleep investment – following periods of sleep deprivation, individuals experience longer and more intense sleep bouts. Yet, most studies of sleep have been conducted in highly controlled settings, disconnected from the ecological and social context that may exert pressures on sleep patterns in conflict with homeostatic regulation. Using tri-axial accelerometry and GPS to track the sleep patterns of a group of wild baboons (*Papio anubis*) at multiple temporal and spatial scales, we found that ecological and social pressures indeed interfere with homeostatic sleep regulation. Baboons sacrificed time spent sleeping when in less familiar locations and when sleeping in proximity to more group-mates, regardless of how much they had slept the prior night or how much they had physically exerted themselves the preceding day. Moreover, we found that the collective dynamics characteristic of social animal groups persist into the sleep period, as baboons exhibited synchronized patterns of waking throughout the night, particularly with nearby group-mates. Thus, for animals whose fitness depends critically on avoiding predation and developing social relationships, maintaining sleep homeostasis may be only secondary to remaining vigilant when sleeping in risky habitats and interacting with group-mates during the night. Our results highlight the importance of studying sleep in ecologically relevant contexts, where the adaptive function of sleep patterns directly reflect the complex trade-offs that have guided its evolution.

Research supported by: National Science Foundation (IIS 1514174 & IOS 1250895), a Packard Foundation Fellowship (2016-65130), and the Alexander von Humboldt Foundation.

Human energetic stress associated with upregulation of spatial cognition

DANIEL P. LONGMAN[1], JONATHAN CK. WELLS[2] and JAY T. STOCK[3,4,5]

[1]School of Sport, Exercise and Health Sciences, Loughborough University, [2]Childhood Nutrition Research Centre, UCL Institute of Child Health, [3]Department of Archaeology, University of Cambridge, [4]Department of Anthropology, University of Western Ontario, [5]Department of Archaeology, Max Planck Institute for the Science of Human History

Evolutionary life history theory has a unique potential to shed light on human adaptive capabilities. Ultra-endurance challenges have emerged as a valuable experimental model in this context, allowing the direct testing of phenotypic plasticity via physiological trade-offs in resource allocation. This is enhancing our understanding of how the body prioritises different tissues or functions when energetically stressed. However, despite the central role played by the brain in both hominin evolution and metabolic budgeting, cognitive plasticity during energetic stress remains unstudied. Here, we analysed variability in performance in three key cognitive domains in athletes before and after competing in 2 multiday ultramarathons (n=48; 29 male, 19 female). We demonstrate that during energetic stress, performance in a spatial working memory task assessing the ability to store location information, and promoting ability to navigate a landscape to locate food and acquire calories, increased (95% CI 0.9, 7.1, p = 0.014). In contrast, reaction time remained unchanged and episodic memory performance decreased (95% CI -3.1, -0.4, p = .013).These results were consistent with the predictions of life history theory, as the function with the greatest immediate survival value was prioritised. We discuss these results with reference to a human evolutionary trajectory centred around encephalisation. Encephalisation affords great plasticity, facilitating rapid responses tailored to specific environmental conditions. Through encephalisation, hominins increased their adaptive capabilities as a phenotypically plastic species, a process we term 'adaptive cognitive flexibility'. This short-term adaptive cognitive flexibility may promote fitness to a greater extent than longer-term less-dynamic adaptive responses.

This work was funded by the European Union's Seventh Framework Programme, Grant/Award Numbers: 617627, FP/2007-2013, awarded to JTS.

Primates on the move: a comparison of student physical activity during an ethno-primatological field school and traditional classroom setting

JAMES E. LOUDON[1], MICHAELA E. HOWELLS[2], TARYN B. APRIL[2] and KATHERINE L. WOOLARD[3]

[1]Department of Anthropology, East Carolina University, [2]Department of Anthropology, University

of North Carolina-Wilmington, [3]School of Social Work, University of North Carolina-Chapel Hill

Field training in biological anthropology has documented educational and professional benefits. Although the physical benefits (e.g., increased exercise) are often discussed they are less well documented. We compared the physical activity of nine students participating in the 2018 *Balinese Macaque Ethnoprimatology Field School* to their activity expenditure in traditional classroom environment. We predicted that the students would exhibit higher physical activity during the field school due to the substantial physical requirements associated with the program (e.g., walking as primary mode of transportation, lengthy follows of nonhuman primates), compared to traditional classrooms (e.g., long periods of inactivity during lectures and studying). During the first days of the three-week field school, we issued students an accelerometer, and recorded their age, sex, height, and weight. Students were issued accelerometers again during their third week of course work in traditional classrooms following the field school. The accelerometer measured calories burned, number of steps, and the number of minutes engaged in four levels of energy expenditure (vigorous, moderate, easy, and very easy) during a 24-hour period. As predicted, during the field school students burned more calories ($P < 0.05$), took more steps ($P < 0.0001$), and engaged in more moderate and easy exercise ($P < 0.0001$) compared to their experiences in the traditional classroom environment. These differences reflect a more consistent but lower intensity physical work through the day compared to intensive purposeful exercise bouts (e.g., gym) in a typically college experience. Taken together, these results document the physical benefits of biological anthropology field schools.

This project was supported by the University of North Carolina-Wilmington's Experiencing Transformative Education through Applied Learning (ETEAL) program and Center for the Support of Undergraduate Research and Fellowships (CSURF).

Sharing circles: Native American Young Adult Perspectives on Genomics and Identity

JUSTIN LUND

Anthropology, University of Oklahoma

Native American identity is fluid, complex, and like all identities, socially constructed. Today, social conceptions of Indigeneity are increasingly playing out in genomics discourses. Genomics does not adequately define Native American identity for many reasons, so genomics discourse around this identity is troubling. As Native identity is increasingly defined by widely accessible genomic technologies, Native Americans continue to have alternatively distinct ways of identifying and belonging. This project discusses with a sample of Native American young people their perspectives on genomics and Native American identity. Sharing Circles, an Indigenous centered approach to understand the stories of Native Americans, were conducted with 18 self-identified Native American students and staff at the University of Oklahoma. Sharing Circles as an alternative to focus groups works to decolonize methodological spaces by being both culturally sensitive and relevant. The perspectives of these young people should also work to decolonize popular understandings of what Native American identity is and is not. The Sharing Circles events resulted in rich discussions that convey a sense of identity that is grounded in ties to tribal communities, relationships with other tribal students on campus, and specific conceptions of traditional and modern tribal identities. Participants expressly challenge genomics as a defining discourse about Indigeneity.

This research was supported by the National Human Genome Research Institute and the Center for the Ethics of Indigenous Genomics Research (RM1HG009042).

Adapiform internal nasal anatomy and implications for crown Primates

INGRID K. LUNDEEN

Department of Anthropology, University of Texas at Austin

The delicate scrolls of bone in the nasal fossa—turbinals—exhibit sometimes dramatic interspecific variability among extant primates. This variability is particularly evident in the numbers of ethmoturbinals and frontoturbinals seen among living strepsirrhines. The fact that turbinals are often not visible or not preserved in fossil crania has historically complicated efforts to reconstruct patterns of turbinal evolution within Primates. However, advances in μCT scanning resolution has substantially increased number of fossil taxa for which turbinal morphology may be directly observed. To date, fossilized turbinals have been described in omomyoids and a stem platyrrhine. Here, I use μCT data to describe turbinal anatomy in Adapiformes, which are often inferred to be stem strepsirrhines. This sample includes two European adapids—*Leptadapis* and *Adapis*—and two North American notharctids—*Notharctus* and *Smilodectes*. Turbinal anatomy preserved in these taxa—particularly in one remarkably well-preserved specimen of *Leptadapis leenhardti* (YPM-011481)—demonstrates that adapiforms had four ethmoturbinals and two frontoturbinals. This finding suggests that the five ethmoturbinals seen in some extant strepsirrhines (e.g., *Hapalemur*, *Daubentonia*) represent derived increases in turbinal number. These observations further suggest that the last common ancestors of both crown primates and crown strepsirrhines probably had nasal fossae with four ethmoturbinals and two frontoturbinals.

The inhibitory cascade model predicts postcanine tooth size in fossil catarrhines from the early Miocene

RISA LUTHER[1], FRANCESCA SOCKI[2], ABIGAIL S. HALL[1] and KIERAN P. MCNULTY[1]

[1]Anthropology, University of Minnesota, [2]Earth and Environmental Science, University of Minnesota

The inhibitory cascade model has been used to predict postcanine dental proportions across multiple mammalian orders, including a broad range of extant primate species and fossil hominins. We computed molar size ratios in a sample of fossil apes and compared these to published data from extant hominoids and cercopithecoids to determine the extent to which this model also explains variation in early Miocene catarrhine lower postcanine dentitions. Likewise, we computed premolar-molar ratios in the same sample to further explore relationships among tooth sizes. Our results show that the inhibitory cascade model of development adequately characterizes the lower molars in these fossils. Moreover, molar ratios more closely align early Miocene apes with extant cercopithecoids rather than hominoids, but statistically the fossils differ from both extant superfamilies. A similar pattern of results was found in premolar-molar ratios, but all three groups' distributions were more similar compared to results for molar ratios. Previous studies have demonstrated the importance of the inhibitory cascade model (and deviations from it) for developing hypotheses about dental development and evolution, and have concluded that the standard inhibitory cascade is likely plesiomorphic in catarrhines and platyrrhines. Our results are consistent with that conclusion and do not implicate unique specializations in the fossil sample. Similarities noted between fossils and extant cercopithecoids suggest that, within the inhibitory cascade model, these ratios may provide additional resolution about the evolution of dental proportions within catarrhines. However, larger fossil samples are needed to verify and clarify the significance of those relationships.

Inferring geographic origins and migration among Middle Formative individuals from the Central Highlands of Mesoamerica using strontium and oxygen isotopes

PAIGE A. LYNCH[1], HEATHER HJ. EDGAR[1], VICTOR J. POLYAK[2], GISELLE CANTO AGUILAR[3], ALEJANDRO ARUGUELLES[4], COREY RAGSDALE[5], YEMANE ASMEROM[2] and KEITH M. PRUFER[1]

[1]Anthropology, University of New Mexico, [2]Earth and Planetary Sciences, University of New Mexico, [3]Investigadora Centro, Instituto Nacional de Antropología e Historia – Morelos, [4]Desarrollo académico, Universidad del Valle de Puebla, [5]Anthropology, Southern Illinois University – Edwardsville

Strontium and oxygen stable isotopes from enamel provide geochemical evidence for mobility in humans post dental development. Studies in Mesoamerica have investigated mobility in large complex states, but few data exist for the Middle Formative (900 - 400 BCE). Zazacatla, located in central Mexico, had a long history of occupation (800 BCE - 1150 CE), and has been proposed to be a key link between Olmec centers in the Gulf, west and south Pacific coasts, and Highlands. The region is marked by temperate climate and high agricultural yields, making it attractive to live. Here, we investigate mobility patterns among individuals buried at Zazacatla. Timing and frequency of individual migration is informative about interactions among Olmec-period sites across Mesoamerica. Previous data from nearby sites show ranges of 0.7053-0.7061 for strontium ($^{87}Sr/^{86}Sr$) and -7.80 to -11.80‰ oxygen ($\delta^{18}O_{enamel}$; VSMOW). We assume individuals buried at Zazacatla have $^{87}Sr/^{86}Sr$ and $\delta^{18}O_{enamel}$ values close to those ranges.

We sampled second or third molar enamel (depending on preservation; N_{total} = 19). Direct dating of tooth root dentin revealed that individuals came from Middle Formative, Classic, and Postclassic periods. Strontium values created two clusters (0.7047-0.7053 and 0.7064-0.7071) and oxygen values ranged from -8.19 to -12.76‰ (VSMOW). Results indicate no consistent migration pattern through time. People originated from three distinct regions within the Highlands of Mexico (Basin of Mexico, Xochicalco, and the Sierra Madre ranges). This suggests individuals at Zazacatla originated in the central highlands/ Basin of Mexico, likely moving north-south rather than east-west from the Lowland Olmec heartland.

Tattooing the integument: Inflammatory and endocrine responses are primed by lifetime tattoo experience

CHRISTOPHER D. LYNN

Anthropology, University of Alabama

This abstract is part of the symposium *Integumentary Anthropology: Examining the Exterior*. This presentation introduces a concept called "allostatic preparation" to provide a framework for investigating plastic changes in endocrine and immune function that adaptively prepare the body for expected stress. Despite constant and critical interactions between human immune and endocrine systems, the adaptive nature of these interactions with regard to cultural variability is difficult to parse. The allostasis concept, meaning stability (of homeostasis) through change, provides an avenue for clarity.

Whereas a large body of research describes "allostatic overload" and the negative health consequences of too much stress, few studies map out "allostatic preparation," or how the body adapts for future expected stress. Experimental research and studies from exercise science suggest that immunosuppression occurs with respect to both novel and chronic stress but that repeated or moderate stressors may build up immune function in specific and non-specific ways. Tattooing provides another model for exploring these systemic interactions in context. I present data from my research collaborations in the U.S. and Pacific comparing immune and endocrine level before and during tattooing in relation to lifetime tattoo experience.

Consistent with an allostatic preparation model, limited tattoo experience is associated with immunosuppression, whereas high tattoo experience is associated with increased immune function. I discuss how the secretory biomarkers immunoglobulin A, cortisol, and C-reactive protein assayed from saliva taken during tattoo sessions are reflective of circulating homeostats of allostasis and lifetime of experience gathered through the human integument.

This research was supported in part by the Wenner Gren Foundation (Grant No. 7985665216) and the University of Alabama (CARSCA).

Variation of bony labyrinth morphology in late Middle Pleistocene Neanderthals from Abri Suard, France

DIEGO LÓPEZ-ONAINDIA[1], ISABELLE CREVECOEUR[1], ADRIEN THIBEAULT[1], ALESSANDRO URCIUOLI[2], MARTA LUCAS-ARAGAY[3], MÉLANIE PRUVOST[1], CLÉMENT ZANOLLI[1], NOHEMI SALA[4,8], ANTOINE BALZEAU[5], CHRISTINE COUTURE-VESCHAMBRE[1] and ASIER GÓMEZ-OLIVENCIA[6,7,8]

[1]UMR-5199 PACEA, Université de Bordeaux, [2]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona (UAB), [3]Departament d'Història i Arqueologia, Universitat de Barcelona (UB), [4]Centro Nacional de Investigación Sobre la Evolución Humana, [5]UMR 7194, Dpt Homme et environnement, Muséum national d'Histoire naturelle (MNHN), [6]Department of Geología, Universidad del País Vasco-Euskal Herriko Unibertsitatea (UPV/EHU), [7]Sociedad de Ciencias Aranzadi, [8]Centro UCM-ISCIII de Investigación Sobre Evolución y Comportamiento Humanos, Universidad Complutense de Madrid

Neanderthals present several autapomorphic bony labyrinth features, while other groups, including modern humans, retain the primitive condition found in early *Homo*. The main distinctive features are the low positioned posterior canal and the relatively small-sized anterior and posterior semicircular canals. Although all these derived features are not observed together before 200 ka, some were already present in the Middle Pleistocene individuals from Sima de los Huesos and Reilingen. Here we describe of the bony labyrinth of two individuals from Abri Suard site (200–150 ka, France): S17 and S53 (the latter being unpublished). We used a series of 2D morphometrics and 3D Geometric Morphometric analyses to compare these two specimens to earlier and later *Homo* specimens.

Both S17 and S53 have a relatively low positioned posterior canal, although less pronounced in S17. The cochlea of S53 is larger and more laterally rotated than S17. The specimens from Abri Suard represent two extremes of the range of the European Middle Pleistocene hominin and Neanderthal variation. While both bony labyrinths plot close to the Late Pleistocene Neanderthals, S53 shares more features with some of the Sima de los Huesos hominins and with classic Neanderthals than S17, which plots closer to Steinheim and Aroeira 3.

The description for the first time of S53 and the contextualization of both Abri Suard's individuals sheds light on the diversity of Middle Pleistocene Neanderthals. The morphological differences observed in this site allow us to further understand the potential evolutionary paths of the lineage.

This research received the support of the MSCA Project N° 895713. Neander-TALe

First enamel nitrogen isotope data of early hominins: Early Pleistocene *Australopithecus* (Sterkfontein Member 4, South Africa) did not consume significant amounts of animal resources

TINA LÜDECKE[1,2], JENNIFER N. LEICHLITER[1,3], NICOLAS N. DUPREY[4], DOMINIC STRATFORD[5], HUBERT B. VONHOF[4], MARION K. BAMFORD[6], GERALD H. HAUG[4] and ALFREDO MARTÍNEZ-GARCÍA[4]

[1]Emmy Noether Group for Hominin Meat Consumption, Max Planck Institute for Chemistry, [2]Senckenberg Biodiversity and Climate Research Centre, Senckenberg, [3]Institute of Geosciences, Johannes Gutenberg University, [4]Department for Climate Geochemistry, Max Planck Institute for Chemistry, [5]School of Geography, Archaeology and Environmental Studies, University of the Witwatersrand, [6]Evolutionary Studies Institute and School of Geosciences, University of the Witwatersrand

Direct evidence regarding when and to what degree our early ancestors incorporated animal resources into their diets is sparse. The strongest, but indirect, evidence for meat consumption are cutmarks on fossil bone material. Yet, meat eating has major implications for the evolution of the hominin lineage, as the consumption of this calorie-dense, high-quality food has been linked to significant adaptations (e.g., brain expansion) in the genus *Homo*. Shifting from a mainly vegetarian diet represents an encroachment of hominins into the large carnivore guild, presenting our ancestors with new competitive pressures.

The understanding of animal resource consumption is crucial to reconstruct the timing of changes in hominin dietary behavior and to evaluate their position in (paleo)food-webs.

Nitrogen isotope ($\delta^{15}N$) data reveal information about an individual's position in the food web and are frequently used in conjunction with carbon isotopes ($\delta^{13}C$) to reconstruct diet. However, $\delta^{15}N$ has thus far only been determined in hominin specimens younger than 120,000 years because large quantities of well-preserved collagen are required. We utilize a biogeochemical method that allows us to perform $\delta^{15}N$ measurements of diagenetically resistant tooth enamel. We present $\delta^{15}N$ and $\delta^{13}C$ data for *Australopithecus*(n=7) from Sterkfontein Member 4. Our data indicates a large variation in $\delta^{15}N$ values between *Australopithecus* individuals, larger than in any other (primate) taxa analyzed from this member. The values however do not overlap with carnivore $\delta^{15}N$ data, pointing to a plant-based diet of these early Pleistocene hominins, providing a first glimpse into the trophic behavior of *Australopithecus*.

This project has been funded by the German Research Foundation Emmy Noether Fellowship DFG LU 2199/2-1 (to T.L.) and the Max Planck Society (MPG).

Evolution of cognitive traits in the hominin clade: a paleoneurological approach

FABIO MACCIARDI[1], ALESSIO BOATTINI[2], GIORGIA MODENINI[2] and FABIO MARTINI[3]

[1]Psychiatry and Human Behavior, University of California, Irvine, [2]Biological, Geological and Environmental Sciences, University of Bologna, Italy, [3]Dipartimento di Storia, Archeologia, Geografia, Arte e Spettacolo (SAGAS), University of Florence, Italy

The evolution of high cognitive functions requires that a neural machinery is in place supporting these functions. Evidences from archeological investigations showing that Neanderthals had a complex behavior indirectly support the hypothesis of their cognitive abilities, but we are also growing our knowledge of their possible neural structure. Past paleoneurological investigations have shown that Neanderthal's brains were different from Anatomically Modern Humans (AMHs) in their shape and regional architecture, despite a similar global size and volume. AMHs present with a globular rather than an elongated brain, due to a marked bulging of the frontal and parietal lobes, and expanded cerebellar interconnections with prefrontal, premotor, and superior-posterior parietal cortices. These local adaptations suggest a marked reorganization of the neural architecture in regions that are relevant for cognitive abilities. Integrating evidence from paleoanthropology, comparative genomics, epigenetics and neuroimaging we set out to identify genes associated with such a specific brain evolution and we found that non-coding, regulatory RNA genes rather than protein coding gene variants are the most important genomic elements that are implicated in these anatomical and possibly functional differences between Neanderthals and AMHs. Our results suggest a complex pattern, where Neanderthals and AMHs share a very high proportion of cognitively-related genomic elements while only a small set of them appear AMH specific, supporting the hypothesis that Neanderthals already had a cognitively ready brain. These shared genomic elements may then be a common feature of hominins, setting the origin of a symbolic thought deeper in time.

The Stockman, the Nurse, and the Engineer: Using historical documents to interpret osteobiographies

JENNIFER E. MACK[1] and WESLEY VANOSDALL[2]

[1]Office of the State Archaeologist, University of Iowa, [2]Department of Anthropology, University of Wyoming

The University of Iowa-Stanford Collection (UI-SC) is an anatomical collection of human skeletal remains representing approximately 1,100 individuals who died in the San Francisco Bay area. Of these, documentation exists for only 230 individuals who died between 1930 and 1952. Research presented in this poster resulted from a pilot project to determine how much information can be gathered about the life histories of identified individuals (n=20) from publicly available records. Three selected biographies were then compared with the results of osteological analyses, which were initially conducted by the second author to avoid confirmation bias.

Documents research using census records, marriage records, voter lists, city directories, newspapers, passenger lists, and other resources available online yielded unexpectedly detailed information for some individuals, while 25% (5/20) could not be found in records at all. Comparison of the documentary and osteological datasets demonstrated that more complete knowledge of an individual's history of residency, migration, occupation, and childbearing can inform interpretations of pathology and occupational stress markers and can increase the research value of remains for isotope studies and other location-specific investigations.

Furthermore, the compiling of personal histories, even with names redacted, provides a humanizing aspect that encourages respectful treatment of individuals in collections. For decades, complete anonymity has protected the privacy of those whose bodies have contributed to important advances in anthropology, forensic science, and medicine. However, memorialization through biographical depiction would better acknowledge their individual contributions, whether donation was elected, nonvoluntary, or through circumstances unknown.

The feasibility of palaeoproteomics for studying ancient hominins from South Africa

PALESA MADUPE[1,2], NOMAWETHU HLAZO[1,2,3], PATRICK L. RÜTHER[5], MEAGHAN MACKIE[1,5], FRIDO WELKER[1], JAZMIN RAMOS MADRIGAL[6], IOANNIS PATRAMANIS[6], FERNANDO RACIMO[6], LAUREN SCHROEDER[2,4], JESPER V. OLSEN[5], REBECCA R. ACKERMANN[2,3] and ENRICO CAPPELLINI[1]

[1]Department of Evogenomics, Globe Institute, University of Copenhagen, [2]Human Evolution Research Institute, University of Cape Town, [3]Department of Archaeology, University of Cape Town, [4]Department of Anthropology, University of Toronto Mississauga, [5]Proteomics Program, Novo Nordisk Foundation Center for Protein Research, University of Copenhagen, [6]Lundbeck GeoGenetics Centre, Globe Institute, University of Copenhagen

Palaeoproteomics allows for the recovery of genetic information beyond the limits of ancient DNA preservation. Dental enamel proteins older than one million years from temperate and subtropical areas can be phylogenetically informative, as recently demonstrated by the analysis of fossil teeth from *Gigantopithecus blacki* (1.9Ma), *Homo antecessor* (900Ka), and *Homo erectus*(1.7Ma). To date, such deep-time studies have been largely limited to Europe and Asia. Here we report on a preliminary study of faunal teeth from Swartkrans and Cooper's Cave, South Africa. The analysis of faunal enamel from *Connochaetes* (N=2), *Damaliscus* (N=1) and *Tragelaphus* (N=1) identified endogenous peptides supporting the confident reconstruction of the proteome sequence with a coverage spanning a few hundred amino acids. Following this preliminary result, extraction of enamel proteins from Swartkrans *Paranthropus robustus* (N=3; ca. 2Ma) samples was attempted. The analyses yielded similarly promising results to what was observed for the fauna, and identified one of the individuals as a male. A preliminary analysis of the molecular damage confirms the endogenous origin of the retrieved sequences. These preliminary results demonstrate that it is possible to recover ancient proteins from African hominin remains, opening the possibility to attempt their phylogenetic placement based on molecular evidence. Such an accomplishment requires the development of dedicated solutions to maximize sequence coverage and the detection of amino acid substitutions not present in modern variability.

This Research is funded through European Comission Horison 2020 Marie Skłodowska Curie Action Innovative Training Network, Grant Agreement number: 861389

The potential role of phenotypic plasticity in the adaptation of nasal turbinates to cold environment

LOUISE MAGNE[1], LAURA MARÉCHAL[1], MAUREEN J. DEVLIN[2] and YANN HEUZÉ[1]

[1]PACEA, UMR5199, Univ. Bordeaux, CNRS, MC, [2]Department of Anthropology, University of Michigan

In humans, the nasal region is the main area of the craniofacial skeleton displaying clear signs of environmental adaptation (temperature, humidity). However, the evolutionary mechanisms supporting such adaptation remain debated including the potential role played by phenotypic plasticity. A recent study showed that beside the nasal aperture and cavity, the inferior nasal turbinates also exhibit ecogeographic variation. Inferior turbinates contribute to homeothermy and water conservation. Individuals living in cold-dry climate tend to possess larger inferior turbinates enhancing air conditioning capacity. To explore the potential role of phenotypic plasticity in such adaptation, male C57BL/6J inbred laboratory mice were exposed from 3-12 weeks of age to 10˚C, 22˚C, and 26˚C (N=8/group). The mice were sacrificed at the age of 12 weeks and subsequently micro-CT scanned. The left respiratory turbinates were segmented and their volume (V), surface area (SA), and SA/V ratio automatically computed. The volume of the inferior respiratory turbinate (i.e. maxilloturbinate, MT) was significantly larger in mice exposed to 10˚C (ANOVA; F=3.88, p=0.0376). Mice raised at 10˚C exhibited a significantly lower MT SA/V ratio (ANOVA; F=6.05, p=0.0094). Our results support the hypothesis that inferior turbinate phenotype has developmental plasticity in response to temperature. Indeed, similar to humans, mice exposed to cold exhibit larger inferior turbinates. However, more work is required to interpret our counterintuitive finding of lower SA/V ratio in cold-housed mice (high SA/V ratio increases thermodynamic exchanges and air conditioning capacity) and the role of phenotypic plasticity in the production of a temperature-adapted phenotype.

This study was partially funded by the French National Agency for Research (ANR) with the program ANR-10-LABX-52 and NSF BCS-1638553

Neanderthal infant growth reconstructed from virtual histology of deciduous teeth

PATRICK MAHONEY[1], GINA MCFARLANE[1], B. HOLLY. SMITH[2,3], JUSTYNA J. MISZKIEWICZ[4,5], PAOLA CERRITO[6,7], HELEN LIVERSIDGE[8], LUCIA MANCINI[9], DIEGO DREOSSI[9], ALESSIO VENEZIANO[10,9], FEDERICO BERNARDINI[11,12], EMANUELA CRISTIANI[13], ALISON BEHIE[4], ALFREDO COPPA[14,15,16], LUCA BONDIOLI[17], DAVID W. FRAYER[18], DAVORKA RADOVČIĆ[19] and ALESSIA NAVA[1,13]

[1]School of Anthropology and Conservation, University of Kent, [2]Center for the Advanced Study of Human Paleobiology, The George Washington University, [3]Museum of Anthropological Archaeology, The University of Michigan, [4]School of Archaeology and Anthropology, Australian National University, [5]School of Social Science, The University of Queensland, [6]Department of Anthropology, New York University, [7]Department of Molecular Pathobiology, New York University College of Dentistry, [8]Institute of Dentistry, Queen Mary University of London, [9]Elettra-Sincrotrone Trieste, S.C.p.A, [10]Department of Archaeology, University of Cambridge, [11]Department of Humanities, Ca' Foscari University, [12]Abdus Salam International Centre for Theoretical Physics, [13]Department of Maxillo-Facial Sciences, Sapienza University of Roma, [14]Dipartimento di Biologia Ambientale, Università di Roma, [15]Department of Genetics, Harvard Medical School, [16]Department of Evolutionary Anthropology, University of Vienna, [17]Servizio di Bioarcheologia, Museo delle Civiltà, [18]Department of Anthropology, University of Kansas, [19]Department of Geology and Paleontology, Croatian Natural History Museum

Modern humans have a slow and extended period of childhood growth but to what extent this ontogenetic pathway was present in Neanderthals is debated. Dental development, linked to the duration of somatic growth across modern primates, is the main source for information about growth and development in fossil primates. Studies of Neanderthal permanent teeth report a pace of development either similar to recent humans or relatively accelerated. Neanderthal milk teeth, which form and emerge before permanent teeth, provide an opportunity to determine which pattern was present at birth. Here, we reconstruct the development of five isolated deciduous teeth of three Neanderthals from Krapina (120-130 ka) in Croatia using phase-contrast synchrotron radiation computed microtomography at the Elettra synchrotron facility in Trieste (Italy).

Results reveal regions of Neanderthal milk teeth formed quickly before birth, and over a relatively short period of time after birth. We estimated that a deciduous central incisor emerged towards the earliest end of the eruption schedules displayed by extant human children. Our data provide evidence that the year after birth was a period of relatively advanced somatic growth for the Neanderthal infants of Krapina. Advanced dental development is consistent with expectations for Neanderthal infant feeding.

The Royal Society, The Leverhulme Trust, Marie Skłodowska-Curie Actions Individual Fellowship, Australian National University, SYRMEP beamline at Elettra Sincrotrone Trieste (Proposal-20180099).

Examining Heavy Metal Exposure in Two Historic San Francisco Cemeteries

DIANA MALARCHIK[1], JELMER W. EERKENS[1], MATTHEW A. RUSSELL[2] and THOMAS OSTRANDER[2]

[1]Department of Anthropology, University of California, Davis, [2]Archaeology, Environmental Science Associates

It was not until the mid-20th century that the harmful effects of lead and mercury became common knowledge. Exposure to lead during childhood impairs one's ability to control emotions, create complex interpersonal relationships, and regulate aggression. While mercury doesn't seem to have a direct effect on neurodevelopment, there is a positive association between mercury exposure and high frequencies of behaviors associated with autism. As a result, lead and mercury exposure, particularly during childhood, have a direct effect on the individual and their social connection to the larger community. We examine heavy metal exposure in conjunction with stable isotopes in first and third molars from individuals dating to the 1850s-1890s buried in the Golden Gate and Yerba Buena Cemeteries, in San Francisco, CA. Results show high levels of Pb and Hg in dental enamel, 10-1000 times higher than pre-contact populations from the same region. High Pb and Hg are consistent with use of metal infused cosmetics and medicines and a growing dependence on metalwork and smelting, and may correlate with changes in individual behavior and poor overall health.

Assessment of morphological cranial and mandibular traits for sex estimation in southern African Holocene San and Khoekhoe populations

SADIYAH MALEK[1], VICTORIA E. GIBBON[1] and JUDITH C. SEALY[2]

[1]Department of Human Biology, University of Cape Town, [2]Department of Archaeology, University of Cape Town

The cranium and mandible are commonly used for sex estimation with high accuracy. Accurate population-specific sex estimation standards do not exist for the southern African Holocene San and Khoekhoe (S-K) population. Due to their markedly small stature, skeletal gracility, and physically active lifestyle, this population exhibits reduced sexual dimorphism. The following study assessed the accuracy of morphological cranial and mandibular traits for estimating sex in a southern African Holocene S-K sample.

Seven cranial and mandibular traits (*i.e.*, nuchal crest, mastoid process, supra-orbital margin, glabella, mental eminence, mandibular shape, gonial eversion/flaring) were assessed in sample of 155 Holocene S-K adults. To determine trait accuracy, cranial and mandibular sex estimates were compared to the individuals' pelvic (Phenice) sex estimate. Results were statistically analysed using chi-squared tests. Combined cranial morphological traits (reported accuracies of up to 93% by Krüger *et al.*, 2015), produced an accuracy of 74% (111/151) for this sample. Of the individual traits, the mastoid process produced the highest classification accuracy (73%, 73/100), followed by

mandibular shape (72%, 79/110), both reaching statistical significance. Whilst accuracies of 79% and 98% have been reported for the nuchal crest and mental eminence respectively in other populations (Inskip *et al.*, 2018), they produced the lowest accuracies in this study, both with 53% (65/123 and 44/83 respectively).

Cranium and mandible morphology, whilst highly sexually dimorphic in other populations, do not conform to existing standards in this population. This suggests the need for methodological adjustments to improve sex estimation accuracies for the southern African Holocene S-K population.

Malek and research were funded by the UCT Ada and Bertie Levenstein Bursary, UCT Vice-chancellors postgraduate scholarship and the National Research Foundation (NRF), South Africa.

Uncovering biocultural histories of marginalized individuals through osteobiography: A case study of the environmental and political-economic causes of linear enamel hypoplasia in early 20th century Mississippi.

SIERRA W. MALIS[1], MOLLY K. ZUCKERMAN[1], LARISSA DANIELS-HILL[2], ANNA J. OSTERHOLTZ[1], JESSE R. GOLIATH[1], NICHOLAS P. HERRMANN[3], WILLA TRASK[4], GRANT HARLEY[5] and DARCIE BADON[1]

[1]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Department of Anthropology, University of South Carolina, [3]Department of Anthropology, Texas State University, [4]Department of Anthropology, Texas A&M University, [5]Department of Geography and Geological Sciences, University of Idaho

Through a contextualized biocultural approach, ecological and political-economic causes were investigated as potential stressors causal to linear enamel hypoplasia (LEH) formation in Burial 1, representing an individual institutionalized at the Mississippi State Asylum (MSA), Jackson, MS (AD 1855-1935). LEHs represent periods of decreased enamel deposition during growth and development and are used to identify periods of prolonged, non-specific, physiological stress. Previous dendrochronological and isotopic analyses indicated Burial 1 was interred post-1926 and resided in northern Mississippi during development. Our results indicate that Burial 1's LEHs formed episodically between birth and six years of age, based on defect location relative to crown development rates. Given an estimated age-at-death of 22-23 years, Burial 1 likely experienced physiological stress prior to institutionalization, between 1906-1909. Although weaning and other generalized stressors (i.e., infection) were potential contributors, the historical record suggests that this stress aligns with several political-economic and ecological events in early 20th century Mississippi that exacerbated already insalubrious conditions for children, the most socially and biologically vulnerable individuals. These include ecologically disruptive events, namely flooding and hurricanes (1906), and political and economic disruption, including boll weevil infestation (1907-1913) and intensifying racial terror, which cumulatively prompted the Great Migration (1910-1970). These intersected with the backdrop of systemic racism, race-based structural violence, intensifying poverty, and regional disease epidemics (e.g., pellagra). An osteobiographical approach enables further humanization of Burial 1, including identification of cumulative hardship during childhood, while contextualizing LEH formation within complex political-economic, social, and ecological experiences.

Human Evolution in the Mariana Islands through of CHamoru Medicine

KAYLANI H. MANGLONA

Department of Biology, University of Colorado Colorado Springs, Department of Anthropology, University of Colorado Colorado Springs

Health in the Mariana islands were historically supported by Indigenous CHamoru healers known as *makana*, who were described by the colonial Spanish as *suruhanu/a*. Despite close geographic location, each island within the Mariana Archipelago maintains differences in microenvironments which may have affected the availability of medicinal botanica and relate to disease prevalence found on excavated skeletons. Due to lack of epidemiological data stemming from the Commonwealth of the Northern Mariana Islands (CNMI), this study aims to understand current perspectives and usage of CHamoru traditional medicine and Western biomedicine as they relate to health on Rota Island, CNMI. 33 individuals located across Songsong and Sinapalo villages were formally interviewed regarding their healthcare experiences as well as opinions on overall public health in the CNMI. Study results indicate that though contemporary *suruhana* continue to struggle with microenvironmental issues regarding plant availability, health and disease prevalence are perceived to be critically attached to regional economic instability (76%), changes in indigenous lifestyle (82%) and consequences of remote healthcare (73%). Postcolonial tensions are exhibited by their perception of traditional medicine as being more efficacious than biomedicine. Participants express preference for traditional medicine to solve every-day acute ailments, but preferred biomedicine for chronic ailments. Specific individuals also suggest that medical choices are actively becoming indicators of class status amongst younger generations that further impact the instability of indigenous medicine. Emergent questions regarding CNMI cultural and environmental preservation, the possibility of complementary medicinal practices, and the current state of CHamoru Indigenous preservation are discussed.

Climatic influence on dietary behavior: Isotopic evidence from pre and post hurricane Cayo Santiago macaques

EVA H.J. MANN[1,2], ALEX R. DECASIEN[3], MICHAEL J. MONTAGUE[6], MICHAEL L. PLATT[6], SUSAN C. ANTÓN[1], RHONDA L. QUINN[4,5] and JAMES P. HIGHAM[1]

[1]Department of Anthropology, New York University, [2]Department of Anthropology/Human Evolutionary Sciences, Rutgers University, [3]Section on Developmental Neurogenomics, National Institute of Mental Health, [4]Department of Sociology, Anthropology & Social Work, Seton Hall University, [5]Department of Earth and Planetary Sciences, Rutgers University, [6]Department of Neuroscience, Perelman School of Medicine, University of Pennsylvania

Stable isotope analysis of primate tissues provides an excellent framework in which to assess the impacts of environmental disaster on primate dietary behavior. We analyzed isotopic differences between free-ranging, Cayo Santiago, Puerto Rico *Macaca mulatta* sampled before (2016, group HH, n=29) and after Hurricane Maria (2018, group KK, n=47) , and assessed isotopic variability within the post-Hurricane group. We analyzed muscle tissue, fecal, and hair $\delta^{13}C$ and $\delta^{15}N$ values, as well as food sources collected on the island in 2018 (species=10). Dietary differences were characterized by modeling $\delta^{13}C$ and $\delta^{15}N$ isotope values as a function of sex and mother-infant dependent status (MIDS) in fecal (n=65), hair (n=60), and fresh muscle (n=67) samples within group KK. Comparisons between the HH and KK group $\delta^{15}N$ and $\delta^{13}C$ values revealed a slight (0.34‰) and significant ($p<0.001$) increase in the average $\delta^{13}C$ values from 2016 to 2018. These results indicate that the vegetative loss from Hurricane Maria led to a modest increase in C_4 food consumption post-hurricane. Behavioral observations and food isotopes suggest these C_4 food items include C_4 grasses and commercial monkey chow. In group KK, males showed lower $\delta^{15}N$ values than females, in fecal (mean=1.48, difference= -0.84‰), muscle tissue (5.29, -0.34‰), and hair isotopes (4.88, -0.24‰), suggesting females consumed more protein rich foods, like monkey chow, than males. Together our results offer new insights into how destructive climatic events affect dietary behaviors in primates, using stable isotope analysis.

Funding to JH and SA from NSF (BCS-1800558 & BCS-1754024), and RLQ (NSF BCS-1455274). CORE Cayo funding from NCRR to CPRC #8-P40-OD012217-25. Funding to MLP and MJM from NIH (NIH R01MH096875).

Pandemic perceptions: a mixed-methods study of young adults during COVID-19

MADELEINE MANT[1], ASAL ASLEMAND[2], ANDREW PRINE[3] and ALYSON HOLLAND[4]

[1]Department of Anthropology, University of Toronto Mississauga, [2]Department of Mathematical &

Computational Science, University of Toronto Mississauga, [3]Emergency Medicine Department, Groves Memorial Community Hospital, [4]Department of Family Medicine, McMaster University

Biocultural anthropological approaches to pandemic research incorporating health behaviours and perceptions of varied groups can help inform public policy regarding pandemic preparedness. Health perceptions of young adults (18-30) are important to target because they have different understandings of disease and risk than older adults. A mixed-methods longitudinal survey (5 iterations, total n=4603) of University of Toronto students' perceptions of COVID-19 ran from March 2020 to September 2021. Overall survey results show a significant relationship between female students and the adoption of new health behaviours. Students who perceived they were not susceptible to COVID-19 noted mitigating factors such as new health behaviours to be a major driver in their perception. In June 2020, 77.8% (n=483) of students indicated willingness to get the COVID-19 vaccine, by September 2020, 79.6% were willing (n=1269), and in March 2021 78.3% were willing (n=835) and 8.7% (n=93) had already received it. Multinomial and binary logistic regression analyses showed that increasing perception of COVID-19 severity predicted the likelihood that a respondent was willing to receive the vaccine. In the September 2020 survey, individuals who noted that they would be encouraged to get the vaccine if their doctor/pharmacist recommended it were 76x more likely to be willing to get the vaccine than those who would not be encouraged by medical advice. Qualitative analyses of interviews (n=108) revealed ongoing and nuanced concerns about vaccines and pandemic measures that must be considered by public health authorities as the COVID-19 pandemic continues to unfold and governments adapt policy for future pandemics.

This research was funded by the University of Toronto COVID-19 Action Initiative.

Polycystic Ovarian Syndrome (PCOS) as an Evolutionary Mismatch Disorder: Preliminary evidence that PCOS may reduce fracture risk among female CrossFit athletes

COURTNEY MANTHEY-PIERCE and TARA CEPON-ROBINS

Department of Anthropology, The University of Colorado Colorado Springs

Polycystic ovarian syndrome (PCOS) is argued to be an evolutionary mismatch disorder. One argument suggests that PCOS hyperandrogenism may have been beneficial to ancestral populations experiencing sporadic nutritional stress by increasing bone mineral density (BMD), however current research is conflicting. Here, we test the hypothesis that PCOS-related hyperandrogenism has a protective effect on BMD, especially during reproductive stress (i.e., pregnancy, childbirth, breastfeeding) or hormonal supplementation (i.e., contraceptives) and leads to reduced fracture occurrence. CrossFit athletes were recruited due to their intense fitness regimen that is often linked to altered nutritional status and increased fracture occurrence compared to the general population. 56 adult women were surveyed and categorized as follows: CrossFit athletes with PCOS (35.7%), CrossFit athletes without PCOS (30.3%), and non-athletes with PCOS (33.9%). Though non-significant (p = 0.338). CrossFit athletes without PCOS reported a higher percentage of fracture occurrence (47.1%) compared to CrossFit athletes with PCOS (20%) and non-athletes with PCOS (10.5%). Chi-square tests revealed no significant relationships between pregnancy, childbirth, breastfeeding and elevated fracture occurrence in any group. However, there were significant relationships between bone fractures and diet at the time of injury (p = 0.009), as well as with hormonal contraceptive usage (p = 0.026) among CrossFit athletes without PCOS, but not in any other group. These results suggest females without PCOS are more likely to experience bone fractures during nutritional stress or hormone supplementation compared to those with PCOS, providing limited support for the hypothesis that PCOS hyperandrogenism may have helped preserve BMD in ancestral populations.

Intra- and inter-individual variation across the peri-menopausal period among Qom women of Argentina

URSZULA M. MARCINKOWSKA[1], MARGARET C. CORLEY[2], MELANIE A. MARTIN[3], RICHARD G. BRIBIESCAS[3] and CLAUDIA VALEGGIA[3]

[1]Department of Public Health, Medical College Jagiellonian University, [2]Department of Anthropology, Yale University, [3]Department of Anthropology, University of Washington

The perimenopausal period is characterized by increasingly variable ovarian hormone levels in response to changes in the hypothalamic-pituitary-ovarian axis. As viable oocytes fail to mature, ovarian cycles become more variable in length and the frequency of ovulation declines until there is complete anovulation. The perimenopausal period represents the last life history transition for women and marks the end of physiological investment in new offspring.

We present here an analysis of urinary progesterone metabolite (uPdG) levels in 24 Qom women (mean age?) who we followed longitudinally across the perimenopausal transition. The Qom are one of the three major indigenous groups in northern Argentina. Traditionally hunter gatherers, they now participate in market economies to varying degrees.

Based on the occurrence of menses, we divided participants into three subsamples: post-menopausal (menses had ceased), pre-menopausal (regular cycles observed) and transitional (amenorrhoeic periods shorter than 6 months). A total of 844 hormonal measurements were conducted and individual hormonal profiles were computed.

We found considerable variation in uPdG levels across all three groups. Inter-individual cycle median levels varied from 248 ng/ml to 5568 ng/ml (SD=1082 ng/ml). Within group variation was also extremely high (SDs = 435 – 1562 ng/ml) and we could not conclude that the cycle median values of the uPdG differed among three menopausal groups.

Despite the challenges of interpreting variation in non-clinical, non-western settings, including these populations within the scope of reproductive biology broadens the range of common variation in women's reproductive physiology.

The role of cartilage in endochondral ossification: a metaplastic paradigm

RALPH MARCUCIO

Department of Orthopaedic Surgery, University of California, San Francisco

This abstract is part of the symposium *Cartilage and craniofacial growth* and places the current understanding of endocondral ossification into historical context. The foundational understanding of endochondral ossification was put forth in the mid-1800's. The history of this field is difficult to fully reconstruct, but here I review seminal developments that drive the evolution of our current understanding. W. Beresford describes the state of the field in "Chondroid Bone, Secondary Cartilage, and Metaplasia". In his account, anatomists in the early 1800's thought cartilage transformed directly into bone through a process called metaplasia, whereby a mature tissue transforms directly into another. In the middle of the century this idea shifted, as Sharpey and Muller stated that cartilage did not turn into bone rather bone replaced cartilage. According to Beresford, anatomists and others gradually accepted this view. However, a plethora of data provided both descriptive and experimental evidence that chondrocytes become osteoblasts that make bone. As recently as 2010, the identity of the bone forming osteoprogenitor cells remained unknown. Nonetheless, the accepted model of endochondral ossification describes that chondrocytes differentiate, undergo hypertrophy, calcify the cartilage matrix, induce vascular invasion, undergo programmed cell death, while cells that make the new bone are delivered to the cartilage by invading vasculature. However, work from our laboratory and other laboratories demonstrates that chondrocytes give rise to osteoblasts that make the new bone, and this may be the mechanism by which endochondral ossification occurs.

Strength in frailty: Interpreting skeletal frailty and resilience in catastrophic and attritional burial contexts from Roman period Oymaaćaç, Turkey

KATHRYN E. MARKLEIN[1,2], ELIZABETH BEWS[3] and DOUGLAS E. CREWS[4,5]

[1]Department of Anthropology, University of Louisville, [2]Center for Archaeology and Cultural Heritage, University of Louisville, [3]Department of Anthropology, University of South Florida, [4]Department of Anthropology, The Ohio State University, [5]School of Public Health, The Ohio State University

Understanding the entangled relationship between frailty and resilience in bioarchaeological contexts requires recognition and analysis of physiological, biological, and biocultural components impacting individual mortality risk. While frailty and resilience oftentimes are evaluated by presence of pathological lesions/conditions, frailty indices provide a complementary cumulative measure of individual lifetime skeletal and dentoalveolar markers to crude prevalence rates (CPR). Archaeological sites, where both attritional and catastrophic burials are identified, like Oymaaćaç, provide unique samples for evaluating the biological, physiological, and biocultural variables that predispose individuals to death under "normal" and "extraordinary" mortality circumstances. In tandem with CPR from six biomarkers (linear enamel hypoplasia, LEH; antemortem tooth loss, AMTL; periosteal lesions, PL; periodontal disease, PD; trauma, and osteoarthritis), 6-biomarker skeletal frailty indices (SFI) were used to analyze adults from catastrophic (n=28) and attritional (n=12) burial contexts (3rd-5th c. CE) at Oymaaćaç, Turkey. Analyses using ANCOVA yielded significantly higher frailty distributions among attritional (SFI: 2.58±0.36) than catastrophic (1.29±0.24) burials, findings explained by significantly higher rates of osteoarthritis, AMTL, and LEH and lower rates of PL and PD in attritional contexts. Although more individuals died before 35 years of age under catastrophic (54.6%) than attritional (30%) circumstances, age-at-death did not contribute to cumulative frailty or CPR differences. However, females (SFI: 1.19±0.29) overall exhibited lower frailty compared to males (2.05±0.31). In addition to illustrating sex-based SFI differences within this agropastoral community, these findings demonstrate both selectivity of inflammatory skeletal markers (PL and PD) in catastrophic contexts, and resiliency represented by cumulative skeletal frailty in specific population samples.

Allometric Scaling: A 50-Year Retrospective

ROBERT D. MARTIN[1,2], ANN M. MACLARNON[3] and KARIN ISLER[4]

[1]Institute of Evolutionary Medicine, University of Zürich, [2]Science & Education, The Field Museum, Chicago, [3]Department of Anthropology, Durham University, [4]Department of Anthropology, University of Zürich

Allometric analysis — non-linear scaling of biological variables to body size — has been radically transformed over the past half century. Theoretical developments, especially in statistical testing, have counterbalanced an initial prevalence of empirical findings. Major advances have resulted, notably in analysing brain:body size relationships and testing influences of behavioural factors. Now is a good time to take stock, recognizing progress achieved while identifying some important neglected aspects. Here, it is particularly relevant to focus on vital contributions made by Swiss zoologist Adolf Portmann (1897-1982) between 1938 and 1962. Because his key papers were all published in German, they are generally poorly known in English-speaking circles. Fortunately, a posthumous English book encapsulating Portmann's work — *A Zoologist Looks at Human Kind* — appeared in 1990, and interest in his research has recently resurged. Notable features in original publications from the Portmann school include a tight focus on reproduction, resulting in clear recognition of the crucial distinction between altricial and precocial offspring types in both birds and mammals, and the first penetrating analyses of scaling of mammalian gestation periods. Portmann's comparative studies of altriciality *versus* precociality, gestation length and brain size (including developmental aspects) directly led to formulation of his seminal hypothesis that during human evolution persistence of a fetal pattern of brain growth throughout the first year of postnatal life emerged as a unique feature. [Portmann hence proposed that human gestation actually lasts 21 months.] Current findings for these topics will be reviewed in hope of offsetting lingering misunderstandings.

Weaning at Altitude: An Investigation Into the Relationship Between Age at Weaning and the Altitude of Ethnographic Populations

MARCOS C. MARTINEZ

School of Human Evolution and Social Change, Center for Bioarchaeological Research, Arizona State University

The ecological stressors placed on high-altitude populations in areas throughout the world have provided natural experimental settings to further our understanding of human adaptation and evolution. To sustain metabolic processes, despite limited oxygen availability and other environmental stressors that influence Hypoxia Inducible Factor (HIFs) expression, such as environmental temperature and infection rates, high-altitude populations have evolved variable adaptive responses. Human adaptive variation extends to reproduction and development, including lactation and breastfeeding structure, and this variability has been reported on for various high-altitude populations in the ethnographic literature. As a cross-cultural test of the prediction that the elevation of a population will be a proximate factor in the observed age at the cessation of breastfeeding, I examine available data on weaning age variation for over 100 populations (n= 106) from the Electronic Human Relations Area Files (eHRAF). Regression analysis reveals that there is no statistically significant relationship between the age at weaning and altitude (Multiple R-squared: 0.003462, F (1,81): 0.2814, p-value: 0.5972). I discuss the implications for understanding these results and explore how human behavioral variation (i.e., infant feeding practices, cultural beliefs regarding child provisioning and weaning, maternal workload across subsistence economies, alloparenting practices, etc.) can help further explain the observed heterogeneity in the breastfeeding structure of different high-altitude populations.

Quantification of nasal airway morphological variation in modern humans

LAURA MARÉCHAL[1], JEAN DUMONCEL[1], WILLIAMS ASTUDILLO ENCINA[2], ANDREJ EVTEEV[3], VIVIANA TORO-IBACACHE[4], RUDOLPH G. VENTER[5] and YANN HEUZÉ[1]

[1]UMR 5199 PACEA, Univ. Bordeaux, CNRS, MC, [2]Imaging Centre, Hospital of the University of Chile, [3]Anuchin Research Institute and Museum of Anthropology, omonosov Moscow State University, [4]Institute for Research in Dental Sciences, Faculty of Dentistry, Universidad de Chile, [5]Division of Orthopaedic Surgery, Department of Surgical Sciences, Faculty of Medicine and Health Sciences, Tygerberg Hospital, Stellenbosch University

Human populations exhibit morphological differences in their nasal cavities that are correlated with eco-geographic factors (temperature, humidity). Less is known about the morphological variation of the nasal airway, which is the negative space defined by the respiratory epithelium lining the nasal cavity. Yet, this key anatomical region is the first to be involved in respiration and air conditioning. To explore climate-related variation of the nasal airway shape, we studied *in vivo* CT scans of 195 (96 females and 99 males) adult individuals from France, South Africa, Russia, Cambodia and Chile. The reconstructed 3D meshes of the nasal airways were analyzed with a landmark-free surface deformation method, that allowed a quantification of the morphological variation. Besides producing a visualization of the mean shapes of the nasal airway for each population, sex and age category, we provided additional information regarding the morphological differences between the groups. Indeed, the results of the PCA highlighted significant inter-population shape differences in the nasal airway. However, no significant intra-population differences (sex and age) were found. Beyond the expected variation in nasal airway main dimensions, paralleling those of the nasal cavity, we also observed that

the meati curvature and the position of the nasal openings were highly variable aspects of the nasal passages. This study is the first to document nasal airway's morphological variation based on a large multi-regional sample. It will enable a population-based approach when addressing the influence of environmental factors on nasal morphology, e.g. in computational fluid dynamics studies.

This study was partially funded by the French National Agency for Research (ANR) with the program ANR-10-LABX-52 and by the Erasmus+ programme of the European Union Bakeng se Afrika (EAC-A05-2017).

Group size, dispersal sex, coalition sex, and female aggression influence the evolution of maxillary canine sexual monomorphism in primates

ERIKA M. MATTHEWS[1] and TODD C. RAE[2]

[1]Department of Anthropology, University of Arkansas, [2]School of Life and Health Sciences, University of Roehampton

The selective pressures that lead to sexual monomorphism in primates is understudied when compared to the investigation of sexual dimorphism within the order. Given some extant species appear to be experiencing a reduction in sex differences, as well as the proposal that some ancestral primates may have exhibited greater degrees of dimorphism than their suggested descendants, understanding the pressures that lead to sexual monomorphism is warranted. This study analyzed the relationship between the degree of sexual dimorphism of the maxillary canine teeth and four distinct social conditions in order to investigate what pressures may influence sex differences across 111 species and subspecies of primate. This was done using a linear model that examined the significance of log-transformed mean group size, female aggression intensity, dispersal sex and coalition sex with log-transformed maxillary canine sexual dimorphism. Small group sizes and high female aggression were associated with a reduction in sex differences of the maxillary canine teeth. These social conditions result in more equal weaponry pressures for the sexes, as smaller groups reduce male intrasexual competition for females and aggressive females are more likely to utilize weaponry in mate or resource defense. Additionally, primates that exhibit female dispersal or male coalition formation were associated with more monomorphic maxillary canine height as weapons aid in immigrating or excluding immigration and coalition formation is less metabolically costly than weaponry. This analysis offers further support that social pressures can greatly influence body form and dimensions, both within our own lineage of hominins and across primates.

A new Levantine Middle Pleistocene paleodeme: the Nesher Ramla *Homo*

HILA MAY[1,2], RACHEL SARIG[2,3], GERHARD W. WEBER[10,5,9], CINZIA FORNAI[4,5,6], MARÍA MARTINÓN-TORRES[7,8], JOSÉ M. BERMÚDEZ DE CASTRO[7,8], YOSSI ZAIDNER[11] and ISRAEL HERSHKOVITZ[1,2]

[1]Department of Anatomy and Anthropology, Sackler Faculty of Medicine, Tel Aviv University, [2]The Shmunis Family Anthropology Institute, the Dan David Center for Human Evolution and Biohistory Research, Tel Aviv University, [3]Department of Oral Biology, The Maurice and Gabriela Goldschleger School of Dental Medicine, Sackler Faculty of Medicine, Tel Aviv University, [4]Vienna School of Interdisciplinary Dentistry, [5]Department of Evolutionary Anthropology, University of Vienna, [6]Institute of Evolutionary Medicine, University of Zurich, [7]Centro Nacional de Investigacion sobre la Evolucion Humana (CENIEH), [8]Department of Anthropology, University College London, [9]Core Facility for Micro-Computed Tomography, University of Vienna, [10]Human Evolution and Archaeological Sciences, University of Vienna, [11]Institute of Archaeology, The Hebrew University of Jerusalem

Several Late Middle Pleistocene (MP) *Homo* fossils are known from the Levant. However, their taxonomic affiliation remains unclear. A newly discovered fossil from the Nesher Ramla (NR) site, Israel, dated to ~130,000 year BP, could shed light on the Levantine MP fossils and their role in human evolution. The aims of this study were to morphologically characterize the NR fossil (including parietal bones and a partial mandible with an intact second molar tooth) and to reveal their association to known *Homo* groups. We compared the NR skeletal remains to a comprehensive sample including Eurasian and African MP *Homo*, Neanderthals, and archaic and recent *Homo sapiens*. Morphological and morphometric analyses were carried out based on linear measurements and 3D landmark configurations. The NR *Homo* revealed a unique combination of Neanderthal and archaic traits: the parietal bone exhibited affiliation to archaic MP *Homo*, while the mandible and tooth were more Neanderthal-like. The distinctive combination of traits shown by the NR fossil and the possible association to other Levantine MP fossils (e.g., Qesem and Zuttiyeh) suggest that the NR *Homo* was probably a late survivor of a Levantine MP paleodeme that existed in the region from at least 400,000 years ago. This paleodeme likely contributed to the evolution of MP *Homo* in Europe and East Asia, and probably interbred with *Homo sapiens* that lived simultaneously in the Levant beginning from 180,000 years ago. Finally, our study supports the hypothesis that the Neanderthal lineage, at least partially, originated from a non-European *Homo* group.

The Dan David Foundation

Movement speed towards shared latrine sites by southern bamboo lemurs indicates cautionary behavior

KEELY Q. MAYNARD[1], STEPHANIE A. POINDEXTER[1] and TIMOTHY M. EPPLEY[2,3]

[1]Anthropology, SUNY University at Buffalo, [2]Conservation Science & Wildlife Health, San Diego Zoo Wildlife Alliance, [3]Anthropology, Portland State University

Moving faster towards known locations is associated with goal-directed travel and spatial knowledge. However, moving at a faster speed can leave you vulnerable as you focus less on vigilance. For southern bamboo lemurs (*Hapalemur meridionalis*) in southeast Madagascar, latrines are a stable non-seasonal entity that can act as spatial landmarks for route utilization. Considering spatial knowledge and the potential risks associated with fast group movement, we predict that *H. meridionalis* will approach more frequently used latrines faster than those less frequently used. If *H. meridionalis* is concerned about intergroup competition (or security), then we predict they will approach shared latrines slower than non-shared latrines. We calculated speed (m/min) across a total of 139 routes used by three groups of *H. meridionalis* focusing on the segments where they approach latrines (n= 418). We categorized latrines by usage frequency and shared utilization between two of the groups. Groups approached frequently used latrines and the infrequently used latrines at about the same speed. On average, groups approached shared latrines at a speed of 3.33 ± 4.21 m/min which was slower than non-shared latrines (4.96 ± 9.9 m/min). Based on our results, cautionary behavior around the shared latrines may influence approach speed and could be indicative of the role these landmarks play in avoiding inter-group agonistic interactions.

American Society of Primatologists, Conservation International Primate Action Fund, Idea Wild, Mohamed bin Zayed Species Conservation Fund (11253008), Primate Conservation Inc., and the Primate Society of Great Britain/Knowsley Safari Park.

Reducing Preterm Birth and Racial Disparities: A Model of Stress-Induced Developmental Plasticity

GABRIELLA B. MAYNE[1], AYISHA BUCKLEY[2] and LUWAM GHIDEI[3]

[1]Anthropology, University of Colorado, Denver, [2]Obstetrics & Gynecology, Maternal Fetal Medicine, Icahn School of Medicine at Mount Sinai Hospital, [3]Obstetrics & Gynecology, Baylor College of Medicine

Preterm birth is a leading cause of neonatal mortality and is characterized by substantial racial disparities. Despite efforts to reduce preterm birth, rates continue to rise while racial disparities persist. Maternal stress is a risk-factor for preterm birth; however, often it is treated as a secondary variable rather than a key target for

intervention. Stress is known to affect several biological processes leading to downstream sequelae. Here we present a model of stress-induced developmental plasticity where maternal stress is a key environmental cue impacting the length of gestation and therefore a primary target for intervention. Developmental plasticity is the biological capacity to alter developmental trajectories in response to environmental cues and results in phenotypic variation, including preterm birth. During pregnancy this plasticity is mediated through the maternal-fetal-placental neuroendocrine stress axis. Black women experience disproportionate and unique maternal stressors related to racism and discrimination. It is therefore not surprising that Black women have disproportionate rates of preterm birth. The downstream effects of racism on preterm birth pathophysiology reflect an appropriate response to stressors through this ancient, environmentally sensitive system. Fortunately, stress does not appear to be an all-or-none variable. Evidence suggests developmental plasticity is dynamic, functioning on a continuum. Therefore, simple, stress-reducing interventions that support pregnant women may tangibly reduce rates of preterm birth and improve birth outcomes for all women, particularly Black women.

New body mass-at-death estimates for KNM-WT 15000 (*Homo erectus*)

ROBERT C. MCCARTHY[1], DEBORAH L. CUNNINGHAM[2] and DANIEL J. WESCOTT[2]

[1]Department of Biological Sciences, Benedictine University, [2]Department of Anthropology, Texas State University

Previous estimates of KNM-WT 15000's body mass-at-death are based on stature-at-death estimates ≥157 cm that can be modeled using equations for modern human adults. Anatomical reconstructions <150 cm fall at or below the lower limit for adult statures used for such purposes and imply unique body proportions and growth characteristics, requiring a different approach. In this study, we used generalized additive modeling (GAM) regression to predict body mass from stature, bi-iliac breadth (BIB), and bi-acromial breadth (BAB) in a worldwide sample of modern human juveniles at yearly intervals between one and 18 years of age. Body mass estimates for KNM-WT 15000 are based on an anatomically-reconstructed stature of 146 cm, BIB of 27.4 cm, and BAB of 35 cm (the latter estimated from preserved clavicle length). We used z-scores to determine the most appropriate age intervals with which to model KNM-WT 15000's body mass using these three morphometric variables. Regression estimates for age intervals between 12–13 and 11–15 years of age range between 37–40 kg (stature), 39–42 kg (stature|BIB), and 41–45 kg (stature|BIB|BAB), with prediction intervals for these values ±1 kg. These estimates are congruent with a 42-kg prediction using a recently-published random effect panel regression equation for the relationship between body mass, stature, and BIB in 4–18-year-old juveniles. Both sets of predictions imply that KNM-WT 15000 had a heavily-built physique and avoid extrapolation from adult values. These GAM regression models can be used to predict body mass in other juvenile hominin specimens.

Funding for this research has been provided by The Dr. Scholl Foundation.

Genetic Approaches to the Paternal Ancestry of Contemporary Afro-Puerto Rican Communities

KATIE MCCORMACK and JADA BENN-TORRES

Anthropology, Vanderbilt University

A 400-year history of European Colonization and the Transatlantic Slave Trade has left an indelible mark on the demographic makeup of the Caribbean, seen in both the diverse identities of Caribbean peoples and the patterns of genetic ancestry in this region today. From the 16th - 19th Centuries, over 3 million enslaved African people were forcibly relocated to the Caribbean. Although genetic research has documented the resulting admixture of African, European, and Indigenous American peoples, much of this work has utilized an island-wide approach that can overlook heterogeneity of modern Caribbean populations by excluding marginalized communities with unique histories that shape their ancestries. This study aims to document these patterns of genetic ancestry in Afro-Puerto Rican communities. Previous work on the maternal ancestry of these communities has found that 68% of individuals had haplotypes of African origin, while less is understood about the paternal ancestry of these communities. To this end, we genotyped diagnostic SNPs for Y Chromosome haplogroups using Pyrosequencing in a sample of 26 self-identified Afro-Puerto Rican men. These results show that a majority of men had haplotypes of African origin, with a minority of haplotypes representing European ancestry. We also document the presence of Indigenous paternal ancestry in Puerto Rico for the first time, demonstrating that both African and Indigenous men have shaped contemporary Afro-Puerto Rican populations. These results indicate patterns of genetic variation distinct from the broader island population, indicating a need for further study of subpopulations whose unique histories are visible in their genetic ancestry.

Identification of Male and Female DNA in Mixed Samples Using an *Amelogenin* qPCR Assay

SAMANTHA M. MCCRANE, MA[1,2] and CONNIE J. MULLIGAN, PHD[1,2]

[1]Anthropology, University of Florida, [2]Genetics Institute, University of Florida

Forensic 'touch' DNA samples are recovered from surfaces that have been touched by single or multiple individuals. These samples can include DNA from primary contributors who directly touched the surface, as well as secondary or tertiary contributors, whose DNA was transferred to the surface through an intermediary, such as the primary contributor. The presence of multiple contributors can create samples with widely varying DNA concentrations. In this study, we utilized a cost-effective quantitative PCR assay that amplifies a sex-specific region in the *Amelogenin* gene so we could distinguish between male (XY) and female (XX) DNA in mixed samples. We created a series of known mixtures of male and female DNA at concentration ratios ranging from 1 female:83 male to 83 female:1 male in order to mimic mixed forensic touch DNA samples. We compared the intensity of fluorescent dye probes indicating X and Y chromosomes to determine if male and/or female DNA was detectable. Male DNA was identified in multiple samples, even when male DNA was a minor contributor (ratios of female:male DNA of 3:1, 1:1, 1:3, 1:9, and 1:83). However, female DNA was only identified in mixed samples with high ratios of female DNA (9:1 and 83:1). Our results help determine the limits of identifying male and female DNA in mixed samples. Furthermore, these results suggest that standard sex determination assays may underestimate female DNA contributions in mixed samples.

A comparison of enamel daily sections rates in deciduous molars from modern-day children living in Aotearoa New Zealand, Britain, Canada, France, and Sweden

GINA MCFARLANE[1], CAROLINA LOCH[2], DEBBIE GUATELLI-STEINBERG[3], PRISCILLA BAYLE[4], MONA LE LUYER[4], NINA SABEL[5], ALESSIA NAVA[1], BRUCE FLOYD[6], MARK SKINNER[7], SOPHIE WHITE[2], ROSIE PITFIELD[1] and PATRICK MAHONEY[1]

[1]School of Anthropology and Conservation, University of Kent, [2]Sir John Walsh Research Institute, Faculty of Dentistry, University of Otago, [3]Department of Anthropology, The Ohio State University, [4]CNRS, Univ. Bordeaux, [5]Department of pedodontics, University of Gothenburg, [6]School of Social Sciences, University of Auckland, [7]Department of Archaeology, Simon Fraser University

The daily enamel secretion rate (DSR) of ameloblasts can be reconstructed from incremental markings retained in teeth. Within

palaeoanthropology, bioarchaeology, and forensic contexts, DSRs are used to establish the pace of dental development, the timing of birth and weaning, and age-at-death in juveniles. Yet compared to permanent teeth, little is known about DSRs of modern-day children including whether rates vary between populations. Here we report DSRs of naturally exfoliated deciduous molars (n = 345) from five populations (Aotearoa New Zealand, Britain, Canada, France, and Sweden).

Each tooth deciduous molar was thin sectioned and examined using a high-powered Olympus BX51 microscope and DP25 digital microscope camera. Mean DSRs were recorded for the inner, mid, and outer regions of cuspal and lateral enamel, excluding the first and last formed 100µm of enamel.

Mean DSRs did not vary significantly between populations, or by sex. Cuspal enamel grew slightly faster than lateral enamel (mean difference 0.16 µm per day; $p < 0.001$). The trajectory of DSRs from inner to outer enamel showed a minor increase that was significant in lateral enamel only ($p = 0.003$).

The DSRs of deciduous molars from modern children are remarkably consistent when compared among populations. Furthermore, while growth rates are faster in cuspal than lateral enamel, DSRs only show a minor increase in pace from inner to outer regions. The trajectory described for deciduous enamel of modern-day children differs to that of permanent molar enamel, which typically displays a steep increase in matrix deposition from inner to outer enamel.

This study was funded by The Leverhulme Trust. The Royal Society provided an equipment grant. The European Union's Horizon 2020 research and innovation programme under the Marie Skłodowska-Curie (AN).

Comparing 3D Estimates of Neck Muscle Function in Primates

FAYE R. MCGECHIE[1], KEVIN M. MIDDLETON[2], CASEY M. HOLLIDAY[2], THIERRA K. NALLEY[3], ELLEN FRICANO[3], NEYSA GRIDER-POTTER[4] and CAROL V. WARD[2]

[1]Department of Organismal Biology and Anatomy, University of Chicago, [2]Department of Pathology and Anatomical Sciences, University of Missouri, [3]Department of Medical Anatomical Sciences, Western University, [4]Department of Cell Systems and Anatomy, The University of Texas Health Science Center at San Antonio

The neck plays an important role in primate locomotion as it orients the visual field. The nuchal region contains several muscles and bones that work together to facilitate a variety of actions: holding up and stabilizing the head, turning the neck, and elevating the arm. Primate positional behaviors, such as prominent bouts of neck rotation, are therefore hypothesized to influence the size, shape, and function of the nuchal musculature. To test this hypothesis, 3D static models of five different primate taxa (*Propithecus*, *Carlito*, *Aotus*, *Cebus*, and *Lagothrix*) were generated using contrast-enhanced computed tomography data from cadaveric specimens. Individual bones and muscles were isolated, muscle forces were estimated, and muscle attachment sites were mapped in *Avizo*. Individual muscle moments, moment arms, and summed moments about the craniocervical joints were calculated and compared using *R*. Results demonstrate that *Propithecus* and *Carlito*, vertical clingers and leapers noted for their prominent bouts of neck rotation, demonstrate overall larger moments of lateral flexion relative to body size when compared to *Lagothrix*, *Aotus*, and *Cebus*. *Carlito* is estimated to generate greater moments of lateral flexion through longer moment arms of the sternocleidomastoid muscle relative to body size, whereas *Propithecus* has greater force-production capacity estimates of both the sternocleidomastoid muscle and anterior scalene muscle. These results highlight the utility of analyzing 3D lever mechanics when investigating form function relationships in the musculoskeletal system. It offers a basis from which osteological correlates of specific muscles can be readily identified and used to reconstruct behavior in extinct primates.

This research was supported by the NSF DDRIG (#1919475), the NSF GRFP, the American Association for Anatomy, the Leakey Foundation Research Grant, and the University of Missouri Life Sciences Fellowship.

Developmental milestones of body systems in the leaping primate *Galago moholi*

BRENNA R. MCGOVERN-LIND[1], KATHRYN A. PROFFITT[1], SCOT EE. KING[1], VALERIE B. DELEON[2] and TIMOTHY D. SMITH[1]

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

Systems of the body develop in a modular manner. For example, neural development in primates is generally rapid relative to other mammals, whereas dental development varies much more. In the present study, we examined development of the skull, teeth and postcrania in a highly specialized leaping primate, *Galago moholi*. Ten cadavers (birth to 97 postnatal days) were scanned using micro computed tomography (CT) with a Scanco vivaCT 75 scanner. Bones, teeth and the cranial cavity (i.e., endocast) were reconstructed with Amira software based on micro CT cross-referenced to histology. Amira was also used to compute endocast volume (as a proxy for brain size). Reconstructions of the wrist and ankle show that ossification is complete at one month postnatally, which is consistent with the known timing at which the species is practicing signature leaping movements . In contrast, brain growth is slightly less rapid, at 75% of adult size by 2 weeks, ~80% by one month, and complete by weaning age. Full deciduous dentition eruption occurs by two weeks, and as juveniles (first permanent teeth erupt) they are accepting food from adults. The modular pattern of development of body systems in *Galago Moholi* provides an interesting view of a "race" to adult morphology for some joints that are critical for specialized leaping and clinging, early dental eruption to begin a transitional diet, but perhaps more prolonged reliance on nursing to support brain growth.

Funded by NSF grant #s BCS-1830894 and BCS-1830919.

Distributions of Colobinae across space and through time in South East Asia

CHRISTINA MCGRATH[1], MARIE VERGAMINI[2,3] and AMY L. RECTOR[3]

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

The Colobinae, or leaf monkeys, are specialized arborealists and leaf eaters distributed geographically across Africa and Asia. They have extraordinary adaptations of sacculated stomachs, sheering teeth, reduced thumbs, and very mobile shoulders. Colobinae diverged ~10.9 million years ago (Ma) from the Cercopithecidae in Africa, and Asian colobines appear in the fossil record in the late Miocene ~8.5 Ma. Though the fossil record is scarce in Asia, we looked to investigate the evolutionary pressures that led to Asian colobine migration and diversification to develop hypotheses about how geographic barriers played direct roles in Asian colobine evolution.

This study used ArcGIS to plot Miocene-epoch to Pleistocene-epoch fossil Colobinae sites with overlapping geospatial information of geographic barriers that may have influenced species distribution. Extant species' presence, distributions, and species diversity were included to assess and compare patterns of distribution over time.

By using geographical histories and current species distribution, results suggest that combining fossil data, extant species' distributions, and relevant biogeographical factors provide some clues for where and when Asian Colobinae adaptions underwent selection. For example, cold climate adaptions in *Rhinopithecus* species are not recent, but they influence distribution and movement of that genus today. These parameters can support powerful hypothesis building about the evolutionary histories of extant species adapting behaviorally and anatomically among mountainous, densely forested South Asia, and plateaus and lowlands of South East Asia.

ABSTRACTS

More severe stress markers in the teeth of *Australopithecus africanus* compared to *Paranthropus robustus*

KATE MCGRATH[1,2,3], IRIS PANSIN[3] and DEBBIE GUATELLI-STEINBERG[2]

[1]Anthropology, SUNY Oneonta, [2]Anthropology, The Ohio State University, [3]PACEA, University of Bordeaux

Stress events like childhood illness and injury create horizontal grooves on the surface of developing teeth. Previous work has shown that more severe stressors increase defect dimensions, while faster enamel growth rates create shallower features on the enamel surface, i.e., defects and normal growth increments called perikymata. Here, we used confocal profilometry to create high-resolution 3D canine surface maps in South African hominin *Australopithecus africanus* (N=15) and *Paranthropus robustus* (N=7). We find more defects in *A. africanus* canines (W=84.5; p=0.022), which are also deeper (F(1,21)=4.82, p=0.04; mixed model used to control for individual effects due to multiple observations per tooth) compared to *P. robustus*. Plane-form defects, representing more severe cellular growth disruptions, are deeper than furrow-form defects (F(1,34)=8.85; p=0.005) and are more common in the *A. africanus* sample. We find no differences in defect width, which has been linked to stress duration, nor differences in perikymata width nor depth. While *Paranthropus* exhibits particularly fast growth and uniquely thick enamel, particularly in their molar teeth, our results suggest that *A. africanus* and *P. robustus* canines do not share the same major differences in normal growth patterns as supported by their similar perikymata dimensions in the current study. However, the higher enamel defect prevalence and deeper defect morphology in *A. africanus* suggests that this species experienced more severe stressors, as evidenced by their abundance of plane-form defects, during early life. Future work will further examine the relationships between perikymata and defect dimensions as well as growth parameters and enamel geometry.

European Union's Horizon 2020 research and innovation program under the Marie Sklodowska-Curie grant agreement No 798117, The Ohio State University President's Postdoctoral Scholar's Program, and The Leakey Foundation

Ranging responses to chainsaw noise and home range use of the northern yellow-cheeked crested gibbon *Nomascus annamensis*

SARAH J. MCGRATH and ALISON M. BEHIE

School of Archaeology and Anthropology, The Australian National University, Acton, Canberra, 2601, Australia

Veun Sai-Siem Pang National Park (VSSP) in north-eastern Cambodia contains one of the world's largest known populations of the Endangered northern yellow-cheeked crested gibbon *Nomascus annamensis*. The population in VSSP is threatened by illegal logging, which is common in the 57,469 ha park, yet the impact of chainsaw noise on the ranging behaviour of *N. annamensis* is unknown. To determine if chainsaw intensity affects the daily path length (DPL) of *N. annamensis,* we use scan sampling and chainsaw intensity data collected during 37 full-day follows of a habituated *N. annamensis* group in VSSP (Group A). We determine Group A's home range size using the 95% kernel density estimation (KDE) and the 100% minimum convex polygon (MCP), and core range using the 50% KDE method, incorporating data collected over 134 days. To understand the severity of logging in Group A's home and core range, we recorded each logged tree encountered while following Group A and conducted seven 500 m transects in the area. There was no significant effect of chainsaw intensity on Group A's DPL. The home range size of Group A using the 100% MCP is 99.93 ha and 85.82 ha using the 95% KDE and the group's core range is 22.74 ha. Nine of the 24 logged trees detected in Group A's home range were within the core range and were logged during the study period. While Group A continued to utilise the area, a network of tracks was created, increasing vehicle access which may result in further logging.

This research was funded by the Australian National University Research Training Scheme, Primate Action Fund, Primate Conservation, Incorporated and the Margot Marsh Biodiversity Foundation.

Total daily energy expenditure and water turnover in a small-scale agro-pastoralist society from northern Kenya

AMANDA MCGROSKY[1], ZANE S. SWANSON[1], ROSEMARY NZUNZA[2], REBECCA RIMBACH[1,3], HILARY BETHANCOURT[4,5], EMMANUEL NDIEMA[6], DAVID R. BRAUN[7,8], ASHER Y. ROSINGER[4,9] and HERMAN PONTZER[1,10]

[1]Department of Evolutionary Anthropology, Duke University, [2]Kenya Medical Research Institute (KEMRI), Nairobi, Kenya, [3]School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, [4]Department of Anthropology, Pennsylvania State University, [5]Department of Anthropology, Northwestern University, [6]Department of Earth Sciences, National Museums of Kenya, [7]Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, [8]Department of Human Evolution, Max Planck Institute of Evolutionary Anthropology, [9]Department of Biobehavioral Health, Pennsylvania State University, [10]Global Health Institute, Duke University

Total daily energy expenditure (TEE; kcal/day), the sum of resting expenditure and that expended in physical activity and digestion, represents the energetic cost of life's essential tasks. Despite major differences in lifestyle and physical activity, fat-free body mass (FFM)-adjusted TEE is typically consistent across modern human populations. By contrast, daily water requirements can vary substantially between populations and little data has examined TEE and water turnover (L/day) in pastoralists, who often face extreme heat, food and water insecurity. Here we report doubly labeled water-derived TEE and water turnover for highly active, semi-nomadic agro-pastoralist Daasanach adults (n=11, semi-random selection) from the vicinity of Illeret on the arid/semi-arid northeastern shore of Lake Turkana (Kenya).

When modeled as a function of FFM, fat mass, age, and sex, Daasanach TEEs (1496–2398kcal/day or 6.3–10.0MJ/day) fall within the range expected of adults in other small-scale societies, as well as both sedentary and active western populations (Daasanach: FFM β=0.64, 95%CI=-0.19–1.47; intercept=-1.17, 95%CI=-4.17–1.83; Western: FFM β=0.79, 95%CI=0.54–1.04; intercept=-0.53, 95%CI=-1.44–0.39). Mean water turnover, however, was higher in the Daasanach (6.41L/day, sd=0.88) than in hunter-gatherer (3.77L/day, sd=0.60) and industrialized samples (4.24L/day, sd=1.13). These data provide insights into the physiology of a highly active population in an arid climate and potential adaptations to extreme environments and water stress. The similar FFM-adjusted TEE of the Daasanach and western populations lends support to the hypothesis that modern human TEE is constrained, with high levels of physical activity necessitating trade-offs in energy allocation away from other demands.

This research was supported by the National Science Foundation (NSF #1852406, NSF ARCH #1624398, NSF REU #1930719, NSF CNH2-S #1924322).

Characterizing Heterospecific Encounters with the Ring-tailed Lemurs (*Lemur catta)* on St. Catherines Island, Georgia, USA

KATHLEEN M. MCGUIRE and MICHELLE L. SAUTHER

Department of Anthropology, University of Colorado Boulder

Encounters between primate and non-primate species (heterospecific interactions) provide important insight into the evolution of sociality, niche partitioning and predator avoidance. The free-ranging colony of ring-tailed lemurs (*Lemur catta)* on St. Catherines Island (SCI) was used to address heterospecific interactions because provisioned social groups have lived in the island's northern forests since 1985 where they have interacted with other animal species. Using data from a larger project on social competence, we investigated the nature of heterospecific encounters in three social groups (January to July 2021), defining these as instances where a group changed their behavioral state in response to another species' clearly-identified presence. Group focal sampling data was used to identify the other animals that groups encountered, supplementing this with

video and field notes. Lemur interactions with deer were also captured during individual focal follows. SCI lemurs most encountered (n=231 events) raptors (57%), deer (20%), raccoons (9%), armadillos (9%), and wild pigs (3%). There was no significant difference in encounter counts among social groups (Kruskal-Wallis: H(2)=0.159, p=0.92). Group behavioral responses consisted of vigilance, startling, antipredator vocalizations, or a sequence of these behaviors. Additionally, during daily provisioning, deer would often wait under feeding platforms for lemurs to drop unwanted food or follow individuals around a feeding site, and several instances (n=16) of individuals both initiating and receiving aggression with deer were observed. Overall, these behavioral findings suggest that the SCI lemurs view other species like raccoons and armadillos primarily as threats and highlight a competitive relationship with deer over provisioned resources.

Funding was provided for by the American Museum of Natural History, Edward J. Noble Foundation, St. Catherines Island Foundation, the University of Colorado Boulder Anthropology Department and Graduate School.

Sleep quality, social support, stress, and personality traits in a sample of Canadian university students during the 2020-2021 online academic year

LEELA MCKINNON, ERICA KILIUS and MING FEI LI

Anthropology, University of Toronto

Background: Sleep is influenced by social support, loneliness, and stress. Individual factors like personality traits may be associated with the tendency to experience loneliness and so should be considered for a better understanding of the effects of social isolation on sleep. The COVID-19 pandemic changed the way individuals could interact over the past academic year, with ongoing isolation measures necessitating decreased in-person contact. Here, we present results from university students on their sleep patterns, loneliness, and stress during online learning. Methods: We surveyed 126 students using the Pittsburgh Sleep Quality Index (PSQI), the Medical Outcomes Study Social Support Survey, the Three-Item Loneliness Scale, the Perceived Stress Scale, and the Ten-Item Personality Inventory to explore the relationship between sleep, social support, loneliness, stress, and personality traits. Results: Average sleep duration over the past academic year was reported to be 7.14 hours (SD=1.30). After controlling for age and gender, results indicate that poor sleep quality as measured by total PSQI score is significantly predicted by higher stress (estimate=0.88, SE=0.35, p = 0.013) and loneliness (estimate=2.78, SE=0.36, p<0.001). Loneliness is predicted by lower perceived social support (estimate=-1.29, SE=0.26, p<0.001) and more introverted personality (estimate=-0.54, SE=0.26, p=0.045). Perceived stress is significantly associated with lower emotionally stable personality (estimate=-2.56, SE=0.54, p<0.001). Significance: Our results highlight the relationship between sleep, perceived social support, loneliness, stress, and personality traits, suggesting that they should be considered together for a more complete understanding of the individual factors that affect sleep and health in response to conditions of social isolation.

This project was funded by the University of Toronto Student Engagement Award.

What is a paleodeme? Theoretical considerations and applications using the East Asian hominin fossil record

CATHERINE E. MCLEAN and DAVID S. STRAIT

Anthropology, Washington University in St. Louis

Populations are fundamental units of evolutionary biology for understanding essential phenomena such as natural selection, speciation, and adaptation. In paleoanthropology, paleodemes are frequently used to represent past populations of hominins in evolutionary studies. Paleodemes are useful units for assessing phylogenetic affinities, evolutionary trends, and dispersal patterns among fossil hominins. Although paleodemes are frequently recognized in paleoanthropology, they are commonly defined using either arbitrary blocks of time and space or morphology, which can create a circular argument when studying variation. Here, we discuss criteria that should be considered when constructing hominin paleodemes, and introduce a new approach using temporal and geographic boundaries that reflect ecology and topography. Specifically, paleodemes were identified corresponding to Marine Isotope Stages and geological basins. We then apply this approach to the East Asian hominin fossil record as an example, resulting in a minimum number of 30 identifiable hominin paleodemes across Pleistocene East Asia. These paleodemes can then be used to facilitate phylogenetic, biogeographic, and other evolutionary analyses. In principle, these fine-scale paleodemes could be combined into coarser units. Ultimately, the scale of the paleodemes should depend on the nature of the research question being addressed. Regardless, however, it is important to define paleodemes using non-arbitrary criteria.

Tales in teeth – dental analyses of childhood health, mortality, and status from the Early and Late Classic Maya Belize (250-900 CE)

CARMELLA C. MCMANUS[1], KIRA J. WILDE[1], JULIE A. HOGGARTH[2] and SAIGE KELMELIS[1]

[1]Department of Anthropology and Sociology, University of South Dakota, [2]Department of Anthropology, Baylor University

Dental tissue has the unique capacity to inform on past life histories in the absence of well-preserved skeletal material and reliable documentary sources. We demonstrate the efficacy of dental analyses in reconstructing information about childhood health, mortality, and status from skeletal samples from Early and Late Classic (250-900 CE) Maya settlements in the Belize Valley. This project is a collaborative study led by two undergraduate women from the University of South Dakota (Anthropology). Dental and skeletal data were derived from the BVAR skeletal collection, resulting in a test sample of 27 individuals. Osteological analyses included age-estimation for adults and nonadults. Dental enamel defects (LEH) were scored and estimated for age of incidence following criteria developed by Reid and Dean (2006). Status was reconstructed from mortuary evidence including household volume and organization, burial location, grave artifacts, and dental modifications (e.g. filing, obsidian and jade inlays). Fishers exacts tests and Kaplan Meier survival analyses were conducted to examine associations and survivorship trends. Results show that there are significant associations between status and LEH (p=0.03) with commoners more likely having endured childhood stress events. Kaplan Meier results (p=0.4) show increased survivorship for individuals with LEH, but this is likely an artifact of selective mortality and sample size. Chronological estimates of enamel defects show that most experienced physiological stress events between the ages of 2-3.6 years, possibly representing diseases, malnutrition, or weaning. Our study demonstrates how dental tissues are versatile in skeletal reconstruction of childhood health and social status where taphonomic damage is extensive.

Student research was supported by the Tuve Fund and the Dean's Opportunity Fund at USD. Travel was additionally supported by the USD College of Arts & Sciences Travel Fund.

Catching their Strides: A comparative analysis of wild platyrrhine walking kinematics on naturally variable substrates

ALLISON MCNAMARA[1], NOAH T. DUNHAM[2], WALKER STANTON[1], JESSE W. YOUNG[3] and LIZA J. SHAPIRO[1]

[1]Anthropology, University of Texas at Austin, [2]Conservation and Science, Cleveland Metroparks Zoo, [3]Department of Anatomy and Neurobiology, Northeast Ohio Medical University

We are just beginning to understand the variability and flexibility of primates' walking gaits when moving through their complex, arboreal habitats. Most gait studies take place in laboratories and focus on single substrate use; however, wild primates use multiple substrates with different characteristics and transition among substrates as they move. This comparative analysis of wild platyrrhine walking gait kinematics integrates

natural locomotor behavior and quadrupedal kinematics to further our understanding of the adaptive context in which primate locomotion and morphology evolved. We collected high-speed video data of platyrrhines in Amazonian Ecuador and Costa Rica (*Alouatta palliata, Alouatta seniculus, Ateles belzebuth, Ateles geoffroyi, Cebus albifrons, Cebus capucinus, Lagothrix lagotricha, Plecturocebus discolor*, *Saimiri sciureus*). We analyzed quadrupedal locomotor bouts of multiple strides, digitized footfall events, and categorized substrate size, type, diameter, and inconsistencies (e.g., offshoot, gap, etc.). We then calculated if and how substrate inconsistencies affect gait symmetry, footfall sequence, and gait kinematics. All species used symmetrical and asymmetrical walking gaits, as well as both diagonal and lateral footfall sequences. Presence of a substrate inconsistency significantly affected gait symmetry of four species (increased symmetry: *Ateles geoffroyi*; increased asymmetry: *Plecturocebus discolor, Lagothrix lagotricha, Saimiri sciureus*), and footfall sequence of three species (increased frequency of lateral sequence: *Alouatta palliata, Alouatta seniculus, Lagothrix lagotricha*). Results highlight intra- and interspecific variability in kinematic adjustments to substrate inconsistencies during walking. This study reveals the importance of studying primate kinematics in natural habitats and expands on laboratory-based investigations of locomotor kinematics and biomechanics.

National Science Foundation BCS-1640552 and BCS-1640453

Skeletodental element abundance in the hominin fossil record

RYAN T. MCRAE and BERNARD A. WOOD

Center for the Advanced Study of Human Paleobiology (CASHP), The George Washington University

To generate and test alpha taxonomic and phylogenetic hypotheses in the hominin fossil record, it is important to appreciate how well represented each skeletodental elements is in the taxa under consideration. This is because it is prudent to focus attention on the taxonomic and phylogenetic valency of elements that are well-enough represented in the hominin fossil record for us to get a reliable estimate of population variation. Surprisingly, there is no existing open-access database from which it is possible to extract this information, so we set out to generate one. We tried to strike a balance between skeletodental element categories that were unhelpfully exclusive or inclusive, finally opting for 92 distinct categories to describe the skeleton and dentition. We initially focused on 10 early hominin taxa whose hypodigms are not especially contentious. We searched the literature for precise information about the hypodigm of each taxon, and assigned each separate fossil discovery into one, or more, of the 92 distinct categories. We intend to make this database available on-line, along with a comprehensive description of each of the 92 categories and links to the papers from which we extracted the data. Our presentation will be an opportunity for the community to make suggestions about how we might improve the utility of a hominin fossil database.

Are we all equal in death? Current barriers to equity and inclusivity in deathcare practices

RAPHAELA M. MELORO

Anthropology, University of Florida

This abstract is part of the symposium *Advances and Challenges in the Identification of Sex and Gender in Human Osteological Contexts*. This presentation reviews current literature and guidelines regarding deathcare practices and forensic identification methods to determine ways in which LGBTQ+ individuals may be marginalized in death. Case studies of recent LGBTQ+ homicides are used to highlight critical challenges to identification efforts under current practices.

Results of the review indicate that key issues in the current deathcare system that may hinder identification efforts mirror those that contribute to the marginalization of LTBTQ+ individuals in life; practices in both areas are typically based on a Euro-centric conceptualization of identity and do not reflect the diversity found in modern cultures nor do they accurately reflect modern understandings of human biology. These key issues include poor relationships between LGBTQ+ populations and law enforcement agencies, the practice of biological profile estimations based on the conceptualization of sex as a binary, and the use of rigid categories on submission forms for databases of unknown decedents.

A path for moving toward an LGBTQ+ inclusive deathcare system is proposed with an emphasis on the use of anthropological principles and methodology in constructing such a system. The role of forensic anthropologists in such a system is highlighted due to the importance of information generated from osteology reports in guiding identification efforts for unknown decedents.

Early humans in South America: First direct radiocarbon dating and morphometric study of "Zuzu" (Serra da Capivara, Brazil)

LUMILA P. MENÉNDEZ[1,2], MARÍA CLARA LÓPEZ-SOSA[1], SERGIO FRANCISCO SERAFIM MONTEIRO DA SILVA[3], GABRIELA MARTIN[4,5], ANNE-MARIE PESSIS[4,5], NIÈDE GUIDON[3,4] and ANA SOLARI[4,5]

[1]Department Anthropology of the Americas, University of Bonn, [2]Evolutionary Biology, University of Vienna, [3]Departamento de Arqueologia, Universidade Federal de Pernambuco, [4]FUMDHAM, Fundação Museu do Homem Americano, [5]INCT-INAPAS, Instituto Nacional de Ciencia e Tecnologia de Arqueologia, Paleontologia e Ambiente do Semiárido do Nordeste do Brasil,

The biological variation of the earliest humans in South America provides clues on the evolutionary processes by which the continent was occupied. We evaluated the craniometric variation of the first direct radiocarbon-dated early Holocene human skeleton from Serra da Capivara. This individual, also known as "Zuzú", comes from the burial 1 of Toca dos Coqueiros, in Brazil. Dental enamel carbonate provided a date of 8,640 + 30 BP (9,526-9,681 cal years BP), which falls within the distribution of direct radiocarbon dates for Brazil. In addition, we performed a morphometric study of the skull using exclusively early and late Holocene samples from Brazil, in order to revisit the sex of the skeleton, and to discuss the evolutionary processes involved in the occupation of the continent. The sex of the individual is estimated as a probable female when compared to late and early Holocene individuals, but as a male when compared to the early Holocene ones. This individual presents the strongest differences with the late Holocene individuals from Guajajara, located nearby, and the strongest similarities with the early Holocene series from Lagoa Santa. Overall, our morphometric results showed solid biological affinities among early Holocene individuals from Brazil as well as a moderate level of morphological variation among them. This suggests that the early Holocene individuals from Brazil were part of the same heterogeneous lineage, possibly a different one from which late Holocene populations diverged. Further studies should take interdisciplinary efforts as well as focus on incorporating more individuals into the comparisons.

German Research Council (DFG, Projektnummer 415489479), Fundação de Amparo à Pesquisa do Estado do Piauí (FAPEPI), and Instituto Nacional de Arqueología, Paleontología y Ambiente del Nordeste de Brasil (INCT-INAPAS).

Locomotor signal in the forelimb of *Sahelanthropus* and OH 36 is unlike known hominins

MARC R. MEYER[1], JASON P. JUNG[2], JEFFREY K. SPEAR[3,4], ISABELLA FX. ARAIZA[3,4] and SCOTT A. WILLIAMS[3,4]

[1]Anthropology, Chaffey College, [2]Biology, California State University, San Bernardino, [3]Anthropology, Center for the Study of Human Origins, New York University, [4]New York Consortium in Evolutionary Primatology, NYCEP

Variation in ulna morphology is known to differentiate specialized locomotor groups. Using elliptical Fourier analysis, we evaluate the ulnar shaft and proximal complex in 13 hominin fossils from *Sahelanthropus*, *Ardipithecus*, *Australopithecus*,

Paranthropus, and early *Homo*. Principal components of shape contours were evaluated against locomotor pattern, body mass, and taxonomy in 418 ulnae representing 88 extant primate species.

Factor analysis confirms that locomotion influences the ulna shaft and proximal complex, differentiating locomotor groups. Apes differ from other primates with the smallest olecranon processes and retroflexed trochlear notches, with *Pan* and *Gorilla* exhibiting the tallest and most robust coronoid processes. Like many primarily terrestrial primates, African apes often possess the retroanconeal incisura.

Analyses of Fourier descriptors place the OH 36 and TM 266 *Sahelanthropus* ulnae within the morphospace of *Pan*, far from the distribution of other hominins. These two fossils are vastly unlike those of known bipeds, with robusticity and curvature only observed among the African apes where ulna contours reflect the role of the forelimb in channeling body weight during terrestrial locomotion. By contrast, the *Ardipithecus* ulna falls closest to A.L. 288-1 and the MH2 *Australopithecus* close to the human distribution.

These findings highlight the derived nature of the forearm in *Ardipithecus* and *Australopithecus* and raise questions about the claimed bipedal status of the *Sahelanthropus* and OH 36 specimens. In the case of *Sahelanthropus*, this evidence may signal that this species retained adaptations for knuckle-walking, or alternatively, signals the presence of a Miocene ape moving in a similar way to chimpanzees.

In juvenile weight estimation, can external breadth measurements replace an internal cross-sectional measurement?

JULIA L. MEYERS and HUGO FV. CARDOSO

Department of Archaeology, Simon Fraser University

The use of distal femoral breadth measurements has been integral to the development of body weight estimation formulae for juvenile populations. More recently, femoral cross-sectional measurements have been shown to provide the most accurate weight estimations. However, less research has been conducted on the applicability of the proximal tibial breadth in creating similar formulae, despite both it and the distal femur being part of the knee joint. The purpose of this research is to examine the reliability of external breadth measurements of the proximal tibia for the estimation of juvenile body weight.

The individuals in this sample were taken from the New Mexico Decedent Images Database (NMDID), ranging from just under 1 to 19 years of age (n= 78). The NMDID collection is curated by the Office of the Medical Examiner of New Mexico and the University of New Mexico.

Distal femoral metaphyseal breadth, femoral mid-shaft J, and proximal tibial metaphyseal breadth were regressed on weight, using linear and non-linear analyses. The distal femur explains the least amount of variation in weight (R^2 ~0.7), followed by J and the proximal tibia which are on par (R^2 ~0.8).

This study suggests that within this population, the tibial breadth is comparable to J for weight estimation purposes, with both being better than the femur. These results indicate that future attempts to develop juvenile weight estimation formulae should consider the proximal tibia. The proximal tibia has the added advantage of providing estimates as reliable as J but not requiring additional radiographic data collection.

This research was partially funded by Julia Meyers' Social Science and Humanities Research Council of Canada Doctoral Fellowship and a Nation Sciences and Engineering Research Council of Canada Discovery Grant.

Host-Pathogen Coevolution through the Lens of Ancient Genomics: A Case Study of the Cariogenic Pathobiont, *Streptococcus mutans*

MEGAN MICHEL[1,2,3], AIDA ANDRADES VALTUEÎA[2], RODRIGO BARQUERA[2], TIAGO FERRAZ DA SILVA[2,4], EVELYN GUEVARA[5], ALISSA MITTNIK[6], KATHRIN NÄGELE[2], ELIZABETH A. NELSON[2,7], GUNNAR NEUMANN[2,3], MARIA SPYROU[2,8], VANESSA VILLALBA[2], KIRSTEN BOS[2], WOLFGANG HAAK[2], COSIMO POSTH[2,8], PHILIPP STOCKHAMMER[2,3,9], ALEXANDER HERBIG[2] and JOHANNES KRAUSE[2,3]

[1]Department of Human Evolutionary Biology, Harvard University, [2]Archaeogenetics Department, Max Planck Institute for Evolutionary Anthropology, [3]Max Planck-Harvard Research Center for the Archaeoscience of the Ancient Mediterranean, [4]Institute of Bioscience, Department of Genetics and Evolutionary Biology, University of São Paulo, [5]Department of Forensic Medicine, University of Helsinki, [6]Department of Genetics, Harvard Medical School, [7]Department of Anthropology, University of Connecticut, [8]Archaeo- and Palaeogenetics Group, Institute for Archaeological Sciences, University of Tübingen, [9]Institute for Pre- and Protohistoric Archaeology and Archaeology of the Roman Provinces, Ludwig Maximilian University

Dental caries has a bioculturally complex pathophysiology, with both diet and oral microbes impacting variation in disease burden across past populations. Changes in human subsistence practices, particularly adoption of carbohydrate-rich agricultural diets, are generally associated with increased caries rates relative to hunter-gatherer diets. Oral pathobionts like *Streptococcus mutans* metabolize diverse carbohydrates, generating acidic biofilms that demineralize enamel and produce caries. However, whether genes contributing to *S. mutans* cariogenicity predate the spread of agriculture or represent coevolutionary adaptations to a changing human dietary niche remains to be explored.

To address this question, we generated the first whole-genome ancient DNA data from 80 geographically diverse *S. mutans* strains spanning the Mesolithic to the modern era. To facilitate genome recovery from highly degraded metagenomic samples, we designed a custom in-solution hybridization capture targeting the pan-genomic diversity present in modern *S. mutans*. After capture, 60/80 samples yielded a mean coverage greater than 3X when mapped to the UA159 reference genome. Comparing modern and ancient strains, we find that many *S. mutans* virulence-associated genes are present as early as the Mesolithic period in Europe, suggesting that some cariogenic phenotypes may have been present across thousands of years of *S. mutans* evolution. Interestingly, we identify several loci whose presence appears to correlate with human subsistence practices; the ComCDE system, which regulates biofilm production, interspecies competition, and genetic competence, is absent in 4/5 geographically and temporally diverse hunter-gatherers. This result highlights ancient genomics as a unique tool for exploring the coevolution of humans and pathogenic microbes.

Visiting the dead: Patterns of grave re-entry in ancient Nubia

CEARRA L. MIHAL[1], BRENDA J. BAKER[1] and SIDNEY G. REMPEL[2]

[1]Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona State University, [2]ASU Bioarchaeology of Nubia Expedition

Anthropogenic postmortem disturbance of graves typically is attributed to looting, which fails to consider culturally sanctioned alternatives for re-entry. Patterns of grave disturbance in ancient Nubia have rarely been analyzed systematically to distinguish sanctioned cultural practices from actual instances of plundering. We hypothesize that small re-entry holes targeting specific areas of the grave and corpse, with limited disarticulation and disturbance represent a culturally sanctioned practice that occurred within memory of the deceased's interment. Alternatively, large re-entry pits, extensive disturbance, and substantial skeletal disarticulation represent illicit grave re-entry.

Grave disturbance was examined in 48 fully excavated graves from five cemeteries dating between the Early Kerma and Napatan periods (radiocarbon dated c. 2200-430 BCE) in the Bioarchaeology of Nubia Expedition (BONE) project area west of Abu Hamed, Sudan. ArcGIS Pro was used to assess the dimensions of re-entry pits in relation to the overall grave dimensions, extent of grave disturbance, and skeletal disarticulation. The percentage of *in situ* skeletal disarticulation (<25%, 25-75%, and >75%) was additionally ascertained from field photographs and documentation, georeferenced drawings of

each burial, and presence/absence of elements in the BONE laboratory. Statistical tests, including correspondence analysis, were performed. The results demonstrate an association between re-entry pit size and skeletal disarticulation, supporting the existence of two different forms of grave re-entry. Such complex taphonomic processes within disturbed graves are frequently ignored and data from them deemed incomplete. This study highlights the biocultural meaning that can be derived from grave taphonomy, challenging preconceptions about "looting" and "useful" bioarchaeological data.

BONE fieldwork was supported by the Qatar-Sudan Archaeological Project (QSAP A.17) and private donor grants to B. Baker.

Dining in Tuva: social correlates of diet and mobility in a nomadic community from Southern Siberia (2nd-4th c. CE)

MARCO MILELLA[1], GINO CASPARI[2,3], ZITA LAFFRANCHI[1], GABRIELE ARENZ[1], TIMUR SADYKOV[4], JEGOR BLOCHIN[4], MARCEL KELLER[5], YULIJA KAPINUS[6] and SANDRA LÖSCH[1]

[1]Department of Physical Anthropology, Institute of Forensic Medicine, University of Bern, [2]Department of Archaeology, University of Sydney, [3]Institute of Archaeological Sciences, University of Bern, [4]Institute for the History of Material Culture, Russian Academy of Sciences, [5]Institute of Genomics, Estonian Biocentre, University of Tartu, Estonia., [6]Volga-Ural Center for Paleoanthropological Research

The traditional notions of "nomadic" cultures as homogenously mobile and economically simple is increasingly displaced by more nuanced interpretations. A large part of the scientific literature on diet and mobility among Eurasian pastoralists is focused on Bronze Age and Iron Age. The relative underrepresentation of more recent contexts in these analyses hampers a full discussion of possible chronological trajectories. In this study we explore diet and mobility at Tunnug1 (Republic of Tuva, 2nd-4th century CE), and test their possible correlation with social differentiation.

We compare demographic patterns of carbon, nitrogen, and sulfur stable isotope ratios ($\delta^{13}C$, $\delta^{15}N$, $\delta^{34}S$) among 65 humans and 12 animals from Tunnug1 using nonparametric tests and Bayesian modeling. We then compare isotopic data with data on perimortal skeletal lesions of anthropic origin and funerary variables.

Results show that: 1) diet at Tunnug1 was largely based on C_4 plants (likely millet) and animal proteins; 2) only few individuals were nonlocals, although their geographic origin remains unclarified; 3) no differences in diet separates individuals based on sex and funerary treatment. In contrast, individuals with perimortal lesions show carbon and nitrogen stable isotope ratios consistent with a diet incorporating a lower consumption of millet and animal proteins.

Our study provides new insights about the socio-ocultural variability of pastoralist societies in Southern Siberia during the early centuries CE. At the same time, they further support the economic importance of millet for these communities.

Embedded Experience: exploring spear throwing performance among adolescent and adult BaYaka forager and Bandongo fisher-farmer males

ANNEMIEKE G. MILKS[1,2], SHEINA LEW-LEVY[3,4] and FRANCY KIABIYA NTAMBOUDILA[5]

[1]Department of Archaeology, University of Reading (UK), [2]Institute of Archaeology, University College London (UK), [3]Department of Human Behaviour, Ecology and Culture, Max Planck Institute for Evolutionary Anthropology (Germany), [4]Department of Comparative Cultural Psychology, Max Planck Institute for Evolutionary Anthropology (Germany), [5]Faculté des Lettres, Arts, et Sciences Humaines, Marien Ngouabi University ((Republic of Congo)

Spears are the earliest evidenced and longest-used weapon used by humans. Yet, spear hunting is poorly understood in comparison to other subsistence technologies. Learning to spear hunt involves the acquisition of motor skills, alongside cooperative and social skills, and environmental knowledge. Both spear thrusting and throwing can involve considerable energy outputs and therefore it is hypothesised that successful hunting of larger prey may necessitate a certain level of body size. It has also been hypothesised that the physiological skills required for successful spear hunting may take longer to acquire than those needed for other weapon technologies, with a particular emphasis on the challenges of accurate throwing, a skill that is learnt over time through integrating perceptual and motor learning. Here we share results from a research project with BaYaka foragers, who currently hunt in the tropical forests of the Congo rainforest basin. We gathered data on how spear hunting skills are learnt during early childhood and adolescence through interviews, focal follows and a competition-style spear throwing experiment involving adolescent and adult male participants. Our experimental data explores possible correlations in the domain of spear throwing between age, skill, and physiology, impact velocities, kinetic energy and accuracy. Our results demonstrate that spear hunting is a complex, embedded skill that is learnt, developed and maintained throughout childhood, adolescence and adulthood through role play, games, practice, direct experience and high-fidelity teaching from peers and from adults.

This research was funded by the Wenner-Gren Foundation (no. 9789) and the Leakey Foundation, and a Social Sciences and Humanities Research Council of Canada Postdoctoral Fellowship (no. 756-2019-0102).

Consequences of parental loss and unstable social environments on offspring survival, feeding and playing in gelada monkeys (*Theropithecus gelada*) at Guassa, Ethiopia

CARRIE M. MILLER[1], NGA NGUYEN[2,3], PETER J. FASHING[2,3] and MICHAEL L. WILSON[1,4,5,6]

[1]Department of Anthropology, University of Minnesota, [2]Department of Anthropology & Environmental Studies Program, California State University, Fullerton, [3]Center for Evolutionary & Ecological Synthesis (CEES), Department of Biosciences, University of Oslo, [4]Department of Ecology, Evolution, & Behavior, University of Minnesota, [5]Institute on the Environment, University of Minnesota, [6]Institute for Advanced Study in Toulouse, Université Toulouse 1 Capitole

In most mammals, mothers raise offspring independently, whereas in humans, fathers often contribute substantially to parental care. To understand factors that might promote increased paternal investment in primates, we examined the effects of maternal loss, paternal loss, and unit instability, on offspring feeding, playing, and survival in gelada monkeys (*Theropithecus gelada*) at Guassa, Ethiopia. Geladas aggregate in herds with a varying number of units. Units contain several females, a leader, and (sometimes) one or more followers, who are often deposed leaders. We found that early loss of either parent, in combination with unit instability, reduced infant survival (maternal loss and unit instability: *Wald Test p-value* < 0.001, *N* = 101 offspring; paternal loss and unit instability: *Wald Test p-value* = 0.002, *N* = 94 offspring). We used an information theoretic model selection approach to identify which variables (season, maternal loss, paternal loss, and unit instability) best predicted the proportion of time immatures fed and played. According to model-averaged parameter (MAP) estimates, maternal loss (MAP = -0.29) best explained feeding patterns, while season (MAP = 1.98) best predicted patterns of play. However, paternal loss and/or unit instability were included as variables in the top two models for each response variable. Thus, in geladas, both parents contribute importantly to offspring survival and well-being. Our results contribute to the growing body of literature describing the degree parents can ameliorate the effects of early childhood adversity on offspring survival. If hominins lived in multi-level societies, similar dynamics may have also promoted increased paternal investment.

This research was funded by the Leakey Foundation, the Wenner-Gren Foundation, and the University of Minnesota.

Fishing for the secrets of vertebrate integument development, regeneration, and evolution

CRAIG T. MILLER, SOPHIE L. ARCHAMBEAULT and TYLER A. SQUARE

Department of Molecular and Cell Biology, University of California, Berkeley

This abstract is part of the symposium *Integumentary Anthropology: Examining the Exterior*. This presentation will summarize studies of integument development, regeneration, and evolution in fish models. These studies reveal that genetic networks that pattern the vertebrate integument are deeply conserved across jawed vertebrates. From fish to mammals, the secreted signaling molecules Ectodysplasin (Eda) and Wnt10a play highly conserved roles in promoting tooth development. In fish models, Eda signaling is sufficient to induce tooth development at many ectopic sites inside and outside of the oral cavity.

Using a combination of quantitative genetics, functional genetics, and gene expression studies, we have uncovered parallels between fish tooth replacement and mammalian hair regeneration (e.g. BMP signaling inhibits regeneration in both). Given the accepted deep homology of hair and teeth as "epithelial appendages," one parsimonious hypothesis is that mammalian hair regenerates using a homologous gene regulatory network that governs tooth replacement in vertebrates, including fish.

Some outstanding questions remain, for example: how pleiotropic are the mutations that control evolved differences in integumentary phenotypes in natural populations? Are these mutations less pleiotropic than the genes themselves? Stickleback fish have repeatedly evolved multiple major integumentary phenotypes. We find that while individual genes can be highly pleiotropic in regulating different features of the integument, specific mutations found in nature appear to be much less pleiotropic and seem to affect a single integumentary phenotype.

This work is supported by the National Institute of Dental and Craniofacial Research (NIDCR) grants DE021475, DE030340, and DE031017.

The Power of the Senses: Using Ecological Niche Modeling to Evaluate the Role of Sensory Drive in the Divergence of Dwarf Galagos (*Paragalago* spp.)

EVAN MILLER[1], AVEREE LUHRS[1], MARY BLAIR[2] and LUCA POZZI[1]

[1]Department of Anthropology, University of Texas at San Antonio, [2]Center for Biodiversity and Conservation, American Museum of Natural History

The *Paragalago zanzibaricus* complex consists of three cryptic dwarf galago species endemic to East Africa: *P. cocos* in Kenya, *P. zanzibaricus* in mainland Tanzania and Zanzibar, and *P. granti*, ranging from southern Tanzania to Mozambique and northern South Africa. Like other galagid primates, the species within this complex produce mate-specific vocalizations that distinguish them from other species, reducing the probability of interspecific mating. It has been hypothesized that sensory drive mediated by environmental change might have been responsible for the speciation event between *P. cocos* and *P. zanzibaricus,* while the evolutionary divergence of *P. granti* can likely be explained by the geographic barrier presented by the Rufiji River. Here, we assessed alternative models of speciation (allopatric vs. ecological/parapatric) and tested the sensory drive speciation hypothesis through the use of ecological niche modeling (ENM) to evaluate the extent of niche overlap in ecological and geographical space. Locality data for the three species and 19 climatic variables were used to generate ecological niche models. The most important variables in the model differ among species: while temperature variables (e.g., isothermality) play a major role for *P. cocos*, precipitation (e.g., annual precipitation) seems critical to explain the distribution of *P. zanzibaricus*. We found evidence for niche differentiation, showing that the members of the *zanzibaricus* complex exist in and respond to aspects of different environments, leading to geographical variation. These results support the hypothesis that environment-driven change in the sensory tuning might have played a critical role in the speciation within this complex.

Funding for work provided by National Science Foundation (BCS 1926105/1926215)

Best Practices for Returning Genomics Research Results to Participants, with a Special Focus on Marginalized Populations

GRACE V. MILLER[1] and KATHLEEN E. GROGAN[1,2]

[1]Department of Biological Sciences, University of Cincinnati, [2]Department of Anthropology, University of Cincinnati

Human genomics research depends upon the trust and voluntary participation of its subjects, yet rarely do participants later hear from researchers about even the most general research findings. This lack of communication about study findings occurs in spite of the majority of participants and researchers supporting the return of research results to participants. Furthermore, when study participants are members of a marginalized group, this lack of communication can further damage trust in science and compound societal marginalization. Multiple barriers hinder this return process, which can differ in part based on the type of genomic result, but these barriers must be balanced with the harm of not following-up with the community. We will discuss the best practices for returning genomic research results to participants, particularly those from marginalized populations, in ways that minimize the potential for miscommunication and emphasize the importance of a strong researcher/participant relationship in marginalized communities. These best practices include engaging the community with the research project from conception to completion, creating a more dynamic and thorough informed consent process, continued researcher participation within the community throughout the project, and tailored results summaries that are tested for clarity with community members. Incorporating these best practices would create a more equitable way of doing research and would empower the communities that are so vital for this research.

Summer Research Mentor Award, Charles Phelps Taft Research Center at the University of Cincinnati

To boldly go where no primatomorph has gone before: Dental topography and enamel thickness illuminate the dietary adaptations of paromomyid plesiadapiforms from Ellesmere Island, Arctic Canada

KRISTEN E. MILLER and K. CHRISTOPHER BEARD

Department of Ecology and Evolutionary Biology, University of Kansas

The Margaret formation of the Eureka Sound Group in the Canadian Arctic Archipelago samples a unique, warm temperate ecosystem with a polar light regime that dates to the early Eocene epoch ~ 53 Ma. Although crown clade primates have never been recovered from the Eocene of Arctic Canada, at least two new taxa of paromomyid plesiadapiforms occur there. Here, we describe these Arctic paromomyids from Ellesmere Island and assess their phylogenetic relationships with respect to other members of this clade. A phylogenetic analysis was completed using a morphological character matrix utilizing 63 dental characters scored for 17 taxa. A parsimony analysis completed using TNT suggests the two new paromomyid species are sister taxa that are highly nested within the *Ignacius* clade. These results suggest the Arctic paromomyids are closely related to mid-latitude North American paromomyids and are not specially related to the European genus *Arcius*. Phylogenetic tree topology also suggests the Arctic taxa dispersed into high northern latitudes long after the initial diversification of North American paromomyids during the Paleocene, coincidental with the increasing temperatures associated with the Early Eocene Climatic Optimum (EECO). Additional research analyzing molar dental topography using the R package molaR along with measurements of labial and lingual enamel thickness on upper incisors, suggest the new Arctic paromomyids may have relied on tough fruits and exudates to survive the long, dark Arctic winters.

Research supported by the David B. Jones Foundation.

Use of Thermal Imaging to Measure Behavioral Thermoregulation of Western Chimpanzees (*Pan troglodytes verus*) in a Savanna-Mosaic Woodland Environment

MCKENSEY R. MILLER[1] and JILL PRUETZ[2]

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

As regions continue to warm, it is becoming increasingly important to understand non-human primates' ability to adapt to changing environmental conditions. However, physiological measurements can be difficult to obtain from primates, especially when invasive methods are not feasible. Recent technologies have become available that can provide insight into the behavioral and physiological mechanisms animals utilize to maintain homeostasis. Thermal imaging is a non-invasive technology that can be used to measure surface body temperature of individuals. We use thermal imaging, microclimate environmental conditions, and behavioral data to measure how chimpanzees' surface hair temperature is affected by behavioral thermoregulation in the Fongoli chimpanzee (*Pan troglodytes verus*) group in Senegal. 734 focal points were collected on adult males (n=12). A mixed effect model was created to measure the effect of environmental conditions, behavior, and habitat choice on surface body temperature. Our results demonstrate that while surface body temperature is largely determined by environmental temperature, habitat selection, behavior, and even individual differences play a small, albeit important, role in the maintenance of homeostasis. Therefore, surface temperature can be used to show how specific behavioral adaptations can alter the thermal load animals experience and eventually respond to using more energetically expensive physiological adjustments.

This research was funded by the Texas State Graduate College, Texas State Department of Anthropology, and the National Science Foundation (Grant # 1840989)

Simulating amelogenesis and resulting perikymata distribution using continuum models

PEARSON W. MILLER[1] and MACKIE C. O'HARA[2]

[1]Center for Computational Biology, Flatiron Institute, [2]Department of Anthropology, Ohio State University

Dental researchers have identified significant variation in perikymata distribution across hominin dentitions. Developmental factors such as Retzius periodicity (RP), daily secretion rate (DSR), and enamel extension rate (EER) have been suggested to influence perikymata distribution patterns in lateral enamel. *H. sapiens* and *H. naledi* have a steep distribution pattern, with widely spaced perikymata occlusally and tight packing of perikymata in the cervical deciles. *Paranthropus* and Neandertals, though, have a relatively flat, more uniform distribution, with limited difference in the number of perikymata per decile. Within *Homo sapiens,* high RP is associated with a less steep perikymata distribution, resulting in a lower percentage of perikymata falling in the cervical half of the crown. To explore how underlying developmental factors (namely, DSR and EER) drive perikymata distribution differences, we construct a data-driven mathematical model of amelogenesis. Under broad assumptions about the behavior of individual ameloblasts, we simulate the enamel forming front to calculate first passage time (secretion), as a function of position within the enamel layer. By identifying striae of Retzius as level sets of this function, we numerically probe the dependence of perikymata distribution on EER, DSR, and total formation time, subject to fixed EDJ length, enamel thickness, and RP. We validate our model by direct comparison with published data. By examining a wide space of possible DSR and EER profiles, we demonstrate that, most obviously, a sharp decrease in EER is essential to achieve increased cervical packing. Thus, we provide a theoretical justification for EER's effect on perikymata distribution.

Use of small mammal tarsals in paleoenvironmental reconstruction

SAMANTHA M. MILLS

Department of Anthropology, University of Wisconsin - Milwaukee

The potential of small mammals for reconstructing paleoenvironments has been overlooked and thus, underutilized. Therefore, the goal of this preliminary study was to test the utility of tarsal bones of small mammals for reconstructing paleoenvironments. Based on the premise that tarsal morphology reflects adaptation to specific ecological niches, I collected morphometric data for a sample of 44 astragali and 46 calcanei from small mammal taxa (defining small mammal as less than or equal to 1,000 grams). The samples came from comparative osteological specimens of adult individuals representing extant species of Rodentia, Lagomorpha, and Primates. Metric data was collected using a Dinolite microscope and DinoXcope imaging software. Pairwise comparisons of tarsal indices were evaluated using One-Way PERMANOVA and PCAs. Results suggest that rodent calcanei are particularly successful at differentiating between arboreal, semi-aquatic, and terrestrial locomotor behaviors, and thus show good potential for use in paleoenvironmental reconstruction.

Human femur microstructure changes with chronology at Bakr Awa, Iraqi Kurdistan

JUSTYNA J. MISZKIEWICZ[1,2] and RAFAŁ FETNER[3]

[1]School of Archaeology and Anthropology, Australian National University, [2]School of Social Science, University of Queensland, [3]Faculty of Archaeology, University of Warsaw

Excavations at Bakr Awa (BA), a historically significant archaeological mound in Iraq, have uncovered a rich source of material and skeletal evidence for human occupations dating back to the third millennium BC. We examined BA human remains from a chronological cross-section to test whether behavioral changes through time can be detected in femoral bone microstructure. With permissions from local Iraqi heritage authorities, posterior femur midshaft cortical bone samples (1 x 2 cm) were extracted and processed into thin sections for n = 13 individuals. The represented time periods were Middle Bronze Age (MBA, n = 4), Iron Age (IA, n = 4), and the Islamic Period (IP, n = 5). Cortical bone Haversian canal geometric properties were collected for a minimum of 86 completed secondary osteons per sample, further corrected by cortical thickness and femoral midshaft circumference. Out of all three periods, the IA samples showed the smallest Haversian canals in combination with the largest femoral midshafts. The MBA samples had the thinnest midshafts with largest Haversian canals. This was consistent when age-at-death and sex were considered. Results indicate that quicker bone remodeling events characterized the IA femora, possibly due to higher mechanical demands associated with town-scape shift food farming and herding behaviors at BA. Slower bone remodeling in the MBA samples could relate to sporadic residential physical regimes. More recent IP physical activities might have been variable in nature as is reflected in the intermediate histology data. Confounding factors, including dietary and environmental, cannot be excluded.

Australian Research Council (DE190100068); Australian National University

The roles of natural selection and drift in the evolution of modern human pelvic form

PHILIPP MITTEROECKER[1,2], NICOLE D.S. GRUNSTRA[2,3], EKATERINA STANSFIELD[1], LUKAS WALTENBERGER[4] and BARBARA FISCHER[1]

[1]Dept. of Evolutionary Biology, University of Vienna, [2]KLI, Konrad Lorenz Institute for Evolution and Cognition Research, [3]Mammal Collection, Natural History Museum Vienna, [4]Austrian Archaeological Institute, Austrian Academy of Sciences

Many studies addressed whether morphological differences among human populations evolved by natural selection or drift. Historically, the role of adaptation has often been overestimated; today we know that most genetic differences

evolved by drift, and also phenotypic evolution involves random processes, even in the presence of selection. In recent years, the human pelvis has received much attention in this regard. Despite a rich literature on the relevance of pelvic geometry for parturition, support of inner organs and the fetus, locomotion, and thermoregulation, some recent papers claimed that population differences in pelvic form mainly arose by neutral evolution, without considerable natural selection. This view, as well as the underlying approach to correlate morphometric and neutral genetic distances, have been taken up in the literature already. By drawing from evolutionary quantitative genetics, we derive a number of expectations for phenotypic traits under neutral and adaptive evolution in geographically structured environments. Importantly, morphometric distances between populations correlate with geographic and genetic distances also under an adaptive scenario, not only under drift. Based on these models, we analyze published data on pelvic canal diameters and show that pelvic canal shape is more evolutionarily conserved than non-pelvic traits. Nonetheless, pelvic dimensions, especially the width of the pelvic inlet, diverged much more across populations than expected under neutral evolution, as inferred from neutral genetic divergence. Furthermore, average pelvic canal form correlates with minimum and maximum temperature across populations. All these results evidence an important role of natural selection in the evolution of modern pelvic form variation.

This work was supported by the Austrian Science Fund (Lise Meitner grant M-2772-B to E.S. and Elise Richter grant V 826-B to B.F.).

Selection for Obstetric Sufficiency Affects Integration of the True Pelvis Among Females in Anthropoid Primates

ELIZABETH A. MOFFETT

Clinical Anatomy & Osteopathic Principals, Rocky Vista University

Natural selection for obstetric sufficiency impacts the morphology of the true pelvis in primates. It is thought that birth-related selection should maintain obstetric diameters of the birth canal, especially among females in taxa that give birth to neonates that have relatively large cranial dimensions relative to dimensions of the maternal pelvis (i.e., have large cephalopelvic proportions). Traits that are under co-selection for obstetric sufficiency should theoretically be morphologically integrated, maintaining high levels of covariation between such traits. This study examines magnitudes and patterns of morphological integration in the birth canals of anthropoid primates. The study sample comprised 828 primate skeletal specimens, including 4 taxa with large cephalopelvic proportions and 2 taxa with small cephalopelvic proportions. Eigenanalysis is used to determine the magnitude of birth canal integration within each species, and Mantel tests of matrix similarity are used to compare patterns of birth canal integration between species. This study does not find any difference between the magnitudes or patterns of morphological integration between taxa that have large cephalopelvic proportions and those with small proportions. However, among taxa with large cephalopelvic proportions, females do have significantly higher magnitudes of integration in birth canal dimensions, but this is not true in taxa with small cephalopelvic proportions. The results of this study are consistent with previous studies examining pelvic integration in humans, and the results demonstrated here indicate that there is an effect of obstetric selection on integration of the true pelvis, but only on females in taxa with difficult birth.

This research was funded by the Wenner-Gren and Louis B. Leakey Foundations.

Patterns of trauma and violence in a Later Stone Age sample from southern Africa

CALVIN G. MOLE[1,2], VICTORIA E. GIBBON[1] and DEANO D. STYNDER[3]

[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

Trauma and violence are a common occurrence in contemporary life. However, systematic analyses of prevalence and patterns of trauma within the Later Stone Age (LSA) in southern Africa are required. Discrepancies exist between ethnographic sources and case studies regarding the nature of violence in the LSA, indicating a need to better understand theories of violence during the LSA. The aim of this study was to assess trauma in the context of the LSA of southern Africa to clarify temporal and geographic patterns in trauma and violence. Crania and post cranial from 65 adult human skeletons from the University of Cape Town Human Skeletal Repository were analyzed for trauma and assessed for likelihood it was caused by violence over being accidental. Trauma was assessed macroscopically using standard forensic and bioarchaeological analytical methods. Ante- and/or peri-mortem trauma was observed in 36 (55%) individuals ranging from 1-5 lesions per individual. The most frequently affected areas included the lateral portions of the cranial vault (29 individuals), face (14 individuals), upper limbs (6 individuals) and ribs (2 individuals). No significant difference in trauma prevalence was observed in skeletons of coastal origin compared to inland, or between skeletons dated to before or after the arrival of pastoralism in the region. While environmental or accidental aetiologies cannot be entirely ruled out, the location and frequency of traumatic lesions indicate at least a moderate level of violence in the LSA of southern Africa. This study adds to the growing body of work disputing the harmless people hypothesis.

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.

Spina Bifida and Community Health in the Piata Cetatii Collection from 14th-17th Century Transylvania

PRISCILLA B. MOLLARD

Anthropology, The University of Massachusetts Amherst

Spina bifida is a congenital neural tube defect involving incomplete fusion of the sacral vertebrae. Its heritability makes it a valuable diagnostic indicator of kinship in archaeological populations, in which high prevalences are interpreted as meaningful indications of endogamy.

Samples from medieval Hungary show *spina bifida* at frequencies of around 4%, while the anomaly is recorded at 51% in Roman Britain, and 15% in 18th-19th century London. Recent investigations of *spina bifida* in 14th-19th century samples from Eastern Romania correspond to medieval Hungarian frequencies, as would be predicted, with rates of around 4%.

Within this framework, the frequency of *spina bifida* observed in the Piata Cetatii collection, a previously unstudied collection of over 800 burials from 14th-17th century Transylvania, stands out as anomalously high. Current research on the collection suggests frequencies of 60% or higher, with new cases being discovered as research progresses. While this could suggest the kinship/endogamy aspect of *spina bifida*, the collection derives from Nagybanya, one of the most important gold mining towns in medieval Transylvania. Nagybanya attracted diverse groups of laborers from throughout Europe, making genetic isolation an unlikely explanation.

The current project explores an alternate hypothesis for the prevalence of *spina bifida* at Piata Cetatii, with an emphasis on community health impacts of medieval gold mining both inside and outside the mines.

The project is supported by the National Science Foundation, the Fulbright Program, and the University of Massachusetts Amherst.

How can calcaneal shape help us infer locomotor behavior in extinct primates? A 3D geometric morphometric approach

ORIOL MONCLÚS-GONZALO[1], DAVID M. ALBA[1], ANNE-CLAIRE FABRE[2] and JUDIT MARIGÓ[1]

[1]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, [2]Dynamik fur Nature, Museum fur Naturkunde

The calcaneus is among the most useful postcranial elements for inferring the positional behavior of extinct primates, which is key to test hypotheses on the paleobiology and adaptations of this group throughout its evolutionary history. With this aim in mind, we quantitatively assessed the phylogenetic signal embedded in the calcaneus based on a wide sample of extant primates using 3D geometric morphometric techniques. The relationship between calcaneal shape and locomotor repertoire was also examined by means of two-block partial least-squares analyses among calcaneal shape and percentages of locomotor behavior compiled from field studies. Allometric effects on calcaneal shape were also examined using phylogenetic generalized least-squares regressions. Our results show that the phylogenetic signal embedded in the shape of the calcaneus and its articular facets indicate a greater importance of function in determining calcaneal morphology. Our results further confirm that calcaneal morphology is significantly correlated with the locomotor repertoire of extant primates and that different regions of this bone are also informative of primate positional behavior. Finally, as shown by previous studies, our analyses indicate that the shape of the distal calcaneus and the sustentacular facet are influenced by body size allometry. Our results confirm that, despite allometric effects, calcaneal shape is very reliable for predicting the locomotor repertoire of extant primates, even when only particular portions are considered. The latter fact highlights the great potential of fossil calcanei (even if fragmentary) for making paleobiological inferences about the positional repertoire of extinct taxa.

Funded by: MCIN/AEI (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).

A Freeware, Equitable Method of Conducting Dental Topographic Analysis

MATTHEW J. MORLEY and MICHAEL A. BERTHAUME

Department of Mechanical Engineering and Design, London South Bank University

Dental topographic analysis (DTA), a methodology for quantifying dental morphology, has been used to infer diet and food item breakdown mechanisms in primates and other mammals. Mesh preparation is the first step in conducting DTA, where meshes are first decimated then smoothed. These steps often occur in expensive proprietary software (i.e., Avizo/Amira), restricting access to researchers and labs which can afford this software. This study compares DTA metrics from meshes processed using proprietary and freeware methods to investigate the feasibility and comparability of these software. We conduct a sensitivity analysis to determine the effects of decimation/smoothing parameters and algorithms on the resultant DTA metrics. 25 platyrrhine and prosimian lower second molars, spanning five dietary categories, were downloaded from morphosource.org. Four DTA metrics – relief index (RFI), Dirichlet normal energy (DNE), orientation patch count rotated (OPCR) and portion de ciel visible (PCV) – were calculated using freeware methods and compared to published values obtained using proprietary software via paired t-tests. The freeware method giving the closest results to the proprietary method showed no significant differences in RFI, DNE or OPCR ($0.396 \leq p$) but a significant difference in PCV ($p < e\text{-}6$), although mean percentage differences in PCV were small (1.43%). We conclude that freeware mesh preparation methods for DTA can provide comparable results to established proprietary methods, and describe a freeware method producing comparable results to the proprietary method which makes DTA accessible to all researchers.

Molar sharpness maintained with wear in the early anthropoids *Apidium* and *Aegyptopithecus*

PAUL E. MORSE[1,2], JAMES D. PAMPUSH[3,4] and RICHARD F. KAY[1,5]

[1]Evolutionary Anthropology, Duke University, [2]Florida Museum of Natural History, University of Florida, [3]Exercise Science, High Point University, [4]Physician Assistant Studies, High Point University, [5]Earth and Climate Sciences, Nicholas School of the Environment, Duke University

The early Oligocene fossil record from the Fayum Depression, Egypt, includes well-documented taxa such as *Apidium phiomense* and *Aegyptopithecus zeuxis*, supported in phylogenetic analyses as a stem anthropoid and stem catarrhine respectively. The dental morphology of these species predates the first appearance of the distinctive cercopithecoid 'bilophodont' pattern and may represent the ancestral anthropoid dental condition. How this architecture functionally interacts with tooth wear remains understudied, as comparing variably worn teeth has proved methodologically challenging. Dental topography overcomes this by quantifying properties of the continuous tooth surface such as occlusal sharpness, expressed in the measurement Dirichlet normal energy (DNE). Studies measuring change in DNE across series of variably worn teeth have found that the platyrrhines *Ateles* and *Plecturocebus* (both frugivores) maintain molar sharpness with wear, while *Alouatta* (a folivore) increases sharpness with wear. We measured DNE on digital surfaces of variably worn M_2s derived from µCT scans of *Apidium* (N=14) and *Aegyptopithecus* (N=11). Due to differences in enamel thickness, wear was qualitatively classified as light (minimal wear on all cusps and crests), moderate (cusp and crest height reduced but still distinguishable), or heavy (cusps and crests no longer distinct, substantial dentin exposure). Analyses of variance of DNE from the convex portions of the tooth crowns within each taxon were insignificant (*Apidium*: p=0.10; *Aegyptopithecus*: p=0.15), indicating occlusal sharpness is maintained with wear. These results parallel the trend exhibited by extant platyrrhine frugivores, indicating that the specializations exhibited by folivorous *Alouatta*—and potentially bilophodont cercopithecoids—are unlikely to characterize early anthropoids.

This research was supported by NSF BCS-2018769 to R.F. Kay, BCS-2018779 to J.D. Pampush, and DBI-1458192 to G.F. Gunnell, A.D. Yoder, R.F. Kay, and D.M. Boyer.

Elastic energy contribution of the hip joint capsular ligaments to human walking mechanics

HAYDEN MOSES[1], MADISON BERG[2] and MATTHEW C. O'NEILL[2]

[1]College of Medicine, Midwestern University, [2]Department of Anatomy, Midwestern University

Human walking involves the use of elastic mechanisms that store and release joint power during a stride at minimal metabolic cost. Inverse dynamics analyses suggest that the hip joint is a potential site of elastic energy storage and release, but the specific tissues involved remain unclear. Here, we test the hypothesis that the hip joint capsular ligaments store and release elastic strain energy over a walking stride and compare those results to estimated strain patterns in bipedal chimpanzees.

Marker data from humans (N=3) and bipedal chimpanzees (N=3) walking at matched dimensionless and dimensional speeds were integrated with three-dimensional musculoskeletal models that included ischiofemoral, pubofemoral and iliofemoral ligaments. Inverse kinematics were used to compute ligament strain patterns over a full walking stride in each species. The known material properties of human hip joint capsular ligaments were used to calculate the instantaneous force, elastic work and power in a human walking stride.

In both species, the strain patterns were distinct among the three hip ligaments. In human walking, the iliofemoral ligament exhibited the largest strains, and had the highest peak stress, force and power. Initial estimates suggest that the hip joint capsular ligaments contribute about 20% of the hip joint positive power to the second double-support period and limb swing. In contrast, the strain in the iliofemoral ligament in bipedal chimpanzees was quite small. Our results indicate that the hip joint capsular ligaments make an underappreciated elastic contribution to human walking, one that is likely evolved within the hominin lineage.

NSF BCS 0935321 and 2018436

ABSTRACTS

Cranial sex estimation with non-traditional linear measurement: A geometric morphometric approach

BENJAMIN H. MOSS

Department of Geography and Anthropology, Louisiana State University

Geometric morphometrics (GM) are criticized for their lack of utility in field studies. This study shows the use of GM for sex estimation and, in turn, how GM can be applied for archaeological and forensic anthropology field work where bulky and expensive equipment cannot be used. GM were used to record 40 landmark data points on 100 human crania (50 M, 50 F) of reported White affiliation from a contemporary southeastern Texas sample, and 780 linear measurements were calculated from all combinations of paired interlandmark distances. Correlations between measurements and centroid size were computed, and 43 measurements that had a correlation greater than 0.85 were selected for stepwise discriminant analysis. Independent measurements were run through discriminant analysis to estimate sex, and 34 individual estimators with classifications above 80% were selected for stepwise discriminant analysis. Results of both discriminant analyses separately produced classification rates of 90% accuracy with males classifying better than females in both analyses. Results suggest that non-traditional linear measurements such as Frontomalar Temporale Right – Condylar Foramen Left are better estimators of sex than sagittal or bilateral measurements (e.g, maximum cranial length, biauricular breadth). The higher classifying measurements were typically found between the face and cranial vault and often obliquely crossed the midsagittal plane. GM provide a useful means of increasing sex estimation accuracy through the analysis of large numbers of measurements, as well as identifying nontraditional measurements that can be taken with calipers in the field and that have higher classification rates than traditional measurements.

Funding provided by the David and Sally Jackman Anthropology Endowment, Nancy J. Berner Student Research Support Fund, and the Torrence and Wyvonne Townsend Innovation Fund, Wichita State University.

Effects of a novel food on female reproductive parameters in wild olive baboons (*P. anubis*)

CORINNA A. MOST[1,2], MONICA L. WAKEFIELD[2,3], DAVID MUIRURI[2] and SHIRLEY C. STRUM[3,4]

[1]Department of Ecology, Evolution, and Organismal Biology, Iowa State University, [2]Uaso Ngiro Baboon Project, Kenya, [3]Department of Sociology, Anthropology, and Philosophy, Northern Kentucky University, [4]Department of Anthropology, University of California San Diego

Female reproduction is influenced by a female's growth rates and general condition, which result from female age, food availability, and amount of surplus energy. Here we present long-term data collected at the Uaso Ngiro Baboon Project (UNBP) on the effects of a novel food, the highly invasive prickly pear cactus *Opuntia stricta*, on the reproductive parameters of female olive baboons (*Papio anubis*). *O. stricta* invaded the study troop's home range from the east beginning in 2005 and slowly became the most frequently consumed succulent and food after grasses and herbs: between 2007 and 2016, *O. stricta* comprised between 22-30% of these baboons' diet. The year-round availability of this calorie-rich food improved female body condition, leading to faster growth and reproduction. Between 2008 and 2016 there was a significant reduction in mean interbirth interval length from 650 to 527 days (n=93, t=-2.68, p=0.01). Age at menarche and first birth also declined from a mean of 1770 and 2532 days in 2008 respectively, to 1731 and 2301 in 2016 (age at menarche: n=29, t=-1.981, p=0.039; age at first birth: n=25, t=-2.205, p=0.044). The spread of *O. stricta* has thus led to a natural experiment demonstrating the link between food availability, female growth, and reproduction in olive baboons. By documenting these animals' responses to ecological change, this research provides valuable insights into the relationship between phenotype, ecology, and evolutionary fitness.

This research was funded between 2005-2016 by the African Conservation Centre, Kenya, ACC-US and DGIS (Dutch Government).

The role of Meckel's cartilage in mandibular development

SUSAN M. MOTCH PERRINE[1], KAZUHIKO KAWASAKI[1], EMILY L. DURHAM[1], HAO ZHENG[2], DANNY Z. CHEN[2], ETHYLIN WANG JABS[3], MENG WU[3] and JOAN T. RICHTSMEIER[1]

[1]Department of Anthropology, Pennsylvania State University, [2]Department of Computer Science and Engineering, University of Notre Dame, [3]Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai

The current paradigm of mandibular development assumes Meckel's cartilage (MC) as a scaffold for mandibular development. MC contributes to the symphysis, malleus, and incus, and the intermediate portion is thought to function as a template for intramembranous mineralization of the mandible. MC development is therefore crucial to shape variation across primate mandibles and to evolution of the uniquely human chin. When *Sox9*, a transcription factor essential in endochondral ossification, is conditionally inactivated in cranial neural crest cells (CNCC) in mice, CNCC-derived cartilages and endochondral bones are absent. However, a small, misshapen mandible develops intramembranously refuting the traditional view of MC as a template for mandibular form and generating new questions. We crossed *Sox9fl/+* and *Wnt1*-Cre2 mice creating a conditional heterozygous inactivation model of attenuated MC growth and segmented MC from PTA-enhanced (PTAe) µCT images (resolution of 4-5 µm) of *Sox9fl/+;Wnt1-Cre2* (N=5) and typically developing littermates (*Sox9fl/+*; N=4) at E14.5. MCs of *Sox9fl/+;Wnt1-Cre2* mice are reduced in length and volume relative to *Sox9fl/+* mice, but widths at the symphysis and proximal end are unchanged. Staining of 8 µm sections of *Sox9fl/+;Wnt1-Cre2* embryos with alcian blue and nuclear fast red shows two separate MC sections, validating a gap (~0.88 mm) observed in PTAe µCT images separating MC into two parts. Histomorphometry reveals increased chondrocyte size in *Sox9fl/+;Wnt1-Cre2* mice, suggesting increased hypertrophy. We are investigating the transcriptome and fate of chondrocytes of MC's intermediate region using spatial transcriptomics and cell lineage tracing to illuminate the potential role of MC perichondrial and mandible mineralization.

This work is funded in part by NICDR grants R01DE027677 and R01DE029832-01A1.

Incorporating Emerging Insights on Psychosocial Stress into Bioarchaeology

REBECCA V. MOUNTAIN[1], CAIT B. MCPHERSON[2,3] and JORDAN A. WILSON[4]

[1]Center for Molecular Medicine, Maine Medical Center Research Institute, [2]School of Anthropology, University of Arizona, [3]Arizona State Museum, [4]Department of History, Georgetown University

Biomarkers of non-specific physiological stress are traditional components of bioarchaeological research. Evidence of stress in the form of enamel defects, diaphyseal stunting, and porotic lesions have typically been interpreted as evidence of malnutrition or disease and are commonly used in individual or population-level assessments of "health". However, recent studies in the fields of psychiatry, neurobiology, dentistry, and others suggest that exposure to psychosocial stress (recurring or sustained exposure to adverse social conditions or negative psychological responses to social conditions) may also produce artifacts in hard tissue via complex interactions with biocultural processes. Psychosocial stress may have profound effects on measures of health and wellbeing across the life course, particularly among marginalized groups or in non-neurotypical individuals, and it is likely that exposure to psychosocial stress shaped the experiences of past peoples. For these reasons, it is essential that we consider the impact of psychosocial stress on the lived experiences of archaeological populations, particularly as it relates to health inequities. Here, we examine recent advances in biomarkers of psychosocial stress in hard tissue, and the applicability of these biomarkers to bioarchaeological research. In addition, we suggest avenues for incorporating emerging insights from the study of psychosocial stress into skeletal analyses. Methods of identifying and interpreting

evidence of psychosocial stress in the archaeological record would allow us to better understand the role of stress events in shaping patterns of morbidity and mortality, and facilitate a more holistic understanding of health in the past.

Evaluating the effects of a high fat, low fiber diet on the composition and biodiversity of gut microbiota in wild olive baboons

MADELYN R. MOY[1], LAURA DIAKIW[2] and KATHERINE R. AMATO[1]

[1]Department of Anthropology, Northwestern University, [2]Department of Wildlife Monitoring, Olderkesi Wildlife Conservancy

Increasingly obese populations are raising concerns about humanity's relationship with food. Host diet has proven to influence the composition and function of the gut microbiota (GM), which subsequently interacts with metabolism, the immune system, and brain to affect host health. Thus, evaluating the GM's evolutionary changes may offer insight into how humans can adapt to changing metabolic and energetic needs. A lack of ancient human soft tissue makes nonhuman primates (NHPs) an excellent model to understand the GM's presumed role in initiating changes in human metabolic pathways over time. To improve our understanding of diet's effect on the NHP GM in a comparative context, this study tested the hypothesis that the wild, NHP GM changes in response to a shift from a low fat, high fiber diet (LFHF) to a high fat, lower fiber (HFLF) diet. Fecal samples were collected from seven wild baboon (*Papio anubis*) social groups in Rwanda's Akagera National Park consuming three diet types: wild (LFHF), limited garbage input (partial HFLF), and unlimited garbage input (HFLF). 16s rRNA sequencing indicate significant GM composition differences across diet groups (weighted UniFrac: Psuedo $F_{2,98} = 7.5$, $r^2 = 0.13$, $p < 0.001$). Only baboons consuming unlimited garbage had lower GM diversity than baboons consuming a wild diet (Shannon: $F_{1,89} = 42.1$, $p < 0.001$), suggesting a diet threshold past which the GM shifts and that low amounts of HFLF foods may not affect. Moving forward, we will compare these data to data from humans and other NHPs consuming HFLF diets.

Sex differences in aggression and status competition in Kanyawara chimpanzees

MARTIN N. MULLER[1], MELISSA EMERY THOMPSON[1], DREW K. ENIGK[1], ZARIN P. MACHANDA[2], EMILY OTALI[3], KRISTIN H. SABBI[2] and RICHARD W. WRANGHAM[4]

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

Across primates, both males and females gain fitness benefits from high rank. In chimpanzees, rank confers increased mating success on males, who engage in costly forms of status competition that include elaborate threat displays and fierce contact aggression. Dominant females enjoy increased access to food and show higher reproductive rates, but little is known about how they acquire and maintain rank. We used long-term data on wild chimpanzees to compare patterns of aggression and rank acquisition between the sexes. Our dataset included >50,000 incidents of aggression observed between 2005 and 2019 in the Kanyawara community, Kibale National Park, Uganda. Males were more aggressive than females throughout adulthood, with prime males showing rates an order of magnitude higher than females. Females rarely formed targeted coalitions, but in males these were associated with both increased rank and higher copulation rates. Male rank and aggression were highly correlated throughout the life course, peaking around age 24, then exhibiting a steady decline. By contrast, females showed no overall relationship between rank and aggression, increased their rank with age, and maintained uniform levels of aggression across most of adulthood. The exception was a peak in aggression during late adolescence and early adulthood (around ages 12-20), which correlated with rank across the adult life course. This suggests that females who were aggressive early in life achieved higher rank but didn't rely on aggression to maintain rank in the same way that males did. Aggression in parous females may be constrained by the vulnerability of dependent infants.

This research was supported by National Science Foundation grants BCS-0849380, BCS 1355014 and IOS-LTREB1052693, NIH grants AI058715 and R01-AG049395, Harvard University, University of New Mexico, and the Leakey Foundation.

Relating Status to Access to Healthcare in Pre-Contact Peru During the Middle and Late Horizon Periods

SAMANTHA MK. MURPHY

Anthroplogy, University of Colorado Denver

Competition for resources has always been crucial to the study of past populations, and while not always included in these studies, access to healthcare should be considered as recourse because it can be vital to the survival of an individual. Resources are normally limited in quality and quantity to the high-status members of the community and if healthcare is considered a resource it will not be available to all. Pre-contact Peru offers an excellent case study as there were complex societies that were highly stratified with limited social mobility, along with advanced medical and surgical practices. By analyzing data from several skeletal research collections for trauma and surgical intervention, access to healthcare was assessed. An attempt was made to determine status based on grave good analysis, however many of these skeletal collections have become separated from initial burial records and therefore have minimal burial context. In an attempt to counter this nutritional markers were used to assess health over time, assuming those of higher status would have better overall health. Early results suggest that most members of the community suffered some kind of trauma over the course of their lifetime and recovered. Access to and quality of surgical intervention do not appear to be restricted based on age, gender or status. This suggests that healthcare was highly accessible and was not a restricted resource as expected. This new research not only assesses responses to disease and trauma in the past, but how communities value different resources and other community members.

Support: University of Colorado Denver Department of Anthropology, Denver Colorado

Pinpointing the timing of impact loading in young adult females: Insights from pQCT-derived tibial cortical and trabecular structure and density

ALISON A. MURRAY[1] and MARTA C. ERLANDSON[2]

[1]Department of Anthropology, University of Victoria, [2]College of Kinesiology, University of Saskatchewan

Though relationships between limb bone structure and mechanical loading have provided fantastic opportunities for understanding the lives of prehistoric adults, the behaviours of children and adolescents in the past, as well as age-related changes in behaviours across the life course, are comparatively poorly understood. The aim of our work was to determine the extent to which *adult* tibial structural and/or densitometric properties retain information about childhood/adolescent loading, through assessing relationships between cortical and trabecular bone parameters and the timing of impact loading relative to menarche in premenopausal adult females. Peripheral quantitative computed tomography (pQCT) was used to quantify geometric and densitometric parameters from the proximal tibial diaphysis (66% location) and distal epiphysis (4% location) among 81 young adult female controls and athletes aged 19-33 years, grouped according to intensity of impact loading both pre- and post-menarche. ANCOVA was used to compare properties among the groups adjusted for age, stature, and body mass. Groups with any pre-menarcheal impact loading exhibited significantly elevated tibial diaphyseal cortical bone size and strength properties relative to groups with no pre-menarcheal loading, regardless of post-menarcheal loading history. In contrast, groups with recent post-menarcheal loading exhibited significantly elevated distal trabecular volumetric bone mineral density relative to groups with none, regardless

of pre-menarcheal impact loading history. In combination, tibial diaphyseal cortical bone and epiphyseal trabecular bone parameters identified differences in the timing of impact loading relative to menarche in premenopausal adult females. This whole-bone approach has potential to more accurately reconstruct lifetime loading histories from adult limb bones.

The research leading to these results has received funding from the European Research Council under the European Union's Seventh Framework Programme (FP/2007-2013)/ERC Grant Agreement n.617627.

Primate gait diversity: Comparing quadrupedal kinematics of lemurids in free-ranging and laboratory environments

LYDIA C. MYERS[1], ALLISON MCNAMARA[1], NOAH T. DUNHAM[2], TAYLOR PHELPS[3], JESSE W. YOUNG[3], TOBIN HIERONYMUS[3] and LIZA J. SHAPIRO[1]

[1]Department of Anthropology, University of Texas at Austin, [2]Department of Conservation and Science, Cleveland Metroparks Zoo, [3]Department of Anatomy and Neurobiology, Northeast Ohio Medical University

Laboratory studies are valuable for testing hypotheses related to the biomechanics and evolution of primate quadrupedal gait but may not fully reflect primate gait diversity in a natural habitat. We filmed quadrupedal walking of three free-ranging lemurids (*Eulemur flavifrons, Eulemur mongoz, Lemur catta*) at the Duke Lemur Center. We quantified the diameter and orientation of locomotor substrates using remote sensors and tested for the effects of substrate variation on gait kinematics (N = 117 strides). We then compared the results to published data on congeneric lemurids filmed in a laboratory setting. Consistent with data reported for lemurids filmed in laboratory settings, free-ranging lemurids preferred diagonal sequence gaits on all substrates, adjusted duty factor in response to substrate orientation, increased walking speed on inclined substrates, and did not adjust duty factor or limb phase in response to substrate diameter. Free-ranging lemurids did not significantly adjust limb phase in response to substrate orientation, though we lack comparable data on lemurids filmed in a laboratory setting. The consistency of gait type and limb phase across substrate types accords with our previous comparisons of wild versus laboratory platyrrhines, as does our finding that free-ranging lemurids use higher duty factors than those in laboratory settings, suggesting slower walking speeds in natural habitats. Future research will extend this analysis to strepsirrhines in their native ranges in Madagascar, where we expect increased variation in both substrate complexity and kinematic response.

Supported by NSF BCS-1921135, BCS-1921314, BCS-1640552 and BCS-1640453.

Oral pathologies of late Holocene populations from Volta Grande do Rio Xingu, Amazonia, Brazil (2,240 – 248 years BP)

LETÍCIA M. MÜLLER[1,2], HILTON P. SILVA[1] and RENATO KIPNIS[2]

[1]Programa de Pós Graduação em Antropologia, Universidade Federal do Pará - Brazil, [2]Archeology, Scientia Consultoria Científica

Archaeological studies based on material culture in the Amazon suggest that the economy of late indigenous groups was centred on consumption of cultivated plants complemented by gathering, fishing and hunting of wild foods. However, the Amazon forest covers a very vast area, with different phytosociology compositions and indigenous societies. It is hypothesized that the cultural responses and practices of different groups to the daily dietary needs be different, and different choices will produce different signatures on the teeth and health of these populations. In this study we approach the dietary patterns through bioarchaeology, with direct observations on the oral pathologies of human remains exhumed in the region of Volta Grande do Rio Xingu (Amazonia, Brazil), during the late Holocene (between 2,240 and 248 BP). A total of 114 teeth and, when present, mandibles, and maxillae of 13 individuals exhumed from five archaeological sites were analysed. Despite the problems with poor preservation of organic material in a Tropical Forest environment, it was possible to observe a high percentage of caries, calculus, and tooth wear. These results are compared with archaeological studies of the Maracá population (ca. 500 years BP) and with data on oral health from recently contacted indigenous groups from the second half of the 20th century. Results indicate that different eating habits can exist within the same type of subsistence pattern; and that different modes of food processing and consumption can trigger greater or lesser occurrence of oral pathologies.

Lessons from the coywolf (*Canis latrans* var.): patterns of mandibular integration in hybrid canids and its implications for the hominin fossil record

LAVANIA NAGENDRAN[1] and LAUREN SCHROEDER[2,3,4]

[1]Department of Anthropology, University of Toronto, Toronto, ON, Canada, [2]Human Evolution Research Institute, University of Cape Town, Rondebosch, South Africa, [3]Department of Anthropology, University of Toronto, Mississauga, ON, Canada, [4]Department of Natural History, Royal Ontario Museum, Toronto, ON, Canada

Morphological integration allows for an organism's form to function as a whole through the coordinated variation of related developmentally or functionally traits. Previous studies of hybrid mammals suggest that hybridization reduces constraint on integration resulting in greater morphological variability, and potentially more evolvable phenotypes. The hybrid eastern coyote and their parental taxa act as ideal models to further investigate this relationship since they naturally occur in the wild. Seventeen landmarks were collected from 3D surface scans of canid right hemi-mandibles (*Canis lupus*, n=30; *Canis latrans*, n=30; *Canis latrans* var., n=30). From the collected landmarks, interlandmark distances were extracted and a resampling technique was applied to control for the number of traits compared to number of specimens. Interlandmark distances were mean-standardized, and distributions of integration coefficient of variation (ICV) values were retrieved. Levels of integration between and within groups were assessed with the Mann-Whitney U test. Results indicate that the hybrid sample expresses an overall reduction of morphological integration compared to wolves in all modules (ramus, corpus, and whole mandible), and a slightly higher level of integration compared to coyotes. Both the corpus and ramus modules depicted significantly lower levels of integration than the whole mandible in all taxa. Overall, in canid mandibles, hybridization seems to reduce integration. A reduction in levels of integration in multiple mammalian taxa may reveal a consistent pattern which could have been expressed by early hybrid hominins as well. This could have been a catalyst for novel variation to evolve during hybridization episodes in human evolution.

Funded by the Connaught Fund New Researcher Award, and a Discovery Grant from the Natural Sciences and Engineering Research Council of Canada

Examining the Influence of Psychosocial Stress on Telomere Length in NCAA Collegiate Swimmers

ANAMIKA NANDA[1] and ROBERT L. TENNYSON[1,2]

[1]Department of Anthropology, University of Washington, [2]Center for Studies of Demography and Ecology, University of Washington

Regular physical activity protects against cellular aging, but a recent study found shorter telomere length (TL) in professional swimmers compared to less active controls. Shorter TL is associated with increased cellular senescence and functional decline with age, suggesting swimmers may be at increased risk for age-related morbidity. Previous studies reported competitive swimmers face high levels of psychosocial stress, which, in turn, is posited to accelerate TL shortening. We hypothesize that competitive collegiate swimmers experience increased psychosocial stress, leading them to have shorter TL despite their active lifestyles.

We are conducting a mixed-methods study to examine whether TL differs between Division-1 and Division-3 NCAA swimmers (N=20 respectively) and their non-athlete counterparts (N=20) and if differences in TL is associated with

psychosocial stress (Total N=60). Collegiate swimmers face a unique set of stressors to perform for scholarships and professional opportunities while simultaneously continuing their responsibilities as students. Accordingly, we are measuring overall psychosocial stress (Cohen's Perceived Stress Scale; PSS) to compare swimmers and non-athletes as well as sports-related psychosocial stress (The Student Athletes' Motivation toward Sports and Academics Questionnaire; SAMSAQ) to compare D-1 to D-3 swimmers. Further, we are conducting semi-structured qualitative interviews to better contextualize how student-athletes perceive how the psychosocial stress they experience impacts their lives and performance.

We expect swimmers to report higher levels of overall psychosocial stress (PSS) and have shorter TL compared to non-athletes. Further, we expect that D-1 swimmers will report higher levels of psychosocial stress (SAMSAQ) and have shorter TL compared to D-3 swimmers.

Effects of forest loss on lemur density in the Kianjavato forest fragments, Southeast Madagascar

PAMELA R. NARVÁEZ-TORRES[1], NICOLA K. GUTHRIE[1], TYPHENN A. BRICHIERI-COLOMBI[2], CRESSANT P. RAZAFINDRAVELO[3], ZACHARY S. JACOBSON[1], FREDO TERA[3], DANIEL RAFIDIMANANA[4], HARISOA M. ANDRIANANTENAINA[4], ELINAH Z. RAHASIVELO[5], MELODY A. PETERSEN[1], HASINALA RAMANGASON[1], LEA RANDALL[2], JANA M. MCPHERSON[2], AXEL MOEHRENSCHLAGER[2], SHEILA M. HOLMES[6], EDWARD E. LOUIS[3,7] and STEIG E. JOHNSON[1]

[1]Department of Anthropology and Archaeology, University of Calgary, [2]Centre for Conservation Research, Calgary Zoological Society, [3]Madagascar Biodiversity Partnership, [4]Faculté des Sciences, Université d'Antananarivo, [5]Faculté des Sciences, de Technologies et de l'Environnement, Université de Mahajanga, [6]Department of Wildlife, Fish and Environmental Studies, Swedish University of Agricultural Sciences, [7]Conservation Genetics Department, Omaha's Henry Doorly Zoo and Aquarium

Madagascar, a globally important biodiversity hotspot with high levels of endemic flora and fauna, has lost over 80% of its native vegetation cover due to slash-and-burn agriculture, selective logging, and burning for pastureland. Madagascar's lemurs are strongly affected by these land-use practices because of their high dependence on forest habitats. We explored the relationship between forest cover change and the densities of lemur species over a five-year period in Kianjavato, Madagascar. We surveyed day-active lemur species on 35 line-transects from 2015 to 2019 and nocturnal species on 21 transects from 2015 to 2016. During this time, we registered four day-active and three nocturnal species and calculated annual densities for each. To quantify how forest cover changed between 2015 and 2019, we generated a land use/land cover (LULC) map from Sentinel-2 imagery using supervised classification for each year. The density of three of the day-active lemur species decreased considerably over the five-year period. *Eulemur rubriventer* population decreased gradually from 1.59 (±0.88) to 0.47 (±0.22) individuals/km^2, *E. rufifrons* from 6.16 (±1.78) to 2.33 (±0.98) individuals/ km^2, and *Varecia variegata* from 7.40 (±2.40) to 1.61 (±0.81) individuals/ km^2. We did not observe a clear trend in the nocturnal species' populations. Using LULC change detection, we found that forest cover also decreased each year. As all lemur species in Kianjavato are threatened with extinction, obtaining reliable density estimates, including changes through time, such as we provide here, are necessary to inform ongoing conservation practices.

This study was supported by the Natural Sciences and Engineering Research Council of Canada, Calgary Zoological Society, Primate Conservation Inc., and Re:wild.

Covariation between cranial vault thickness and endocast shape in present-day humans and Neanderthals

SELIM NATAHI, SIMON NEUBAUER, ZEWDI J. TSEGAI, JEAN-JACQUES HUBLIN and PHILIPP GUNZ

Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

While cranial vault thickness (CVT) is often used to discuss the taxonomic assignment of fossil specimens within the human lineage, the evolutionary processes accounting for its variation remain elusive. Numerous hypotheses have been proposed to interpret CVT arrangements, whether they relate to systemic, metabolic, biomechanical, allometric factors and/or to brain evolution. As they reach similar brain volumes via different developmental trajectories, comparing the CVT of present-day humans and Neanderthals allow us to evaluate whether brain development is likely to affect CVT. Here we document the CVT arrangements among these two groups and we test if differences are likely to be explained by variation in brain shape.

We have used a sample of computed-tomographic scans consisting of 75 present-day humans and 6 Neanderthal adult individuals. Their respective endocranial shapes were quantified using landmarks and semilandmarks-based geometric morphometrics. The CVT was calculated at different semilandmarks positions and the cubic root of the endocranial volume was used for standardizing size in each measurement. Finally, the covariation between the shape of the endocast and CVT measurements was subsequently explored via two-block partial least squares analysis.

Our results demonstrate that Neanderthals tend to display a thicker cranial vault, but this variation is still comprised within the range of present-day humans. The distinctive globular shape of present-day humans is characterized by thinner parietal walls. These results suggest that the differences in brain development in these two groups partly explain their respective CVT arrangements.

This work was funded by the Fyssen Foundation and the Max Planck Society

Forest fire smoke exposure increases oxidative stress and inflammation in a wild great ape

DANIEL J. NAUMENKO[1,2], CAITLIN A. O'CONNELL[3,4], LAURA KIELY[5], DOMINICK V. SPRACKLEN[6], REBECCA S.A. BRITTAIN[4,7], SRI SUCI UTAMI ATMOKO[8] and ERIN R. VOGEL[4,7]

[1]Department of Anthropology, University of Colorado Boulder, [2]Institute of Behavioral Science, University of Colorado Boulder, [3]Department of Anthropology, University of Pennsylvania, [4]Department of Anthropology, Rutgers, the State University of New Jersey, [5]Department of Chemical and Environmental Engineering, University of California Riverside, [6]School of Earth and Environment, University of Leeds, [7]Center for Human Evolutionary Studies, Rutgers, the State University of New Jersey, [8]Fakultas Biologi, Universitas Nasional

Annual peat-swamp forest fires in Indonesia emit large amounts of hazardous smoke with deleterious effects for local human populations. However, there is a dearth of evidence on how this smoke impacts the health of local flora and fauna. We examine if exposure to particulate matter ($PM_{2.5}$) released from these fires induces oxidative stress and inflammation in wild Bornean orangutans. Combining urinary biomarkers (2009-2016) of oxidative damage (8-OHdG, N=384), antioxidants (TAC, N=206), and intracellular inflammation (neopterin, N=518) with a satellite-based measure of daily $PM_{2.5}$ emissions adjusted for peat depth and moisture (FINNpeatSM, 2004-2019), we test whether accumulated exposure to smoke results in increased oxidative stress and inflammation. Using a generalized additive mixed model, we found that oxidative damage significantly increased with increasing cumulative exposure to $PM_{2.5}$ up to 9 weeks (edf=3.88, p<0.0001), with antioxidants increasing in tandem, likely as a defense against oxidation (edf=1, p<0.001). However, neopterin did not predict oxidative damage, accounting for smoke and antioxidants in the model (full model R^2_{adj}=0.37). $PM_{2.5}$ alone significantly explained 7% of oxidative damage despite an effective antioxidant defense (edf=4.5, p<0.001). Neopterin alone was found to increase with increasing $PM_{2.5}$ exposure (edf=1.96, p<0.0001) though only 4% of variation in inflammation was explained by particulate matter. These results demonstrate, for the

first time, that smoke exposure from annual peat-swamp fires results in negative health impacts via oxidative stress and inflammation for wild orangutans and highlights the need for preventative measures to protect this critically endangered species and their ecosystems.

This research was funded by USAID (APS-497-11-000001), L.S.B Leakey Foundation, National Science Foundation (BCS-0643122), Rutgers University (E.R.V), Center for Human Evolutionary Studies (E.R.V./D.J.N.), and NERC studentship (NE/L002574/1 to L.K.).

Time-resolved trace element variations in dental enamel of contemporary children with known dietary history through Laser-Based Mass Spectrometry (LA-ICPMS): implications for ancient dietary reconstructions

ALESSIA NAVA[1], FEDERICO LUGLI[2,3], PATRICK MAHONEY[1], GINA MCFARLANE[1], LUCA BONDIOLI[2], STEFANO BENAZZI[2], CHRISTOPHER M. DEAN[4] and WOLFGANG MÜLLER[5,6]

[1]School of Anthropology and Conservation, University of Kent, [2]Department of Cultural Heritage, University of Bologna, [3]Department of Chemical and Geological Sciences, University of Modena and Reggio Emilia, [4]Department of Earth Sciences, Natural History Museum, [5]Institute of Geosciences, Goethe University, [6]Frankfurt Isotope and Element Research Center (FIERCE), Goethe University

Human growth and development, from the earliest phases of ontogenesis, is shaped by dietary behaviour – including that of the mother during pregnancy. Understanding the time and mode of dietary transitions in early life in past human populations is therefore pivotal in disentangling biocultural adaptations through time and has been the subject of a number of high-profile recent studies. Early life changes in diet are identifiable by time-resolved variations of trace elemental compositions in dental enamel using mainly strontium-calcium (Sr/Ca) and barium-calcium (Ba/Ca) ratios. Little is known about the way that Ba is incorporated into forming enamel, relative to Sr, or the way other trace elements relate to maternal/infant diet.

This study presents the histologically-controlled spatial distribution of dietary-related trace elements along the enamel-dentine junction of 20 naturally exfoliated deciduous teeth of contemporary infants with well known dietary and biological life history. Results show that it is possible to trace back at the highest temporal resolution (sub-weekly), the major dietary events during infancy. Different teeth from the same individual consistently report the same dietary history. Using Sr/Ca ratios, breastfeeding vs formula feeding and the onset of weaning are easily detectable as changes in the elemental profile slope.

The Royal Society and The Leverhulme Trust (PM, RG110435, RPG-2018-226), Marie Skłodowska-Curie (AN, H2020-MSCA-IF-2018-842812-WEAN-IT), ERC Horizon 2020 (SB, 724046-SUCCESS), Heraeus Foundation and Deutsche Forschungsgemeinschaft (WM, DFG-INST-161/921-1, INST-161/923-1)

Untangling Carbohydrate and Protein Source Contributions in the Diets of a Neotropical Foraging-to-Farming Population using Carbon Stable Isotope Analysis of Amino Acids

NADIA C. NEFF[1,3], KEITH M. PRUFER[1,3], GERALDINE BUSQUETS-VASS[2,3,4], ERIN E. RAY[1,3], EMMA ELLIOTT SMITH[5], DOUGLAS J. KENNETT[6] and SETH D. NEWSOME[2,3]

[1]Anthropology, University of New Mexico, [2]Biology, University of New Mexico, [3]Center for Stable Isotopes, University of New Mexico, [4]Centro de Investigación Científica y Educación Superior de Ensenada, Unidad La Paz, [5]Anthropology, Smithsonian Institution, [6]Anthropology, University of California Santa Barbara

The middle-late Holocene in the neotropics saw shifts in environmental conditions, subsistence strategies, and social complexity culminating in agricultural societies. Well-preserved and directly dated human skeletons (n=27) from three sites including two continual-use rockshelters and a civic-ceremonial center following the emergence of inequality span the transition from egalitarian forager-horticulturalists to socially stratified farmer economies in southern Belize. Carbon isotope ($\delta^{13}C$) analysis of amino acids (AA) is a powerful tool that allows researchers to identify source(s) of C_3- or C_4-based proteins and carbohydrates in human diets. We used isotopic discrimination between nonessential-essential AA $\delta^{13}C$ values ($\Delta^{13}C_{NESS\text{-}ESS}$) as a proxy for the relative contributions of C_3 vs. C_4 sources to total ($\delta^{13}C_{NESS}$) diet and the protein ($\delta^{13}C_{ESS}$) portion of diet.

$\Delta^{13}C_{NESS\text{-}ESS}$ suggests protein source similarities with minimal carbohydrate source diversity during the middle Holocene, generally indicating C_3-based diet with nominal individual variation. With the increasing dietary importance of maize (~4.7kybp), carbohydrate sources became highly uniform among individuals while dietary protein varied between C_3- and C_4-based sources, correlating with increased domestic plant use in egalitarian groups as some began incorporating maize-fed animals into their diet. As populations became reliant on farming, dietary variation became stratified with three identifiable groups: those that sourced protein and carbohydrates from a C_4-base (maize-fed animals and maize), those that derived carbohydrates from maize and proteins from C_3 sources (wild animals), and those with similar C_3-based dietary strategies to earlier horticulturalists. These data indicate strong relationships between dietary change and social relations, and economies.

This research is part of an ongoing project investigating human-environmental interactions in the Maya Mountains of Southern Belize and is funded by the National Science Foundation and the Alphawood Foundation.

Viral infection and life history trade-offs in wild chimpanzees

JACOB D. NEGREY[1], MELISSA EMERY THOMPSON[2], KEVIN E. LANGERGRABER[3,4], ZARIN P. MACHANDA[5], JOHN C. MITANI[6], MARTIN N. MULLER[2], EMILY OTALI[7], RACHNA B. REDDY[8], RICHARD W. WRANGHAM[8] and TONY L. GOLDBERG[9]

[1]Department of Pathology, Wake Forest School of Medicine, [2]Department of Anthropology, University of New Mexico, [3]School of Human Evolution and Social Change, Arizona State University, [4]Institute of Human Origins, Arizona State University, [5]Department of Anthropology, Tufts University, [6]Department of Anthropology, University of Michigan, [7]Kibale Chimpanzee Project, Makerere University Biological Field Station, [8]Department of Human Evolutionary Biology, Harvard University, [9]Department of Pathobiological Sciences, University of Wisconsin-Madison

For energetically limited organisms, life history theory predicts trade-offs between reproductive effort and somatic maintenance. Immune investment should therefore vary according to an organism's reproductive strategy and attendant energetic demands. As obligate intracellular parasites, viruses may be especially useful biomarkers for studying life history trade-offs in long-lived organisms such as humans and chimpanzees (*Pan troglodytes*). We conducted a longitudinal study of chimpanzee gastrointestinal viromes at two long-term field sites in Kibale National Park, Uganda. We used metagenomic methods to analyze viromes, which included many poorly characterized viruses, and found considerable variation related to demographic, physiological, and ecological conditions. First, increased viral load (number of viral sequences shed) accompanied explicit episodes of illness. Second, viral richness (number of unique viral species shed) increased with age in males but not females, suggesting that males experience late-life immune consequences for heightened early-life reproductive investment. Third, female reproductive status influenced viral richness, with females shedding more viral species during early lactation, an especially costly reproductive stage, than when cycling or pregnant. Finally, viral richness and load were greater in the study community located nearer to human settlements and with a lower-quality diet, suggesting that local ecological conditions affect chimpanzee physiology and, thus, viral shedding.

These results indicate that patterns of virus shedding are largely consistent with life history theory, making viruses promising biomarkers for investigating physiological trade-offs related to infection.

This research was primarily supported by the National Institutes of Health [Award R01AG049395], with additional support from the Leakey Foundation, National Geographic Society, National Science Foundation, and Wenner-Gren Foundation.

Paleogenomics, pathogens and critical perspectives on infectious disease

ELIZABETH A. NELSON[1], KRYSTAL S. TSOSIE[2] and RICK W. A. SMITH[3]

[1]Anthropology, University of Connecticut, [2]Native BioData Consortium, Eagle Butte, SD, [3]Department of Sociology and Anthropology and Women and Gender Studies, George Mason University

The rapidly advancing field of paleogenomics has brought about an explosion of genomic information, much centered on what human genomes can tell us about the past. However, humans have an immeasurably intertwined evolutionary history with microbes including those that are considered symbiotic and pathogens. As agents of infectious disease, pathogens have shaped human biology, society and history. They have caused epidemics and pandemics, they have led to the stigmatization and "othering" of individuals, they have been weaponized for political and colonial agendas, and they have caused the decimation of populations. Yet, much of what we know about the past has been shaped by colonial expectations of population health and disease, leading to false narratives and an incomplete understanding.

Applied to the study of ancient disease (paleopathology), ancient DNA methods have permitted high-resolution analyses of pathogen evolution and diversity revealing unexpected infectious disease histories and challenged preconceived notions. However, few studies attempt to transcend dominant analytical frameworks and comprehensively analyze and interpret human-pathogen genomic results within biocultural contexts to evaluate factors and structures influencing pathogen emergence, success, and the propagation of health disparities. Paleogenomics is perfectly positioned to provide critical perspectives of infectious disease emergence and evolution by providing complex retrospective views of how large-scale environmental and socio-cultural forces influence pathogen emergence and distribution. This talk discusses what aspects of ancient disease research are obscured by dominant research designs and structure, the promise of genomic based paleopathology as translational and relevant and offer considerations for the field moving forward.

Exploring Juvenile Growth Stunting in Limb Length and Body Proportions

JENNIFER S. NELSON[1], LESLEY HARRINGTON[1], EMILY HOLLAND[2] and HUGO FV. CARDOSO[3]

[1]Department of Anthropology, University of Alberta, [2]Department of Anthropology, Brandon University, [3]Department of Archaeology, Simon Fraser University

Juvenile bone size is a frequently used indicator of growth environment quality during childhood, with changes in length being linked to several biocultural factors related to socioeconomic status. Differentiating between growth stunting and genetically accumulated short stature can be difficult, particularly when analyzing absolute bone lengths in archaeological samples. An alternative approach commonly applied in clinical contexts is the use of body proportions, which might provide a different measure for assessing growth in past populations.

This study explores how growth and biocultural environment quality are differentially captured using these two methods. By comparing how assessments of reduced bone length and changing limb proportions vary in their measures of diminished growth, it is intended that our understanding of juvenile development will be furthered, and choice of methodological approach refined.

Diaphyseal length measurements and limb indices (crural, brachial, intermembral) were calculated for impoverished children (n=56) from the Certosa collection, aged between birth and 11 years. These were compared to Maresh reference data using age and sex-specific z-scores.

Absolute lengths show a significant growth deficit relative to the reference population (mean z-score= -2.43). All limb indices differ significantly ($p<0.01$) from the reference data. Absolute limb length and indices z-scores differ significantly ($p<0.01$).

Although both approaches detect diminished growth in the sample population, the differences in their measures of growth stunting demonstrate that growth quality is not reflected equally. Analysis of limb proportions may help differentiate short stature linked to thermoregulation or generational factors from reduction in size due to poor growth environment quality.

Funding for this project was provided by SSHRC - Social Sciences and Humanities Research Council of Canada

Implications of Univariate Subadult Craniometric Growth Patterns in Biological Anthropology

BRIANA T. NEW[1], CHRISTOPHER A. WOLFE[1], LOUISE K. CORRON[1], KATE SPRADLEY[2] and KYRA E. STULL[1]

[1]Anthropology, University of Nevada, Reno, [2]Anthropology, Texas State University

Small subadult sample sizes often restrict research on modern human cranial variation from the perspective of population differentiation, sexual dimorphism, or ontogenetic variation. Examining the timing of subadult cranial growth trajectories and assessing when maturity is reached for cranial size can assist in improving parameters of the subadult biological profile and estimating the developmental timing of cranial pathologies or defects. This research assessed cranial growth patterns of 26 interlandmark distances (ILD) using a sample of 571 male and female subadults aged from birth to 20 years from the Subadult Virtual Anthropology Database (SVAD).

Multivariate Adaptive Regression Splines (MARS) with 10-fold cross-validation were used to capture the nonlinear growth trajectory of each ILD by sex. Results were evaluated through ontogenetic the life history stages (LHS) of infancy, childhood, juvenile, adolescent, adulthood, as well as three cranial regions (neurocranium, basicranium, splanchnocranium). Overall, growth trajectory timing for males and females is comparable for all cranial regions prior to adolescence but diverges during adolescence and increases in magnitude with age. Differences were identified in the timing of size maturity for the cranial regions: the neurocranium tends to peak in early childhood, the basicranium stabilizes in infancy with a secondary peak during the juvenile/adolescent LHSs, and the splanchnocranium develops consistently through ontogeny before stabilizing around puberty. These results provide a quantifiable examination of cranial growth from a large subadult sample with applications and implications for multiple subfields in biological anthropology.

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

When the cold gets under your skin: The effects and role of brown adipose tissue activity in Samoans

ALEXANDRA NICLOU[1], LUPESINA VESI[2], MARIA ARORAE[2], NEW CALEDONIA NASERI[2], KIMA FAASALELE SAVUSA[2], TAKE NASERI[3], JAMES P. DELANY[4], STEPHEN T. MCGARVEY[5], ANNA C. RIVARA[6], NICOLA L. HAWLEY[6] and CARA OCOBOCK[1,7]

[1]Department of Anthropology, University of Notre Dame, [2]Obesity, Lifestyle and Genetic Adaptations (OLaGA) Study Group, Apia, Samoa, [3]Samoa Ministry of Health, Apia, Samoa, [4]AdventHealth Orlando, Translational Research Institute, [5]International Health Institute & Department of Anthropology, Brown University, [6]Department of Chronic Disease Epidemiology, Yale School of Public Health, [7]Eck Institute for Global Health, University of Notre Dame

Brown adipose tissue (BAT), a heat generating organ associated with glucose disposal, contributes to human cold acclimatization and

adaptation in temperate and cold climate populations. The thermogenic and metabolic effects of BAT in tropical populations, however, are unknown. In this study we inferred BAT activity in adults with obesity in Apia, Samoa (N=61, female: n=38). BAT activity was inferred by simultaneously measuring metabolic rate (MR) and heat dissipation at BAT (supraclavicular area) and non-BAT locations (sternum) at room temperature (avg: 26˚C) and after a 30-minute mild cold exposure (13-16˚C), achieved by pumping water through a cooling garment. MR and heat dissipation were measured using a portable calorimetry unit and thermal imaging camera, respectively. Paired Student T-tests showed that while MR did not change significantly after cooling (P=0.281), heat dissipation measurements in the sternum and supraclavicular area did (both: P<0.001). Unpaired T-tests demonstrated that differences in surface temperatures between exposures were significantly greater at the sternum compared to the supraclavicular area (P<0.001), suggesting greater heat dissipation in BAT locations through BAT activation. Furthermore, fasting glucose levels significantly decreased after cooling (P<0.001), suggesting glucose uptake by BAT upon activation. Despite a blunted MR response, BAT may thus be activated in Samoans during mild cold exposure, possibly contributing to non-shivering thermogenesis in tropical populations. Preliminary evidence of BAT activity in adults with obesity highlights its possible capacity for glucose disposal decreasing the risk of associated metabolic diseases in Samoans and raises questions about the evolution of a potentially cold-adaptive trait in Polynesians.

Support: NSF grant 1945331, The Wenner-Gren Foundation grant 4424030281, Notre Dame Graduate Student Research Award, NIH grant HL140570.

Using ancient DNA to revisit the historical record of Latin America and the Caribbean

MARIA A. NIEVES-COLÓN

Department of Anthropology, University of Minnesota Twin Cities

Ancient DNA (aDNA) directly queries the genetic diversity of ancient and historic human populations. Such data can be used to investigate the experiences of peoples who have been historically marginalized or excluded from the written documentary record. As such, aDNA is especially relevant for understanding the history of the Americas, a region where settler colonial perspectives are overrepresented in the written historical record; often serving as the hegemonic frameworks from which past events are reconstructed and understood. In this talk, I will use two examples to argue that aDNA, when coupled with other lines of evidence, can be an important tool for revisiting Latin American and Caribbean history. First, I will discuss how aDNA and modern genetics research in the Caribbean unsettled historical narratives about the fate of Indigenous Caribbean peoples, their responses to colonization and their relationship with present-day islanders. Second, I will present ongoing pilot research which combines aDNA and bioarcheological approaches to investigate the African Diaspora to Latin America, by reconstructing the lives of enslaved laborers buried in an 18-19th century sugar plantation in coastal Peru (n=30). This community-engaged research project seeks to provide a new perspective towards histories of African captivity and diaspora in Latin America by centering the experiences of African and African-descendant communities in narratives of Peruvian history, heritage, and identity. Overall, this presentation will stress how integrative aDNA research can problematize our understandings of history by constructing more inclusive narratives of the Latin American and Caribbean experience.

This research is supported in part by the University of Minnesota Department of Anthropology Wilford Funds Endowment Award

Positional behavior adaptations in the mammalian cervical spine

ABIGAIL C. NISHIMURA[1], MICHAELA C. WINKELER[2,3] and GABRIELLE A. RUSSO[2]

[1]Interdepartmental Doctoral Program in Anthropological Sciences, Stony Brook University, [2]Department of Anthropology, Stony Brook University, [3]College of Medicine, Albert Einstein College of Medicine

The neck plays an important role in head stability and mobility, and accordingly, cervical vertebrae exhibit adaptations to positional behaviors in mammals. Researchers studying neck and head posture have focused particular attention on cervical vertebral morphology in primates in order to make inferences about fossil hominins. Less research has taken advantage of a broad comparative approach in which other mammalian taxa can be used to evaluate positional behavior adaptations in the neck. Here, we test cervical vertebral functional hypotheses using a comparative mammalian sample of rodents and marsupials (N=34 species) including species with independently-evolved forms of bipedal hopping, i.e., ricochetal locomotion. We quantified and compared C5–T1 vertebral morphology across our sample by segmenting and landmarking individual cervical vertebrae. Five body mass-adjusted linear metrics and one angle were extracted from the landmarks, each having previously proposed links to mobility or muscle force generation. Compared with quadrupedal marsupials, bipedal marsupials had significantly shorter vertebral bodies (craniocaudally) from C5–C7. Compared with non-burrowing rodents, burrowing rodents had significantly shorter C5–C6 vertebral bodies. The only arboreal rodent species in the sample (*Eliurus webbi*) exhibited taller C5 and C6 uncinate processes than all terrestrial rodents. Future analyses will incorporate primate taxa and phylogenetically-informed 3D geometric morphometric analyses. Taken together, the results of this study are of interest to mammalogists as well as paleoanthropologists. This work can help to refine interpretations of hominin cervical vertebral fossils, thereby elucidating the transition to upright bipedalism in the human lineage.

Funding support was provided by the NSF (BCS-1919764) and the Leakey Foundation.

A new distribution area of bushbabies, *Galagoides demidovii* (*Galagidae*, Primates) in Kinshasa, D.R. Congo

JERRY B. NKENKU and JEAN M. MALEKANI

Department of Biology, University of Kinshasa

The biodiversity of the city of Kinshasa is among the least known in primate species. Two species of bushbabies are cited in the geographical area of Kinshasa: Demidoff's Dwarf Galago *Galagoides demidovii* and Thomas's Dwarf Galago *Galagoides thomasi*. Due to the strong extension of urbanization and human pressure, forests are shrinking and research is more oriented towards more wooded areas teeming with the most imposing primate species such as gorillas, chimpanzees, bonobos. Our preliminary study carried out in the CECFOR forest located in the municipality of Mont-Ngafula, in the vicinity of the city of Kinshasa, in the Democratic Republic of Congo in the period from December 2020 to June 2021, revealed the presence of a population of *Galagoides demidovii* hitherto ignored in this area of the city of Kinshasa. In an area of 188 hectares, we counted, during four nights, 30 bushbabies on three line transects of different lengths. Analysis of images taken while exploring the site reveals the probable presence of other galago species. Further research will allow us to verify this hypothesis in the near future.

Sacroiliac Joint Variation in Humans and Non-Human Primates: A Comparative Analysis of Sacroiliac Joint Size Using CT Imagery

ERICA NOBLE and JOHN HAWKS

Department of Anthropology, University of Wisconsin-Madison

The sacroiliac joint (SIJ) serves as the connection between the os coxa and the sacrum. In modern humans, the SIJ articular surface has a larger area than other hominoids, when compared to measures of sacrum size. Modern humans also have a larger SIJ than hominins such as Australopithecus, and it is not clear whether the larger body size of humans explains the entire difference or if there are additional factors that have influenced SIJ size. This study compares SIJ size and form among the living primates to examine the effect of body size and form of locomotion on the joint.

Using computed tomography (CT) scans of 13 species of primates including humans with 9 landmarks along the SIJ, iliac spine, and acetabulum, we compare the size and shape of the SIJ to the rest of the pelvis. The results show that variation in SIJ size in different primate lineages is influenced by both body mass and locomotor pattern. We apply these results to an examination of the SIJ of U.W. 102a-138, a fossil ilium of *Homo naledi* found in the Lesedi Chamber, South Africa, which combines an australopithecine-like ilium and a modern human-like SIJ.

Sicilia al centro: Ancient DNA analysis of key sites from medieval Sicily

IAN T. NOBLE, AURORE MONNEREAU, NATHAN WALES and MARTIN CARVER

BioArCh, Department of Archaeology, University of York

Sicily, a highly contested border zone and staging area for cultural interaction between North Africa, Asia Minor, and Europe was left vulnerable to the expanding Arabic empire following the relocation of the Roman empire's capital to Constantinople, initiating the Byzantine period. While archaeological contexts indicate a cultural mosaic, genetic impacts of these successive conquests remains unclear. By compiling and analyzing genomic data from sites at major port cities Agrigento and Palermo, and San Miceli church in rural Salemi, we contributed to the "Sicily in Transition" (SICTRANSIT) project investigating impacts of imperial colonization on Sicilian people.

EDTA/Proteinase K extraction with silica-based spin columns was used to extract DNA from 10 individuals sourced from three sites in Sicily associated with the medieval period between the 5th – 12th century CE. Individuals 4, 7 (female, male; Salemi), 9, and 10 (sex unknown; Palermo) yielded sufficient coverage for principal component analysis (PCA) and were analyzed using mitochondrial and Y chromosome haplogroups. Only individual 7 returned mitochondrial coverage: haplogroup H, a maternal lineage present in Europe since the last glacial maximum. Individuals 7 and 10 matched Y chromosome haplogroups G2a and J1a, respectively, paternal lineages found across Eurasia, and North Africa. In PCA, individuals showed affinity with populations from Europe, Asia Minor, and North Africa. These preliminary results indicate dynamic systems of genomic diffusion between Sicilian and surrounding geographic populations. Future studies expanding sample size for population-level analyses will expand our understanding of how successive waves of people to the island interacted with previous populations.

European Research Council grant 693600

Preferential routing of C_4 dietary carbon reflected in chimpanzee and baboon $\delta^{13}C$ values

REBECCA S. NOCKERTS[1], DAVID L. FOX[3], ROBERT O'MALLEY[5], DEUS MJUNGU[4], D.ANTHONY COLLINS[4] and MICHAEL L. WILSON[1,2]

[1]Department of Anthropology, University of Minnesota, [2]Department of Ecology, Evolution, and Behavior, University of Minnesota, [3]Department of Earth and Environmental Sciences, University of Minnesota, [4]Gombe Stream Research Center, Jane Goodall Institute, [5]DoSER, AAAS

Tissue $\delta^{13}C$ values provide important measures of C_3 vs C_4 consumption, but challenges remain in understanding how preferential routing of food molecules in the body affect those values. We examined variation in bulk hair keratin, bone collagen, and bone carbonate $\delta^{13}C$ between chimpanzees (*Pan troglodytes*) and baboons (*Papio anubis*) of Gombe National Park, Tanzania. These populations have broadly overlapping diets but vary in how much time they spend consuming grasses and sedges.

As expected based on observed diet, chimpanzee (-24.0 ± 1.0‰, n=7) and baboon (-21.6 ± 0.7‰, n=11) bulk hair $\delta^{13}C$ values differed significantly (t=6.0, df=15.6, p<0.0001). Chimpanzee (-22.4 ± 0.3‰, n=30) and baboon (-20.9 ± 0.7‰, n=16) bone collagen $\delta^{13}C$ values also differed (t=8.6, df=18.6, p<0.0001). Bone carbonate values in the chimpanzees (-16.5‰ ± 0.5‰, n=30) and baboons (-16.0‰ ± 0.9‰, n=16) differed only slightly, though still significantly (t=2.2, df=20.3, p=0.04).

We hypothesize that the variation in $\delta^{13}C$ values reflects the protein content of each population's preferred C_4 food resources as well as the extent to which they consume such foods. Preliminary results indicate that the young grass leaves the baboons regularly exploit are high in protein compared to the grass pith consumed by the chimpanzees.

The potential for proteinaceous C_4 food resources to be preferentially routed to proteinaceous tissues should be considered when interpreting the extent of C_4 consumption in fossil primates using carbonate $\delta^{13}C$ values.

Funding and logistical support were generously provided by The Leakey Foundation, The Wenner-Gren Foundation, The University of Minnesota, a GWU/SI Opportunity Research Grant, and The Jane Goodall Institute.

The University of Iowa Stanford Collection: past, present, and future

LARA NOLDNER

Office of the State Archaeologist, University of Iowa

The University of Iowa Stanford Collection (UI-SC) is one of many anatomical collections with partial documentation for individuals representing marginalized and historically underrepresented communities. As part of an invited symposium organized by this author, the goal of this poster is to bring more awareness to the UI-SC and get feedback from participants on proposed research agendas aimed at better contextualizing the collection in a collaborative, inclusive, and transparent manner. Previous research results and data presented will provide a comprehensive summary of what we know of the collection's context, and topics that require further research will be highlighted. Of the roughly 1100 individuals, 230 (31 females, 197 males, 2 unknown) have associated documentation: 85.6% are European/European American, 9.7% East Asian, 3.1% Central American, and 1.5% African American; age at death ranges from 46-91 years for females and 27-96 years for males; year of death ranges from 1930-1952; places of death include two almshouses, an asylum, and a county hospital; most individuals have ambiguous occupations like housewife and laborer, respectively, but 32% of females and 44% of males have more specific jobs listed, including some indicating specialized education and higher socioeconomic status (SES). These data and more will be highlighted in relation to the author's preliminary research on what skeletal evidence of labor can add to our knowledge of individuals' lives. Complimentary posters on tracing UI-SC individuals' personal histories with archival sources, and examining evidence of pre- and post-mortem treatment based on race, ancestry, and place of death, will follow this presentation.

The historic legacy of race-corrections in medicine: medical harm of slavery-era assumptions about "inferior Black lungs" for recovering COVID-19 patients.

AMY L. NON, MEREDITH A. ANDERSON and SAMANTHA FLORES

Anthropology, University of California, San Diego

Social scientists concur that race is a social construction, and a poor proxy for genetic differences, but race has become firmly embedded within standard biomedical practice. Physicians routinely use race within diagnostic algorithms to assess risk and guide clinical decisions, including race adjustments built into the spirometer used to measure lung function. In fact, these race adjustments are influenced by historic legacies of racist assumptions about "inferior lungs" of Black Americans dating back to the time of slavery, and lack rigorous evidence to support these claims. It is broadly assumed that these lung capacity differences are due to innate biological differences between racial groups, without supporting genetic evidence. Black lungs are assumed to have 10-15% lower capacity than White lungs, and thus Black patients must demonstrate a greater reduction in lung function to warrant treatment. This bias may exacerbate racial disparities in recovery from COVID-19, a disease that

disproportionately affects racial/ethnic minorities. Here we quantify the clinical consequences of spirometry race adjustments for ~200 recovering COVID-19 patients in San Diego, California. We re-calculate lung function without the race-adjustment and quantify changes in lung damage classification. Of the preliminary sample (n=40), we find 27.5% are unknown/other/mixed race, which are not classifiable with existing binary-race spirometry equations. We find race-adjusted mean percent predicted forced vital capacity is higher among White patients than all other racial groups (83.3% vs 78%). We discuss implications for these findings to influence follow-up treatments in COVID-19 recovery, and to further exacerbate racial disparities in COVID-19.

A case of a large pedunculated-type osteochondroma on the lower leg of an adult female from late medieval Ilok, eastern Croatia

MARIO NOVAK[1], IGOR ERJAVEC[2], SVEN SEIWERTH[2], IVOR JANKOVIC[1], MARIO CARIC[1], ANDREA RIMPF[3], SINISA KRZNAR[4], IVANA SAVIC PAVICIN[5], MARIN VODANOVIC[5], HRVOJE BRKIC[5] and MISLAV CAVKA[6]

[1]Center for Applied Bioanthropology, Institute for Anthropological Research, [2]School of Medicine, University of Zagreb, [3]., Ilok Town Museum, [4]., Institute of Archaeology, [5]School of Dental Medicine, University of Zagreb, [6]University Department of Diagnostic and Interventional Radiology, University Hospital Centre Zagreb

Osteochondroma is one of the most common benign tumors of the bone. Causes for the disease are yet unknown, but there are indications that they may be linked to abnormality in the growth plate and possibly mutation in EXT1, EXT2 and EXT3 genes. Cases of reported osteochondroma range from prehistoric to contemporary examples, are not limited geographically, and no evidence for sex predominance has been reported.

Here we present a large pedunculated-type solitary osteochondroma on the medio-posterior part of the right fibula found in a skeleton of an adult female from the medieval site (12^{th}-15^{th}/16^{th} century) of Ilok-Krstbajer in eastern Croatia. In order to gain more insight into this pathological change we used multiple lines of inquiry: (i) macroscopic analysis, (ii) X-ray and Multislice computerized tomography, (iii) micro-CT, and (iv) biopsy and patohistological analysis. To minimize damage of surrounding tissue and to better visualize area of sampling, biopsy was done under CT-guidance.

The cauliflower-shaped growth is 50 mm long in sagittal and 57.41 mm in transverse diameter with the tumor exhibiting a bulbous, rough superior surface, and a flat, smoother inferior surface. The observed trabecular bone within the mass densifies outward, along with the tumor's expansion. The histological features are consistent with a chondromatous lesion (enchondroma or osteochondroma) with reactive/reparatory changes indicating a trauma relatively short ante-mortem.

The gross morphology of the tumor together with X-ray/CT scans and patohistological analysis support the diagnosis of a proximal fibular osteochondroma making it a unique case in an archaeological population.

This research has been supported by the Croatian Science Foundation (project IP-2020-02-9423).

Is *Paranthropus boisei* an environmental specialist compared to early *Homo*? Evaluating the faunal evidence from the Koobi Fora Formation, Kenya

KAEDAN O'BRIEN[1,2], NICHOLAS HEBDON[3] and J. TYLER FAITH[1,2,4]

[1]Anthropology, University of Utah, [2]Natural History Museum of Utah, University of Utah, [3]Biological Sciences, Chapman University, [4]Origins Centre, University of the Witwatersrand

Since the discovery of *Paranthropus boisei* alongside early *Homo* at Olduvai Gorge and Koobi Fora, paleoanthropologists have attempted to understand the different evolutionary paths of these two hominin lineages since their divergence in the Pliocene. Conventional wisdom is that their prolonged phase of sympatry in eastern Africa reflects very different adaptive strategies, with early *Homo* characterized as the ecologically flexible generalist and *Paranthropus* as the less versatile specialist. If correct, this should imply differences in their use of ancient landscapes, with *Homo* occurring in a broader range of environments compared to *Paranthropus*. In this study, we use the fossil record of large mammals from the Koobi Fora Formation dated to 2.0-1.4 Ma to quantitatively evaluate the ecological breadth of faunal assemblages associated with *Homo* and *P. boisei*. We also evaluate the more common large mammal genera to determine where each falls on a spectrum of generalist to specialist with regard to environmental associations. Both *Homo* and *P. boisei* occur in faunal assemblages indicating a similarly broad range of environmental settings, and both can be considered generalists relative to coeval mammalian species. This suggests that a primary ecological difference between these two hominin genera concerns their diet rather than their use of different environments.

Age and sex related variation in urinary neopterin in wild Bornean orangutans

CAITLIN A. O'CONNELL[1,2], DANIEL J. NAUMENKO[3,4], MARIA A. VAN NOORDWIJK[5], REBECCA S.A. BRITTAIN[2], SRI SUCI UTAMI ATMOKO[6,7] and ERIN R. VOGEL[2]

[1]Anthropology, University of Pennsylvania, [2]Anthropology, Rutgers University, [3]Anthropology, University of Colorado Boulder, [4]Institute of Behavioral Science, University of Colorado Boulder, [5]Anthropology, University of Zurich, [6]Faculty of Biology, Universitas Nasional, [7]Primate Research Center, Universitas Nasional

Life history theory predicts that tradeoffs among growth, maintenance, and reproduction will result in variation in immune function over the life span. Humans have been shown to experience *inflammaging*, displaying an increase in inflammatory biomarkers with age as adaptive immune function declines. While it has been argued that this phenomenon is unique to modern humans and perhaps captive primates as a result of altered lifestyles, age-related increases in markers of inflammation have been documented in other mammals as well. Previous studies from wild chimpanzees have reported mixed results in support of this: Ngogo chimpanzees exhibited increased urinary neopterin, a marker of inflammation via macrophage activity, with age as well as marked sex differences, while Kanyawara chimpanzees lacked differences in neopterin with age or sex. Here we examined urinary neopterin in wild Bornean orangutans at the Tuanan Research Station from 2009-2017 using 587 urine samples from 52 individuals. Preliminary analysis using a generalized linear mixed model revealed that neopterin did not vary among age-sex classes as expected, but among adults, males had significantly higher levels of inflammation than females (β=6.113, t=69.64±.088, p<0.001). We consider our results in the context of orangutan socioecology compared to other apes. These findings highlight the need for long-term sampling on individuals over their lifespan to better understand inflammaging and whether it is unique to the human ageing process.

This research was funded by USAID (E.R.V., APS-497-11-000001), L.S.B Leakey Foundation (E.R.V.), A.H. Schultz Foundation (M.A.N.), National Science Foundation (E.R.V., BCS-0643122), Rutgers University (E.R.V), Center for Human Evolutionary Studies (E.R.V.)

Features of catarrhine molars associated with durophagy

MACKIE C. O'HARA[1], SIMON CHAPPLE[2], MARK HUBBE[1], PATRICK MAHONEY[2], W. SCOTT MCGRAW[1], GARY T. SCHWARTZ[3], MATTHEW M. SKINNER[2,4] and DEBBIE GUATELLI-STEINBERG[1,2]

[1]Department of Anthropology, The Ohio State University, [2]School of Anthropology and Conservation, University of Kent, [3]School of Human Evolution and Social Change, Arizona State University, [4]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Dental features associated with hard-object feeding include enlarged teeth, flat or more bunodont molars, thick enamel overall, and/or thick enamel concentrated across occlusal basins and cusp tips. The present study investigates the extent that tooth size, tooth shape, and enamel thickness distribution are associated across a range of primates differing in their reliance on

durophagy. Because enamel thickness is considered more evolvable than tooth morphology, we test the hypothesis that aspects of enamel thickness distribution will show stronger association with durophagy than other elements of tooth morphology (e.g., tooth size, shape, strength). We analyzed 2D histological and virtual mesial slices of upper (n=188) and lower (n=212) M1-2s from 13 primate groups (4 cercopithecoids; 5 extant hominoids, including 2 humans populations; 4 fossil hominins), with each clade including at least one hard-object feeding taxon. Blomberg's K values revealed significant phylogenetic signals in multiple measures of tooth size and enamel thickness, as well as absolute crown strength. Consistent with the idea that enamel thickness is highly evolvable, lower molars of durophagous species have thicker proportional enamel across their occlusal basins, particularly on the lingual aspect, providing protection from fracture. Interestingly, upper molars do not show a consistent pattern of association between the molar features analyzed and durophagy, which could be due to the inherently larger size of upper molars, allowing them to better withstand high loads. Compared to other aspects of tooth size and shape, we conclude that shifts in enamel thickness distribution are more frequently associated with durophagy across catarrhine molars.

This research was supported by the Wenner-Gren Foundation, NSF GRFP DGE-1343012, NSF BCS-1945008, the European Research Council (ERC) under the European Union's Horizon 2020 (ERC-2018-COG-819960), and Max Planck Society.

Center of Pressure Location on the Foot During Bipedal Walking

MIGUEL OCHOA[1], STEVEN G. LAUTZENHEISER[2] and PATRICIA A. KRAMER[1,3]

[1]Anthropology, University of Washington, [2]Anthropology, University of Tennessee, [3]Orthopaedics and Sports Medicine, University of Washington

For bipedal locomotion, the foot must be able to conform to different substrates in order to support and stabilize the body, but also be rigid enough to act as a lever to propel the body forward during toe off. Recent work using force-sensing insoles suggests that the center of pressure (CoP) location of the ground reaction forces (GRF's) of braking and propulsion phases of stance differ. The CoP of the peak GRF during propulsion is consistently located under the medial metatarsal heads, while the location of the CoP during peak braking is variably located from the posterior hindfoot to the forefoot. This work was limited, however, in that the location of foot landmarks were assumed from the insole. We sought to confirm this result in subjects where the position of the CoP and tarsals were measured simultaneously. Kinetic data (motion and GRFs) of 26 individuals were collected using a ten-camera Qualisys system with four Kistler force plates. Participants walked unshod for 10 meters at a self-selected normal pace. Marker locations, GRFs and CoPs were measured. After controlling for foot length, we used Levene's test to assess whether the distribution of the locations of the CoP at peak braking force are different from those at peak propulsive force. We found that braking CoPs are more dispersed than propulsive CoPs ($p<0.001$, n=497 stance phases). Our results confirm that the peak force during propulsion occurs under the medial metatarsal heads, but that the peak force during braking is more dispersed

(Wo)man the hunter: The Physiological Evidence Ignored

CARA OCOBOCK[1] and SARAH LACY[2]

[1]Anthropology, University of Notre Dame, [2]Anthropology, California State University Dominguez Hills

"Popular pictures drawn of the past are too often little more than backward projections of cultural sex stereotypes onto humans who lived more than million years ago," (Zihlman, 1981, p. 76). Foundational feminist anthropologists like Adrienne Zihlman and Sarah Blaffer Hrdy have made valiant efforts in moving the field forward to better recognize the critical role of women in human evolution. However, the myths of "Man the Hunter" and male biological superiority persist in interpretations and reconstructions of human evolution. Although there are uncontroversial average biological differences between females and males, the potential physiological advantages females may possess are less well-known and less well-studied. Here we review and present emerging physiological evidence that women may be better metabolically suited for endurance activities such as running, which could have profound implications for understanding subsistence capabilities and patterns in the past. We will discuss the role of estrogen and adiponectin as respective key modulators of glucose and fat metabolism, both of which are critical fuels during long endurance activities. We will also discuss how differences in overall body composition, muscle fiber composition, the metabolic cost of load carrying, and self-pacing may provide females with increased endurance activity capacities. Highlighting these potential advantages provides a physiological framework that compliments existing archaeological (see Lacy and Ocobock, this conference) and cultural work reassessing women's endurance and hunting capabilities as well as the sexual division of labor. Such a holistic approach is critical to amending our current understanding of hu(wo)man evolution.

A review of techniques and landmarks used in geometric morphometric studies of human crania

TRINE B. OLSEN[1], JULIE HANSEN[1], MARIE LOUISE S. JØRKOV[1], DANIEL GARCÍA-MARTÍNEZ[2] and CHIARA VILLA[1]

[1]Department of Forensic Medicine, University of Copenhagen, [2]Department of Biodiversity, Ecology, and Evolution, Complutense University of Madrid

We evaluated the precision of three techniques used for collecting cranial 3D landmarks for geometric morphometric studies, and reviewed the applicability of some of the most common landmarks used in this context.

Sets of 65 landmarks were acquired from 14 archaeological crania using 3D digitizer, and from 3D models generated from CT scanner and surface scanner using Viewbox. Data were collected by two observers to investigate both intra-and inter-observer error. Individual landmark scatter was analyzed using standard deviations in Euclidean space. Landmarks were analyzed with regards to data collection technique, type, and placement on the cranium.

Intra-observer landmark scatter ranged from 0.07-2.19mm for 3D digitizer, 0.09-4.46mm for CT scans, and 0.09-5.45mm for surface scans. Inter-observer landmark scatter ranged from 0.05-7.46mm for 3D digitizer, 0.06-10.44mm for CT scans, and 0.05-9.92mm for surface scans. Type 1 landmarks were more precise than type 2 landmarks for both intra- and inter-observer datasets. Landmarks found on the face were most precise for CT scans and surface scans, while the most precise landmarks found with the 3D digitizer were on the calvarium. The most variable landmarks for all three techniques were found at the extremes of curves and on structures with high levels of anatomical variability, e.g. the edge of the orbit and the sphenoid spine.

Cranial landmarks can be found with high levels of precision using both 3D digitizer, and CT scans, and surface scans. It is however recommended to consider landmark choice when designing geometric morphometric studies.

Developing a quantitative means of assessing the biological integrity of fossil enamel for dietary and paleoecological reconstructions of early hominins

GEORGIA OPPENHEIM and JOHN KINGSTON

Department of Anthropology, University of Michigan

Reconstructing the diet and environment of human ancestors through isotopic analysis provides insights into the evolutionary history and adaptations of our species. The foundational premise of this research is that the biogenic (*in-vivo*) isotopic dietary signal can be retrieved intact from fossilized tooth enamel, providing

perspectives on dietary and habitat preferences of fossil taxa (hominins, associated fauna). But, there is still uncertainty about post-depositional chemical modifications to enamel (diagenesis) and the pre-treatment methods that attempt to remedy this impact. Methods must be developed to systematically characterize the chemical nature of enamel, including the specific crystalline sites that yield the biogenic dietary signals during fossilization and the effects of pretreatments. This project analyzes the chemical composition of variably pre-treated fossil and modern enamel of different African herbivores using x-ray photoelectron spectroscopy. This approach, which provides data on structural and elemental shifts in enamel, complements isotopic analysis and is a means of assessing how changes in chemical properties of enamel affect the isotopic values of teeth, providing information on diagenesis. Analysis has shown that carbon occupies discriminate sites within the enamel structure and can be used to assess variable substitution in tooth enamel. Data also indicates variation in the relative elemental abundances in modern and fossil enamel and that pre-treatment methods alter the relative amounts of certain carbon bonds in fossil samples. Given the centrality of isotopic analysis for reconstructing the diet and environment of early hominins and their communities, this systematic assessment of diagenesis is critical to accurately reconstructing hominin paleoecology.

Safe at The College?: 1918 Influenza in the Student Army Training Corps (SATC) at the University of Missouri

CAROLYN M. ORBANN and ERIN WALTON

Department of Health Sciences, University of Missouri

The Student Army Training Corps (SATC) was a short-lived Federal program to allow active-duty military men to enroll in colleges in the fall of 1918. In that semester, the University of Missouri's SATC chapter boasted more than 700 men. These members experienced some of the earliest flu-related illness and death in the city of Columbia, Boone County, Missouri.

A collection of 1918 billing records from UM hospital to the War Department sheds light on the progress of the pandemic in this population and has been analyzed in conjunction with death certificate data at the county level, supporting information from newspapers, as well as other special collections. The authors calculated hospital admission rates, readmission rates, and case fatality rates in this population of 18–30-year-old men. In all, over 450 SATC recruits were hospitalized with flu-related diagnoses, and seven men died.

It is rare to have both illness and death data from the 1918 pandemic, particularly in a semi-civilian, small-town context. We will discuss our findings on the impact of the flu in the SATC population, as well as showing how their story fits into the larger context of the pandemic in Boone County. This project demonstrates an innovative strategy for using multiple lines of historical evidence to better understand the 1918 flu and its effects on a community.

Support: NSF RAPIDD Grant No. BCS-2031703.

Without a net: comparing mouse locomotor modes to study arboreality and its impact on musculoskeletal functional morphology

JASON M. ORGAN[1,2] and CRAIG D. BYRON[3]

[1]Anatomy, Cell Biology & Physiology, Indiana University School of Medicine, [2]Anthropology, Indiana University Purdue University Indianapolis, [3]Biology, Mercer University

For the last several years, our labs have collaborated on a musculoskeletal biomechanics research program rooted in the scholarship and mentorship of Dr. Christopher Ruff. The experiment utilizes a unique climbing mouse model that enhances musculoskeletal morphological properties like bone cross-sectional geometry and muscle cross-sectional area, and mechanical properties like bone toughness and skeletal muscle contractile force, through multi-directional, off-axis, low-intensity loading. The model consists of two types of enclosures: a fine-wire (climbing) enclosure that mimics a narrow-branch arboreal niche and requires mice to develop enhanced balancing and pedal grasping to move above branch between nest sites, food, and water; and a parking deck-like (control) enclosure that prevents pedal grasping but is vertically stratified like the fine-wire enclosure. Mice (C57BL/6 and CD-1(ICR)) are raised from weaning to maturity in one of these enclosures. At sacrifice, several bones and muscles are excised and undergo a battery of mechanical and physiological testing, high resolution imaging, and preparation for histological examination. Climbing in the simulated fine branch arboreal environment enhances morphological characteristics like cross-sectional geometry of the first metatarsal and caudal vertebrae and larger anatomical cross-sectional area of tail muscles. Mechanical properties of the musculoskeletal system are similarly enhanced: femora are stronger and tougher in four-point bending, and leg muscles contract with higher force and fatigue slower. These experiments are foundational to understanding musculoskeletal plasticity in the evolution of derived types of fine-branch arboreality from more ancestral forms.

Funding for this work provided by the IUPUI Biomechanics and Biomaterials Research Center, Ralph W. and Grace M. Showalter Research Trust Fund, Mercer Office of the Provost, and Mercer Seed Grant.

The Taphonomy of Status: Medieval church burial at Đurđevac-Sošice (Croatia), the creation of group identity, and inequality

ANNA J. OSTERHOLTZ

Anthropology and Middle Eastern Cultures, Mississippi State University

Death in the medieval period was seen as the great equalizer, experienced equally by all members of society. Burial, however, was performed quite differently, depending on the social class of the decedent and their family. Individuals were interred in church subfloors, often disrupting older burials. Elements dislodged during these excavations were added to the burial fill of the later burials, thus ensuring that the individuals remained a part of the ritual space. Burial within the church added the body to the physical structure of the Church. The community, while attending church services, would have experienced the olfactory consequences of burial within the church structure. This phenomenological experience of the body while in ritual services, cemented concepts of equality (the high status decompose just like the low) as well as inequality (the high status became part of the church architecture, closer to the alter and its relics.

Excavations of the interior of the church at Đurđevac-Sošice in eastern Croatia (in use from the 11th—16thcenturies) have uncovered over 240 identified burial cuts throughout the interior of the church as well as a large commingled collection derived from the burial fill of identified graves.

This presentation will explore the concepts of identity and phenomenology and how the process of successive burials created the taphonomic indicators for class-based identity through a preliminary analysis of a non-representative sample of the burials as well as the commingled remains focusing on demography and indicators of health.

Whole genome capture of oral pathogenic bacteria from Great Ape dental calculus

ANDREW T. OZGA[1], TANVI HONAP[2,3], CECIL M. LEWIS JR.[2,3] and ANNE C. STONE[4,5]

[1]Department of Biological Sciences, Nova Southeastern University, [2]Department of Anthropology, University of Oklahoma, [3]Laboratories of Molecular Anthropology and Microbiome Research, University of Oklahoma, [4]School of Human Evolution and Social Change, Arizona State University, [5]School of Life Sciences, Arizona State University

Oral diseases, such as periodontitis and dental caries, affect humans as well as our closest evolutionary cousins, the Great Apes, and are primarily caused by oral microbial dysbiosis. Dental calculus (calcified dental plaque) can yield genomic information about the host, along with commensal and pathogenic oral microbiota.

However, oral pathogens are often present in such low abundance that sufficient genomic information cannot be recovered through shotgun metagenomic sequencing. As a solution, the field of ancient genomics has begun to utilize target capture technology. Until recently, oral pathogen capture has only been used to study human strains; thus, there is little information on strains present in other Great Apes. Here, we report the successful capture of ten oral pathogen genomes from museum acquired dental calculus samples from chimpanzees, gorillas, and orangutans. We recovered near-complete genomes (between 70% and 90% of the reference sequence) for four *Treponema denticola* strains (mean coverage 80 to 193-fold) and six *Tannerella forsythia* strains (mean coverage 256 to 467-fold), which are both associated with the Red Complex of periodontal pathogens. We then reconstructed oral pathogen strains from previously published ancient and modern human oral metagenome datasets to compare strain-level and gene content variation across species. We also report that many individuals contain multiple strains of each oral pathogen species. This research has implications for our understanding of strain-level differences within a single oral cavity as well as the microbial evolutionary changes in non-human primates compared to human populations.

This research was funded by a grant from the National Science Foundation (NSF BCS-2045308).

The activity budget of a mother aye-aye (Daubentonia madagascariensis) postpartum

LISA M. PACIULLI, LAUREN BOYD, ANTONIO ALVA, IRIS HORTON, CHASEN STEPHENSON and DAVID WATTS

Department of Biological Sciences, NC State University

Nonhuman primate mothers typically divide their time foraging and feeding, nursing, and resting. Very little is known about how aye-aye (*Daubentonia madagascariensis*) mothers spend their time because they are primarily solitary, nocturnal, and live in cocoon-like nests, which makes them difficult to observe. In this study, a Duke Lemur Center (Durham, N.C.) aye-aye mother's behavior was video-recorded for five days postpartum using motion-sensor cameras placed in key areas of her enclosure including inside of nest boxes. The resulting video was uploaded to Google Drive, and the mother's behavior was noted using 2.5-minute instantaneous focal animal sampling. All occurrences sampling was also employed to record instances and durations of grooming, nursing, and playing. Preliminary results show that the most common behaviors exhibited by the mother aye-aye were grooming (27%), sleeping (22%), nest construction (15%), traveling (14%), and resting (9%). The mother may have groomed herself and her offspring a lot after the birth to clean them. Sleeping and resting are common behaviors of mothers postpartum to regain the strength they lost during gestation, birthing, and lactation. Thus, the mother aye-aye seemed to spend her time similar to other nonhuman primate postpartum mothers. With fewer than 30 aye-ayes in captivity in the U.S. and decreasing populations in the wild, learning more about aye-aye mother behavior could help inform captive aye-aye management, breeding programs, and conservation efforts. Future research should consist of data collection on more aye-ayes for a longer period of time.

The Bioarchaeology of Violence during the Yayoi Period in Western Japan

BRIAN D. PADGETT[1,2] and NORIKO SEGUCHI[3,4]

[1]Department of Anthropology, The Ohio State University, [2]SNA International, Defense POW/MIA Accounting Agency, [3]Faculty of Social and Cultural Studies, Kyushu University, [4]Department of Anthropology, University of Montana, Missoula

Evidence of violence has been observed at many sites in Japan dated to the Yayoi period (~900 BCE – 300 CE), though the implications have not been explored in depth. In this study, it was hypothesized that the frequency of violent trauma, and the weapons employed, would not significantly differ among sites dated to the Yayoi period. Analysis of skeletal trauma at sites in western Japan revealed changes in the conduct of inter-group conflict from the Early to the Late Yayoi period.

Evidence indicates that during the Early Yayoi period, female adults were targeted more frequently than males, and perimortem injuries were most often due to direct blunt force trauma. Patterns of trauma suggest that lithic and blunt weapons were gradually replaced by bronze weapons. Perimortem violent trauma among female remains nearly disappeared during the Middle Yayoi. Demographic shifts in the targets of violence suggest more formalization of inter-group conflict during the Middle Yayoi, though any proscriptions against attacking certain classes of individuals are not reflected in the Late Yayoi dataset.

Intergroup conflict for political power contributed to the emergence of a state society. This research demonstrates how patterns of violence reflect changes in social structure. The development of a code of conduct for the application or restraint of violence is an important indicator of the changing belief systems of the Yayoi people, and is relevant to the ethnogenesis of the Yamato people, the predominant ethnic group in Japan today.

Funded by MEXT KAKENHI Grant Number JP19H05737: "Genetic diversity and physical changes associated with human dispersal and the development of complex societies" and The Ohio State University Alumni Association.

The evolution of cumulative culture in the hominin lineage

JONATHAN PAIGE[1,2,3] and CHARLES PERREAULT[2,3]

[1]Center for Archaeological Research, University of Texas, San Antonio, [2]Institute of Human Origins, Arizona State University, [3]School of Human Evolution and Social Change, Arizona State University

Cumulative culture is the ability to accumulate, new, modified, or improved practices, technologies, and beliefs across generations. It underlies the behavioral diversity of our species and our unique capacity to adapt to novel environments. Cumulative culture may also have been a driver in the evolution of hominin brain size, life history, and body morphology across the Pleistocene. However, the evolutionary history of cumulative culture is not well understood, and claims range from it being absent even among Neanderthals, to it being a primitive feature of the genus *Homo*.

We analyzed the complexity and diversity of stone tool production sequences among archaeological assemblages (N = 550) to identify when hominins began relying on tools that would have been unlikely to evolve without some form of cumulative culture. We compared technological complexity and diversity found in stone tool assemblages to that of the technologies produced by non-human primates lacking cumulative culture, as well as to that observed in randomized flaking experiments.

We found that hominins began relying on technologies unlikely to be discovered through randomized flaking behaviors, and more complex than non-human primate tool-making behaviors by ~2 million years ago. We also found *H. sapiens* and *H. neanderthalensis* in the Pleistocene show similar technological complexity, and technological variability. Both findings suggest that hominins relied on some form of cumulative culture by ~2mya, while a modern human-like capacity for cumulative culture may have been shared with the last common ancestor of *H. sapiens* and *H. neanderthalensis*.

This project was supported by the Leakey Foundation, and a dissertation writing fellowship from the School of Human Evolution and Social Change, Arizona State University.

Ancient Skeletons *In Situ*: Evaluating Diagenesis at a Covered Open-Air Excavation Display and Community Museum in Central Thailand

GINA PALEFSKY[1], THANIK LERTCHARNRIT[2], ROBIN B. TRAYLER[3] and SORA L. KIM[3]

[1]Department of Anthropology & Heritage Studies, University of California, Merced, [2]Faculty of Archaeology, Silpakorn University, [3]Department of Life & Environmental Sciences, University of California, Merced

Human bone collagen is routinely analyzed for radioisotopic dating and paleodietary studies using stable isotope analysis, but its utility is contingent upon preservation. In addition to numerous taphonomic factors that affect diagenesis post-deposition, curation and display of human skeletal remains post-excavation may also influence collagen preservation or degradation. Here, we present an assessment of diagenetic alteration of human bone collagen from the archaeological site of Ban Pong Manao, an Iron Age settlement and cemetery in central Thailand. Following excavations in the early 2000s, most excavated human skeletal remains were housed at the on-site research and storage center, while a subset were chosen to remain *in situ* under covered open-air excavation units for public display and community tourism. We analyzed samples from both post-excavation contexts (*in situ*, n=12; museum storage, n=21), and assessed whether different curation techniques affected the degree of diagenetic alteration. We measured collagen yield, carbon and nitrogen wt%, and atomic C:N ratios. Results show that while collagen yields varied, ranging from 0.6 to 9.3 wt% (n=33), differences between contexts were not significant (p=0.2), and all samples fell within accepted ranges for each criteria. Contrary to initial hypotheses, the *in situ* display of human skeletal remains in covered open-air excavation units has had little if any effect on collagen preservation at Ban Pong Manao. These preliminary findings highlight how community stewardship upholds aspects of bioarchaeological preservation ethics, protecting collagen, despite outdoor exposure in a tropical monsoon climate.

This research was funded by the Wenner-Gren Foundation for Anthropological Research, American Philosophical Society, and University of California, Merced Center for the Humanities.

Variation in the Platyrrhine Pterygoid Process using Linear and Angle Measurements

STEPHANIE PALMER[1], CLAIRE E. TERHUNE[2], CLAIRE A. KIRCHHOFF[3] and SIOBHÁN B. COOKE[1,4]

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

Studies have found variation in the osteological correlates of masticatory musculature that are related to masticatory biomechanics, diet, and socioecology; however, analyses of the basicranium, specifically the origin of the pterygoid muscles, and how they may also relate to these factors has not been thoroughly explored.

Here, we examined variation in the morphology of pterygoid plates and basicranium in a dietarily diverse sample of platyrrhines: *Sapajus apella* (n= 44), *Cebus capucinus* (n= 53), *Alouatta seniculus* (n=53), and *Ateles geoffroyi* (n=41). Linear measurements of the length and angle of the pterygoid plates relative to the basicranium were taken on surface scans using Checkpoint software and scaled by skull length. Results of statistical analyses show the lateral pterygoid plate lengths differ between *Alouatta* and all other species, but in no other species pairs. Sex differences in lateral plate length were found within *Alouatta* and *Cebus* but not *Ateles* and *Sapajus*. Lateral pterygoid angles differed between all species pairs except between *Alouatta* and *Ateles* and differed between males and females within *Sapajus*.

These data demonstrate variation in pterygoid morphology among genera and between sexes. While the driving force for this variation is unclear, these results show that it is worthwhile to consider this region when discussing variation and evolution of the masticatory system and basicranium. Future work will expand upon the taxa sampled, will quantify variation of the lateral pterygoid plate and fossa, and will address covariation of the lateral plate morphology with the entire skull through geometric morphometric methods.

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

Cleaning is the hardest part: best practices for chemically defleshing fixed, irregular human bones

ANNIE S. PANAGEAS[1], BOBBIE LEEPER[2], PAMELA MARSHALL[1], LISA LUDVICO[1], MICHAEL JENSEN-SEAMAN[3] and ANNE BURROWS[4]

[1]Department of Forensic Science and Law, Duquesne University, [2]School of Natural and Health Sciences, Seton Hill University, [3]Department of Biological Sciences, Duquesne University, [4]Department of Physical Therapy, Duquesne University

Accurate sex determination of human skeletal remains is highest when the pelvis and skull are present, but these are not always available. Small and irregular bones are more often present so developing techniques to establish sex of human skeletal remains using these bones is important. Accurate measurements of these bones depend on clear visualization of landmarks, so cleaning these bones must be done completely but not so aggressively that they are damaged. The present study focused on assessing the best cleaning methods for select human irregular and small bones using chemical defleshing techniques. We gathered the hyoid, the medial and intermediate cuneiforms, and other select small bones from 30 human cadavers. We tested four cleaning methods for each bone using sodium carbonate solution: 1) chemical defleshing with bones being immersed prior to the solution reaching boiling point, with no prior manual cleaning, 2) chemical defleshing with bones being immersed after the solution reached boiling with no prior manual cleaning, 3) and 4) options 1 and 2 but with prior manual cleaning of the bones. Results indicated that immersing the hyoid bone in the solution prior to the boiling point sometimes resulted in them becoming overly porous with 25% of them becoming too damaged to measure. All bones without prior manual cleaning were successfully cleaned. Results revealed that chemical defleshing cleaning techniques for these bones should be tailored to the individual bone and that prior manual cleaning of the bones is not necessary.

A virtual repository of Lower Siwalik Miocene fossils from Ramnagar (Udhampur District, Jammu & Kashmir), India

BIREN A. PATEL[1,2], CHRISTOPHER C. GILBERT[3,4,5,6], RAMESH K. SEHGAL[7,8], NINGTHOUJAM P. SINGH[7], ANNA DI[2], DEEPAK CHOUDHARY[9], WASIM A. WAZIR[9], CHRISTOPHER J. CAMPISANO[10,11] and RAJEEV PATNAIK[9]

[1]Integrative Anatomical Sciences, University of Southern California, [2]Human and Evolutionary Biology, University of Southern California, [3]Anthropology, Hunter College of the City University of New York, [4]PhD Program in Anthropology, Graduate Center of the City University of New York, [5]NYCEP, New York Consortium in Evolutionary Primatology, [6]Division of Paleontology, American Museum of Natural History, [7]Biostratigraphy Group, Wadia Institute of Himalayan Geology, [8]AcSIR, Academy of Scientific and Innovative Research, [9]Geology, Panjab University, [10]Institute of Human Origins, Arizona State University, [11]School of Human Evolution and Social Change, Arizona State University

Vertebrate fossils have been known from Lower Siwalik Miocene deposits surrounding the town of Ramnagar (Udhampur District, Jammu & Kashmir) in northwest India since Barnum Brown's American Museum of Natural History (AMNH) expedition in 1922. These fossils included dentognathic specimens of *Sivapithecus* and other Chinji Formation-aged mammals. Paleontological fieldwork has continued sporadically in the Ramnagar region ever since, and in that time, a large number of vertebrate fossils have been recovered by many different researchers and institutions, including the recently discovered primates *Kapi* and *Ramadapis*. Ramnagar fossils are currently housed in several institutions across India and the United States, thereby making it challenging to comprehensively study the entire collection. Consequently, a full understanding of important questions related to the taxonomy, paleobiology, paleoecology, and biochronology of the Ramnagar fauna cannot be readily obtained. Moreover, without answers to these questions, correlations and comparisons cannot be accurately made to other similar aged fossil localities in the Siwaliks (i.e., Potwar Plateau, Pakistan) and elsewhere in Eurasia. Therefore, the goal of this collaborative project is to establish and grow a 3D

digital repository of all fossil specimens from the Ramnagar region for continued comprehensive study. We employ µCT, surface scanning, and photogrammetry to virtually bring together specimens from the AMNH, Panjab University, Wadia Institute of Himalayan Geology, and Yale Peabody Museum. Thus far, >100 specimens have been digitized and made openly accessible on the MorphoSource web platform. Here we highlight some of the best-preserved specimens, including recovered primates and micromammals, and discuss their scientific importance.

Funding generously provided by the U.S. National Science Foundation (BCS-1945618, BCS-1945736, BCS-1945743) and the Leakey Foundation.

Infant baboons reduce costly social behaviors but grunt more during challenging times

SAM K. PATTERSON[1], SHIRLEY C. STRUM[2,3] and JOAN B. SILK[4,5]

[1]Anthropology, New York University, [2]Anthropology, University of California, San Diego, [3]Uaso Ngiro Baboon Project, Kenya, [4]School of Human Evolution and Social Change, Arizona State University, [5]Institute for Human Origins, Arizona State University

Experiences during early development can shape phenotypes into adulthood. Among female baboons, early life adversity negatively affects the extent of social connectedness and interaction style in adulthood. Some of the negative effects of early adversity on social development might be mitigated if infants are able to increase low-cost social behaviors or if partners initiate more interactions with them. Here, we investigate the influence of environmental challenges on sociality in wild olive baboon infants (*Papio anubis*) from Laikipia, Kenya. We collected behavioral data from 51 infants to quantify frequency of play, degree of independence, and rates of social interactions and vocalizations. We paired these behavioral data with ad libitum data on environmental challenges (i.e., encounters with humans, domestic dogs, and unfamiliar male baboons). As the number of environmental challenges increase, infants are less independent (ß= -0.27), approach others less (ß= -0.04), groom others less (ß= -0.20), and play less (ß= -0.22). However, as the number of environmental challenges increase, infants grunt to others more (ß= 0.10). We suggest that grunts, which function as signals of benign intent, might be used by infants to develop and maintain social relations when other forms of sociality are too costly or risky. These results demonstrate that there are immediate consequences of early life adversity for infants that may affect their social development, but also reveal that infants may make behavioral adjustments to reduce negative impacts of early life adversity.

Funding provided by the National Science Foundation (DDRI, GRFP, SPRF), the Leakey Foundation, and SHESC and IHO at Arizona State University.

Subadult dental variation and biological structure at precolonial Tlatelolco

KATHLEEN S. PAUL[1], KELLY E. BLEVINS[2], JOSEFINA MANSILLA LORY[3] and JANE E. BUIKSTRA[4]

[1]Department of Anthropology, University of Arkansas, USA, [2]Department of Archaeology, Durham University, UK, [3]Dirección de Antropología Física, Instituto Nacional de Antropología e Historia, Mexico, [4]Center for Bioarchaeological Research, School of Human Evolution and Social Change, Arizona State University, USA

During the height of the Aztec empire (1300-1521 CE), the twin urban centers of Tlatelolco and Tenochtitlan were characterized by a high degree of social complexity and population density. Tlatelolco boasted one of the largest interregional marketplaces in Mesoamerica, which made it a central point of migration and—presumably—biological exchange. While Tlatelolco has been the focus of intensive bioarchaeological research, few studies have considered *intrasite* patterns of biological affinity. Additionally, most biodistance studies have excluded subadult individuals, yet infants, children, and adolescents make up an appreciable portion of Tlatelolco's bioarchaeological record. Here, we present a reconstruction of Tlatelolco's biological structure with a focus on the subadult population. After pre-analysis data treatment, 25 deciduous dental measurements (crown and cervical) representing 79 individuals were subjected to principal components analysis and hierarchical clustering. UPGA agglomeration of Euclidean distances resulted in eight distinct groupings. Groups 1 and 2 contained 92% of the sample, while the other six groups contained only a single individual. Spatial, contextual, paleopathology, and dismemberment/defleshing patterns did not clearly map onto the biodistance output, with one exception: approximately half of the individuals in Group 1 were recovered from Patio Sur—a context thought to represent a sacrificial or ceremonial event. The results suggest that a) the Patio Sur mortuary event disproportionately impacted individuals of a specific (sub)population affinity, and b) subadult biological variation explains a limited amount of the broader contextual structure of Tlatelolco. Future work will explore these patterns using morphology of the deciduous and mixed dentitions.

Fulbright-García Robles Fellowship (K. Blevins)

Cross-sectional geometry and bilateral asymmetry of Omo I humeri

OSBJORN M. PEARSON[1], IAN J. WALLACE[1], TEA JASHASHVILI[2,3], KRISTIAN J. CARLSON[2], STUART J. WARDEN[4,5] and JOHN G. FLEAGLE[6]

[1]Department of Anthropology, University of New Mexico, [2]Clinical Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, [3]Department of Geology and Paleontology, Georgian National Museum, [4]Center for Translational Musculoskeletal Research, Indiana University, [5]Department of Physical Therapy, School of Health and Rehabilitation Sciences, Indiana University, [6]Department of Anatomical Sciences, School of Medicine, Stony Brook University

As one of the earliest anatomically modern humans, Omo I's humeral cross-sectional geometry is of interest. Computed tomography scans of Omo I were made in Addis Ababa and compared to data from the literature on other Middle-Late Pleistocene hominins, Holocene humans, and data on professional baseball pitchers collected by Warden. Analyses focus on J and %CA and Imax/Imin for the 35% and 50% levels, measured from the distal end. We used 368 mm as the estimated length of Omo I's humeri. Results show Omo I has comparatively low asymmetry for all of the variables at both levels, unlike the highly lateralized male humeri of Neandertals, Gravettians, and baseball pitchers, but resembling Late Pleistocene females and recent, sedentary people. Omo I has remarkably thick cortical bone (50% level %CA: 91.3%, 85% [R,L]; 35% level: 89.2%, 80% [R,L]), exceeding the of Neandertal males' values but matched by the highest values among the professional pitchers. Omo I's Imax/Imin values show only moderate AP flattening of the shaft (50% level: 1.2103, 1.3088 [R,L]; 35% level: 1.3260, 1.3141 [R,L]). Raw values for J (mm^4) (50% level: 16061.8, 13764.5 [R,L]) reflect Omo I's large size; but values for J standardized for bone length and body mass resemble those of the dominant arm of Neandertal males. Both of Omo I's humeri feature an expanded area for the attachment of the brachioradialis and brachialis muscles. In sum, Omo I's humeri show low asymmetry and suggest vigorous, bilateral activity.

NSF BCS-9817950, NSF BCS-0097112, L.S.B. Leakey Foundation, National Geographic Society, Australian National University, NIH R01 AR057740

Title: Evolutionary déjà-vus: Why did size reduction evolve multiple times within primates?

ANNA PENNA[1], JAMES P. HERRERA[2] and LUCA POZZI[1]

[1]Anthropology, University of Texas San Antonio, [2]Duke Lemur Center SAVA Conservation, Duke University

It is largely accepted that the order Primates has followed a trend of increasing body size over time. However, extreme size reduction has convergently evolved in various primate clades. Examples of clade-wide convergence can be interpreted as lineages independently reaching similar adaptive peaks on a macroevolutionary adaptive landscape, thus offering a unique opportunity to test hypotheses about how natural selection can shape organisms to their environments. Here we used phylogenetic comparative methods to investigate whether small-sized species have remained small throughout their evolutionary history or have convergently reached similar adaptive peaks. We compiled body mass data from the literature for 754 living and fossil primates and plesiadapiform species to model size evolution. Using a comprehensive dated phylogeny we first estimated ancestral state to evaluate body mass change over time in each of the living miniaturized lineages. Our results show that mouse lemurs and marmosets have rapidly reduced in size since the late Oligocene, while dwarf galagos, lorises and tarsiers showed much slower decrease rates since the mid-Eocene, suggesting that both strong directional and stabilizing selection led to the evolution of similar phenotypic outcomes. We then compared the fit of seven different evolutionary models in explaining the observed body mass variation in the primate phylogeny, and lastly tested if small-sized lineages evolved under the same evolutionary regime. The favored model was punctuated evolution, suggesting that major size changes occurred in cladogenetic events. This result was also supported by our analysis of regime shift, which recovered unique regimes for each miniaturized lineage.

Funding citation: Penna, A. is supported by National Science Foundation (BCS 2120691), Pozzi is supported by National Science Foundation (BCS 1926105)

Comparison of hind limb kinematics in *Lemur catta* climbing and descending a 45˚ oriented substrate

BERNADETTE A. PERCHALSKI[1], ANGEL ZEININGER[2] and DANIEL SCHMITT[2]

[1]Basic Medical Sciences, University of Arizona College of Medicine Phoenix, [2]Evolutionary Anthropology, Duke University

The mechanics of climbing are well studied in primates. In contrast, little is known about the mechanics of descent despite its importance in arboreal locomotion. Rump-first descent is qualitatively described as the kinematic 'reversal' of quadrupedal climbing. This study tests that prediction by directly comparing the kinematics of ascending and descending. *Lemur catta* (n = 4) were filmed traveling on a thin (3.18 cm) wooden pole oriented at 45˚. Symmetrical strides (33 ascents, 16 descents) were collected to measure stride length and speed, total hind limb excursion, and knee angle at touchdown and takeoff. Welch's t-test was used for statistical comparison. The predicted kinematic 'reversal' is observed in the knee angle at touchdown and takeoff. During ascent, the knee is flexed at touchdown (mean 75.3˚) and extended at takeoff (mean 149.3˚), while this is reversed in descent (touchdown mean 149.2˚, takeoff mean 84.2˚). The degree of knee flexion was significantly greater during ascent ($p < 0.01$), with no differences in extension. Descents were significantly slower ($p < 0.01$), had smaller hind limb excursions ($p < 0.01$) and shorter stride lengths ($p < 0.01$). During ascent primates used diagonally sequenced gaits, but in descent they often relied on an unsequenced gait that featured relatively long hind limb contact periods and aerial forelimbs. Therefore, kinematic reversal of the hind limb joint angle appears to be just one of several gait modifications primates make during rump-first descent, and further study is needed to fully understand the role of the forelimb in this behavior.

Funding for this research was provided by the Duke Lemur Center Director's Fund and the National Science Foundation (NSF BSC 1751686).

Ancient DNA-based insights into the diet-related evolutionary ecology of Pleistocene hominins

GEORGE PERRY

Anthropology and Biology, Pennsylvania State University

Ancient DNA data from Neandertals, Denisovans, and archaic anatomically modern humans can be used to complement our understanding of hominin dietary ecology through i) direct inference of archaic hominin diet-related phenotypes, ii) indirect inference of those phenotypes by identifying the effects of previously-introgressed alleles still present among modern humans, iii) determining the evolutionary timing of relevant hominin-specific genetic changes, iv) identifying evidence of consumed foods from dental calculus, and v) studying DNA signatures from soil samples from occupation layers of hominin-inhabited sites. I will review the current landscape of this knowledge in addition to detailing results from our reanalysis of published Neandertal and Denisovan genome sequence data to infer the timing of five human gene presence/absence changes that may be related to particular hominin-specific dietary changes. For example, we found that pseudogenizing (gene loss) mutations in the *TAS2R62* and *TAS2R64* bitter taste receptor genes and the *MYH16* masticatory myosin gene occurred after the hominin-chimpanzee divergence but before the divergence of the human and Neandertal/Denisovan lineages, whereas salivary amylase gene (*AMY1*) duplications were not observed in the Neandertal and Denisovan genomes, suggesting a relatively recent origin for the *AMY1* copy number gains that are observed in modern humans.

Sexual dimorphism in a sample of semi-commensal chacma baboons (*Papio ursinus*) from South Africa

RYAN PHELAN[1], SHAHRINA CHOWDHURY[2,3,4], ESME BEAMISH[5], LARISSA SWEDELL[3,4,6,7], MICHAEL PLAVCAN[8], DEBRA GUATELLI-STEINBERG[1] and SCOTT MCGRAW[1]

[1]Department of Anthropology, The Ohio State University, [2]Department of Anthropology, Brooklyn College–CUNY, [3]Department of Anthropology, CUNY Graduate Center, [4]Department of Anthropology, New York Consortium in Evolutionary Primatology, [5]Department of Anthropology, Institute for Communities and Wildlife in Africa (iCWild), University of Cape Town, [6]Department of Anthropology, Queens College–CUNY, [7]Department of Archaeology, University of Cape Town, [8]Department of Anthropology, University of Arkansas

The determinants of sexual dimorphism continue to be investigated. Here we investigate sexual dimorphism in a skeletal sample of 28 (20 males, 8 females) chacma baboons (*Papio ursinus*) from South Africa. The sample comprises individuals living in proximity to humans that were euthanized due to raiding and other issues related to baboon-human conflict. Body weights of several males exceed the largest on record. We use dental measurements to test the hypotheses that (a) body weight and canine size are correlated in males, (b) male body weights correlate more strongly with canine than with second molar crown size, and (c) this sample exhibits greater sexual dimorphism relative to museum collections of the same species. These associations are expected for at least 3 reasons: (1) higher testosterone levels during development, often associated with aggression and increased muscle mass, increase both body and canine sizes; (2) males with larger canines are better able to access human-derived foods and increase their body weights; and (3) in *P. cynocephalus*, food-enhanced males have longer canines at younger ages. While the canine dimensions of our sample fell within the range of museum collections of *P. ursinus* and other baboon taxa, sexual dimorphism in canine mesiodistal and crown height dimensions exceeded that of comparative published samples. Correlations between male body weight and tooth size were in most cases greater for maxillary canines than for second molars or mandibular canines. Our results support an association between maxillary canine size, body weight, food enhancement and behaviors related to baboon-human conflict.

Amara West: A dental insight into Egyptian-Nubian interactions in the New Kingdom

EMMA LW. PHILLIPS[1,2], JOEL D. IRISH[1] and DANIEL ANTOINE[2]

[1]School of Biological and Environmental Sciences, Liverpool John Moores University, [2]Department of Egypt and Sudan, The British Museum

Egypt invaded and ruled much of Nubia in the New Kingdom (c.1550–1069 BCE). Consequently, the level of integration between populations during this period has been highly debated. Amara West was the Egyptian administrative center in Upper Nubia during the later stages of Egyptian rule (c.1294–1069 BCE). It contained two cemeteries, thought to be for elite and non-elite individuals. This study investigates whether these New Kingdom inhabitants of Amara West were: 1) Egyptian immigrants, 2) Nubians, 3) both, or 4) if admixture may be indicated. Additionally, assessments were made concerning whether interment in either cemetery suggests specific biological affinities.

Thirty-six nonmetric ASUDAS traits were recorded in a total 144 individuals, for comparison with those in 12 Nubian and Egyptian samples dating from the Old Kingdom (2613-2494 BCE) through Roman periods (200–400 CE). Inter-sample bio-distances were calculated using the mean measure of divergence (MMD) statistic, with multi-dimensional scaling used to visualize affinities.

The Amara West assemblage shows similar levels of affinity to both Nubian (mean MMD=0.07) and Egyptian samples (MMD=0.08, p≤0.05). After the assemblage was divided by cemetery, both samples (elite and non-elite) presented high levels of affinity to both Egyptians (MMD=0.032-0.21, p≤0.05) and Nubians (MMD=0.05-0.10, p≤0.05). The non-elites are significantly different from several Egyptian samples. These data suggest both Egyptians and Nubians inhabited Amara West, along with potential admixture. Furthermore, the statistical differences observed in the non-elite cemetery could indicate ethnicity played a part in cemetery choice at Amara West.

Support from the Wellcome Trust (British Museum grant 097365/Z/11/Z), Liverpool John Moores University (Matched-Funded PhD Scholarship), and the National Science Foundation (BNS-9013942, BNS-0104731).

The efficacy of a priori grouping in cold adaptation studies

ERIN F. E. PINKSTON, MARIANNE J. COOPER and NOREEN VON CRAMON-TAUBADEL

Buffalo Human Evolutionary Morphology Lab, Department of Anthropology, University at Buffalo, SUNY

Given the recent global expansion of tropically-adapted *Homo sapiens*, morphological studies of the cranium have investigated potential selection in response to expansion into different climatic zones. While studies indicate morphological evolution in the human cranium is primarily subject to neutral evolution, the midfacial region shows potential adaptation to extreme cold climates. In studies of cold adaptation, however, a priori classification systems used to designate which populations are potentially cold-adapted vary. Here, we explore how effective non-climatic variables used to designate populations as potentially cold-adapted are for determining which populations experience extreme cold climates. 22 populations from Howells' dataset were designated as either potentially cold-adapted or non-cold-adapted using latitude and geographic region as proxies for climate. Averaged annual vapor pressure and minimum, mean, and maximum temperatures for the geographic locations of the populations were then analyzed using Principal Components Analysis (PCA), grouping populations by similarities in climate. The a priori designations were then compared to the PCA, which indicated that using latitude or geographic region as a classifier resulted in populations in a variety of climatic zones falling under the "cold-adapted" designation. This observation emphasizes the need to use climatic data rather than non-climatic variables as proxies for climate when assigning a priori designations in cold adaptation studies.

When studying human sociality, we need to distinguish intergroup relationships from long-distance relationships

ANNE C. PISOR[1] and CODY T. ROSS[2]

[1]Department of Anthropology, Washington State University, [2]Department of Human Behavior, Ecology, and Culture, Max Planck Institute for Evolutionary Anthropology

Intergroup relations—usually intergroup conflict between ethnic groups, but sometimes also intergroup relationships (IRs)—dominate the literature on human sociality. This focus has obscured our characterization of other integral features of human sociality—like long-distance relationships (LDRs), which are often conflated with IRs. While both IRs and LDRs can provide resource access, LDRs likely predate IRs in human evolution and are especially effective for managing correlated resource shortfalls and accessing clumped resources not locally available. To illustrate why IRs and LDRs should be studied separately, we draw on a case study from rural Bolivia. This case study demonstrates how (1) differences in socioecology and the outcomes of past interactions and (2) researcher expectations with respect to IRs can bias both data collection and data interpretation, in turn impacting our characterizations of human sociality. We close by outlining areas of LDR research that will improve our understanding of human sociality.

The Max Planck Society for Evolutionary Anthropology, the US National Science Foundation (DDRIG 1357209), the Wenner-Gren Foundation (Dissertation Fieldwork Grant 8913), UCSB Broom Center, and UCSB Anthropology provided funding.

Come together over me: The role of the chondrocranium in dermal bone formation of the skull

M. KATHLEEN PITIRRI[1], SUSAN M. MOTCH PERRINE[1], HAO ZHENG[2], DANNY Z. CHEN[2], KAZUHIKO KAWASAKI[1] and JOAN T. RICHTSMEIER[1]

[1]Department of Anthropology, Pennsylvania State University, [2]Department of Computer Science & Engineering, University of Notre Dame

Although a major focus of bioanthropology is quantification of skull variation throughout primate evolution, investigations have largely ignored the chondrocranium that proceeds the bony skull in development. The difficulty in studying the chondrocranium, initially composed of cartilage, is partly due to the transient nature of this complex structure during embryogenesis. The chondrocranium appears prior to the appearance of cranial bones but as development progresses, chondrocranial elements either dissolve as cranial dermal bones ossify intramembranously to form the dermatocranium, ossify into endochondral bone, or remain cartilaginous. While the relationship between elements of the chondrocranium and skull bones that ossify endochondrally is clear, the relationship between bones of the dermatocranium and their associated chondrocranial elements is less certain. To evaluate the hypothesis that the chondrocranium serves as a scaffold for the dermatocranium during embryogenesis, we present morphometric analyses of the mouse chondrocranium from embryonic day (E)13.5 to E17.5, and the dermatocranium from E15.5 to E17.5, in mice carrying a mutation in fibroblast growth factor receptor 2 (*Fgfr2*), which is associated with Crouzon syndrome in humans. Our results reveal significant differences in chondrocranial morphology between mice carrying the *Fgfr2* mutation and unaffected littermates prior to the development of dermatocranial bones and differences in integration of the dermatocranium and chondrocranium. Our results suggest that dermatocranial variation is driven by variation in the chondrocranium, and that studying chondrocranial variation across Primates is critical to understanding dermatocranial variation in primate evolution.

Funding: NICHD grant P01HD078233 & NIDCR grant R01DE027677

Paternity, group size, sexual selection, and sexual dimorphism in primates

J. MICHAEL PLAVCAN

Anthropology, University of Arkansas, Fayetteville

It is widely accepted that sexual size dimorphism (SSD) and canine dimorphism (SCD) in primates are products of sexual selection, especially through male-male agonistic competition. While most comparative tests corroborating this hypothesis rely on surrogate measures of sexual

selection such as competition levels, breeding system, or the operational sex ratio, recent analyses of paternity skew find no support for the hypothesis. However, these analyses fail to account for the interaction between breeding system, group size and paternity skew. Thus, monomorphic monogamous males often sire 100% of offspring, as do some resident males in dimorphic small polygynous groups. While such data seemingly corroborate the sexual selection hypothesis, statistically paternity skew for the two breeding systems is equal, thereby rejecting the hypothesis. This analysis evaluates the relationship between these variables and dimorphism using comparative paternity and morphological data for 50 primate species. Paternity skew is estimated as the percentage of offspring sired by dominant or resident males. While raw skew is not associated with female group size or dimorphism, it is strongly negatively correlated with female group size excluding monogamous species. Female group size is associated with dimorphism in both traits, but multiplying female group size by paternity skew to correct for the dependency of skew on female group size results in stronger correlations for SCD, but not SSD. The results strongly suggest that female group size and breeding system play a critical role in the relationship between paternity skew and the evolution of sexual dimorphism in primates.

Predicting environmental and ecological drivers of human population structure

EVLYN PLESS, ANDERS ECKBURG and BRENNA HENN

Department of Anthropology, UC Davis

Landscape, climate, and culture can all structure human populations, but few methods are designed to disentangle the importance of these many variables. We present a machine learning method for identifying the variables which best explain migration rates, as measured by the coalescent-based program MAPS which uses shared identical-by-descent tracts to infer and extrapolate spatial migration across a region of interest. We apply our method to 30 human populations in eastern Africa with high density SNP array data. The unparalleled diversity of ethnicities, languages, and environments in this region offers a unique opportunity to explore the variables that shape migration and genetic structure in humans. We explored more than twenty spatial variables relating to landscape, climate, and presence of tsetse flies (an important disease vector). The full model explains ~41% of variance in migration rate – precipitation, minimum temperature of the coldest month, and altitude were found to be the most important variables. Among the three groups of tsetse flies, the most important was the fusca group which vectors livestock trypanosomiasis. We also performed a selection scan on a subgroup of the populations who live in Ethiopia at relatively high altitudes. We did not identify well-known high-altitude genes, but we did find signatures of positive selection related to metabolism and disease (e.g. PNPLA2 and IRF4). We conclude that environment and landscape shaped the migration and adaptation of human population in east Africa, but cultural factors not captured in our model likely contributed as well.

The use of actualistic studies to model an early hominin scavenging niche

BRIANA POBINER

Anthropology, Smithsonian Institution

This abstract is part of the symposium *Current and multidisciplinary perspectives on hominin diets and trophic level during the Pleistocene*. This presentation reviews actualistic studies of passive scavenging from free-ranging predators in modern east African ecosystems undertaken to infer the types and amounts of carcass resources that could have been available to passively scavenging hominins. The quality of a passive scavenging opportunity provided by a carcass can be measured by the amount of edible tissues remaining after initial carcass consumption by predators and the length of time a carcass persists as a source of scavengable food. I compare variables that can affect the quality of a scavenging opportunity across these studies, including carcass size, carcass habitat, initial consumer body size, initial consumer feeding group size, ability of the initial consumer to expose edible tissue, and ecosystem predator: prey ratio. I present data from my published research and that of others to demonstrate that the quality of scavenging opportunities is not uniform within or across ecosystems, and that some ecological settings afford higher quality scavenging opportunities than others. I also identify opportunities for further exploration of a passive scavenging niche using actualistic studies.

What behavioral and biological traits are constraining social state evolution across Lorisiformes?

STEPHAINE A. POINDEXTER[1,2], KEELY Q. MAYNARD[1], VINCENT NIJMAN[2] and K.A.I. NEKARIS[1,2]

[1]Anthropology, SUNY Buffalo, [2]Nocturnal Primate Research Group, Oxford Brookes University

Among primates, Lorisiformes are consistently the most informative in identifying ancestral states through phylogenetic-based models, including those focused on social state evolution. We know that most of the current primate social states are conserved throughout evolutionary history, but our understanding of what traits are correlated with each social state, and which if any may act as constraining factors is limited. Here, we looked at Lorisiformes social states and five biological and behavioral traits to see if they displayed any signs of correlated evolution. We pulled our dataset from published observations of body size, sleep group sizes, sleep site type, vocal cohesion, and infant care in 20 species (10 Galagidae; 10 Lorisidae). We used Pagel's binary tests for correlated evolution, which uses discreet variable pairings to determine if the paired traits evolved independently or dependently. Among all of the pairings in our dataset, we only found evidence of correlated evolution between species using a dispersed family group and their use of specific sleeping sites (e.g., forked branches). While sleeping sites are highly variable based on the environment, our results likely reflect their need for security and tolerance for conspecifics. Social tolerance is known to constrain social state evolution in other primates, as we expand our understanding and perception of social cohesion, tolerance, and behaviors in these nocturnal primates, we may find a similar trend.

Effects of exercise on spatial variation in subchondral and trabecular bone properties

JOHN D. POLK[1,2,3], HYUNGGWI SONG[4] and MARIANA E. KERSH[4]

[1]Anthropology, University of Illinois, [2]Biomedical and Translational Science, University of Illinois, [3]Anthropology, University at Albany, [4]Mechanical Science and Engineering, University of Illinois

This research evaluates how exercise influences spatial variation in trabecular and subchondral bone properties across the joint surface, and with increasing depth, in the medial femoral condyle. These properties are commonly used to make behavioral inferences in hominins. We hypothesized that exercise would cause increased thickness and density and more strongly affect bone closest to the articular surface.

We compared bone properties from exercised, and non-exercised groups of sheep. Condyles were microCT scanned to quantify subchondral and trabecular thickness, and density, trabecular bone volume fraction (BV/TV), and degree of anisotropy (DA). We compared medial, central and lateral regions of the condyle at subchondral as well as superficial, intermediate and deep trabecular layers.

Subchondral and trabecular thickness increased with exercise on the medial but not the lateral side of the condyle, and the effect dissipated with depth. Density increased on the subchondral surface but more markedly on the lateral side of the condyle. Subtle postural differences were apparent in the density of the shallowest trabecular region, but not in deeper trabecular layers. The most anisotropic bone is found laterally, and this pattern was maintained with depth. Spatial variation in BV/TV largely follows thickness.

These results demonstrate that the spatial response of bone is heterogeneous and exercise increases thickness and density but not in the same places. Exercise effects dissipate with increasing depth. These patterns of bone growth are essential for making inferences about hominin behavior and guide choices in which regions of bone will be most informative for providing behavioral information.

This research was supported by the National Science Foundation (1638756)

The Demography of Violence: Patterns of Interpersonal Violence in a Middle Bronze Age Population from Northeastern Serbia

KATHERINE M. POMPEANI

Forensic Anthropology, Defense POW/MIA Accounting Agency

Violent conflict in Middle Bronze Age (ca. 2000-1500 BCE) populations in Central Europe is assumed to have been widespread, but there is limited physical evidence as to the effect of interpersonal violence and warfare on demographics. This study presents a skeletal analysis of trauma from the cemetery at Ostojićevo, Serbia (1920-1550 BCE). Skeletal remains (n=229) were analyzed for sex, age, and evidence of trauma. Biological sex was assessed skeletally in individuals ≥18 years and inferred from body position in subadults (<18 years). Analysis of sex-specific survivorship found no significant difference in overall survival time between males and females. Sharp- and blunt-force weapon injuries to the cranial vault present the most unequivocal evidence of interpersonal violence at Ostojićevo. Additionally, two individuals exhibited complex antemortem injury patterns. There is no skeletal evidence of violent trauma in individuals <12-15 years and in females <40 years. The highest prevalence of violent trauma occurs in males 30-40 years (25%). Total prevalence of violent trauma is 12.5% in males and 3.6% in females. The pattern of trauma attributed to interpersonal violence suggests one-on-one encounters rather than organized warfare with skeletal patterns of trauma indicating cultural appropriate methods of combat. This study has implications for documenting the cultural and demographic realities of violence in Middle Bronze Age communities.

This work was supported by an Andrew W. Mellon Predoctoral Fellowship and the University of Pittsburgh.

What do Living and Recent Hunter-Gatherers Tell Us about Ancestral Diet and the Human Trophic Level?

HERMAN PONTZER[1,2] and BRIAN M. WOOD[3]

[1]Evolutionary Anthropology, Duke University, [2]Duke Global Health Institute, Duke University, [3]Department of Anthropology, UCLA

This presentation is part of the symposium *Current and Multidisciplinary Perspectives on Hominin Diets and Trophic Level during the Pleistocene. Homo* is a hunting and gathering genus, and this subsistence strategy characterized hominin populations throughout the Pleistocene. Living hunter-gatherer communities have therefore played a central role in reconstructing the diets and trophic level of Paleolithic populations. Here, we review ecological and ethnographic data from living and recent hunter-gatherer communities to understand how hunter-gatherer diets vary over time, geography, and economy. Among tropical and temperate populations, the proportions of animals and plants vary widely among groups and over time. Populations in colder climates, those that depend more heavily on fishing, and those that incorporate some degree of pastoralism rely more heavily on animal foods. Populations in warmer climates, and those that incorporate some degree of farming, depend more heavily on plants. Macronutrient proportions in living hunter-gatherer groups are carbohydrate-dominated. The remarkable variability in hunter-gatherer diets across time and space belies the notion of a singular, narrow ancestral diet, and supports the view that hominins throughout the Pleistocene were strategic omnivores, subsisting on variable and locally adapted diets.

The accuracy of photogrammetry for the recording of antemortem cranial depression fractures using low-cost and open-source software

KERI PORTER

Department of Anthropology, University of Notre Dame

Within bioarchaeology and paleopathology, digitally recording human skeletal remains holds significant promise for long-term preservation, long-distance collaboration, digital analysis, and education. Of the many potential applications, the digital recording and analysis of traumatic fractures could be significant for increasing standardization in trauma analysis and enhancing our understandings of violence and lived experience in the past. Compared to other methods for digital modeling, photogrammetry is portable, user-friendly, and cost-effective. Additionally, photogrammetry does not require that skeletal remains be present during model construction if suitable photographs exist. Despite these potential benefits of photogrammetric modeling, few investigations into this technology have occurred. This research contributes to studies of photogrammetry in biological anthropology by investigating the accuracy of this technology for recording antemortem cranial depression fractures (CDFs). Using the Mississippi State Asylum skeletal collection, dry bone measurements of CDFs were compared to those on photogrammetric models. Models were constructed and analyzed using affordable and open-source software to encourage accessibility in research. Results showed that maximum length and width measurements for each lesion could be digitally recorded to a statistical accuracy. Maximum depth could not be recorded within the tools provided by the software. Therefore, photogrammetry should not be used for the initial recording of CDFs when dry bone recording is possible. However, photogrammetric modeling could still be useful in research when dry bone remains are not available or as a reference for researchers after initial studies when access to skeletal collections is no longer possible or convenient.

Frontal sinus variation in Later Stone Age crania from South Africa

NICHOLAS W. POST[1], CARRIE S. MONGLE[1,2,3] and FREDERICK E. GRINE[1,4]

[1]Department of Anthropology, Stony Brook University, [2]Turkana Basin Institute, Stony Brook University, [3]Division of Anthropology, American Museum of Natural History, [4]Department of Anatomical Sciences, Stony Brook University

The frontal sinus (FS) exhibits considerable variation in size and shape between individuals and among recent human populations. Although volumetric data have been recorded from CT scans for numerous (n = 37) samples of Middle Eastern, European, Asian and American populations, only four samples have been documented for the entire African continent - one sample of Nubian language speakers from Sudan (n = 35), two samples of Bantu language speakers from West Africa (n = 13 and n = 27), and one sample of living South African Nguni speakers (n = 330).

This study documents FS volume in a sample (n = 102) of radiocarbon dated (range of 10.1 - 0.56 ka) adult crania from Later Stone Age archaeological contexts in South Africa. Previous 3DGM analyses of these crania have demonstrated distinctly Khoesan morphology, indicating population continuity. Sex could be determined for 85 individuals based on associated pelves. The sample was divided into five temporal bins of approximately equivalent size (average = ~20 individuals) to evaluate possible chronological trends in FS volume.

Sinuses were manually segmented from CT scans using Avizo 9.7 to measure FS volume, with the inferior margin of the FS defined by a horizontal plane coincident with the cribriform plate. Relative FS volume was determined using the geometric mean of four linear measurements for each cranium. Neither absolute nor relative FS volume shows significant sexual dimorphism in this sample. Similarly, there is no apparent temporal trend in FS volume over the span of the Holocene.

This work was generously supported by The Leakey Foundation and The Wenner-Gren Foundation.

Comparative Trauma Analysis Between Erie County Poorhouse and Colorado State Insane Asylum

ROXAYN L. POVIDAS and JENNIFER F. BYRNES

Department of Anthropology, University of Nevada Las Vegas

Skeletal trauma is one line of bioarchaeological evidence that structural violence can inscribe itself into human bodies. Previously collected skeletal trauma data from two samples: the Erie County Poorhouse cemetery (1851-1913) (ECPH), located in Buffalo, New York, and the Colorado State Insane Asylum cemetery (1879-1899) (CSIA), located in Pueblo, Colorado was utilized for this analysis. The crania and upper limb skeletal elements from skeletally mature adults were included in this study, as these regions are typically where violent-intent trauma would be located. ECPH individuals with 75% or more completeness of the individual skeletal element were included. 304 individuals from ECPH and 166 from CSIA were included to determine if institutionalization put individuals at a greater risk for interpersonal violence and/or abuse. Results indicated that there was no significant difference in cranial trauma between institutions (p=0.25) or sex (ECPH p=0.056, CSIA p=0.53). The only skeletal trauma that appears to have a pattern related to sex was upper limb trauma with ECPH males being more likely than females to show evidence of upper limb trauma (p=0.0003). The same could not be said for CSIA due to there being no upper limb trauma within the female sample. Additional archival research inferences will be made to link trauma patterns within the skeletal samples to institutionalization and abuse within a structural violence framework. This research focused on two disenfranchised groups that identified marginalizing social mechanism that likely contributed to the trauma patterns present in the samples.

Unlocking the past: museomics of African galagids

LUCA POZZI[1], KAYLA PRINGLE[1], ANNA PENNA[1], KATHRYN M. EVERSON[2], DAVID W. WEISROCK[2] and MARY E. BLAIR[3]

[1]Anthropology, The University of Texas San Antonio, [2]Biology, University of Kentucky, [3]Center for Biodiversity and Conservation, American Museum of Natural History

Our understanding of primate phylogenetics is often limited by our ability to obtain high-quality data from wild populations. Developments in sequencing techniques have recently unlocked genetic access to millions of specimens housed in museum collections, providing an exciting alternative to overcome issues with sampling wild populations. Galagids are among the least studied primates and the lack of both comprehensive taxonomic and geographic sampling and genetic data has hindered our understanding of their evolutionary history. Here, we discuss the promise and challenges of using museum collections to study galagid evolution. We extracted over 150 specimens dated between 1912 and 1974 and we found that sample age was not a significant factor for determining DNA concentration (R2=0.035; F=2.335, p=0.1314). We used target sequence capture to generate data at the genomic level. The final dataset contained 334 loci and a total of 1,108,850 bp. A total of 48 lorisiform specimens were included in the dataset, representing 13 galagid and 7 lorisid species. The level of support for the monophyly of the family Lorisidae improves by increasing the number of loci included in a species tree analysis. Phylogenetic analyses confirm known phylogenetic relationships among galagid genera with high support; however, a few species were not recovered as monophyletic suggesting that either some museum specimens were mislabeled, or the current taxonomy does not reflect species diversity adequately. Future work will be focused on obtaining additional data for specific taxonomic groups to further advance our understanding of cryptic diversity within the Galagidae.

Funding for work provided by National Science Foundation (BCS 1926105/1926215)

The causes and consequences of women's status in Himba pastoralists

SEAN P. PRALL[1] and BROOKE A. SCELZA[2]

[1]Department of Anthropology, University of Missouri, [2]Department of Anthropology, University of California, Los Angeles

Gender inequalities in status are a common feature of many populations, but while the drivers of men's status have been well-studied, evolutionary perspectives on women's status are underdeveloped. Here we combine demographic data with a dataset of peer ratings (n>10,000) from Himba pastoralists, a group with a high degree of female autonomy. Specifically, we explore (1) the determinants of women's status, (2) how status determinants differ for men and women, and (3) how women's status impacts fitness-related outcomes. Perceptions of generosity, intelligence, and respectfulness best predicted women's status (pr[b>0]>95%), with neither wealth nor fertility being meaningful predictors. Multilevel models comparing men and women showed some sex differences, with fertility, attractiveness, and wealth better predicting men's status. Surprisingly, although men tend to reach higher status at older ages, men were no more likely than women to be rated influential by their peers. Women's status had several important effects on outcomes related to reproductive success. Women's status predicted residuals for children's height (pr[b>0]=99%), particularly for younger children (pr[b<0]=97%), but not weight. Status also predicted estimates of women's desirability as a partner (pr[b>0]=99%). In marital and non-marital partnerships, women's and men's status was positively correlated (rho = 0.29), and in a multilevel model, women's status predicted the status of their partner (pr[b>0]=99%). These findings highlight the diverse social drivers of women's status, particularly community perceptions of prosociality, and highlight how the motivations for attaining status relate to reproductive success, including child health and procurement of high-quality partners.

This work was funded by the National Science Foundation (BCS-1534682) to B.A.S.

Capitate morphometrics and evolutionary modeling with implications for the knuckle-walking hypothesis

THOMAS C. PRANG

Anthropology, Texas A&M University

The positional behavior of the human-chimpanzee last common ancestor (LCA), although critically important for interpreting the evolution of human bipedalism, is currently unknown due to a lack of relevant fossil material. Previous investigators have presented various competing hypotheses for the positional behavior of the LCA, but they can be collapsed into hypotheses about evolution from an essentially African ape-like ancestor, or a more "generalized" ancestor lacking postcranial features associated with vertical climbing, suspension, and terrestrial quadrupedalism. The evolution of terrestrial features in the postcranial skeleton of African apes and humans is a focal aspect of questions surrounding the positional behavior of the LCA. This study evaluates the long-standing knuckle-walking hypothesis using evolutionary modeling and ancestral estimations of capitate morphology. The comparative data set includes five linear capitate metrics representing early fossil hominins, extant hominoids, cercopithecoids, and platyrrhines (N = 374). Principal components analysis (PCA) was used to reduce the dimensionality of the data for subsequent analyses. Evolutionary models were fit to the principal components to infer evolutionary shifts in capitate shape across the anthropoid phylogeny hypothetically associated with locomotor behavior. The results show that recent humans, African apes, and early fossil hominins occupy a derived selective regime associated with the intrinsic radioulnar expansion of the capitate head, plausibly associated with knuckle-walking hand postures utilized among extant African apes. When interpreted within the context of recent analyses demonstrating that early hominins retain suspensory hand and heel-strike plantigrade foot morphologies, these results are consistent with human evolution from a knuckle-walking ancestor.

This research was supported by a Wenner-Gren Dissertation Fieldwork Grant

Coloring inside the invisible lines: A novel method for reconstructing the endocast for an incompletely ossified skull

KATHRYN A. PROFFITT[1], BRENNA R. MCGOVERN-LIND[1], SIAN EVANS[2], VALERIE B. DELEON[3] and TIMOTHY D. SMITH[1]

[1]School of Physical Therapy, Slippery Rock University, [2]Monkey Jungle, DuMond Conservancy, [3]Department of Anthropology, University of Florida

Digital endocasts of subadult primates are complicated by the incomplete ossification of the skull at early ages. For example, micro CT does not allow visualization of the cartilaginous nasal capsule prior to ossification. Here, we present a novel method for isolating unossified boundaries of the endocranial contour. DiceCT scans provide imaging of unossified tissues, including some cartilaginous structures. Superimposition of semi-transparent diceCT scans on micro CT scans in Photoshop allows the investigator to observe complete endocranial contours, including the unossified material. Using Amira software, these hybrid scan slices were employed to segment an endocast of a newborn owl monkey (*Aotus nancymaae*) whose nasal capsule had not yet reached full ossification. The endocast of the newborn was then volumetrically compared to those of endocasts segmented from infant and adult Aotus specimens. Most notably, the method allowed us to establish the plane of the cribriform plate and the lesser wings of the sphenoid, both of which were unossified in the newborn. Preliminary findings indicate that at birth, *Aotus* has an endocranial volume that is about 50% of the adult volume, and by two weeks the endocranial volume is nearly 90% of adult volume. Since most primates have a partially cartilaginous nasal capsule at birth, this new method resolves issues of "hidden" skeletal boundaries that are inherent to traditional microCT of subadults. This method may also significantly improve the accuracy with which researchers reconstruct an endocast.

Funded by NSF grant #s BCS-1830894 and BCS-1830919.

Marginalizing Melanin: Historical Pigmentation-Based Prejudices Obscuring Research on the Microevolution of Skin Pigmentation

YEMKO PRYOR and JOHN LINDO

Department of Anthropology, Emory University

For centuries Black, Indigenous, and other non-European populations have experienced oppression based upon the level of melanin present in their skin. Although researchers are aware of the selective advantages of highly melanated skin, historical racism and White supremacy have contorted research on this adaptive trait for centuries. Here we present the historical racial biases plaguing methodological approaches used by Anthropologists exploring this adaptive trait, elucidating the ways in which White supremacy has hindered skin pigmentation research. Additionally, analysis of loss of pigmentation-associated genetic variants in Neandertals and ancient Eurasians in comparison to modern Eurasians, has indicated a nuanced understanding of the "vitamin D theory." This highlights the need for incorporation of epigenetic analysis in further interrogating the bio historical significance of this phenomenon. Finally, by incorporating analyses of ancient Indigenous Andean genomes, we further the knowledge around the evolutionary histories of skin pigmentation phenotypes and adaptation to high UV environments in historically marginalized populations; further dispelling racist paradigms built upon the exclusion of individuals containing higher levels of melanin.

This work is supported by the NSF-BCS-1926075, the NAS Ford Foundation Predoctoral Fellowship, and the NSF-GRFP.

A virtual reconstruction of the cranium of *Pierolapithecus catalaunicus*

KELSEY D. PUGH[1,2], JOSEP FORTUNY[3], BRIAN M. SHEARER[2,4,5], ASHLEY S. HAMMOND[1,2], SALVADOR MOYÀ-SOLÀ[3,6,7], DAVID M. ALBA[3] and SERGIO ALMÉCIJA[1,2,3]

[1]Division of Anthropology, American Museum of Natural History, [2]New York Consortium in Evolutionary Primatology, (NYCEP), [3]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, [4]Department of Cell Biology, NYU Grossman School of Medicine, [5]Department of Foundations of Medicine, NYU Long Island School of Medicine, [6]Institució Catalana de Recerca i Estudis Avançats, (ICREA), [7]Unitat d'Antropologia Biològica, Departament de Biologia Animal, Biologia Vegetal i Ecologia, Universitat Autònoma de Barcelona

There are ongoing debates about the systematics of Miocene apes, particularly their relationships to extant apes, which are complicated by the deformation and fragmentary preservation of many fossils. Damage to the holotype cranium of *Pierolapithecus catalaunicus* (IPS21350.1; 12.0 Ma, northeastern Spain) has fueled debates about the affinities of this taxon, as well as about its distinctiveness from other fossil apes known from nearby deposits of similar age. The central role these taxa have played in discussions of ape evolution makes it critically important to better understand their phylogenetic relationships.

Here, we present a CT-based virtual reconstruction of IPS21350.1. Subsequently, we use generalized Procrustes analyses (GPA) followed by principal components analysis (PCA) and cluster analysis (using UPGMA) of 106 three-dimensional craniofacial landmarks to compare this preliminary reconstruction to extant anthropoids. By repositioning and mirror-imaging facial fragments, it was possible to correct for major distortions and gain a better understanding of facial height, breadth, and geometry, as well as orbital shape and dimensions. In the PCA, the virtual reconstruction of IPS21350.1 plots nearest to great apes. Features that align this specimen with great apes on PC1 include increased prognathism, the higher position of the orbits relative to the nasal aperture, and alignment of the frontal processes of the maxillae, inferior nasals, and orbits. Cluster analysis of all PC scores places the reconstructed cranium as sister to extant hominids. This position is consistent with proposals that *Pierolapithecus* represents a stem hominid. Future analyses will incorporate other fossil ape crania from the Vallès-Penedès Basin.

MCIN/AEI (PID2020-116908GB-I00, PID2020-117289GB-I00, PID2020-117118GB-I00), and Generalitat de Catalunya (CERCA Programme and Consolidated Research Groups 2017 SGR 086 and 2017 SGR 116).

Birthweight predicts epigenetic age acceleration during the first three years of life

EDWARD B. QUINN[1,2], CHU J. HSIAO[1,2,3], FELICIEN M. MAISHA[4,5] and CONNIE J. MULLIGAN[1,2]

[1]Department of Anthropology, University of Florida, [2]Genetics Institute, University of Florida, [3]MD-PhD Program, University of Florida, [4]Emerging Pathogens Institute, University of Florida, [5]Maisha Enyanya

The Developmental Origins of Health and Disease hypothesis posits that early life experiences become biologically embedded in ways that affect adult health and mortality. Accelerated biological aging may be one way that early life experiences become biologically embedded. DNA methylation data can be used to estimate epigenetic age, a measure of biological age that is highly correlated with chronological age. Discrepancies between epigenetic age and chronological age are known as epigenetic age acceleration (EAA). EAA predicts risk of many chronic diseases as well as overall mortality among adults. Little is known about the emergence of EAA in the first few years of life. We hypothesized that maternal prenatal psychosocial stress and birthweight would moderate the trajectory of EAA in the first three years of life. We used repeated measurements (n=65, observations=150) of EAA collected from birth to three years among children in the Democratic Republic of Congo. We fit linear mixed-effects models to estimate the longitudinal trajectory of EAA. Low birthweight (<2500 grams) predicted increased EAA in the first three years of life, while high birthweight (≥2500 grams) predicted decreased EAA ($p<0.05$). None of our maternal prenatal psychosocial stress measures predicted the emergence of EAA (all $p>0.05$). Our results suggest that prenatal factors that impact birthweight may become biologically embedded through EAA, potentially impacting disease risk decades later.

Funding: NSF BCS-1231264, BCS-1719866, NICHD F30HD097935

ABSTRACTS

How much power can athletes produce? Taking a closer look at kinetic movement, muscle force, and lower limb morphology

KARYNE N. RABEY[1,2], ALISON A. MURRAY[3,4] and JAY T. STOCK[5,6]

[1]Surgery, University of Alberta, [2]Anthropology, University of Alberta, [3]Anthropology, University of Victoria, [4]Archaeology, University of Cambridge, [5]Anthropology, Western University, [6]Archaeology, Max Plank Institute of the Science of Human History

The ability to make behavioural inferences from skeletal remains is crucial for understanding the habitual behaviours of past populations. Interpreting loading experienced by bone during life using skeletal remains however is challenging and more rigorous methods are needed.

This study seeks to build a more accurate picture of the relationship between muscle function and bony structures by also exploring the forces generated by the lower limbs of various athletes (n = 113) and control (n = 38) individuals ranging from the ages of 18-65. Athletes varied from high-impact activity (running, soccer) to lower-impact (rowing). All subjects were asked to jump on a force plate where ground reaction forces and velocity were recorded. Their dominant limb was scanned using pQCT, where bone, muscle, and fat cross-sectional areas could be measured at the thigh and calf. Bivariate correlations were used to assess femoral and tibial bone structures with soft-tissue and performance variables (significance at $p<0.05$).

Results showed that polar second moment of area and cortical thickness were highly correlated with vertical peak power, velocity, and all soft-tissue areas in high-impact female runners for both thigh and calf. In male runners, similar significant results were found but, in the calf, only. Interestingly, peak forces and bone structures from soccer players and rowers were similar to the control group, but significantly differed in muscle area.

The interplay between performance, muscle, and bone was portrayed differently between sexes, activity, and location. These results continue to show the complexity when interpreting behavioural signature on skeletal remains.

European Research Council under the European Union's Seventh Framework Programme (FP/2007-2013)/ERC Grant Agreement n.617627

Mammalian trabecular bone patterns through ontogeny in relation to life history traits

ANNA J. RAGNI

Department of Biological Sciences, California State University Los Angeles

Trabecular bone architecture is known to respond to changes in loading and is thus informative of locomotor behavior. Nevertheless, we still do not know to what extent other factors, such as life history traits, may also be influencing trabecular structure. Here, trabecular bone architecture is measured in the radius and tibia of mammalian taxa through development and compared to documented life history traits. I hypothesize that changes in trabecular measures through ontogeny are related to the length of the juvenile period, gestation length, weaning age, and age at first reproduction. I also hypothesize that systemic trends of trabecular measures remain constant through development and that changes in trabecular measures through ontogeny show phylogenetic signal. Sixty-eight individuals across thirty-four species of mammals were microCT scanned at high resolution. Volumes of interest (VOI) were collected in homologous areas of the distal radius and distal tibia and analyzed in Volume Graphics StudioMax. Phylogenetic generalized least squares analyses show few and isolated significant relationships between changes in trabecular bone through development and life history traits. Ontogenetic changes in trabecular measures are correlated between the radius and tibia. Lastly, changes in trabecular thickness and degree of anisotropy through ontogeny showed significant but weak phylogenetic signal. These results show that life history traits do not necessarily need to be considered when interpreting trends in developmental trabecular data. Furthermore, systemic trends through ontogeny support known relationships in the adult skeleton, and phylogeny should be taken into account when interpreting ontogenetic trabecular results.

This work was funded by a Peter Buck Postdoctoral Fellowship

Co-creating a genomics project benefit-sharing plan: Results from a case study in Madagascar

RINDRA RAKOTOARIVONY[1], SARAH LEBARON VON BAEYER[2,3] and ERIN E. BURKE[3]

[1]Department of Anthropobiology and Sustainable Development, University of Antananarivo, [2]Department of Anthropology, Tufts University, [3]Division of Anthropology & Ethics, Variant Bio, Inc.

There is a well-established discourse about appropriate ways for anthropologists to engage with diverse communities around research and the particular sensitivities associated with genomic studies. However, rarely does that discourse touch upon sharing the benefits of genomic discoveries with participants. One way to ensure that groups receive tangible benefits is to design collaborations that include distribution of funds to communities in the short- and long-term. Specifically, Variant Bio has built a benefit-sharing model so that communities receive a portion of project budgets upon the conclusion of sample collection (short-term benefits) and 4% of revenue plus 4% of equity value if they are acquired or go public (long-term benefits). Here, we present the pilot results of an extensive co-design process for a genomics collaboration between the University of Antananarivo, Variant Bio, and three partner communities in Madagascar. The project was designed in two parts: the first phase included qualitative research to solicit and document suggestions, questions, and concerns about the study design, as well as suggestions for initiatives to support with benefit-sharing funds. The data from these semi-structured stakeholder interviews was analyzed and condensed into a short list of initiatives. In the second phase, study participants were surveyed to collect quantitative data on preferred initiatives to support. In this way, funds go towards causes identified as meaningful by community members themselves. Compensating partner communities through benefit sharing is one way in which researchers can work towards co-designing ethically grounded and culturally relevant partnerships in anthropological genetics research.

This work was funded by Variant Bio, Inc. Seattle, Washington USA.

Colonized Bodies and Descendant Voices: Collaborative Narratives and Learning to Decolonize the Past Through Bioarchaeological Work in Belen, New Mexico

CLAIRA E. RALSTON[1], PAMELA K. STONE[2] and DEBRA L. MARTIN[1]

[1]Department of Anthropology, University of Nevada, Las Vegas, [2]Department of Sociology and Anthropology, Mount Holyoke College

Our project focuses on excavation and analysis of burials from the first colonial mission church cemetery in Belén, NM. Belén, a frontier land-grant settlement, was populated by a diverse community of Spanish and mixed-heritage individuals, including many Native-American freed servants known as Genízaros. This historic cemetery (*c.* 1793-1900) is potentially the largest known colonial-era cemetery of Genízaros. Our work presents a unique opportunity to explore the history of this marginalized community and its people, who have been mostly invisible in colonial and historic narratives. Our goal for this project is collaboration with the descendant community, who invited us to excavate and study this cemetery, and to focus our research questions and interpretations so as not to reproduce colonialist narratives and perceptions of the past. Through our analyses the bones are brought forward to stand in testimony of individuals' lived experiences and as a voice to their stories, which have been silenced by colonial programs of marginalization and assimilation. Further, by working directly with the descendants of the individuals buried here and by actively engaging and collaborating with them in

every step of our research process, we expressly integrate their voices, questions, and positions as stakeholders in how their ancestors' stories are told and how their remains are taken care of. Our project offers a model for how ethical and impactful community-engaged bioarchaeological research can be done, and how we, as scientists, in collaboration with the communities in which our work takes place, can work to decolonize narratives about the past.

This material is based upon work supported by the National Science Foundation under Grant No. 2051184.

Dietary trends in the post-colonization medieval Prussian region

MARISSA RAMSIER[1], ARIEL GRUENTHAL-RANKIN[1,2], KATHERINE GADDIS[1,3] and ARKADIUSZ KOPERKIEWICZ[4]

[1]Anthropology, Humboldt State University, [2]Anthropology, Binghamton University, [3]Anthropology, University of Nevada, Las Vegas, [4]Archaeology and Ethnology, University of Gdansk

During the medieval period, the region that is now northeastern Poland was inhabited by Indigenous Prussians and settlers from Poland and Germany recruited by the Teutonic Order during the Baltic Crusades. Whereas the environmental impacts of this era are well documented, less is known about how the colonization and prolonged conversion process affected Prussian people.

Here, we present the first isotopic analysis of medieval Prussian diet, utilizing carbon values from bioapatite ($\delta^{13}C_{ap}$) and collagen ($\delta^{13}C_{coll}$) from 21 individuals from the cemetery at the rural settlement of Bezławki (14th-15th c.). For $\delta^{13}C_{ap}$, we compare results to a limited sample from the roughly contemporaneous cemetery at Równina Dolna (n=5).

First molar (M1) $\delta^{13}C_{ap}$ values ranged from -14.92 to -12.74 (mean -13.97) for Bezławki and -14.12 to -12.83 (mean -13.58) for Równina Dolna. For Bezławki third molars, $\delta^{13}C_{ap}$ signatures were similar to M1s but averaged slightly less negative. For Bezławki M1s, $\delta^{13}C_{coll}$ ranged from -20.83 to -18.95 (mean -20.11) with more variation among females; spacing between $\delta^{13}C_{ap}$ and $\delta^{13}C_{coll}$ ranged from 5.08 to 7.02 (mean 6.16).

Within the context of additional local and regional isotopic and environmental data and historical records, these findings indicate a predominant reliance on C_3 resources, with moderate variation indicating possible limited consumption of C_4 resources such as millet, animals foddered on at least partial C_4 diets, or aquatic resources. These results are framed within the changing biocultural landscape of medieval Prussia.

Further associations between humeral head curvature and habitat use in cercopithecids

ANDREW RAPOFF[1], TYLER HUMMER[1], NOAH DUNHAM[2], ERIN E. KANE[3], W. SCOTT MCGRAW[4] and DAVID J. DAEGLING[5]

[1]Mechanical Engineering, Union College, [2]Conservation and Science, Cleveland Metroparks Zoo, [3]Anthropology, Boston University, [4]Anthropology, Ohio State University, [5]Anthropology, University of Florida

Primate limb morphologies reflect both locomotor tendencies and habitat use, e.g., humeral head curvature correlates with locomotion and gross substrate preferences among extant taxa and has been used to infer terrestriality for several Miocene catarrhines. We previously found such correlations in two quadrupedal cercopithecids (the terrestrial *Cercocebus atys* and arboreal *Piliocolobus badius*) in anteroposterior and mediolateral planes. Herein, we extend our analysis over the entire humeral head in a fully three dimensional manner. We used surface coordinate data obtained previously using a laser scanner on humeri from *C. atys* and *P. badius* individuals (3 females and 3 males each). Herein, we used various custom codes to create a mesh for each humeral head from the coordinate data, to isolate each articular surface and then to extract curvatures over each surface. In general, curvatures in the *P. badius* samples exhibit more variability than those of *C. atys*. Further, the female samples in both species are less variable than their male counterparts. Curvatures in the anterior regions change rapidly over relatively short distances and display regions of local flatness. Curvatures in the posterior regions change more gradually. Curvatures in the mediolateral planes resemble those in the anterior regions, with rapid changes over short distances and areas of local flatness. Although we have found broad associations between humeral head curvature and positional behavior, we recognize the need for additional field data to test various hypotheses of habitat use in these extant taxa as we expand our knowledge of humeral head shape.

Supported in part by NSF BCS-0921770, BCS-0922414, BCS-0922429 and BCS-60017683.

Biodistance between flexed and extended burials at the Greek colony of Chersonesos

HANNES RATHMANN[1,2], ROMAN STOYANOV[3] and RICHARD POSAMENTIR[4]

[1]Paleoanthropology, Senckenberg Centre for Human Evolution and Palaeoenvironment, University of Tübingen, [2]DFG Center for Advanced Studies "Words, Bones, Genes, Tools", University of Tübingen, [3]Centre of Classical and Oriental Archaeology, HSE University Moscow, [4]Institute of Classical Archaeology, University of Tübingen

The ancient city of Chersonesos (today Sevastopol) was founded in the 5th century BC on the coast of the Crimean Peninsula in the northern Black Sea region, allegedly by Greek colonists from Heraclea Pontica. Numerous archaeological investigations tackled the question of how Greek colonists interacted with local Taurian tribes and whether both groups were buried together at Chersonesos. Relying on burial traditions as an indicator of the ancestry of the deceased, it was hypothesized that individuals buried in flexed positions were Taurian, whereas individuals buried in extended positions were Greek. In this study, we test the hypothesis that individuals in flexed and extended burials are biologically different by directly analyzing the skeletal remains. For this, we collected three different types of phenotypic data, namely, cranial metrics, dental metrics, and dental non-metric traits. We combine the three data types in a single analysis and estimate Gower distance coefficients among 8 flexed and 13 extended burials. The estimated distances are visualized in a principal coordinates analysis (PCoA) and show a large amount of overlap between the two groups. To statistically corroborate this finding, we perform distance-based permutational multivariate analyses of variance (PERMANOVA) and dispersion (PERMDISP). Both analyses reveal that group centroids and group dispersions do not differ significantly between the two groups. We therefore reject the suggestion that burial position and ancestry of the deceased are associated. This result has implications for further archaeological research at Chersonesos and other Greek colonies of the northern Black Sea region.

Senckenberg Nature Research Society; Ministry for Science, Research and Arts of Baden-Württemberg ("Interdisziplinäre Analyse kultureller Kontakte in antiken Randzonen"); German Research Foundation ("DFG FOR 2237" and "DFG INST 37/706-1 FUGG").

Uncovering the Holocene roots of contemporary disease-scapes: bringing archaeology into One Health

KRISTEN M. RAYFIELD[1,2,3], ALEXIS M. MYCHAJLIW[1,2,4], ROBIN R. SINGLETON[1,2], SABRINA B. SHOLTS[3] and COURTNEY A. HOFMAN[1,2,3]

[1]Laboratories of Molecular Anthropology & Microbiome Research, The University of Oklahoma, [2]Department of Anthropology, The University of Oklahoma, [3]Department of Anthropology, National Museum of Natural History, Smithsonian Institution, [4]Department of Biology & Environmental Studies, Middlebury College

The rise in global zoonotic disease events in the 21st century has motivated academic researchers, health professionals, and policy makers to seek solutions from meaningfully integrating animal ecology, conservation biology, and human health. While progress has been made, these contemporary approaches have left the archaeological record—an archive of the

long-term human-environment interactions—largely untapped, hindering our understanding of the dynamic and contingent nature of how anthropogenic activities alter ecosystems and disease-scapes over time. Simultaneously, technological advances in -omic sequencing are changing our understanding of ancient pathogens. Building on previous research, our review fills the gap in studies of past human health and disease and generates new research avenues spanning the Late Pleistocene to present. Zoonotic diseases are frequently attributed to contemporary human-animal interactions through landscape alterations, industrialized food production, and wildlife consumption and trade. Yet, anthropogenic effects on ecology and biogeography of animals and the environment as a whole extend to the Pleistocene when ancient peoples hunted megafauna and burned landscapes. Here we apply niche construction theory within a One Health framework to explore the deep history of disease-scapes. We highlight how new biomolecular tools can be coupled with paleoecological reconstructions to holistically evaluate past human impacts on environments and exploitation of animal populations. Combining zooarchaeological, bioarchaeological, and paleoecological data within a One Health frame, we argue how humans, as niche constructors, have facilitated new host species and disease-scapes of zoonotic pathogens. As such, we show that human-mediated ecosystems have fostered disease dynamics from the Holocene to the Anthropocene.

Public Engagement with a Localized Unidentified and Missing Persons Repository: Community Collaboration as a Contributing Component to the Identification of Trans, Non-binary, and Intersex Individuals

SOPHIA I. RECK[1], TERESA V. WILSON[2], EMILY F. MICHON[3] and GINESSE A. LISTI[4]

[1]Department of Geography & Anthropology, Louisiana State University, [2]Department of Geography & Anthropology, Louisiana State University, [3]Department of Geography & Anthropology, Louisiana State University, [4]Department of Geography & Anthropology, Louisiana State University

Current methods in the forensic disciplines are insufficient for consistently identifying trans, nonbinary, intersex, and other gender non-conforming individuals. To better understand the identification process in general, case files with positive identifications (n=96 from 2015 to 2020) from the Louisiana State University Forensic Anthropology and Computer Enhancement Services (LSU FACES) Laboratory were analyzed to determine what factors contributed to a putative identity for each case. Of the examined variables, a putative identity established from the recovery location of the decedent was found to result in the highest percentage of positive identifications (63.5%). This finding emphasizes the importance of locally centered identification efforts.

The Louisiana Repository for Unidentified and Missing Persons Information Program is a state-level collection of databases administered by the LSU FACES Laboratory. The public interface of this repository offers data regarding unidentified and missing persons in Louisiana; however, public knowledge and accessibility of such a database may limit the resolution of any given case. Focused community engagement, specifically with the trans, non-binary, and intersex communities in Louisiana, could produce a synergetic relationship founded on the common goal of the identification of unknown decedents. This project will address types of collaboration including, but not limited to, engaging with local advocacy groups, missing and unidentified persons awareness events, determining how to better utilize media to raise awareness of unidentified and missing persons, and the education of various forensic practitioners and law enforcement agencies.

Earliest fossil evidence of *Theropithecus oswaldi* lineage from Galili Formation

HAILAY G. REDA[1], STEPHEN R. FROST[1], EVAN A. SIMONS[2], JAY QUADE[3], HASSEN SAID[4] and SCOTT W. SIMPSON[5,6]

[1]Department of Anthropology, University of Oregon, [2]Department of Anthropology (Courtesy Researcher), University of Oregon, [3]Geosciences, University of Arizona, [4]Ethiopian Studies, Addis Ababa University, [5]Anatomy, Case Western Reserve University, [6]Laboratory of Physical Anthropology, Cleveland Museum of Natural History

Theropithecus is represented by a single extant species but is widespread and abundant in the fossil record. Specimens from Kanapoi demonstrate it dates to at least 4.2 Ma. Other materials have also been reported from ~3.9 Ma at Koobi Fora and the Middle Awash. However, these could be attributed to neither *T. oswaldi* nor *T. brumpti*. Specimens confidently assigned to the *Theropithecus oswaldi* lineage have been recovered from 3.8-3.6 Ma deposits from Woranso-Mille. Here we describe new cranial, mandibular, and dental specimens from Galili, Ethiopia demonstrating the origin of the *T. oswaldi* lineage by at least 3.9 Ma.

Methods employed were traditional morphological description, dental metrics, and shape analysis for 893 crania using 3D-GM, following Frost et al., 2003. Galili crania show affinity to *T. o. cf. darti* due clear presence of anteorbital drop, deep face, strong post-orbital constriction, and well-marked temporal lines converging to form a sagittal crest. Further, absence of maxillary ridges, maxillary and mandibular corpus fossae, and lack of upturned zygomatic arches strengthen this affinity. Molar morphology from Galili also indicates incipient *Theropithecus* features including relatively well-separated cusps with slight columnar arrangement, but compared to later populations show low crown and cusp heights with less complex enamel foldings. Both cranial and dental materials are smaller than younger *T. o. cf. darti* samples from Woranso-Mille and Hadar. Galili cranial shape is similar to *Papio*, suggesting longer face relative to nuerocranium. Combining the cranial, mandibular and dental analyses, Galili materials represent an early form of *T. o. cf. darti*.

Bonobo mothers intervene less than chimpanzee mothers in their offspring's conflicts

RACHNA B. REDDY[1,2], LIRAN SAMUNI[1] and MARTIN SURBECK[1]

[1]Department of Human Evolutionary Biology, Harvard University, [2]Department of Psychology, Harvard University

Many primate mothers intervene when their offspring are targeted with aggression. Such agonistic support can protect offspring and increase their status but poses a risk to mothers. We investigated maternal intervention tendencies in bonobos and chimpanzees, our two closest relatives with similarly long dependencies on mothers despite fundamental differences in female status. Chimpanzee females are subordinate to males while bonobo females hold high social status and may face lower costs for intervening in offspring conflicts. We recorded conflicts involving 22 bonobo offspring in Kokolopori Bonobo Reserve, DRC and 66 chimpanzee offspring in Ngogo, Kibale National Park, Uganda (n = 221 bonobo conflicts, 216 chimpanzee conflicts; offspring age 1-16y). In contrast to our expectation, chimpanzee mothers intervened more frequently than bonobo mothers on behalf of daughters and sons of all ages (49% vs. 9% of all conflicts) despite receiving more frequent retaliation than bonobo mothers for doing so. Bonobo mothers reacted little to aggression against their offspring even when offspring screamed persistently or received injuries. In bonobos compared to chimpanzees we also observed fewer individuals other than mothers to provide support during these incidents. These differences could not be explained by the nature of aggression toward offspring or the identity of aggressors. Our results suggest that agonistic support during development may improve chimpanzee but not bonobo fitness. They also suggest a distinction in species' underlying emotional and

cognitive motivations to intervene during conflict, a propensity that may lead to increased escalation of conflicts in chimpanzees compared to bonobos.

Research was supported by the National Geographic Society (CRE-9742-15), the National Science Foundation (BCS-1613392, DGE-1256260), the Nacey Maggioncalda Foundation, the Leakey Foundation, the the University of Michigan and Harvard University.

Analyzing the effects of a Master Online Course on DFW rates in an online environment

JOHN C. REDMOND[1], AMANDA L. ELLWANGER[1], BETHANY L. TURNER[2] and JENNIE E. BURNET[2]

[1]Cultural & Behavioral Science, Georgia State University, [2]Department of Anthropology, Georgia State University

Online learning in the presence of the Covid-19 pandemic has necessitated the development of new approaches to student success in the online environment. One technique thought to improve student success is the Master Online Course (MOC). In this study, we analyzed DFW rates to examine the effectiveness of a MOC in Anthropology, with specific attention given to the biological component of the course. The MOC included new navigation, content, and deliverable components and was piloted in Fall 2020 and again in Spring 2021. DFW rates for the MOC were compared to the pre-MOC courses. Following the same instructor, teaching multiple courses the mean DFW rates were averaged at 55.95 with a mean standard deviation of 35.8 for Spring 2019 (n=2) and 54.4 for Fall 2019 (n=2) with a mean standard deviation of 21.91. For Fall 2020 (n=5), we found a mean DFW rate average of 44.4 with a standard deviation of 17.73 and 44.34 average DFW rate with a standard deviation of 17.39 for Spring 2021 (n=5). The compared results indicate that the development of a MOC can improve student success measured by DFW rates in an online environment.

Sporadic torpor use of wild slow lorises in a montane rain forest ecoregion

KATHLEEN D. REINHARDT[1,2,3], JULIA NOWACK[4], I WIRDATETI[2,5] and ANNA NEKARIS[2]

[1]Department of Anthropology and Archaeology, University of Calgary, [2]Nocturnal Primate Research Group, Oxford Brookes University, [3]Centre for Ecological and Evolutionary Synthesis, University of Oslo, [4]School of Biological and Environmental Sciences, Liverpool John Moores University, [5]Department of Biology-LIPI, Universitas Jakarta

While heterothermy is most often associated with small animals that must cope in temperate and arctic environments, it has become apparent that many non-Holarctic species are also capable of expressing this phenotype. In particular, recent discoveries of tropical heterotherms have increased in the past decade, including primates. To date, *Nycticebus pygmaeus* is the only Asian primate species for which heterothermy has been confirmed, leading to the question of whether there might be more species of this genera to use torpor. Its larger sister species, *Nycticebus javanicus* (850 - 1100 g) is heavily impacted by anthropogenic land use of its typical lowland forest habitat. Populations must move to higher elevations where forest habitat remains, with lower temperatures and less predictable resources. As part of a long-term study, we monitored the skin temperature (Tsk) of eleven *N. javanicus* individuals in a wild population in Cipaganti, West Java (1254 to 2365 m asl) between June 2015 and April 2017. Six individuals (2 female, 4 male) displayed sporadic torpor bouts across 7 months of the year. All individuals that displayed torpor use were capable of lowering Tsk to a minimum of 21 - 25˚C. Torpor bouts ranged from 2.5 to 4.8-h in duration, with bouts only exceeded 3-h in duration during the dry season. Our data suggest *N. javanicus* is another heterothermic primate that expresses torpor opportunistically, as well as the largest recorded daily heterotherm in the Order Primates. We suggest more species of the lorisids family be tested for this phenotype.

Comparing primate body mass datasets: Cautionary implications for evaluating drivers of sexual size dimorphism in platyrrhines

SAM RETTKE[1], ANTHONY DI FIORE[2,4], EDUARDO FERNANDEZ-DUQUE[3,4] and LIZA SHAPIRO[1]

[1]Department of Anthropology, The University of Texas at Austin, [2]Department of Anthropology and Primate Molecular Ecology Laboratory, The University of Texas at Austin, [3]Department of Anthropology, Yale University, [4]College of Biological and Environmental Sciences, Universidad San Francisco de Quito, Cumbayá, Ecuador

Even after 50 years of comparative analyses, debate regarding hypotheses for the drivers of primate sexual size dimorphism (SSD) continues. This lack of consensus remains underscored by a paucity of high-quality and consistent body mass data, particularly for platyrrhines. We compared five commonly used sources of platyrrhine body masses to assess variability between datasets and how this variability contributes to the evaluation of SSD hypotheses. Additionally, we cross-referenced SSD ratios for two species, *Lagothrix lagotricha* and *Plecturocebus cupreus*, sampled at the Tiputini Biodiversity Station (TBS) against these datasets to determine how data on wild-captured adult animals at a well-characterized site fit with "expected" values from the literature. Although on average platyrrhines exhibit a slightly male-biased degree of SSD (12-17%) regardless of dataset, SSD ratios for 19 of 52 species found in two or more of the published sources varied by more than 10%, and 12 of the 19 represented genera differed substantially across datasets in their average and/or range of SSD. These differences not only influence generalizations that can be made about SSD within certain taxa, but also complicate assessment of the relative importance of such predictors as body mass, primary diet, male-male competition level, and phylogeny used in multivariate comparative analyses. Lastly, we found that SSD ratios from TBS could be either higher *or* lower than previously reported for each taxon, depending on the dataset referenced, further highlighting the need to carefully consider the factors related to SSD (and body mass more generally) when selecting data for comparative purposes.

Field data were collected under NSF BCS-1638822.

Socioeconomic conditions, and not genetics alone, explain progression of nonalcoholic fatty liver disease

MARIA C. RIEMAN-KLINGLER[1,2], JINHO JUNG[3], KALEB N. TESFAI[3], ROHIT LOOMBA[3,4] and AMY L. NON[1]

[1]Department of Anthropology, University of California, San Diego, [2]School of Medicine, University of California, San Diego, [3]NAFLD Research Center, Division of Gastroenterology and Hepatology, Department of Medicine, University of California, San Diego, [4]Division of Epidemiology, Department of Family Medicine and Public Heath, University of California, San Diego

Nonalcoholic fatty liver disease (NAFLD) is the leading cause of chronic liver disease globally, with an estimated prevalence of over 25%. The genetic *PNPLA3* risk variant and *HSD17B13* protective variant have been a focus of investigations surrounding the etiology and progression of NAFLD, and exhibit a higher and a lower respective frequency among Hispanics. However, little is known about socioeconomic factors influencing NAFLD progression or its increased prevalence among Hispanics. We cross-sectionally analyzed 264 patients to assess the role of genetic and socioeconomic variables on the development of advanced liver fibrosis in individuals with NAFLD. Adjusting for age, sex, BMI, and *PNPLA3* genotype, lower education (i.e., having less than a college degree) was associated with 3.3 times higher odds of advanced fibrosis (95% CI: 1.21-8.76, p=0.019), an effect comparable to that of possessing the *PNPLA3* risk variant. Of note, the effect of *PNPLA3* genotype on advanced fibrosis was attenuated to non-significance after adjustment for education and other socioeconomic markers. Additionally, the protective effect of the *HSD17B13* variant was no longer significant after adjustment for education (OR: 0.39 [95% CI: 0.13-1.16, p=0.092]), while lower education predicted advanced fibrosis with an odds ratio of 5.19 (95% CI: 1.61-16.75, p=0.006). Adjusting for education attenuated the effect of both genotype and Hispanic ethnicity on advanced fibrosis,

suggesting that social factors—rather than genes or ethnicity alone—may be driving disease severity within some populations. This study reveals the importance of including socioeconomic variables when considering the role of genetics in complex disease.

This work was supported by NCATS (5UL1TR001442), NIDDK (U01DK061734, U01DK130190, R01DK106419, P30DK120515, R01DK121378, R01DK124318), NHLBI (P01HL147835), and NIAAA (U01AA029019).

Portrayals of Wild Primates in Documentary Films: Reason for Concern?

CRYSTAL M. RILEY KOENIG[1,2], BRYAN L. KOENIG[3] and CRICKETTE M. SANZ[4,5]

[1]Department of Interdisciplinary Studies, Southern Utah University, [2]Department of History, Sociology, & Anthropology, Southern Utah University, [3]Department of Psychology, Southern Utah University, [4]Department of Anthropology, Washington University in St. Louis, [5]Congo Program, Wildlife Conservation Society

Documentaries are the primary means by which many people observe the behavior of wild primates. By influencing layperson perceptions of wild primates, documentaries could impact viewer conservation-related beliefs and behaviors and therefore the wellbeing of wild primates. To investigate such portrayals, we examined 210 documentaries depicting the four species that were most represented in documentaries: rhesus macaques, chimpanzees, ring-tailed lemurs, and mountain gorillas. For each documentary, we continuously coded behavior, conducted scan samples of age-sex classes at three-minute intervals, and made ad libitum observations of inaccuracies and misleading content. We expected that representation of age-sex classes and activity budgets in documentaries would differ from those reported in the primary literature for the same species in the wild. In addition, we expected inaccurate depictions for every species. For ring-tailed lemurs, adult males were underrepresented in documentaries. For macaques, chimpanzees, and gorillas, representation of age-sex classes did not differ from observations in the wild. Documentary depictions of activity budgets differed from researcher accounts of wild primate behavior for rhesus macaques, chimpanzees, and mountain gorillas, but not for ring-tailed lemurs. In general, documentaries overrepresented traveling and social behaviors such as play and grooming. Documentaries may have emphasized traveling because such footage allows storyline narration, whereas the emphasis on social behavior was likely due to the appeal of such footage to audiences. Inaccuracies were documented for all four species, with rhesus macaques having the most inaccuracies. We propose that primatologists have an ethical imperative to enhance the accuracy of primate portrayals to audiences.

The conservation value of anthropogenically-modified habitat for the endangered moor macaque (*Macaca maura*) in Sulawesi, Indonesia

ERIN P. RILEY[1], ALESSANDRO ALBANI[2], ALISON A. ZAK[1], LAVINIA GERMANI[2], JESSICA M. ROTHMAN[3], MONICA CAROSI[2] and PUTU OKA NGAKAN[4]

[1]Anthropology, San Diego State University, [2]Sciences, Roma Tre University, [3]Anthropology, Hunter College of CUNY, [4]Forestry, Hasanuddin University

Human-induced land use change has resulted in substantial loss and degradation of habitat for many primates. This reality points to the need to characterize the habitat within anthropogenic landscapes in order to assess its potential conservation value and ways to make it more hospitable. The moor macaque, an endangered primate endemic to Sulawesi, Indonesia, has been observed in a wide array of habitats, but little is known about the quality of these habitats. The objective of this study was to compare the habitat quality of two forests known to be occupied by moor macaques: karst forest in Bantimurung-Bulusaraung National Park and unprotected anthropogenically-modified forest. We defined habitat quality in terms of forest composition and structure and the nutritional environment of the habitat. We assessed forest composition and structure by analyzing vegetation data collected from a total of 65 vegetation plots at the two sites. Fruit samples from 15 known food species were collected at each site and analyzed for macronutrient composition. While macaque food species richness, diversity, and overall stem density were greater in the protected area forest, total basal area and mean diameter-at-breast height were greater in the anthropogenically-modified forest. Mean metabolizable energy, the proportional contributions of digestible neutral detergent fiber to non-protein energy, and the proportions of protein, lipids, total nonstructural carbohydrates of macaque fruit were similar between the two sites. These results suggest that anthropogenically-modified habitats should not be overlooked for their potential conservation value. To further augment their value, conservation efforts should focus on forest restoration.

American Institute for Indonesian Studies; San Diego State University; Safari Ravenna Zoo

Can hominid mandibles and partial mandibles be accurately identified to taxon?

CHRIS A. ROBINSON

Department of Biological Sciences, Bronx Community College, CUNY, Doctoral Program in Anthropology, The Graduate Center, CUNY, New York Consortium in Evolutionary Primatology

The mandible is one of the most commonly recovered elements in the hominin fossil record and mandibular characters have been included in most lists of characters used to differentiate hominin species. However, some researchers have argued that mandibular characters are not as reliable as others for studies of alpha taxonomy due to their greater plasticity. There has also been debate over which region of the mandible is most effective for differentiating amongst taxa. In this study 69 landmarks and 435 semi-landmarks were collected on virtual models derived from microCT scans of 150 extant hominid mandibles. The landmarks were subjected to Procrustes superimposition and the resulting dataset was used in principal components and discriminant function analyses to examine the extent to which mandibles from different species and genera could be distinguished. The same analyses were then run separately on the symphysis, corpus, and ramus landmark datasets. Using the full dataset, only one mandible was incorrectly attributed to genus after cross validation. 98-99% of specimens were correctly classified to genus when the data were only derived from one of the three mandibular regions. Gorillas were identified to the correct species in all cases using the full dataset. Using the corpus and ramus datasets 98% of gorillas were accurately identified to species while this percentage dropped to 88% when only symphyseal landmarks were included in the analysis. The results suggest that even partial mandibles could be accurately identified to species if there are sufficient amounts of landmark data collected.

This research was funded by NSF BSC 1515053

Linking mammalian herbivore diets and (paleo)environments: implications for hominin paleoecology

JOSHUA R. ROBINSON[1,2], JOHN ROWAN[3], W. ANDREW BARR[4,5] and MATT SPONHEIMER[6]

[1]Archaeology Program, Boston University, [2]Geography-Anthropology Program, University of Southern Maine, [3]Department of Anthropology, University at Albany, State University of New York, [4]Center for the Advanced Study of Human Paleobiology, The George Washington University, [5]Department of Anthropology, The George Washington University, [6]Department of Anthropology, University of Colorado at Boulder

Changing proportions of woody versus grassy vegetation cover in ancient African ecosystems has been central to environmental hypotheses of human evolution for over a century. In recent years, carbon isotopes of fossil herbivore teeth have become widely used to make inferences about woody cover with many studies implicitly or explicitly assuming that various herbivores are ecological 'integrators' whose carbon values directly reflect the abundance of C_3 (trees, shrubs) or C_4 (tropical grasses) vegetation. Despite this conventional wisdom, a strong link between the carbon values of herbivore enamel and ecosystem vegetation structure has not been rigorously tested. Using multidecadal Landsat estimates of C_3 woody cover and a large dataset of 1643

samples of recent herbivores across thirty African ecosystems, we find that the intrataxonomic variation in carbon values for most herbivores are poor predictors of woody cover. This pattern is even clearer when removing forests (> 80% woody cover) from our analyses, which numerous lines of evidence suggest are poorly represented in the African fossil record. One exception to this pattern are elephants, which show the strongest relationship (*R2* = 0.564) between enamel carbon values and woody cover, meaning that they might provide a reliable proxy for woody cover in the fossil record. However, we suggest that a community-based approach whereby carbon values of different herbivore taxa are weighted by abundance and dietary intake and then combined into a single measure is more likely to provide a better understanding of the environmental context of hominin evolution.

Understanding the social functions of genito-genital rubbing in female bonobo relationships

MICHELLE A. RODRIGUES[1], EMILY R. BOEVING[2] and JESSICA T. WALZ[3,4]

[1]Department of Social and Cultural Sciences, Marquette University, [2]Department of Psychology, Florida International University, [3]Department of Sociology, Criminology, and Anthropology, University of Wisconsin-Whitewater, [4]Department of Women and Gender Studies, University of Wisconsin-Whitewater

Understanding female bonobos' unique social adaptations requires exploring the social and sexual significance of genito-genital (GG) rubbing. The social bonding hypothesis posits that GG rubbing in bonobos solidifies social bonds, whereas the tension-regulation hypothesis proposes that GG rubbing mitigates tension and reduces agonism risks. If GG rubbing serves primarily to strengthen social bonds, we predict it to be strongly associated with grooming and huddling; however, if it serves primarily to reduce tension, we expect it to be associated with other behaviors that may mitigate stress, such as play, and potentially agonism. Here, we test between these hypotheses using matrix correlations of female-female dyadic behaviors in captive bonobos living in managed fission-fusion social organization at the Columbus Zoo. Using non-parametric matrix correlations, we found that GG rubbing was significantly correlated with huddling (Dietz *r*=0.788, p=0.023), but not with other the other behaviors. To control for relationships between behaviors, we ran Multiple Regression Quadratic Assignment Procedure, with GG rubbing as the dependent variable and grooming, play, huddling, and agonism as the predictor variables. Huddling was the only significant predictor of GG rubbing (*r*=0.930, p<0.001, N=5, 1,000 permutations). Our results support the social bonding hypothesis, and we consider why huddling may be a stronger predictor of GG rubbing than grooming. However, GG rubbing may serve multiple functions in female bonobo relationships. Future considerations of evolutionary functions of female bonobo sexuality should consider how female pleasure and preferences play a role in structuring these behaviors.

Can infraorbital depth of the maxilla be used to predict activity pattern in fossil primates?

BENJAMIN RODWELL[1] and E. CHRISTOPHER KIRK[1,2]

[1]Department of Anthropology, The University of Texas at Austin, [2]Department of Geological Sciences, The University of Texas at Austin

The link between orbit size and activity pattern in primates is well established, with most nocturnal taxa having relatively larger orbits than diurnal taxa. This relationship has been used to infer activity pattern in fossil primates but requires crania with well-preserved orbits, which are rare in the fossil record. Following the observation that some nocturnal primates have relatively shallow maxillae compared to diurnal primates, some researchers have attempted to reconstruct activity pattern based on maxillary infraorbital depth. Because this previous research used a comparative sample that was restricted to extant haplorhines, it is currently unknown whether extant strepsirrhines exhibit a comparable relationship between maxillary depth and activity pattern. If such a relationship does exist, it could be valuable for reconstructing activity pattern in fossil taxa because isolated maxillae preserve part of the orbit are more common than intact crania. Here, we present data on the parasagittal depth of the maxilla using a broad comparative sample of primates. and principal components analyses indicate that extant strepsirrhines and tarsiers tend to have shallower maxillae relative to molar area than extant anthropoids. Nevertheless, nocturnal primates tend to have shallower maxillae compared with diurnal taxa, with only minimal overlap in relative maxillary depth between the two groups. Relative maxillary depth in the omomyoid *Shoshonius* is most consistent with nocturnality, which matches results previously obtained using relative orbit size. These findings suggest that relative maxillary depth is potentially a useful metric for inferring activity pattern in fossil primates.

How closely does chimpanzee diet predict environmental fruit availability at Gombe National Park?

SHANNON L. ROIVAS and IAN C. GILBY

School of Human Evolution and Social Change, and Institute of Human Origins, Arizona State University

Tropical forests are facing disturbance at an alarming rate, and remaining habitats will undergo the transformative process of ecological succession for the next several decades to centuries. This process can alter the types of foods available and their ultimate abundance and distribution, which, in turn, shape habitat suitability and population viability for frugivorous primates.

Gombe National Park, Tanzania has experienced succession following its protection from anthropogenic disturbance in 1968, providing an opportunity to study the consequences of landscape change for frugivorous primates. Previous analyses indicate dramatic vegetation expansion within the park following its establishment and consequently, that chimpanzee diet has varied in a manner consistent with expected plant community composition across succession.

Regular phenological data collection began at Gombe 24 years after initiation of the standardized chimpanzee behavioral data protocol, limiting our ability to directly measure the availability of key food species and its impact on chimpanzees during the first two decades of succession. While diet is frequently used as a proxy for food availability, the strength of this relationship at Gombe has not been sufficiently established. Using 108 months of phenology and feeding data from 25 individuals, we characterized the correlation between environmental fruit availability and consumption of 11 important fruit-producing species. Preliminary results indicate that the proportion of time spent feeding on fruit of a given species is a significant predictor of fruiting likelihood, and that the diets of older individuals are better indicators of environmental fruit availability, potentially due to increased foraging familiarity or competitive ability.

Data collection: Jane Goodall Institute, Construction of the long-term database: NSF (DBS-9021946, SBR-9319909, BCS-0452315, IIS-0431141, IOS-LTREB-1052693)

Cranial fluctuating asymmetry and reproductive fitness in the Cayo Santiago Rhesus macaques

ASHLY N. ROMERO[1], DAVID R. MITCHELL[2] and CLAIRE E. TERHUNE[1]

[1]Anthropology, University of Arkansas, [2]College of Science and Engineering, Flinders University

Fluctuating asymmetry (FA) refers to random deviations from bilateral symmetry and is frequently used as a proxy for developmental instability, which has in turn been suggested to hold an association with reproductive fitness. However, any links observed between FA and fitness are tenuous at best. If FA is indeed related to reproductive fitness, then this supports the idea that FA is genetically controlled to some degree and not as firmly related to environmental stress as many studies suggest. Investigations

concerning a number of phenotypic traits from a range of species have found both decreased fecundity associated with FA or found no effect. We tested the association between offspring count and craniofacial FA in 112 female *Macaca mulatta* from Cayo Santiago, Puerto Rico to expand this research into nonhuman primates. Using geometric morphometric shape analysis, we placed 38 fixed landmarks across the cranium and calculated an individual FA score for each individual. We then regressed offspring count on age to calculate "age-adjusted" residuals that control for differences in fitness related to age at death. A regression of FA scores on the age-adjusted offspring residuals revealed that there is no statistically significant relationship between these variables. These results support the idea that FA, and therefore developmental instability, do not affect reproductive fitness in rhesus macaques, meaning that FA and developmental instability are more likely a consequence of environmental stress rather than genetic determination, at least in this species.

Funding provided by the University of Arkansas Department of Anthropology and Fulbright College of Arts and Sciences.

Lessons from Portmann on the benefits of human infant helplessness

KAREN R. ROSENBERG

Anthropology, University of Delaware

Adolph Portmann described a continuum of life-history strategy in birds and mammals ranging from altricial to precocial, exemplified by "blind kittens and frisky colts." Altricial species typically have short gestations, large litters, eyes and ears closed at birth, lacking hair (or feathers), unable to regulate their body temperature, move around independently or feed themselves. Precocial species are generally born with hair (or feathers), after longer gestations, in small litters, with well-developed sensory organs and able to locomote, thermoregulate and feed themselves.

Portmann recognized that as primates, humans are precocial, but have a prolonged childhood beginning with an immature state at birth. He distinguished this unusual constellation of features as "secondary altriciality." He noted that because of this distinctive mosaic "in humans, maturation processes, which did indeed begin within the mother's body, go through their most important phases in combination with the experiences offered by a much richer environment with many sources of stimulation to the organism capable of development." Portmann anticipates the point made here that while culture permits us to give birth to these helpless and costly young (mitigating obstetrical and metabolic challenges), their birth with functioning sensory systems into stimulating cultural environments enhances the development of social and emotional relationships with caregivers, as they soak up language and culture. This mosaic of helplessness combined with the ability to absorb information and interact with others, enables infants to learn and engage in intense social and emotional relationships. Adaptation to these challenges also creates opportunities that shape our biocultural evolution.

The effects of wildfire smoke on behavior and energetics in wild Bornean orangutans (*Pongo pygmaeus wurmbii*) in Central Kalimantan, Indonesia

GABRIELLE ROSENTHAL[1,2], ANDREA DIGIORGIO[1,3], DANIEL J. NAUMENKO[4], TIMOTHY BRANSFORD[5], SRI SUCI UTAMI ATMOKO[6] and ERIN R. VOGEL[1,2]

[1]Department of Anthropology, Rutgers University, [2]The Center for Human Evolutionary Studies, Rutgers University, [3]Princeton Writing Program, Princeton University, [4]Institute for Behavioral Sciences, University of Colorado, Boulder, [5]Animal Studies Discipline, Eckerd College, [6]Falkutas Biologi, Universitas Nasional Jakarta

Wildfire events in Southeast Asia have increased in frequency and intensity with climate and land-use change, affecting both human and wildlife populations. Wildfires release particulate matter that has been shown to have negative health effects in humans, including respiratory and cardiac diseases. However, little research has focused on the effects of wildfires on non-human primates and other fauna. We examined how an intense wildfire season in 2015 affected the behavior and energetic status of adult male and female wild Bornean orangutans (*Pongo pygmaeus wurmbii*) at the Tuanan Research Station in Central Kalimantan, Indonesia. We analyzed activity budgets from 5,207 full-day focal animal follows using GAMMs to determine if orangutan behavior differed before, during, and after the fire period. Additionally, using urine samples we measured cortisol levels (n=482), ketone bodies (n=1923), and C-peptide of insulin (n=482) as indicators of energetic stress and balance. We found that orangutans spent more time resting during and after the fires compared to the pre-fire period. Preliminary analyses showed that during and after the fires, orangutans had higher cortisol levels ($p<0.001$), lower C-peptide levels ($p=0.003$), and a greater presence of ketone bodies compared to the pre-fire period. Our results indicate that orangutans are significantly impacted by wildfires and likely experience health effects such as increased immune function costs and energetic stress. This study contributes to a more complete understanding of the threats faced by wild orangutan populations due to wildfires and more generally the health implications of wildfire smoke on primates.

Research was funded by The Leakey Foundation, The National Science Foundation, The Center for Human Evolutionary Studies, and Rutgers University.

Distribution, population density and behavior of Taita Dwarf Galago

HANNA ROSTI[1,2], JANNE HEISKANEN[3], SIMON BEARDER[4], PETRI PELLIKKA[3,5] and JOUKO RIKKINEN[1,2,5]

[1]Faculty of Biological and Environmental Sciences, University of Helsinki, [2]Finnish Museum of Natural History, [3]Department of Geosciences and Geography, University of Helsinki, [4]Nocturnal Primate Research Group, Oxford Brookes University, [5]Taita Research Station, University of Helsinki

We studied habitat preferences and behaviour of dwarf galagos (*Paragalago* sp.) recently rediscovered from the Taita Hills, Kenya. Small populations survive in the two largest remnants of moist montane forest. Inspection of several smaller forest fragments failed to provide evidence of additional survivors. Acoustic data on the two remaining populations were obtained with AudioMoths and analyzed in relation to forest structure data obtained by airborne LiDAR and by foot. Distances to nearest road, house and forest edge were calculated. A Zero-inflated negative binomial GLMM were implemented with calls as the response variable and indicator for relative population density. Our results demonstrate that Taita dwarf galagos are sensitive to human disturbance and tend to avoid forest edges. In Ngangao Forest (120 ha) population density was highest in the most pristine part of the forest. Unfortunately, the size of this population has recently diminished to such an extent that it is nearly extinct. The calls of Taita dwarf galagos resemble those of Kenya coast dwarf galagos (*Paragalago cocos*). However, some differences do exist between the Taita animals and those recently observed by us at the Kenyan coast, and even between the two populations in the Taita Hills. In addition to other data, we present the first ever photographs of Taita dwarf galagos from Mbololo Forest (185 ha) and compare them to those from Ngangao Forest and the Kenya coast. We conclude that DNA studies are urgently needed to resolve the taxonomical status of both surviving populations of Taita dwarf galago.

Field work was funded by Kone Foundation and University of Helsinki. Ministry of Foreign Affairs of Finland (BIODEV), Academy of Finland (TAITAWATER) and University of Helsinki funded lidar data collection.

Nutrient balancing in wild primates provides insights into potential diets of Pleistocene hominins

JESSICA M. ROTHMAN

Dept of Anthropology, Hunter College of the City University of New York

This abstract is part of the symposium "Current and multidisciplinary perspectives on hominin diets and trophic levels during the Pleistocene". Dietary studies of extant nonhuman primates provide key comparative data for the

reconstruction of extinct hominin diets and dietary adaptations. A pressing question is how hominins met their nutritional needs while foraging across diverse landscapes in the Pleistocene, and how the nutritional quality of diets changed over time. Recent studies on extant nonhuman primates demonstrate that viewing nutrition in a multidimensional context is important for deciphering nutritional goals, and single currency models are not supported. I review recent studies and propose that different primate feeding guilds balance macronutrient intake in disparate ways according to environmental nutrient availability and digestive constraints. For example, there is building evidence that omnivorous/frugivorous primates regulate protein in their diets and maximize nonprotein energy, while primates with leafy diets avoid fiber, regulate nonprotein energy and consume excess protein. Primates often seek specific environmentally limited micronutrients such as sodium and copper, and use dietary and behavioral strategies to mitigate the negative effects of plant secondary metabolites. There is large interspecific and intraspecific variability in nutritional concentrations of primate foods from the first trophic level, which can obscure traditional perspectives of food quality. As the potential dietary spectrums of Pleistocene hominins are revealed, data from recent extant primate studies provide new insight into the potential nutritional value of food sources and the nutritional strategies that could have been used to balance multiple nutrients while foraging across diverse landscapes.

NSF 1521528 provided funding for this research.

Social and biological transgenerational underpinnings of adolescent pregnancy

AMANDA ROWLANDS, EMMA C. JUERGENSEN, ANA PAULA PRESCIVALLI COSTA, KATRINA G. SALVANTE and PABLO A. NEPOMNASCHY

Maternal and Child Health Lab, Faculty of Health Sciences, Simon Fraser University

Adolescent pregnancy (occurring < age 20) is considered a global problem that creates and perpetuates inequities, affecting all women. Indeed, approximately 13 million adolescent girls give birth each year. This reproductive outcome is linked to increased morbidity risks during gestation, birth, and early post-partum, and is the leading cause of death among girls aged 12-19 years old worldwide. Currently adolescent pregnancy is more often treated as an individual problem linked to individual behaviors. Interventions resulting from this approach, however present very low efficiency levels. Here we propose a different approach. We merged three theoretical frameworks: "Life History theory", "Eco-Social theory", and "Developmental Origins of Health and Disease". We then used the emerging combined theory to conduct a thorough literature review and discuss adolescent pregnancy's ecological, social, and biological determinants. We focused our attention on two key developmental milestones associated this reproductive outcome: age at girls' first menstrual bleed (menarche) and age at first sexual intercourse (coitarche). Our analysis of the literature suggests that risks for adolescent pregnancy may be influenced by exposures taking place early during development, starting at gametogenesis. These risks are compounded by interactions between socio-structural and ecological factors, including housing and food security, family structure, and gender-based power dynamics. We use this new emerging theory to identify specific biological mechanisms mediating the links between socio-ecological risks, reproductive development, and pregnancy, and explain how this evidence should be used to inform socio-structural interventions aimed at reducing adolescent pregnancy risk.

The remains of the cartilage: ontogenetic transformation of the nasal capsule in rodents

IRINA RUF

Abteilung Messelforschung und Mammalogie, Senckenberg Forschungsinstitut und Naturmuseum Frankfurt, Germany

The ethmoid bone is a complex element of the mammalian cranium and the remnant of the nasal capsule of early ontogenetic stages. However, the ontogenetic transformation of the cartilaginous precursor, the nasal capsule, into the adult ethmoidal region by resorption, ossification, appositional bone growth as well as dermal bone replacement is still not well understood to date.

Rodentia provide a suitable model organism to elucidate the fate of the cartilaginous precursor of the ethmoid bone as ontogenetic series are easily available in several species and different developmental patterns (altricial, precocial) are represented. Based on histological serial sections of perinatal stages as well as µCT scans of selected adults, 23 muroid species were investigated. The results were compared to other rodent clades (especially Caviomorpha) and selected members of Euarchontoglires.

In rodents, resorption of the nasal capsule (tectum nasi, paries nasi, cartilago paraseptalis anterior) and ossification of turbinals, nasal septum, lamina transversalis posterior and lamina cribrosa already start before birth and follow a distinct pattern observed in many rodents and other Euarchontoglires (e.g., *Oryctolagus cuniculus*, *Tupaia* spp.). However, the ethmoidal region of altricial rodent species is less mature at birth than in precocial ones, e.g., Caviomorpha. Furthermore, the ethmoid bone can comprise more structures than generally defined as observed in some Muroidea. These are ossified remnants of the tectum nasi and of the cupula nasi posterior. In contrast, the anterior nasal cartilages as well as the anterior part of the septum remain cartilaginous in order to support a flexible rhinarium.

This study was partly funded by the Landesgraduiertenförderung Baden-Württemberg.

Comparative morphology of two Late Pleistocene human femora from Trinil, Indonesia

CHRISTOPHER B. RUFF[1], ADAM D. SYLVESTER[1], NENI T. RAHMAWATI[2], RUSYAD A. SURIYANTO[2], PAUL STORM[3], MAXIME AUBERT[4], EDUARD POP[5], JOOST BATTENBURG[6], SOPHIA B. COBAN[7], SOFWAN NOERWIDI[8], FRANK HUFFMAN[9], WILLEM RENEMA[5], SHINATRIA ADHITYATAMA[4] and JOSEPHINE C. JOORDENS[5]

[1]Functional Anatomy and Evolution, Johns Hopkins University School of Medicine, USA, [2]Laboratory of Bioanthropology and Paleoanthropology, Universitas Gadjah Mada, Indonesia, [3]Groningen Institute of Archaeology, University of Groningen, The Netherlands, [4]Australian Research Center for Human Evolution, Griffith University, Australia, [5]Naturalis Biodiversity Center, The Netherlands, [6]Leiden Institute of Advanced Computer Science, Leiden University, The Netherlands, [7]Department of Mathematics, The University of Manchester, UK, [8]National Research Center for Archaeology, Indonesia, [9]Department of Anthropology, The University of Texas, USA

Two human right partial femora were discovered by T. Jacob at the site of Trinil, Java in 1978, but have remained largely unknown and undescribed. They have recently been dated by U-series to 26-33ka, consistent with their assumed stratigraphic placement in the site. Trinil 9 and 10 each preserve most of the diaphysis and are similar in general size. Trinil 10 shows significant surface abrasion, so we focus here on the morphology of the better preserved Trinil 9. The specimens were micro-CT scanned at the FleXRay Laboratory located at CWI, Amsterdam (The Netherlands) and structural properties at several locations along the diaphysis were determined using MomentMacro. The reconstructed length of Trinil 9 is about 417 mm, giving an estimated stature of about 157 cm. Body mass, determined from midshaft cortical area and bone length, using a reference sample of 151 Pleistocene through early Holocene hominin femora as well as comparisons to the penecontemporaneous Deep Skull femur, is estimated to be about 51 kg. Regarding cross-sectional shape, Trinil 9 shows evidence for relatively increased anteroposterior bending strength, and in this respect is similar to East Asian Late Pleistocene males including those from Luijiang, Zhoukoudian Upper Cave, and Tam Hang, as well as more recent male hunter-gatherers, suggesting that it was also male and had an active lifestyle. This morphology contrasts strongly with that of East

Asian and African Early and Middle Pleistocene femora. These new femora add to the evidence for active, small-bodied hunter-gatherers in the Late Pleistocene of Southeast Asia.

Funded by the Dutch Research Council (NWO) Talent Programme grant no. 0.16.Vidi.171.049.

Variation in lateral meniscal insertion anatomy in the human knee

C. KINLEY RUSSELL

Center for Functional Anatomy & Evolution, The Johns Hopkins University School of Medicine

The knee joint has been the focus of a substantial amount of research in biological anthropology because of its function in posture and locomotion. Menisci play an important role in knee function, yet meniscal structure has historically been incorporated in a very limited way in the interpretation of the relative extension or rotational capacity of fossil hominin knees. The inference of human-like knee function from proximal tibial morphology requires a greater understanding of meniscal insertion variation in modern humans. Here I examine the presence and size of meniscotibial and meniscofemoral insertions of the posterior horn of the lateral meniscus in relation to biological sex and body size in a human cadaveric sample.

The knees of 62 individuals (34 female, 28 male) were dissected to expose the posterior insertions of the lateral meniscus and linear measures were collected using calipers. The posterior meniscotibial insertion was present in all sampled individuals while the presence of anterior (aMFL) and posterior meniscofemoral ligaments (pMFL) was variable (pMFL: 58%, aMFL: 65%, both: 27%, neither: 5%). Females are significantly more likely to possess a pMFL than males (p=0.02) and this result cannot be attributed to differences in body size. The posterior meniscotibial insertion is significantly larger in individuals without meniscofemoral ligaments (p=0.04). These results suggest that biological sex must be taken into account when interpreting variation in the knee and that the cumulative insertional footprint of the posterior horn may be important for controlled mobility of the lateral meniscus.

A new ekgmowechashalid primate (Adapiformes) from the Naduo Formation (late Eocene) of Guangxi Zhuang Autonomous Region, China

KATHLEEN L. RUST[1], XIJUN NI[2] and K. CHRISTOPHER BEARD[1]

[1]Department of Ecology and Evolutionary Biology & Biodiversity Institute, University of Kansas, [2]Key Laboratory of Vertebrate Evolution and Human Origins, Institute of Vertebrate Paleontology and Paleoanthropology, Chinese Academy of Sciences

Adapiform primates are a diverse clade with a Holarctic distribution throughout the Eocene. While most families go extinct by the early Oligocene, adapiforms in Asia survive well into the Miocene. Here, we share results from morphological and phylogenetic analyses bearing on a new ekgmowechashalid adapiform recovered from the Naduo Formation (late Eocene) of Guangxi Zhuang Autonomous Region, southern China. The discovery of this new taxon informs the origin and evolution of *Ekgmowechashala*, an enigmatic adapiform known from the early Arikareean of South Dakota, Nebraska and Oregon. Several partial dentaries preserving premolars and molars (P_2-P_3, M_1-M_2) and one maxillary fragment preserving M^2 document the new taxon. The Chinese Eocene taxon shares multiple derived character states with *Ekgmowechashala* (mesially canted lower premolars, low tooth crowns with bulbous cusps and crenulated enamel, the presence of lower molar metastylids, and a duplicated protocone on M^2) but is primitive in other respects, suggesting that it is distinct but closely related to *Ekgmowechashala*. Morphological comparisons with additional Asian adapiforms (*Gatanthropus*, *Muangthanhinius*, and *Bugtilemur*) reveal further shared dental features, supporting close affinities among these taxa within a monophyletic Ekgmowechashalidae, a clade that has been previously recovered in other studies.

Our results reinforce earlier findings, recovering a monophyletic Ekgmowechashalidae that includes relatively basal taxa (*Bugtilemur*, *Muangthanhinius*, and *Gatanthropus*) as well as the highly autapomorphous clade comprising *Ekgmowechashala* and the new Chinese Eocene taxon. Our study elucidates a complex biogeographical and evolutionary history for *Ekgmowechashala*, revealing several dental morphoclines that clarify the sequence of morphological evolution within Ekgmowechashalidae.

This research was supported by the University of Kansas, the David B. Jones Foundation, the Chinese Academy of Sciences, and the National Natural Science Foundation of China.

The biocultural fetus: internalizing Portmann's "Social Womb"

JULIENNE N. RUTHERFORD

Human Development Nursing Science, University of Illinois Chicago

This abstract is part of the symposium "*Building on the legacy of Adolf Portmann: Interdisciplinary approaches to human evolution and development*." A tacit assumption in anthropological discussions of human infant development is that the influence of the social world on offspring is minimal until birth into a "social womb" of family and societal connection. It is within that exteriorly-conceptualized womb that the process of becoming human as cultural entity begins. This perspective supposes a clear dichotomy between fetus and infant and obscures the dynamic interactions among fetus, mother, and external environment. In this presentation I will frame intrauterine support systems as internalized social womb, by connecting the human fetus to the external world of culture. The offspring is deeply connected to its environment by a series of tissue systems. First, the embryo is nourished by secretions of the endometrial glands, glands that begin their development in the fetal life of the mother and mature and transform as a consequence of the ovarian cycle in adulthood. These processes precede the existence of the offspring and are shaped by maternal nutrition and psychosocial stress, states that are very much socially, culturally, and structurally driven. Later, when the placenta matures sufficiently and takes over nutritive and endocrine control, maternal blood brings sustenance and signals in real time to fetal tissue. Buffering mechanisms do shield the fetus from direct exposure to exterior life, but the placenta is not a sealed capsule for the fetus. The fetus is influenced by cultural processes long before birth.

Some data presented here were supported by NIH R01 HD076018 (PI Rutherford)

Employing Spherical Harmonics in Assessing the Variation and Covariation of Sphenoidal Sinus Shape in *H. sapiens*

KATHARINE G.J. RYAN and BENJAMIN AUERBACH

Anthropology, University of Tennessee, Knoxville

The evolutionary potential and shape variation of the human sphenoidal sinus are unknown. Moreover, a consensus about the function or evolutionary forces that influence variation of paranasal sinuses among humans remains unestablished. One initial approach to address this lies in determining the covariance of sinus shape with surrounding morphology. The sphenoidal sinus is centrally located within the basicranium, at the intersection of the three cranial fossae and adjacent to the synchondroses, the location of cranial base angulation. The angulation of the cranial base and its relative orientation with the face is a distinctive, derived trait in *Homo sapiens* and is important to our understanding of the evolution of our species.

Here we preliminarily analyze the covariance of sphenoid sinus and basicranial shape. The sphenoidal sinuses of 120 human crania were segmented (Avizo) from CT scans. We quantified the three-dimensional shape variation of sphenoidal sinuses using spherical harmonic analyses (SHARM, Matlab), producing coefficients comparable to traditional landmarks placed virtually on the basicranial surface. Landmarks were chosen that capture the general shape of the sphenoid body, sella turcica, and surrounding cranial anatomy. Two-Block Partial Least Squares (2B-PLS) analyses revealed no significant

covariation (p=0.59) between the shape of the sphenoidal sinus and its surrounding bony architecture. This indicates the establishment of sinus shape occurring independently of the surrounding bone. We will be exploring this further with additional sets of landmarks (representing different developmental regions of the cranium) to determine if pneumatization of the sinus covaries or is independent of the overlying bony anatomy.

Diet quality in elusive species: Using near-infrared spectroscopy to predict diet quality in *Otolemur crassicaudatus*

CHRISTINA M. RYDER[1], MICHELLE L. SAUTHER[1], FRANK P. CUOZZO[2,3], RAVEN JAYNE[1] and MATT SPONHEIMER[1]

[1]Department of Anthropology, University of Colorado, Boulder, [2]Mammal Research Institute, University of Pretoria, [3]Lajuma Research Centre

Determining the accurate diets of small mammals is essential to understanding their ecology. Nocturnal and cryptic, *Otolemur crassicaudatus* is challenging to follow and observe at close range, which impedes the understanding of diet. Traditionally, dietary data collection is labor-intensive, time-consuming, and quite expensive, and most nutritional analyses require a well-equipped laboratory. Near-infrared (NIR) reflectance spectroscopy is a promising non-invasive method to predict diet among *O. crassicaudatus* and other elusive species. Chemometric analysis of overtone and combination bands in the NIR region characterize the molecular content and can be used to model nutritional properties. In collaboration with research to noninvasively understand diet in wild nocturnal primates, fecal samples of *O. crassicaudatus* were collected across an entire year (2017 to 2018) at the Lajuma Research Centre South Africa. A subset of freeze-dried fecal samples (n = 118) were transported to the University of Colorado, Boulder, for NIR, stable isotope, and traditional nutritional analyses. A chemometric model built using partial least squares regression of the samples in the calibration set (R2=0.79) produced a three-factor model and was then validated with a leave-one-out cross-validation (R2=0.77, RMSEP=0.53, slope =0.77). This preliminary work suggests NIR is very good at characterizing protein content in freeze-dried, ground *O. crassicaudatus* fecals, but we need to field test our method with unprocessed samples. Future work on our project will thus demonstrate NIR analysis to be a powerful non-invasive and cost-effective tool to assess wildlife feeding ecology.

The National Science Foundation, USA (BCS 1638833), The University of Colorado-Boulder.

Playing with purpose: sex differences in social play among wild adult chimpanzees (*Pan troglodytes schweinfurthii*)

KRIS H. SABBI[1,2,3], MEGAN F. COLE[2], SOPHIA E. KURILLA[3], ASHLEY MENANTE[5], ISABELLE G. MONROE[4], MELISSA EMERY THOMPSON[2,6], MARTIN N. MULLER[2,6], EMILY OTALI[6], RICHARD W. WRANGHAM[5,6] and ZARIN P. MACHANDA[1,3,6]

[1]Anthropology, Tufts University, [2]Anthropology, University of New Mexico, [3]Biology, Tufts University, [4]Biology, University of New Mexico, [5]Human Evolutionary Biology, Harvard University, [6]Kibale Chimpanzee Project, Fort Portal, Uganda

Social play is common among young primates and thought to function primarily as a learning tool that helps immature individuals gain and practice motor, spatial, and social skills. Albeit far less common compared to infants and juveniles, adult chimpanzees are known to play socially both in captivity and the wild. However, the function of adults' social play remains unclear, as they have presumably mastered the skills that they could gain through such play. In this study, we use 9 years of all-occurrence data on social play by adult chimpanzees of the Kanyawara community in Kibale NP, Uganda (N=3396 play bouts, 42 individuals aged 12-58 years) to test the hypothesis that social play serves different purposes for adult females and males. We predicted that females would play primarily as partners to their dependent offspring, whereas males would play with peers as a component of social bonding. Adult females played more frequently than males (GLMM, β=0.98+0.44, p=0.03), and nearly half of all their play was with their offspring (47%). Play between two adults occurred less frequently (N=791 bouts, 23%), however, males were more likely to play with other adults compared to females (GLMM, β=0.56+0.22, p=0.01). While our results largely confirmed our predictions, we also observed substantial individual variation that was not well-explained by demographic factors. This supports the interpretation that social play serves sex-specific functions for adult chimpanzees on average, but that individual social strategies and styles, including the use of social play, may vary among members of the same sex.

Supported by NSF grants 1355014, 9807448, 0416125, 1926653, NCS-FO-1926352, and NCS-FO 1926737; NIH grants AI058715 and R01AG049395; Harvard University, Tufts University, The University of New Mexico, and the Leakey Foundation.

Survey of exercise behavior and pregnancy outcomes in highly active women

SRISHTI SADHIR[1] and HERMAN PONTZER[1,2]

[1]Evolutionary Anthropology, Duke University, [2]Duke Global Health Institute, Duke University

Energy investment in high levels of physical activity trades off with energy investment in reproduction to influence fecundity and pregnancy outcomes. U.S. pregnancy guidelines recommend 150 mins/week of exercise for positive pregnancy outcomes, including lower likelihoods of hypertension, excessive gestational weight gain, and macrosomia. We predict that women with higher running mileages will report lower fecundity and a higher incidence of menstrual disorders. We also predict that women with higher running mileages during pregnancy will (i) reduce their mileages over gestation, and (ii) report lower birthweights and lower incidence of gestational metabolic disorders. We implemented an online survey targeting women with non-pregnant running mileages of at least 10 miles/week and who have been pregnant or plan to become pregnant. Of N=194 respondents, n=154 ran at some point during pregnancy, while n=94 ran into their third trimesters. Mean running mileage decreased over pregnancy (30.7 miles/week, pre-pregnancy to 10.5 miles/week, third trimester). Compared to more sedentary populations, survey respondents had a higher incidence of irregular periods (23.7%, p<0.01) but less reported difficulty becoming pregnant (1.7%, p<0.001), a lower incidence of miscarriage or stillbirth (2.8%, p<0.001), and fewer reported disordered eating (2.8%, p<0.01). Third-trimester runners had a lower incidence of preterm birth (2.1%; p<0.01). Higher third trimester mileage was associated with normal gestational length i.e., lower frequency of preterm birth (LRT: $x^2 = 9.54$, p<0.01). These results suggest that our highly active sample is healthier than more sedentary populations and lend some support for a tradeoff between physical activity and reproduction.

Trabecular bone growth is linked to brain development, locomotor ontogeny, and body size

JAAP PP. SAERS[1], ADAM D. GORDON[2], TIM M. RYAN[3] and JAY T. STOCK[4]

[1]Department of Archaeology, University of Cambridge, [2]Department of Anthropology, University at Albany, SUNY, [3]Department of Anthropology, Pennsylvania State University, [4]Department of Anthropology, Western University

Introduction: We examine the ontogenetic trajectories of trabecular bone structure in the calcaneus of humans, chimpanzees, gorillas, and Japanese macaques. We test a model where trabecular bone volume fraction is the product of an interaction between neuromaturation and body size via age-related variation in locomotor loading conditions.

Results: Using biomechanical data from a study on human locomotor ontogeny we show that body mass normalized force-time-integrals and peak plantar pressure predict age-matched trabecular bone volume fraction in humans. We also show that interactions between neuromuscular maturation (and by proxy percentage of adult brain size) and body weight strongly predict these biomechanical variables (R^2>0.98).

We then show that the interaction between the onset of locomotion, percent adult brain size, and body weight is the best model to explain age-related patterns in trabecular bone volume fraction in all four primate species (highest R^2 and lowest AIC).

Finally, using piecewise linear regressions we show that distinct changes in the slope of age-related variation in bone volume fraction correspond to the age of the onset of locomotion and the age at which adult-like locomotion is achieved.

Conclusion: These results indicate that ontogenetic trajectories of trabecular bone can not only be used to infer behaviour, but serve as a valuable indicator of neuromuscular maturation and life history events like locomotor onset and the achievement of an adult-like gait.

A detailed histological study of chacma baboon developmental enamel defects

JAMAL K. SALAYMEH[1], JIMMY ERKENS[1], ESME BEAMISH[2], W. SCOTT MCGRAW[1], DEBBIE GUATELLI-STEINBERG[1] and KATE MCGRATH[1,3]

[1]Department of Anthropology, The Ohio State University, [2]Institute for Communities and Wildlife in Africa (iCWild), University of Cape Town, [3]Department of Anthropology, SUNY Oneonta

Stress events such as malnutrition and illness disrupt normal tooth growth creating grooves that are visible on the tooth surface (i.e., linear enamel hypoplasia or LEH). External LEH defects often co-occur with internal manifestations of stress called accentuated lines. However, it is unclear whether the two defect types always co-occur. Monkeys are described as having fewer enamel defects than hominoids, but previous research shows that faster-growing teeth exhibit shallower LEH defects that are harder to macroscopically identify, and only a few histological studies of monkey teeth exist. Here, a male chacma baboon (*Papio ursinus*) first permanent incisor histological thin section was analyzed. We found a higher prevalence of internal accentuated lines (AL; N=48) compared to external LEH defects (N=10). The defect types co-occurred in all instances of LEH, but there is an abundance of AL that do not co-occur with LEH defects, complicating the interpretation of any single event in terms of the cellular responses of ameloblasts to stress. The spatial distribution of AL is more consistent, ranging from 3-10/decile, while LEH defects are confined to the cervical half of the crown. We found that monkeys indeed exhibit faster growth rates (mean=24 microns/day) compared to extant apes and humans, peaking (49 microns/day) toward the cusp. The underlying striae angles are shallow compared to hominoids (11-16 degrees), creating shallower LEH defects and helping to explain the discrepancy and distribution of AL versus LEH defects. Future work will expand the sample size and incorporate associated records for individual baboons.

Funding provided by The Ohio State University President's Postdoctoral Scholar's Program

Multiregional Lead Isotopic Linear Patterns and Evaluating Lead Contamination in Ancient Human Tooth Enamel

JOHN R. SAMUELSEN[1,2] and ADRIANA POTRA[3]

[1]Arkansas Archeological Survey, University of Arkansas, [2]Department of Anthropology, University of Arkansas, [3]Department of Geosciences, University of Arkansas

Lead (Pb) isotopes can be used to evaluate ancient human geographic origins but are relatively underutilized compared to the more commonly employed strontium (Sr) isotopic technique. Issues preventing large-scale adoption of the Pb isotopic technique include anthropogenic and soil contamination of tooth enamel and clear demonstrations of regional differentiation of human remains based on local geology (rather than exposure to pollution). Ancient human teeth from a Caddo skull-and-mandible cemetery at the Crenshaw site in southwest Arkansas were tested for Pb and Sr isotope ratios to determine their geographic origins and to test for evidence of Pb contamination. Multiregional Pb isotopic linear patterns constructed from ancient animal teeth (180 teeth from 28 ancient sites) were constructed for several surrounding regions to construct a background signature. Trace elemental analysis of tooth enamel and burial soils showed that only a few human teeth were contaminated with soil Pb when the proper procedures were closely followed. However, the results suggested that currently established enamel concentration thresholds may need modification and that some elements may not be useful for detecting Pb contamination. The multiregional Pb isotopic linear patterns from surrounding regions, when combined with Sr isotopes, clearly regionally differentiated human remains from these other regions. The addition of Pb linear patterning analysis was able to establish the remains are local to southwest Arkansas and non-local to all other tested regions when Sr alone failed. The results also caution that skull burial rituals can be related to ancestor worship rather than interregional warfare.

This study was funded by the National Science Foundation Doctoral Dissertation Research Improvement grant (grant #1830438) and the Department of Anthropology, University of Arkansas.

Revisiting the evolution of human "hairlessness"

AARON A. SANDEL

Department of Anthropology, University of Texas at Austin

Of all the unusual traits exhibited by humans, our hair is one of the most distinct. From head to toe, save for the very tops of our heads, humans have exposed skin. Numerous hypotheses have been proposed to explain human "hairlessness." I discuss several reasons why prior hypotheses have failed to adequately account for the human hair phenotype. First, humans are not actually "hairless," but are predominantly covered with small, unpigmented vellus hairs rather than thick, pigmented, terminal hairs. This well-known fact was ignored by early scholars surmising about the evolution of the human integument. Second, high quality comparative data have rarely been included in models of human hair evolution. Phylogenetic comparative analyses suggest that primates in general, and apes in particular, have relatively less dense visible hair than many other mammals. Third, high quality data on human hair that includes biological variation and an anti-racist approach have largely been missing. With these considerations in mind, I propose a novel hypothesis for the human hair phenotype that builds on "the expensive brain" hypothesis. I discuss the possible mechanism, development, evolutionary history, and function of our hairless appearance. This abstract is part of the symposium Integumentary Anthropology: Examining the Exterior.

MorphoPASSE Skull Sexing Observer Error

DANIELA SANTAMARIA VARGAS[1], MARY E. ST. JOHN[2], JEFRY R. GARCIA-BERNABE[2] and ELIZABETH A. DIGANGI[2]

[1]Department of Medicine, Research Foundation for The State University of New York, [2]Department of Anthropology, Binghamton University

Estimating sex is a fundamental aspect of forensic anthropological work. Nevertheless, examining traits of human remains can be subjective. MorphoPASSE is a free software program designed to estimate sex using the human skull and pelvis. However, its results can be influenced by observer error. The objective of this project was to compare the results between three different observers with distinct osteological experience who analyzed the same sample using the "score" system established in the MorphoPASSE manual. The sample was composed of 45 individuals of known sex who were part of a postmortem gunshot research collection. Each observer blindly scored five morphological traits from each skull following the MorphoPASSE manual, then re-scored ten individuals. The scores were run through MorphoPASSE and a statistical percentage of sex probability was generated.

Inter- and intra- observer error were calculated using Cohen's Kappa statistical test. Results varied between researchers where the most experienced observer had 1.000 in the intraobserver error test while the observer with the least experience had a result of .167. For the interobserver error, two researchers had results in the same range (.553 and .513) while the third obtained a result of .465. These results demonstrate that scoring skull traits is related to the user's experience, and that MorphoPASSE manual definitions can be improved to increase the accuracy of less experienced researchers. Assessment of sex will likely always have a certain level of subjectivity, underscoring the importance of observer error testing.

The collection used here was procured through the support of NIJ-2016-DN-BX-0155.

Bipedality in chimpanzee: insights into the contextual origins

LAUREN SARRINGHAUS[1,2] and LAURA MACLATCHY[2]

[1]Evolutionary Anthropology, Duke University, [2]Anthropology, University of Michigan

Habitual terrestrial bipedality is a hallmark of the human lineage, but the context under which this behavior evolved is debated. Extant apes have been invoked as models to variously suggest that the antecedent of terrestrial bipedality was terrestrial quadrupedalism or arboreal bipedalism. Bipedal feeding postures have been cited as important to the origins of anatomical specializations for bipedalism, as have load carrying, enhancing vision and appearing more threatening. These debates remain active because of data scarcity. To contribute contextual data that may illuminate the circumstances that favor bipedalism, we opportunistically filmed wild chimpanzees (Ngogo, Kibale forest, Uganda) documenting duration, context, and substrate height of bipedal bouts (locomotion N = 99, posture N = 126) with similar sample sizes in arboreal and terrestrial settings. Among adults, bipedal behavior occurred most often during foraging both arboreally and terrestrially. However, the contribution from other contexts, such as visibility and antagonism, was greater in terrestrial contexts. For subadults, the most common context was terrestrial play and both foraging and play arboreally. There was no separation between postural bipedalism and locomotor bipedalism in terms of context. Unlike some communities of chimpanzees, Ngogo chimpanzees rarely carried objects when bipedal. The length of bipedal bouts ranged from 0.13 - 41.7 s, with an average of less than 4 s in duration. Short bouts of bipedalism may be largely missed in focal follow samples, and argues for increased use of video for documenting this rare, but important, behavior in wild primates.

We thank the National Science Foundation NSF-1850328 and the Leakey Foundation for funding this research.

The impact of demographic and socioeconomic factors on rural vs. urban experiences during the 1918 influenza and COVID-19 pandemics

LISA SATTENSPIEL[1], CAROLYN M. ORBANN[2], HAILEY K. RAMIREZ[1], SEAN PIRRONE[1], JANE A. MCELROY[3], AARON BOGAN[4], CHRISTOPHER K. WIKLE[4], GIOVANNA GUIDOBONI[5] and XIU-FENG WAN[6]

[1]Anthropology, University of Missouri, [2]Health Sciences, University of Missouri, [3]Family & Community Medicine, University of Missouri, [4]Statistics, University of Missouri, [5]Electrical Engineering & Computer Science and Mathematics, University of Missouri, [6]Molecular Biology & Immunology, Electrical Engineering & Computer Science, and Bond Life Sciences Center, University of Missouri

Most studies of pandemics have assessed their effects in urban centers of the world, but the constraints and issues facing rural people during a pandemic are different from those of their urban counterparts. We compare the disease experiences of rural and urban populations during both the 1918 influenza and COVID-19 pandemics in the state of Missouri, USA. Data on deaths from 1918-1920 reported in the online Missouri Digital Heritage database are supplemented by socioeconomic and demographic data available from the 1910 US Census and other sources. Data on both cases and deaths during the COVID-19 pandemic obtained from the Missouri Department of Health and Senior Services and online sources have been supplemented by recent estimates of social variables from the U.S. Census Bureau and other sources. To improve the comparability of results, variables available for both time periods at the county level (e.g., age-sex distribution, rural/urban status, number of primary care physicians) were used in the study. Analyses comparing rural vs. urban counties with regards to influenza mortality rates and COVID-19 case and mortality rates are presented. These indicate that although urban counties experienced more deaths during both pandemics and more cases during the COVID-19 pandemic, rural counties were much more heavily impacted when numbers are adjusted for county population levels. We suggest this may be due to greater rural-urban social and economic disparities in health care in the 21st century than in the early 20th century, even though the quality of health care overall is substantially better now.

This project is supported by NSF RAPIDD Grant No. BCS-2031703.

The effect of body size on the behavioral ecology of two sympatric bushbabies in an Afromontane habitat

MICHELLE L. SAUTHER[1], JAMES B. MILLETTE[1], FRANK P. CUOZZO[2,3], CHANNEN LONG[4] and VÜMBONI HARRY MSIMANGO[5]

[1]Anthropology, University of Colorado - Boulder, [2]Mammal Research Institute, University of Pretoria, [3]Lajuma Research Centre, [4]Department of Paraclinical Sciences, University of Pretoria, [5]School of Environmental Sciences, University of Venda

Body size broadly affects biological, life history and behavioral traits. Although few in number, temperate-living primates are dominated by large-bodied haplorrhine genera and there are few temperate strepsirrhine primates. This research compares two non-heterothermic nocturnal sympatric Afromontane galago species, *Otolemur crassicaudatus* and *Galago moholi*, living within a temperate seasonal habitat (Lajuma Research Centre, South Africa). These species differ dramatically in body size (*O. crassicaudatus* 1090g; *G. moholi* 150 g). Using professional grade thermal imaging cameras (Model T600, Flir® Systems) we determined how encounters by species (84 encounter walks across 11 months, total encounters: *Otolemur* = 208, *Galago* = 206) varied relative to ambient temperature, humidity, moon phase and luminosity, night length, insect and gum availability. Compared to the smaller *Galago, Otolemur* encounters were reduced at the hottest temperatures [(X^2 (1, 85) = 4.69, p < 0.034)]. *Galagos* appear lunarphilic with encounters greater during periods of higher luminosity [(X^2 (1, 413) = 8.07, p < 0.045)], and greater during the full moon [X^2 (1, 46) = 5.29, p < 0.038]. In contrast, *Otolemurs* appear lunarphobic, with greater encounters during the new moon [X^2 (1, 66)= 4.66, p < 0.030]. *Galago* encounters were highest on nights with greater insect availability [(X^2 (1, 358)= 4.66, p < 0.03)]. *Valichellia* sp. gum availability, humidity and night length showed no effect. Results add to our understanding of temperate primate ecology, and expand our understanding of how body size mediates behavior in these nocturnal primates.

The National Science Foundation, USA (BCS 1638833), The University of Colorado-Boulder.

Association between age and cognition in modern Hadza foragers

M. KATHERINE SAYRE[1], GENE E. ALEXANDER[2,3,4,5,6,7], ELIZABETH CASHDAN[8], HERMAN PONTZER[10,9], LAYNE VASHRO[8], BRIAN M. WOOD[11,12] and DAVID A. RAICHLEN[1]

[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, University of Utah, [9]Department of Evolutionary Anthropology, Duke University, [10]Duke Global Health Institute, Duke University, [11]Department of Anthropology, University of California Los Angeles, [12]Department of Human Behavior, Ecology, and Culture, Max Planck Institute for Evolutionary Anthropology

Changes in cognitive function are considered a typical aspect of human aging. However much research on cognitive aging has focused on people living in industrialized populations who do not represent the range of lifestyles that modern humans engage in, limiting our ability to identify common features of human brain aging. Here, we examine cognitive performance across the lifespan in The Hadza, a contemporary subsistence-oriented population living in northern Tanzania, whose lifestyles often involve behaviors linked with healthy aging including high levels of physical activity. While many Hadza adults engage in traditional physically active foraging practices, many others live in more market-integrated villages, and engage in less foraging. We recruited 204 participants (n_{female}=102, n_{male}=102; 15-90 years old) from 13 camps to perform two tests of cognitive function: the Corsi Block Task, a measure of spatial working memory, and the Finger Tapper, a measure of psychomotor processing speed. We examined whether the relationship between age and performance differed for adults who engage in different amounts of foraging. We found that the association between age and Corsi score differed for Hadza adults based on camp residence, with stronger age-related effects in village-living adults. Conversely, the association between age and Finger Tapper score did not differ for Hadza adults living in different types of camp. Engagement in variable amounts of traditional foraging may impact key features of cognition in Hadza adults, and these results can help us further understand how aspects of lifestyle associated with foraging affect human cognitive aging.

Funding provided by the National Science Foundation [NSF-BCS 2051519, 1440867, 1440841, 1440671], The L.S.B. Leakey Foundation, the National Institute on Aging [AG019610, AG067200], and Max Planck Institute for Evolutionary Anthropology

Hidden Kin: The role of extramarital partners in the lives of Himba women

BROOKE A. SCELZA[1] and SEAN P. PRALL[2]

[1]Anthropology, UCLA, [2]Anthropology, University of Missouri

Extramarital partnerships are highly stigmatized in many societies and often excluded from studies of family dynamics and social support. However, in many societies extramarital sex is common, and these partnerships can have an important impact on resource security and health outcomes. Here we combine data from a ten-year ethnographic and demographic study of partnerships among Himba pastoralists with a survey of Himba attitudes on concurrency (n=115). Contrary to the conventional wisdom surrounding concurrency, Himba form enduring bonds with nonmarital partners that often last decades and account for a substantial proportion of births (n=121 individuals, 302 partnerships). Consensus analysis shows that Himba exhibit cultural consonance about the roles, rights and obligations of extramarital partners, with significant agreement (p<0.01) on 15 of 24 statements about concurrency. These statements highlight the primary role of husbands, but also show that women rely on nonmarital partners for resources, both at regular intervals and in times of emergency. These results are supported by quantitative measures of resource transfers. On average, women received gifts from husbands more recently than boyfriends (ùõΩ = -1.47, CI = -1.87 - -1.06) and there are positive effects of concurrency on food security (ùõΩ = -0.48, CI = -0.79 - -0.19). Our data show that extramarital relationships are imbued with a set of rights and obligations that, while distinct from those of marital partners, situate them within larger social structures. We conclude that while extramarital partners are considered separate from the formal kinship structure, they are an integral part of Himba families.

This work was funded by the National Science Foundation (BCS-1534682)

Frail Males on the American Frontier: The Role of Environmental Harshness on Sex Ratios at Birth across a Period of Rapid Industrialization

RYAN SCHACHT

Department of Anthropology, East Carolina University

While sex ratios at birth (SRB) have been shown to vary within and across populations, after over a century of research, explanations have remained elusive. A variety of ecological, demographic, economic, and social variables have been evaluated, yet their association with SRB has been equivocal. Here, in an attempt to shed light on this unresolved topic within the literature, we approach the question of what drives variation in SRB using detailed longitudinal data spanning the frontier-era to the early 20th century in a population from the US state of Utah. Using several measures of environmental harshness, we find that fewer boys are born during challenging times. However, these results hold only for the frontier-era and not into a period of rapid economic and infrastructure development. We argue that the mixed state of the literature may result from the impact and frequency of exogenous stressors being dampened due to industrialization.

Integumentary Bioarchaeology: A Case Study in reconstructing the lived experience of Chimú Era human sacrifices from the North Coast of Peru (1450 CE)

BENJAMIN J. SCHAEFER[1,2], GABRIEL O. PRIETO[3] and JOHN VERANO[4]

[1]Anthropology, Wellesley College, [2]Anthropology, University of Illinois at Chicago, [3]Anthropology, University of Florida, [4]Anthropology, Tulane University

Historically, bioarchaeologists examined health and stress by focusing on nutrition and diseases that were able to be examined macroscopically on bone and teeth. The conceptualizations of stress and health in bioarchaeological research as antithetical entities based on skeletal indicators of stress render many studies as typological in nature, unfortunately. In doing so, this reinforces an interpretive moiety based on binaries to reinforce 'stressed/healthy' or 'not stressed/healthy' through skeletal indicators and artifacts, and lacks an intersectional interpretation beyond the typological models. Bioarchaeological research gives insight into links between early life stressors, later life health outcomes, and mortality risk in a variety of contexts. This paper pushes the field of bioarchaeology by using archaeologically recovered hair, via cortisol, to reconstruct the lived experiences in the months leading up to ritual execution. Hair growth is mediated by biological, environmental, dietary, and physiological factors and does not remodel after formation. Therefore, hair preserves a linear incremental biomarker of a variety of experiences such as perceived violent encounters to indirectly infer psychosocial stressors. On average, about 1cm of hair represents about a month's growth cycle, lending the ability to see incredibly small windows of time in a way generally unavailable to bioarchaeologists. This case study presents preliminary results suggesting that the cortisol levels fluctuated outside (low range: 17 nMol/L; high range: 4383 nMol/L) the typical ranges for cortisol (200-600 nMol/L).

Massachusetts Cultural Council - Tyringham

Beauty is not only skin deep: using biocultural methods to support transgender identification in forensic anthropology

JENNA L. SCHALL[1], TRACY L. ROGERS[1] and JORDAN C. DESCHAMPS-BRALY[2]

[1]Department of Anthropology, University of Toronto Mississauga, [2]Plastic and Craniofacial Surgery, Deschamps-Braly Clinic

This abstract is part of the symposium *Advances and Challenges in the Identification of Sex and Gender in Human Osteological Contexts.* This presentation explores potential avenues for supporting the accurate identification of transgender individuals in forensic anthropology. The growing body of knowledge on transgender research is

becoming increasingly more relevant and necessary as gender-affirming surgeries become more accessible for both trans women and men. To further develop recent research which looked at the impacts of facial feminization surgery (FFS) on craniometric methods of sex assessment, this research addresses the significance of ancestral affiliation to fully understand the range of FFS that may be encountered in forensic casework.

Given that populations and cultures have varying standards of beauty and what is considered to be the "feminine face," ethno-specific FFS modifications have been developed. As previous projects have been conducted blind to ancestral affiliation, this research allows the examination of how these surgical procedures differ between ethnically diverse groups, and how this can further support the identification of trans individuals of different bio-geographical backgrounds.

The goals of this presentation are to identify standards of feminine beauty and how these compare in different ethnographic groups and assess how this is integrated into FFS. Given the epidemic of fatal violence against the trans community, particularly toward those who are Black and Latinx, this research is critical in order to facilitate legal identification in a manner that is respectful to the personal identity of the deceased.

This presentation draws on research supported by the Social Sciences and Humanities Research Council of Canada.

Malaria in the Marshes. Studying the distribution of malaria through cribra orbitalia in the medieval Netherlands

RACHEL SCHATS

Laboratory for Human Osteoarchaeology, Faculty of Archaeology, Leiden University

Malaria is known to have had—and still has—a massive impact on health. Although currently absent in the Netherlands, written records indicate that the disease was endemic here from the 17th to the mid-20th century, mainly in the coastal regions. Unfortunately, due to the paucity of historical data concerning this disease, we know very little about the spread and impact of malaria prior to the 17th-century, hampering our interpretations of past societies. Several palaeopathological studies suggest that cribra orbitalia, a skeletal indicator of anemia, can be used as a marker for malaria in the archaeological record. Although cribra orbitalia is commonly viewed as a non-specific stress marker, there appears to be a strong correlation between this orbital lesion and malaria. This research investigates the spatial distribution of cribra orbitalia in the medieval Netherlands and its potential link to malaria. In total, 1702 individuals from 20 different medieval sites (500-1600 CE) have been studied for the presence or absence of cribra orbitalia and lesion expression. Results show a greater prevalence of cribra orbitalia, in adults and non-adults, in the areas deemed malarial based on paleogeographic maps and 20th-century malaria distribution data (12% vs. 23%, $p<0.001$), yet, no differences in lesion expression are observed. This study suggests that malaria may have been an important contributing factor to the prevalence of cribra orbitalia and that it was likely an influential disease in the low-lying coastal areas of the Netherlands with a substantial impact on health and life expectancy.

Dutch Research Council (NWO) and the Leiden University Fund/Stichting Elise Mathilde Fund

Disentangling phylogenetic, physiological, and ecological influences on the human gut microbiome using primatized gnotobiotic mice

LAURA D. SCHELL, CAROLINE E. DIGGINS and RACHEL N. CARMODY

Department of Human Evolutionary Biology, Harvard University

Human and nonhuman primate gut microbiomes differ in composition and functional capacity. Nevertheless, given profound differences between humans and nonhuman primates in physiology, sociality, and ecology – which all affect the gut microbiome – it is unclear the extent to which gut microbiome differences are ascribable to phylogeny versus physiology versus ecological factors like diet. To develop a model for disentangling these effects, we generated 'primatized' gnotobiotic mice by transplanting gut microbial communities from geographically co-located humans, chimpanzees, and gorillas into germ-free mice. Transplantation enabled characterization of differences in microbiome composition and functional capacity while controlling for host genotype, physiology, development, sociality, environmental exposures, and diet. Mice reliably hosted the gut microbiomes of all three species during the 4-week study; if anything, transplantation led to exacerbation of interspecies differences rather than convergence. However, despite their equivalent phylogenetic relatedness to all three donor species, mice were especially faithful hosts of the human gut microbiome, as indexed by the proportion of donor taxa detected in recipients post-transfer and donor-recipient microbiota dissimilarity. Feeding recipients the donor diet did not increase transfer fidelity, suggesting that improved hosting of the human microbiome was not a byproduct of murine diets being most similar to human diets, and may instead reflect an increased degree of physiological convergence between mice and humans. Taken together, our model and preliminary results offer novel lenses through which to probe human-microbiome co-evolution and distinguish human gut microbiome characteristics that reflect our unique evolutionary history as opposed to our unique physiology or lifestyle.

This research was conducted with funding from the National Science Foundation and the Harvard University Deans Competitive Fund

A review of the general ecology and physiology of the lesser African bushbaby (*Galago moholi*): new information, changing paradigms and future research opportunities

JUAN SCHEUN

Life and Consumer Sciences, University of South Africa, Zoology and Entomology, University of Pretoria

The African lesser bushbaby (*Galago moholi*) is a nocturnal prosimian found throughout southern Africa. Despite the large distribution range and least concern status (International Union for Conservation of Nature) of the species, very little information regarding the thermoregulatory and feeding ecology, as well as reproductive and stress-related physiology of the species was known. However, several long-term studies monitoring the general ecology and physiology of the species has increased the available information considerably. New research found that behavioural and physiological mechanisms allow the species to survive low temperatures within southern Africa. Furthermore, several studies have provided new information on the feeding ecology of the species. Here the feeding ecology of the species has shifted from an insectivore or gummivore to a generalist feeder, able to utilise a wide range of resources. This has far-reaching implications for the species and may allow them to survive a changing environment due to climate change or suboptimal habitats (e.g. urban landscape). Finally, several studies have monitored the reproductive and stress physiology of the species in response to natural (e.g. seasonality, reproduction) and anthropogenic factors (e.g. urbanisation); such information is of utmost importance in understanding the reproductive ecology and response this species will have to a changing environment. The data collected will not only provide important information for the species but also offer possible insight into the feeding, thermoregulatory, reproductive and stress ecology of closely related species. This offers an ideal starting point for new research to be conducted on similarly evasive prosimian species in Africa.

Dental microwear texture analysis at the Gobero site complex (Middle-Late Holocene), Niger

CHRISTOPHER W. SCHMIDT[1], PAUL C. SERENO[2] and GRACE F. HOLMES[3]

[1]Anthropology, University of Indianapolis, [2]Organismal Biology and Anatomy, University of Chicago, [3]Anthropology, University of Manitoba

The locality Gobero in the southern Sahara (Niger) preserves more than 200 burials spanning ~5,000 years during the African Humid Period. Two sustained successive phases of occupation, referred to as Kiffian (9,700-8,200 BP) and Tenerean (7,200-4,500 BP), are separated by an arid horizon recognized across the Sahara. Dental remains from both occupations provide an opportunity to use dental microwear texture analysis to assess diet and compare the temporally calibrated records for enamel isotopes, barbed bone points for fishing, the vertebrate fauna from middens and the nearby paleolake, and palynomorphs. These other lines of evidence indicate both groups remained fisher-hunter-gatherers, as opposed to cattle pastoralists, and that C4 plants during the second occupation were predominant. We applied standard DMTA methods to dental replicas from 11 individuals (5 Kiffian, 6 Tenerean). Data collection used a white-light confocal profiler at 100X; horizontal data spacing was 0.17, and vertical spacing was 0.20 microns. Texture calculations were made with scale-sensitive fractal analysis software. Texture variables included complexity, anisotropy, and textural fill volume. Microwear results support the interpretation of both occupations as fisher-hunter-gatherers, as opposed to cattle pastoralists or farmers, but shows a significant difference between occupations. Tenereans had a higher complexity. Using binary logistic regression, these two groups clustered 82% of the individuals tested, each including a single individual of the other group with atypical complexity. Overall, the diet among Kiffians appears to have been softer than among Tenereans, which may indicate more reliance on terrestrial foraging or C4 plants during the younger occupation.

DMTA funding provided by the National Science Foundation (BCS-0922930).

Why do large apes trot? The ontogeny of trotting gaits in gorillas and its implications for understanding hominoid locomotion

DANIEL SCHMITT[1], BERNADETTE PERCHALSKI[2], ROSHNA E. WUNERLICH[3] and ANGEL ZEININGER[1]

[1]Evolutionary Anthropology, Duke University, [2]College of Medicine, University of Arizona, [3]Biology, James Madison University

Gait selection by primates has been an important part of discussions about primate locomotor evolution. Primates are thought to differ from other mammals in adopting diagonal sequence (DS) gaits, in which the timing of ipsilateral footfalls exceed 50% of the stride duration (limb phase, D), and in avoiding running trots. Yet walking trots (D=50%, no aerial phase) are common in large-bodied apes. Although trotting provides long periods of contralateral limb support, it can also generate interference between ipsilateral limbs. Using an ontogenetic model, we test the hypothesis that the use of walking trots is related to body shape in gorillas. Seven gorillas ranging in age from 5 to 30 years were video-recorded moving freely in a level outdoor enclosure at the NC Zoo. The majority of gaits were walking trots, at or within 5% of D=50% (mean=54, 47-64 for <8 years; mean=48, 44-55 for >8 years; $p < 0.0001$; persisting after correction for speed). Younger individuals behaved in a more primate-like fashion using DS gaits and trots (D ≥ 50%), while older individuals used lateral sequence gaits and trots (D ≤50%). As gorillas age, their body mass increases causing the abdomen to become relatively larger and the hindlimbs relatively shorter, both hypothetically limiting potential for limb interference. In this study, gait selection appears to be related to overall body shape in large apes. Trotting may be a good solution for animals with limited limb interference providing stability especially at heel strike in these primates.

This research was supported by NSF BCS 1517561.

Assessment of endocranial differences between *Pan troglodytes* and *Pan paniscus*

P. THOMAS SCHOENEMANN[1,2,3] and RALPH L. HOLLOWAY[4]

[1]Cognitive Science Program, Indiana University, [2]Department of Anthropology, Indiana University, [3]Research Scientist, Stone Age Institute, [4]Department of Anthropology, Columbia University

Proper interpretation of differences in endocranial form between hominin fossil specimens requires comparisons with modern species. Bonobo (*Pan paniscus: Pp*) vs. common chimp (*Pan troglodytes: Pt*) differences are particularly interesting in this regard: They are our closest living relatives, and they are one example of within-genus variation (having split ~3 MYA). We applied functional neuro imaging methods to compare endocrania in 23 *Pp* and 34 *Pt* endocasts (from RLH). Species shape averages were rigidly aligned and distances measured from corresponding surfaces. Non-rigid diffeomorphic mappings were also derived, allowing calculation of localized scaling coefficients (Jacobians). The average distance from *Pt* to *Pp* was 1.98 mm (SD: 1.07, range: -1.10 to 6.68). The average Jacobian was 1.10 (*Pt* 1.10x larger than *Pp* at each point on average; SD: 0.92). For comparison, the same analyses comparing endocasts of KNM-ER 1813 and KNM-ER 1805 – two hominin fossils generally assumed to be the same species – resulted in similar differences: Average = 1.64 mm (SD: 2.28, range: -8.43 to 8.49); average Jacobian: 1.09 (SD: 0.88). Comparison with analyses on size-equated virtual endocrania (focusing on shape) will be discussed. The pattern of differences highlights more protruding anterior prefrontal areas - but less so for orbital prefrontal and parietal areas - in *Pt* vs. *Pp*. Possible behavioral significance of these differences in *Pan* will be discussed. Although *Pan* comparisons are species averages, whereas these fossils are ostensibly within species, the differences are similar. What this might mean for interpreting hominin fossils will be addressed.

This research was supported in part by grant 52935 from the Templeton Foundation titled: "What Drives Human Cognitive Evolution?" (N. Toth, K. Schick, P. Todd, C. Allen, P.T. Schoenemann, co-PIs).

Biomolecular Evidence for Stress and the Death Experience in Ancient Nubia

SARAH A. SCHRADER

Faculty of Archaeology, Leiden University

One of the challenges bioarchaeologists face when analyzing and interpreting skeletal remains is that bones remodel relatively slowly and, thus, reflect a lived experience from years prior to death. Biomolecular analysis of archaeological hair offers a unique opportunity to examine the months leading up to death via sequential longitudinal sampling, and when coupled with skeletal analysis, can offer important insights into life history. Here, I combine hair cortisol (psychosocial stress), hair nitrogen (physiological stress), and skeletal indicators of stress (physiological stress, employing the Index of Frailty) in an Ancient Nubian/Kushite population from the site of Abu Fatima (*ca*. 2500-1500 BCE; *n*=16). The aims of this study are two-fold: (1) to elucidate stress in the months and years leading up to death, what I refer to as Death Experience, and (2) couch results within an interpretation of the osteological paradox.

Results suggest that, in this relatively small sample, there is variation between hair cortisol, hair nitrogen, and skeletal indicators of stress within and between individuals (cortisol 54-2,656 ng/g, $\bar{x}$ 1,109±968 ng/g; nitrogen $\delta^{15}N_{ker}$ 8.73-15.59‰, $\bar{x}$ 12.17±1.85‰). This is not surprising, but does present an opportunity to examine, in a more refined way, how people experienced stress in the past and how this may have been related to their death. Biomolecular analysis of hair can unhide some aspects of hidden heterogeneity; we are able to (1) examine stress directly prior to death, (2) establish a lifecourse timeline of stress, and (3) assess biochemicals (e.g., hormones), which until recently were undetectable.

American Association of Physical/Biological Anthropologist's Professional Development Grant and Leids Universiteits Fonds Bakels Grant

Traumatic Injury at an Epiclassic Period Central Mexican Shrine Site

MADISON L. SCHULZ and SOFÍA PACHECO-FORÉS
Department of Anthropology, Hamline University

Introduction: Our project focusses on the central Mexican Epiclassic (600-900 CE) of Non-Grid 4 site, shrine where repeated ritual human sacrifices took place. During the Epiclassic period, central Mexico was in a state of sociopolitical upheaval and reorganization. A minimum of 180 individuals were recovered from the site, represented primarily by skulls and cervical vertebra.

Objective: Our objective was to study patterns in sharp force trauma on the remains and connect it to ritual activities.

Methods: We used an inventory and photographs of the recovered remains to collect the data on observed sharp force trauma and compiled composite diagrams. We used archaeological and ethnohistoric data to contextualize our findings.

Results: There were a total of 268 cut marks recorded in the inventory and visible in the photographs. The composite diagrams along with the inventory showed a pattern of trauma concentrated on the C1-C2 vertebrae, along with the mandible. Of all of the observed cut marks, 40% were on the mandible, 35% on the C1s and 8% on the C2s. The data show that 19% of all recovered mandibles, 21% of recovered C1s and, 21% of recovered C2s had cut marks on them.

Conclusion: The data support a ritual sequence of throat slitting and postero-anterior decapitation at Non-Grid 4. Our data along with the archaeological artifacts and ethnohistoric data support the hypothesis of the sacrifices to appease the deities and obtain political power at the Non-Grid 4 site.

The Genetic Landscape of Samegrelo, Western Georgia (Caucasus)

THEODORE G. SCHURR[1], RAMAZ SHENGELIA[2], ARAM YARDUMIAN[3], IAIN MATHIESON[4], MICHEL SHAMOON-POOR[5], DAVID CHITANAVA[6], SHORENA LALIASHVILI[6], IRMA LALIASHVILI[6], REDATE KIBRET[3] and YANU KUME-KANGOLO[7]

[1]Anthropology, University of Pennsylvania, [2]History of Medicine, Tbilisi State Medical University, [3]History and Social Sciences, Bryn Athyn College, [4]Department of Genetics, University of Pennsylvania, [5]Department of Anthropology, Binghamton University, [6]Laboratory for Anthropologic Studies, Ivane Javakhishvili Institute of History and Ethnology, [7]Department of Biology, University of Pennsylvania

To elucidate the population history of the Caucasus and Eurasia, we conducted a survey of genetic diversity in Samegrelo (Mingrelia). We collected DNA samples and genealogical information from 485 Mingrelian individuals residing in 30 different locations after obtaining informed consent from them. In the Laboratory of Molecular Anthropology at Penn, we generated mtDNA control region sequences for all 485 participants (female and male) and Y-STR haplotypes for the 372 male participants. We also analyzed all samples for variation at over 750,000 autosomal SNPs using the GenoChip 2.0+ microarray. The resulting data were compared with those from populations in Anatolia, the Caucasus, the Near East, and Europe. Overall, Mingrelians exhibited greater mtDNA haplogroup diversity than Svans, having low frequencies of East Eurasian haplotypes (A, C, D, F, G) and high frequencies of West Eurasian haplotypes (H, HV, I, J, K, N1, R1, R2, T, U, W), including some of the highest frequencies and diversity of X2 and X4 mtDNAs yet detected. From a Y-chromosome standpoint, Mingrelians possessed a number of haplogroups, including E1b1b, G2a, I2, J1, J2, L, Q, R1a, and R1b. By contrast, Svans had largely G2a haplotypes, although with a few of them belonging to J2, I2, N, and R1a. Analysis of autosomal SNP data further revealed that Mingrelians were genetically similar to each other although not closely related, and grouped with other Caucasus populations in PCA plots. We discuss the implications of these data for the reconstruction of Georgian and Caucasus population history.

This project is supported with funds from the National Science Foundation (BCS-1824826), the National Geographic Society (HJ-041R-17), and the University of Pennsylvania.

Low Reproductive Skew among Flanged Male Orangutans in Gunung Palung National Park, Borneo, Indonesia

AMY M. SCOTT[1,2], GRAHAM L. BANES[3], WURYANTARI SETIADI[4], JESSICA R. SARAGIH[4], TRI WAHYU SUSANTO[5], TATANG MITRA SETIA[5] and CHERYL D. KNOTT[1,6]

[1]Department of Anthropology, Boston University, [2]Department of Natural Resources and the Environment, University of New Hampshire, [3]Wisconsin National Primate Research Center, University of Wisconsin, [4]Genome Diversity and Disease Laboratory, Eijkman Institute for Molecular Biology, [5]Department of Biology, Universitas Nasional, [6]Department of Biology, Boston University

Male orangutans exhibit bimaturism—two mature morphs—flanged and unflanged males. Flanged males are larger, have cheek pads (flanges) and large throat sacs, and produce long calls. Previous orangutan paternity studies found variation between the reproductive success of each morph and in the degrees of reproductive skew. Here we present the first paternity data from completely wild orangutans with known mothers. We hypothesized that (1) flanged males would have higher reproductive success than unflanged males due to flanged male dominance and female preference and (2) a single male would not monopolize paternity due to the temporal and spatial distribution of fecund females. We used fecal DNA samples collected in Gunung Palung National Park from 2008-2019 to genotype 42 orangutans (13 offspring born 2002-2015, their 10 mothers, and 19 candidate fathers) at 12 microsatellite loci. Parentage analyses were performed with both exclusionary and likelihood approaches, in CERVUS 3.0 and COLONY 2.0.6.7. Paternity could be inferred for six offspring. Four flanged males fathered five offspring, and the remaining male's morph was unknown at the time of conception. Thus, in this completely wild setting, we observed flanged males to have higher reproductive success and that paternities were not monopolized. Encounter data from the same period found that unflanged males are more likely than flanged males to be displaced by another male while in association with sexually active females (Fisher's Exact Test, N=34, P=0.044). This result highlights the importance of flanged male dominance over unflanged males for maintaining associations with potentially fecund females.

Funders include Boston University, Leakey Foundation, National Science Foundation (No. DGE-1247312, BCS-1638823, BCS-0936199), Disney Conservation Fund, and US Fish and Wildlife Service (98210-8-G661, 96200-9-G110, F18AP00898, 96200-0-G249, F12AP00369, F13AP00920, F15AP00812).

Tooth morphology and population affinity: testing rASUDAS2 on modern African and European-derived samples

G RICHARD SCOTT[1], DAVID NAVEGA[2], JOAO COELHO[3], TATIANA VLEMINCQ-MENDIETA[1], DORI KENESSEY[1] and MARIN A. PILLOUD[1]

[1]Anthropology, University of Nevada Reno, [2]Life Sciences, University of Coimbra, [3]Anthropology, Oxford University

The web-based application rASUDAS was first developed from samples and trait frequencies in *The Anthropology of Modern Human Teeth*. Since 2015, the method has undergone two major modifications. The beta version included 15 crown and six root traits. The current version, rASUDAS2, includes four new traits and seven back-up traits (e.g., if shoveling is not scored on UI1, UI2 expression can be used). Trait frequencies used in the Bayes algorithm were derived from archaeological samples. To test applicability to modern samples, rASUDAS2 was used to calculate posterior probabilities for African and European-derived samples. Based on 12 to 25 traits, every individual has a probability that it can be assigned to one of seven major geno-geographic groups: Western Eurasia, East Asia, American Arctic, non-Arctic American, Southeast Asian, Australo-Melanesian, and Sub-Saharan Africa. For the modern African sample (n = 159), the highest probability of group assignment was 68.6% for Sub-Saharan African and 22.0% for Western Eurasian. Assignments to the remaining five groups were low (0.6 – 4.4%). For the modern European-derived sample (n = 161), Western Eurasia had the highest

probability of group assignment (75.2%) followed by Sub-Saharan Africa (13.0%). Samples of mixed African and European ancestry yielded almost identical results of 40% Sub-Saharan African and 30% Western Eurasian. Three of four individuals from Africa and Europe can be correctly assigned to their associated ancestral geographic group. For Africans and Europeans, assignment to an Asian or Asian derived group is unlikely (<10%).

Research supported by National Institute of Justice Award [2017-DN-BX-0143].

Food mechanical properties are correlated with relative premolar and incisor size but not relative molar size among anthropoid primates

JEREMIAH E. SCOTT

Department of Medical Anatomical Sciences, Western University of Health Sciences

There is little doubt that the physical properties of foods influence mammalian dental form. While links between aspects of primate tooth shape and broad dietary categories have been demonstrated by many studies, the functional significance of tooth size remains unclear. This study tests the hypothesis that tooth size is related to food mechanical properties. Data on tooth size, mandibular length, and dietary elastic modulus (*E*) and toughness (*R*) for sixteen anthropoid species were taken from the literature. Crown areas for incisors, premolars, and molars were estimated by multiplying each tooth's mesiodistal and buccolingual diameters. Relative tooth size was quantified by dividing the square root of crown area by mandibular length. Correlations between relative tooth size and food mechanical properties were computed using phylogenetic generalized least squares. Among females, relative incisor and premolar sizes are moderately positively correlated with measures of dietary *R*, and relative premolar size is moderately to strongly positively correlated with measures of dietary *E*; relative molar size is uncorrelated with dietary *E* and *R*. Males exhibit a similar pattern, but the correlations are weaker and mostly nonsignificant. These results support the idea that tooth size is evolutionarily sensitive to food mechanical properties: species that consume mechanically challenging diets have relatively large premolars and incisors. The pattern of correlation along the toothrow provides clues about functional differentiation between regions, especially within the postcanine dentition, where the lack of significant correlations for relative molar size is an unexpected contrast with the strong signal found in the premolars.

Survivability versus rate of recovery for skeletal remains in forensic anthropology

SHELBY SCOTT[1] and RICHARD L. JANTZ[2]

[1]Department of Anthropology, Forensic Science Program, University of Toronto, [2]Department of Anthropology, The University of Tennessee

Survivability, the ability of a skeletal element to withstand taphonomic processes, has often been equated to recoverability, and further misused to infer the likelihood that a forensic anthropologist will recover a particular skeletal element at a scene. Consequently, there exists a tendency for forensic researchers to utilize notions of survivability when providing evidence for the necessity of various research endeavours. These types of inferences are problematic in that the factors impacting survivability are not always applicable in a forensic context; the ability of a bone to survive taphonomic processes may not align with the likelihood of recovery.

Empirical recovery rates are presented from two different contexts, with data derived from the Forensic Anthropology Data Bank based on cases performed by the late J. Lawrence Angel (1914-1986) and cases done by the University of Tennessee (UT). Results indicate that the cranium, mandible, and femur are the most recovered skeletal elements in a forensic anthropology context, with comparatively lower recovery rates for bones of the hand and foot, the sternum, manubrium, and patellae.

Analyses of these data indicate that recovery rates may be influenced by factors beyond survivability, such as the experience and training of recovery personnel, deposition, and geography. Thus, it is proposed that researchers consider actual rates of recovery when providing rationale for forensic anthropology research endeavours, in addition to citing a rationale that is based on inferences of survivability. This ensures that the theoretical framework of future forensic anthropology research stems, primarily, from the premise of practical application.

Postural repertoire of free-ranging aye-ayes (*Daubentonia madagascariensis*) at Torotorofotsy, Madagascar

TIMOTHY M. SEFCZEK[1,2], EDWARD E. LOUIS, JR.[1,3] and W. SCOTT MCGRAW[2]

[1]Conservation Genetics, Omaha's Henry Doorly Zoo and Aquarium, [2]Anthropology, The Ohio State University, [3]MBP, Madagascar Biodiversity Partnership

Aye-ayes (*Daubentonia madagascariensis*) are the most anatomically specialized primates. The manner in which continuously growing incisors, clawed digits, and highly modified third fingers are employed during percussive foraging is well known; however, postures associated with feeding are less established. We studied the postural behavior of two aye-ayes from May – December 2017 in Torotorofotsy, Madagascar, an eastern tropical moist evergreen forest. During nightly follows, we used bout sampling to quantify postures of an adult female (N=488 bouts) and juvenile male (N=335 bouts) during feeding and resting. We collected contextual information on strata and substrate characteristics. Chi-square (α=0.05) was used to test for associations between posture, strata, and support use. During our observational period, feeding (81% female, 71% male) occurred more than resting. The most common postures were bimanual cling (35.5%, 23.9%) and unimanual cling (29.1%, 36.1%). These orthograde postures were used most during feeding (bimanual cling: 42.6%, 32.6%; unimanual cling: 35.8%, 50.2%); sitting (37.4%, 44.8%) and laying (46.2%, 43.8%) were the most common resting postures. Pronograde postures, e.g., tripedal crouch and crouch, were employed less often (21.2%, 17.2%). Support use during feeding and resting differed significantly in both individuals ($p<0.001$): most resting occurred on branches (47.3%, 34.4%), while feeding occurred primarily on vertical trunks (60.7%, 69.9%). Strata use during feeding and resting also differed significantly in both individuals ($p<0.001$): both activities occurred most often in the canopy (feed: 67.3%, 90.0%; rest: 79.1%, 78.1%). Aye-aye's frequent use of orthograde postures on trunks underscores the vertical component of their positional repertoire.

Omaha Zoo Foundation, Margot Marsh Biodiversity Foundation, Conservation International, Global Wildlife Conservation, San Diego Zoo, Ahmanson Foundation, Columbus Zoo, Primate Conservation Inc, Cleveland Zoo, Sacramento Zoo, OSU AGGRS/Larsen Grant

Rate heterogeneity among craniodental characters in hominins

YEGANEH SEKHAVATI and DAVID S. STRAIT

Anthropology, Washington University in St. Louis

Estimating the rate of change in morphological characters through time is essential to understanding macroevolutionary processes. Though many models assume that the rate of change is the same among all characters, this assumption needs to be explicitly tested. Moreover, the rate of morphological change can affect estimates of ancestral character states. For example, it has been suggested that maximum parsimony can offer a reasonable estimate of ancestral states when the rate of evolution is low, but parsimony performs poorly when the rate of morphological change is high. Consequently, to estimate the evolution of each character, it is crucial to estimate the rate of transitions between states. Here, we estimated the rate of morphological change and compared five models with different assumptions about rate using maximum likelihood methods in the R package *phytools*. We used 106 discrete craniodental characters from the character matrix of a recently published cladogram of early hominins. Their cladogram was time-calibrated using

the minimum branch length method. For most characters (68), a rate homogeneity model with one parameter to estimate all transitions was the best approximating model. 31 characters were estimated to have different rates for gaining and losing a character state, including cranial capacity and foramen magnum shape. Although rate homogeneity is seen in most craniodental characters, many do not evolve in this fashion. Failure to account for rate heterogeneity could potentially lead to biased estimation of macroevolutionary processes, and adequate modeling of rate variation should be an important direction of future studies in paleoanthropology.

Presence of former leader males improves infant survival in geladas

SHARMI SEN[1], AMY LU[2], NOAH SNYDER-MACKLER[3,4], THORE J. BERGMAN[5,6] and JACINTA C. BEEHNER[1,5]

[1]Anthropology, University of Michigan, [2]Anthropology, Stony Brook University, [3]Center for Evolution and Medicine, Arizona State University, [4]School of Life Sciences, Arizona State University, [5]Psychology, University of Michigan, [6]Ecology & Evolutionary Biology, University of Michigan

Few non-human primate species exhibit evidence of true paternal care, but offspring may still benefit from their fathers in less obvious ways. For instance, the mere presence of a father can protect infants from injury or death by competitors. In geladas (*Theropithecus gelada*), males gain reproductive opportunities by challenging and defeating the dominant ("leader") male of a polygynous "reproductive unit", composed of multiple adult females, their offspring, and sometimes subordinate "follower" males (which can include former leaders). Following takeovers, the new leaders frequently commit infanticide; however the risk of infanticide might be reduced by former leaders, who often remain in the unit as followers (35 out of 51 leader males in our study population remained as followers post takeover). Here, we examined whether the presence of the former leader during the first year following a takeover offered protection for vulnerable infants (less than 1 year old). We collected data during 51 takeovers (2006-2019) from a wild population of geladas living in the Simien Mountains National Park, Ethiopia. Controlling for unit size (number of adult females) and number of other follower males (non-former leaders) in our generalised linear mixed models, we found that infants in units with former leaders were less likely to die in the year following a takeover compared to infants in units without former leaders [odds ratio=0.034, 95%CI= 0.004-0.238, p<0.001***]. Future analysis will examine whether former leaders exhibit any parental behaviors or if their presence alone is enough to reduce infant deaths.

This study was supported by the National Science Foundation (grant#: BCS-2018489, IOS-1854359, IOS-1353110, IOS-1255974), Baldwin Fellowship and research grant from Leakey Foundation(grant#: AWD012312, AWD011197) and the University of Michigan.

The biomechanics of tooth strength: Testing the efficacy of simple models for predicting fracture in geometrically complex teeth

RACHEL S. SENDER and DAVID S. STRAIT

Department of Anthropology, Washington University in St. Louis

Teeth must simultaneously fracture foods in the oral cavity while avoiding being fractured themselves. This study tested the validity of a biomechanical model used to describe tooth strength in which the tooth is represented by a simple dome. Finite element analysis (FEA) was used to determine whether the predictions of the dome model applied to the complex geometry of an actual tooth. A finite element model (FEM) was built from microCT scans of a human M3. The FEM was subjected to three loading regimes simulating 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 entire occlusal surface. Our results corroborate the broad strokes of the dome model with respect to the distribution and orientation of tensile stresses, but document heterogeneity of maximum principal stress orientation across the height of the lateral enamel. This implies that high magnitude tensile stresses might not necessarily cause fractures to fully propagate between cusp tip and cervix. The crown is most at risk of failing during hard object biting on a single cusp. Hard object biting on multiple cusps can drive cusps apart from each other, creating potentially dangerous tensile stresses in fissures. This finding departs from multi-dome tooth models. Geometrically simple biomechanical models are valuable tools for understanding tooth function but do not fully capture aspects of biomechanical performance in actual teeth whose complex geometries likely reflect adaptations for strength.

This research was supported by a grant from the National Science Foundation's Biological Anthropology directorate (NSF-BCS-1627206).

The effect of demographic variation on correlations between developing teeth in humans

VALERIE SGHEIZA

Anthropology, University of Illinois at Urbana-Champaign

Most research in human dental age estimation has focused on point estimates of age. Correlations between developing teeth have received less attention. The effect of demographic variables on these correlations is unknown. I tested the effect of combining reference samples within demographic variables on the residual correlation matrix. The sample consisted of Moorrees et al. (1963) scores of left mandibular permanent 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. A multivariate cumulative probit model was fit to each sex/ancestry group (n=220), each sex (n=440), and each ancestry (n=440). Sampling was therefore considered across two demographic levels: separate sex AND ancestry (level 1) and separate sex OR ancestry (level 2). The correlation matrices from each model fit were then compared between levels by performing a Bartlett's test for difference from the identity matrix on the difference between each level 1 matrix and corresponding level 2 matrix. If combining across levels of demographic variables has no effect on the correlation matrix, the difference between a level 1 and level 2 matrix should be the zero matrix. There were four comparisons with significant chi-square values: Bangladeshi girls from Bangladeshis (p=0.0033, matrix mean<0), European girls from Europeans (p<0.0001, matrix mean<0), Bangladeshi boys from boys (p<0.0001, matrix mean<0), and European boys from boys (p<0.0001, matrix mean>0). Combining across demographic variables generally decreased correlations overall where the difference in correlation matrices between sampling levels was significant.

Validation of a Method for Determining Age At Death Using the Acetabulum

ZOE G. SHAW and DAWN MULHERN

Department of Anthropology, Fort Lewis College

Many methods for determining age at death available to forensic anthropologists can lose accuracy when dealing with individuals over 60. A method that determines age at death from the acetabulum and auricular surface of the pelvis, developed by Rouge-Maillart et al. (2009) uses a scoring system to rank degenerative changes that contribute to a composite score. While this method proved useful in determining age at death, it used a historic Portuguese population. This study tests this method on a modern, forensic population. Using a sample of 152 individuals aged 15-101, scores were determined for the criteria from Rouge-Maillart et al. (2009). Scores were compared to age at death in a Spearman's correlation test and probability tables. The auricular surface and acetabulum criteria were isolated and the scores from the methods were compared through a Spearman's correlation test. Results yielded correlations between age and score, with an r-value of .539 when testing the auricular

surface in isolation, r-value .661 for the acetabulum alone, and r-value .640 for the combined scores. While these show that a relationship exists between age at death and the scores, the utility of this method is apparent in the fact that the general pattern does not change as age at death increases above 60 years of age, contrary to what's typical of many aging methods. The testing of this method on a modern, U.S. sample attests to its possible applicability to U.S. forensic anthropology.

The long and short of it: comparing chronic and acute stress from dental microstructures in Late Archaic children, Ohio

JAKE R. SHIELDS and SAMANTHA H. BLATT

Department of Anthropology, Idaho State University

There is more than one way the body responds to stress. While enamel defects are nonspecific, incremental stress indicators, Wilson bands (WB) and linear enamel hypoplasia (LEH) represent different temporal strategies to stress, acute and chronic, respectively. These could represent not only different causes, but likely different social and biological responses to stress. However, few studies have evaluated both acute and chronic stress indicators from enamel, which requires multiple histological methods.

We compared frequencies, ages-of-occurrence, and durations of acute and chronic stress in the enamel of three Late Archaic children from the Duff Site, Ohio (3390-3220 B.P.). LEH from casts (n=25) were identified and quantified using the microscopic metric method from scanning electron micrographs and known periodicities. WB were identified by decile from thin sections (n=20) and their ages-of-occurrence were calculated. Both LEH and WB (N=45) were recorded in 16 teeth.

Incisors exhibited the highest frequency of WB and LEH (55%). The highest prevalence of WB occurred between the ages of 2-4 years (35-38%) with lowest prevalence from 5-7 years. However, duration was longer for stress that occurred later. While a similar pattern of occurrence and frequency is seen with LEH, the ages-at-occurrence of WB versus LEH are not comparable and WB are not necessarily ancillary to LEH. Frequency of acute stress in these children from a foraging community may be indicative of seasonal nutritional availability or seasonal migration. Future analyses will include the skeletal indicators of stress to develop osteobiographies of early childhood.

This project was supported by a Wenner-Gren Dissertation Fieldwork Grant (Gr. 8390).

How was the abductor function of gluteus medius muscle acquired in the evolution of bipedalism? A comparison of the moment arms of gluteus medius during quadrupedal and bipedal walking in Japanese macaque (*Macaca fuscata*)

TETSUYA SHITARA[1], KOHTA ITO[1], TAKAFUMI FUJIWARA[1], RYOSUKE GOTO[2], EISHI HIRASAKI[3] and YOSHIHIKO NAKANO[1]

[1]Graduate School of Human Sciences, Osaka University, [2]Faculty of Health Sciences, Gunma Paz University, [3]Primate Research Institute, Kyoto University

The human gluteus medius (Gmed) muscle is essential for the generation of the robust bipedal gait, where its abduction prevents the pelvis from rolling in the frontal plane by counteracting the rotation around the hip joint during single support phase. The novel abductor function of Gmed in human lineage may have been acquired with the morphological changes in the pelvis and femur. However, limb posture —the orientation of the thigh relative to the hip— also changes which, in turn, should influence muscular function. The aim of this study is to test the hypothesis that limb postural differences between bipedal and quadrupedal walking affect the function of Gmed without great morphological modification. We test this by comparing the moment arms of Gmed during quadrupedal and bipedal walking in Japanese macaques (*Macaca fuscata*). Models of muscle arrangement were constructed by digitizing cadaveric specimens (n=8). Models were paired with three-dimensional kinematics during quadrupedal and bipedal walking measured from a Japanese macaque (n=1) in order to reconstruct limb posture, and time changes of muscle moment arm lengths were calculated. Gmed of Japanese macaques had extensor, abductor and medial rotator moment arms in both modes of locomotion. Gmed possessed a large medial rotator moment arm during quadrupedal walking but a large abductor moment arm during bipedal walking. The difference in the function of Gmed between quadrupedal and bipedal walking may be related to the difference in limb posture and implies that behavioral change toward bipedalism could precede morphological changes in the pelvis and femur.

This work was partly supported by the Cooperative Research Program of the Primate Research Institute, Kyoto University (2020-B-74).

The Smithsonian survey of human remains of African American individuals at the National Museum of Natural History: Confronting the past and changing the present

SABRINA B. SHOLTS and AMANDA LAWRENCE

National Museum of Natural History, Smithsonian Institution

The history of the Smithsonian Institution is deeply intertwined with the history of the United States, including the development of biological anthropology. Largely resulting from research and collecting practices from the late 19th to mid-20th centuries, the Anthropology Department at the Smithsonian's National Museum of Natural History (NMNH) holds the human remains of approximately 30,000 people who lived across continents and whose stories span millennia. Many of these individuals and their communities were exploited and marginalized by colonial power imbalances and structural inequalities of the era, which were reinforced by anthropological concepts of racial typology and socio-historical evolution. As a critical step in reckoning with this legacy, in 2021 the Museum conducted a survey to identify the human remains of African American individuals in its collections. Our survey team of NMNH staff and contractors searched collections records and physically assessed remains for indicators of African ancestry in people who died in the United States since the beginning of European colonization. We identified a total of 1,011 African American individuals whose remains are part of NMNH's permanent holdings, the majority of which are part of anatomical (65%, 657 individuals) and archaeological/historical (34%, 344 individuals) collections. Among the African American individuals identified by the survey, 233 individuals were alive during slavery in the United States, based on available information. In this paper, we discuss notable findings and examples from specific collections/series of remains identified by this survey, and the consequent actions taken by the Smithsonian with respect to ethical returns and stewardship.

This work was supported by funding from the Smithsonian Institution.

Health impacts of intergenerational households and childcare on Bangladeshi immigrant UK grandmothers

SOFIYA SHREYER[1], LYNNETTE L. SIEVERT[1], SHANTHI MUTTUKRISHNA[2], TANIYA SHARMEEN[3], KHURSHIDA BEGUM[4], OSUL CHOWDHURY[5] and GILLIAN R. BENTLEY[4]

[1]Anthropology, University of Massachusetts - Amherst, [2]Obstetrics and Gynaecology, University of Cork, Ireland, [3]Nuffield Department of Medicines, University of Oxford, UK, [4]Anthropology, Durham University, UK, [5]Parkview Medical College, Sylhet, Bangladesh

The health repercussions for older adults of living in intergenerational households and/or participating in childcare are not well understood. In this study, we explored whether Bangladeshi immigrant women, aged 35-59, living in London (n=100) have health-related differences in relation to: 1) having grandchildren in the household, 2) number of grandchildren in the household, and 3) the amount of time dedicated to childcare.

Health-related variables included body mass index (BMI), waist-to-hip ratio (WHR), symptom burden (compiled from a checklist of common symptoms), disease burden (compiled from a checklist of common diseases) and stress (measured as a 6-point scale from no stress to extreme stress). Linear regression and ordinal linear regression analyses (as appropriate) were completed in SPSS and models were adjusted for age and current financial status. Childcare was defined as minutes per week dedicated to child-minding and walking children to school. Thirty-six women lived in the same household as their grandchildren. Comparing women with and without grandchildren in the household, we found that women living with grandchildren had a significantly higher BMI (26.5 kg/m2 vs. 28.6 kg/m2, p=0.03), but did not differ in other health-related variables. Number of grandchildren in the household was positively associated with women's BMI (p=0.03) and stress levels (p=0.02). We found no health-related differences in relation to the amount of time that women dedicated to childcare. Our findings suggest that, for our population, living in intergenerational households and being involved in childcare does not carry significant health benefits for grandmothers, and may actually be detrimental.

Trunk muscle endurance, strength and flexibility in rural subsistence farmers and urban industrialized adults in western Kenya

BENJAMIN E. SIBSON[1], VICTORIA A. TOBOLSKY[1], TIMOTHY M. KISTNER[1], NICHOLAS B. HOLOWKA[1,2], JOSPHINE JEMUTAI[3], TIMOTHY K. SIGEI[4], ROBERT MANG'ENI OJIAMBO[5], PAUL OKUTOYI[6] and DANIEL E. LIEBERMAN[1]

[1]Department of Human Evolutionary Biology, Harvard University, [2]Department of Anthropology, University at Buffalo, [3]Pemja Primary School, Pemja Primary School, [4]Department of Mathematics, Physics, and Computing, Moi University, [5]Division of Biomedical Sciences, University of Global Health Equity, [6]Department of Orthopaedics, Moi University School of Medicine

High trunk muscle endurance, strength, and moderate flexibility reportedly help maintain musculoskeletal health, but there is evidence for tradeoffs among these variables as well as sex differences in trunk muscle endurance and strength. To test if these observations extend similarly to men and women in nonindustrial and industrial environments, we investigated intra-individual associations and group and sex differences in trunk muscle endurance, strength, and flexibility among 74 (35 F, 39 M; age range: 18-61 yrs.) adults from the same Kalenjin-speaking population in western Kenya. We specifically compared men and women from an urban community with professions that involve minimal manual labor with rural subsistence farmers, including women who frequently carry heavy loads on their heads. Trunk muscle endurance, strength, and flexibility were measured with exercise tests and electromyography median frequency (EMG-MF) analysis. We found a positive correlation between trunk extensor strength and endurance (R = 0.271, $p \leq 0.05$) and no associations between strength or endurance and flexibility. Rural women had higher trunk extensor and flexor endurance, EMG-MF-determined longissimus lumborum endurance, and trunk extensor strength than urban women (all $p \leq 0.05$). Rural women had higher trunk extensor and flexor endurance than rural men (both $p \leq 0.05$). Urban women had lower trunk flexor and extensor endurance than urban men (both $p \leq 0.01$). High levels of physical activity among nonindustrial subsistence farmers, particularly head carrying among women, appear to be associated with high trunk muscle endurance and strength, which may have important benefits for helping maintain musculoskeletal health.

Harvard University: Department of Human Evolutionary Biology Funds; American School of Prehistoric Research

Modern human upper premolar shape does not reflect their geographical origin

PETRA G. ŠIMKOVÁ[1], LISA WURM[2], CINZIA FORNAI[1,3,4] and GERHARD W. WEBER[1,5,6]

[1]Department of Evolutionary Anthropology, University of Vienna, Austria, [2]Clinic of Small Animal Surgery and Reproduction, Ludwig-Maximilians University, Munich, Germany, [3]Vienna School of Interdisciplinary Dentistry – VieSID, Klosterneuburg, Austria, [4]Institute of Evolutionary Medicine, University of Zurich, Switzerland, [5]Core Facility for Micro-Computed Tomography, University of Vienna, Austria, [6]Human Evolution and Archaeological Sciences HEAS, University of Vienna, Austria

Dental shape variation within and between modern human populations has not yet been fully explored. We contributed to this topic by investigating upper third and fourth premolars (uP3 and uP4) from a geographically heterogenous sample using geometric morphometrics in combination with 3D imaging techniques.

High-resolution micro-CT scans of 74 uP3s and 73 uP4s from Europe, Africa, South America, Oceania, Southeast Asia and the Near East were obtained. Four sets of landmarks representing the dentinal crown and the dental outlines were collected. Intra- and inter-population variation was assessed via Principal Component Analysis. Covariation between premolars as well as within premolar features was assessed using Two-Block Partial Least Squares analysis. Size variation was evaluated using the Kruskal Wallis test based on the natural logarithm of Centroid Sizes. Additionally, non-metric traits were scored.

We observed an extensive overlap of tooth shapes in all populations in every analysis. However, we detected significant size differences between populations (p=0.02). Premolars varied between mesio-distally narrow- and tall-crowned with reduced base, and broad- and short-crowned with expanded base. Pairwise covariation between upper premolars was high (r1=0.84). The analysis of non-metric traits did not reveal significant differences between populations.

This study showed that shape variation in upper premolars is not associated with their geographical origin. The high shape covariation between premolars is remarkable, since uP3s possess a tearing function as canines, while uP4s participate in grinding as molars. Our data can serve as reference for further studies on modern human or extinct hominin dental variation and taxonomic assessment.

The Effects of Physiological Stress on the Accuracy of Age Estimation Through Transition Analysis in the Hamann-Todd Collection

ALLYSON M. SIMON[1,2] and MARK HUBBE[2]

[1]Department of Applied Forensic Sciences, Mercyhurst University, [2]Department of Anthropology, The Ohio State University

The accuracy of age-at-death estimates from skeletal remains is affected by numerous biological and environmental variables. Although physiological stress influences the biological age of individuals, research on its impact on the accuracy of age estimation is still scarce. This study analyzed stature, frequency of linear enamel hypoplasias (LEH), and antemortem tooth loss (AMTL) in the Hamann-Todd Collection (n=221) to assess if physiological stress is related to greater age estimation inaccuracy when using transition analysis (TA). Due to the socioeconomic status of the individuals represented in the Hamann-Todd Collection, a large portion of the sample is expected to have experienced moderate to severe physiological stresses during their lifespan. Yet, limited research has examined the prevalence and patterns of physiological stress markers in the collection. Here, we found that at least one LEH was present in 43.9% of the sample. However, regression analyses and independent t-tests, respectively, indicate stature and LEH are not significantly related to TA error. Severe AMTL was present in 23.3% of individuals, with white individuals and females displaying significantly higher frequencies of severe AMTL than the rest of the sample (x^2 test; p<0.001). White females displayed the highest frequency of severe AMTL (50.7%). In contrast with the results obtained for stature and LEH, independent t-tests revealed that individuals with severe AMTL did render significantly higher TA errors (p<0.001). These results strongly suggest that age estimation methods must be further refined to incorporate a better understanding of how physiological stress and health status affect skeletal age estimates.

Surgery before sedentism: Probable trepanation during the early prehistoric period in southeastern north america

DIANA S. SIMPSON

Anthropology, University of Nevada, Las Vegas

Trepanation is regarded as one of the earliest surgical procedures practiced throughout the world, however examples from prehistoric North America are often considered ambiguous, few in number, and are generally limited to the later prehistoric/sedentary periods. In contrast, this study considers a case example of extended survival following probable trepanation during early prehistory (5,000-3,000 BP) at the Little Bear Creek Site (1CT8) in North Alabama.

It is argued that trepanation was performed on this adult male individual through the scraping method, possibly in response to an antemortem traumatic cranial injury. Trepanation is indicated by an ovate perforation of the frontal bone which demonstrates internal beveling, striations, and kerf marks still partially visible on the defect margins. Based on the presence of observable remodeling, and reactive, spiculated bone surrounding the perforation, it is argued that this individual survived for some time after surgical intervention.

Further consideration of the physical and cognitive impacts of the initial cranial injury and subsequent trepanation suggest a possible link to the atypical burial treatment and extensive mortuary assemblage recovered in association with this individual. Ethnographic and ethnohistoric comparison suggest they may have occupied a specialized identity within the community, possibly as a tattooist, shaman, or ritual practitioner. This case not only provides evidence for the presence of complex health care practices in the early prehistoric southeast, but also supports the broader argument for a complex system of performance, ritual, and identity well before sedentism.

Using weighted spherical harmonics to detect functional locomotor signals at the distal femoral articulation

ZANA R. SIMS and CATHERINE J. LLERA MARTÍN

Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

The femur has been used to estimate functional and behavioral signals from fossil material at key points during primate evolution: transitions to arboreality and bipedalism. As a habitually loaded bone, its articular surfaces facilitate joint mobility and transmit forces from the axial skeleton out to distal elements. Owing to this relationship, the femur is often the focus of functional studies and is central to questions regarding locomotion. The purpose of this study is to quantify the morphology of the entire distal femoral articulation across primates to detect which morphological features are functionally associated with locomotion.

A sample of 92 surface meshes was downloaded from MorphoSource, or surface scanned. A shape analysis of the distal femoral articulation was undertaken using spherical harmonics. This Fourier-based method models continuous surfaces as a sum of 3D trigonometric functions on the surface of a sphere. The coefficients associated with the functions are used in a principal component analysis to test for shape differences between locomotor groups. Average models were generated for each group to assess morphological differences attributable to a locomotor signal.

The first three PCs explain 60.08% of the morphological variation in this sample, and distinct locomotor groups are clustered. Arboreal quadrupeds are readily distinguishable from leapers, as are leapers from slow climbers. Relative to the rest of the sample, terrestrial and suspensory clingers are less defined, likely resulting from small samples. These results indicate that a locomotor signal is discernable using the entire distal articulation and may be applicable to incomplete fossil material.

Supported by NSF DGE-1746891

Three-dimensional kinematics of the bipedal chimpanzee pelvis and hind limbs near the walk-run transition speed

AMANDA SINCLAIR[1], BRIGITTE DEMES[2], NATHAN E. THOMPSON[3], SUSAN G. LARSON[2], BRIAN R. UMBERGER[4] and MATTHEW C. O'NEILL[5]

[1]College of Veterinary Medicine, Midwestern University, [2]Department of Anatomical Sciences, Stony Brook University School of Medicine, [3]Department of Anatomy, New York Institute of Technology, [4]School of Kinesiology, University of Michigan, [5]Department of Anatomy, Midwestern University

The three-dimensional (3-D) kinematics of the human pelvis and lower limbs are well characterized across a wide range of speeds, including near the transition from a walking to a running gait. However, comparable 3-D data are only available for a single walking speed in bipedal chimpanzees. Here, we present new 3-D kinematics of the pelvis and hind limbs of bipedal chimpanzees near their predicted walk-run transition speed.

Three-dimensional marker data were collected from three bipedal chimpanzees walking along a level runway. A four-camera motion capture system recorded the movement of reflective anatomical and segment marker clusters, which were digitized using ProAnalyst software (Xcitex, Inc.). Marker data were then integrated with scaled, subject-specific musculoskeletal models of the pelvis and hind limbs of each chimpanzee. An inverse kinematics approach was used to solve for segment and joint angles in OpenSim.

The average dimensionless velocity (v') and Froude number (Fr) were 0.67 ± 0.05 and 0.47 ± 0.07, respectively, which closely approximates the human walk-run transition in dimensionless form (i.e., v' = 0.7; Fr = 0.5). Compared to a moderate speed, bipedal chimpanzees walk with slightly more limb flexion overall. In addition, bipedal chimpanzees walk with a small increase in anterior pelvis tilt and small decrease in hip abduction, on average. Overall, this confirms the distinctive 3-D pelvis and abducted, flexed hind limbs of bipedal chimpanzee gait are conserved from moderate to fast-speed walking.

NSF BCS 0935321 and 2018436

Genetic ancestry defies social organization in human populations of western Himalaya, India

ABHISHEK SINGH[1,2], VIVEK SAHAJPAL[3], SATISH KUMAR[1] and MUKESH THAKUR[2]

[1]Forensic Biology and Biotechnology, National Forensic Sciences University, Gandhinagar, [2]Centre for DNA Taxonomy, Zoological survey of India, Kolkata, [3]DNA division, State forensic science laboratory, Shimla

The human populations of Indian Himalayan region are the amalgamation of several castes with different cultures, languages, and ethnicity. With the practice of strict social organization and the gotra system, majority of populations follow caste endogamy but gotra exogamy. This further indicates the possibility of their conserved genetic pool of caste system. However, the genetic makeup of these populations with the social organization has been poorly assessed in fragments and thus requires a comprehensive study throughout the distribution in the western Himalayan region. In the present study, highly polymorphic 20 autosomal STR markers were used to investigate the genetic structure and affinities among 789 individuals of eight populations with different ethnicity belonging to western Himalaya, India. Overall, we obtained 1461 alleles with 9.13±0.28 alleles per locus. No significant difference was observed between the heterozygosity estimates. The results suggest that the populations of western Himalaya possess close genetic affinity irrespective of their different language, social organization, and ethnicity. The structure analysis revealed a lack of population sub-structure within or between the populations indicating a deep ancestral mixture. In comparison to the other neighboring populations of the Indian Himalayan region, the phylogenetic analysis and PCA plot clustered the populations in three different groups of Western, Central, and Eastern following the geography of the Himalayan

region. These genetic patterns suggest that despite the strict social organization of the caste system, the populations of western Himalayas share a close genetic ancestry.

Testing Data Imputation and Machine Learning Techniques on a Global Odontometric Reference Sample

CASSIE E. SKIPPER and MARIN A. PILLOUD

Department of Anthropology, University of Nevada, Reno

Machine learning (ML) techniques are widely used within data science; however, their popularity in anthropology has not risen as rapidly. As skeletal data from across the globe are included in ever more research projects, our analytical methods must also advance to meet the needs of these burgeoning datasets. Dental crown measurements collected by T. Hanihara (described in Pilloud et al. 2014), served as the dataset for this analysis (n=5,631). The largely archaeological data derive from three continents (Asia n = 3719, Africa n = 858, and Europe n = 1055). This project tests the continental population affinity and sex estimation accuracies of multiple ML methods in Python. These include: Logistic Regression, Linear Discriminant Analysis (LDA), k-Nearest Neighbors (k-NN), Support Vector Machine (SVM), Non-Linear Kernel SVM, Naïve Bayes, Decision Trees, Random Forest, and Gradient Boosting. Imputation methods were also tested as this dataset has nearly 50% missing data. These include: Variable Mean, k-NN, and Iterative imputation.

Accuracy rates for sex estimation reached 80.4% (Iterative imputation, LDA). The maximum prediction rate for population affinity was barely better than chance (39.3%; Iterative imputation, Non-Linear Kernel SVM). However, estimates for combined population affinity and sex improved to 49.2% (Iterative imputation, Logistic Regression). Naïve Bayes consistently produced some of the lowest accuracy rates, while Non-Linear Kernel SVM produced some of the best. The results suggest a need to expand our datasets while incorporating ML techniques. The low accuracy rates for population affinity estimation identify further and necessary discourse in our field surrounding this practice.

This research is supported by the National Institute of Justice Graduate Research Fellowship (2020-R2-CX-0020).

Effects of climate and other habitat variables on African cercopithecid community structure

IRENE E. SMAIL

Department of Integrative Anatomical Sciences, University of Southern California

Cercopithecid primates inhabit a variety of habitats across Africa today, and their overlapping ranges result in many regions where multiple sympatric taxa co-occur. As past and present environmental factors have been shown to influence mammalian community structure at broad scales, this project focuses on how these factors contribute to variation in the diets and dental adaptations of cercopithecid communities (taxocenes) specifically.

Dental metric data were collected from 538 wild-shot specimens representing 42 species of extant African monkeys and observational feeding data were collected from the literature to calculate taxocene dental and dietary niche areas for 49 localities based on published species lists. Akaike's Information Criterion was used to evaluate linear regression models of taxocene niches against a suite of modern and Holocene climatic and habitat variables, anthropogenic impacts, and species richness counts for potential resource competitors.

Environmental variable effects were consistent across the top 95% of model weights for both dental and dietary regression models. Anthropogenic impacts appeared in the fewest models (<15%), followed by competitor species richness (33 – 40%) and measures of canopy height and canopy cover (35 – 40%). Modern and Holocene climate variables appeared in the most models (40 – 60%). Holocene precipitation, modern temperature seasonality, and canopy height are associated with smaller taxocene niche areas while modern precipitation and canopy cover are associated with larger niche areas. These results support previous findings on the role of climate factors in shaping primate community structure and implicate non-climate variables like canopy cover and potential competition.

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.

Grip strength and mating success in US adults

CAROLINE B. SMITH and EDWARD H. HAGEN

Anthropology, Washington State University

Previous research posits that the dramatic male bias in upper body strength is due to sexual selection, either from advantages conferred by greater strength in male-male contests or female preference for stronger mates. Others have proposed that strength is a cue of important mate qualities, such as health or immune function. The sexual selection hypothesis is supported by studies that have found that grip strength is associated with both mating success and reproductive success in men. Although there is some evidence that strength is associated with reproductive success in women, the relationship between female strength and mating outcomes is poorly understood.

Using data from the 2011-2012 phase of the National Health and Nutrition Examination Survey (NHANES), a large representative sample of the US (N = 3328), the current study found that grip strength was a significant positive predictor of several outcome measures of adult mating success (partnership status, lifetime number of sexual partners, and past year number of sexual partners), e.g., 3-5 more lifetime partners in those with strength 1 SD above vs. 1 SD below the mean, even controlling for numerous anthropometric, socioeconomic, hormone, health, and physical activity related confounds. However, there was either no significant sex difference in the effect of grip strength, or the effect in females was smaller than males but still positive. Hence, grip strength is positively related to mating success for females as well as males, contrary to some versions of the sexual selection hypothesis. We discuss possible explanations for these findings.

Comparative Morphology of the Hominid Inner Ear Otolith System

CHRISTOPHER M. SMITH[1,2,3], ASHLEY S. HAMMOND[3,4], SERGIO ALMÉCIJA[3,4,5] and JEFFREY T. LAITMAN[1,2,3,6]

[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]New York Consortium in Evolutionary Primatology, [4]Division of Anthropology, American Museum of Natural History, [5]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, [6]Department of Otolaryngology, Icahn School of Medicine at Mount Sinai

The semicircular canals of the bony labyrinth of the petrosal temporal bone inform the evolution of primate positional behavior and phylogeny. However, the evolutionarily more ancient vestibular otolith organs (utricle and saccule, detecting linear acceleration and gravity) remain largely unexplored. This study utilizes a novel morphometric model to examine the otolith system of the inner ear in extant hominids.

Virtual 3D models of 82 right and left bony labyrinths from five extant hominid species were created from micro-CT scans (including modern *Homo sapiens,* n=58; *Pan troglodytes,* n=8; *Gorilla gorilla,* n=8; *Pongo pygmaeus,* n=8). Principal Components Analyses of Procrustes-superimposed landmark coordinates were used to assess overall shape variation. Planes of otolith organ angulation were analyzed using a set of landmarks that best reflected the internal anatomy of the vestibule. A pairwise Wilcoxon rank sum test

with a post-hoc Bonferroni correction was used to assess significant interspecific differences and the presence of any right-left asymmetries in the angulation of the otolith organs.

Results show significant differences in the configuration of the hominid otolith system. The greater utricle and greater saccule ("greater" indicating the utricle and/or saccule plus their periotic structures) are considerably closer together with a more acute angulation in modern *Homo sapiens* as compared to the condition in the great apes ($p<0.004$). These findings indicate that humans exhibit key structural differences in a prime sensory system. Such findings may have implications in understanding phylogenetic and functional differences.

This research was supported by an NSF Doctoral Dissertation Research Improvement Grant (award #: 2051335), the MCIN/AEI (PID2020-116908GB-I00), and the Generalitat de Catalunya (CERCA Programme).

Hadza hunter-gatherers with greater exposure to other cultures preferentially share with generous campmates

KRISTOPHER M. SMITH[1] and COREN L. APICELLA[2]

[1]Department of Anthropology, Washington State University, [2]Department of Psychology, University of Pennsylvania

Humans have an evolved partner choice psychology that tracks the reputations of others and motivates people to seek out the best available cooperative partners. Previous research has largely focused on choosing the most cooperative partners; however, the benefits a potential partner generates for others is a function of both willingness to cooperate and ability to generate benefits in the first place. Moreover, preferences for either trait should be flexible and responsive to local socioecological conditions, such as the variance of each trait in the population. Here, we test the flexibility of partner choice psychology among Hadza hunter-gatherers of Tanzania. Ninety-two Hadza ranked their campmates on generosity and foraging ability and then played a game in which they could direct finite resources to those campmates. We found that Hadza with greater exposure to other cultures, such as via schooling or participating in the market economy, shared more preferentially with campmates they ranked higher on generosity, whereas Hadza with lower exposure showed no preference to sharing with generous campmates. However, this moderating effect was specific to generosity—regardless of exposure, Hadza showed only a small preference for sharing with better foragers. We suggest this change in preferences is due to high exposure Hadza having more experience cooperating with others in the absence of strong norms of sharing, and thus greater variance in willingness to cooperate among social partners, placing a greater emphasis on choosing more cooperative partners. These results highlight the flexibility in human partner choice psychology.

This work was supported the University of Pennsylvania's MindCORE (Mind Center for Outreach, Research and Education) program.

Fine-scaled oxygen isotope variation in tooth enamel: milk does not trump seasonality

TANYA M. SMITH[1,2], JANAÍNA N. ÁVILA[1,3], DANIEL R. GREEN[4,5] and IAN S. WILLIAMS[3]

[1]Griffith Centre for Social and Cultural Research, Griffith University, [2]Australian Research Centre for Human Evolution, Griffith University, [3]Research School of Earth Sciences, Australian National University, [4]Department of Human Evolutionary Biology, Harvard University, [5]Lamont-Doherty Earth Observatory, The Earth Institute, Columbia University

Oxygen isotope compositions ($\delta^{18}O$) in tooth enamel are of considerable interest in bioarcheology and paleoanthropology for their reported relationship to milk intake during infant nursing as well as seasonal variation due to meteorological cycles. In 2018 we presented near-weekly $\delta^{18}O$ values measured with the Sensitive High Resolution Ion Microprobe – Stable Isotopes (SHRIMP-SI) over the first 2.75 years of life in a Neanderthal first molar (M1) that showed strong annual trends and maximum $\delta^{18}O$ values long after exclusive milk intake. These results suggested that hypothesized isotopic enrichment due to milk intake is minor at best, and does not hinder paleoenvironmental reconstructions. Here we report SHRIMP-SI $\delta^{18}O$ values prior to, during, and after nursing in 10 nonhuman primate dentitions (4 wild baboons, 6 captive macaques). Comparisons of M1s with successively-forming teeth reveal maximum $\delta^{18}O$ values after species-typical ages for cessation of suckling (weaning) in 5 of 6 individuals. We also find short term 1-2 per mil $\delta^{18}O$ fluctuations within a few weeks of physiological disruptions including birth (7 of 9 individuals) and severe illness (4 of 4 individuals); these shifts in tooth chemistry are similar in magnitude to previous inferences of human nursing cessation and prehistoric environmental variation from coarsely-drilled bulk samples. Reported $\delta^{18}O$ decreases in bulk sampled serially-forming human teeth may be due to natural variation in environmental water sources rather than the cessation of isotopically enriched mothers' milk. Ongoing elemental studies will further clarify the determinants of $\delta^{18}O$ variation and instill greater confidence in environmental reconstruction from primate dentitions.

This work was funded by the Australian Academy of Science, Australian National University, Australian Research Council (DP210101913), Griffith University, and Harvard University.

Mitosis and chondral modeling in the nasal capsule of perinatal primates

TIMOTHY D. SMITH[1], JAMES J. CRAY[2] and VALERIE B. DELEON[3]

[1]School of Physical Therapy, Slippery Rock University, [2]Department of Biomedical Education and Anatomy, The Ohio State College of Medicine, [3]Department of Anthropology, University of Florida

Based on mouse models of nasal capsular cartilage (NCC) growth, the prenatal nasal capsule is shaped by complex clonal chondrocyte activity. Whereas this may typify some mammals during early cartilage growth, primates appear to be more variable at birth. Rather than persisting as a largely complete cartilaginous template at birth, as in mice, the nasal capsule is highly fragmented in most newborn primates. Here, we examine the nasal capsule of newborn and early infant primates regionally to document early postnatal persistence of the NCC, and we present preliminary evidence of the expression of proliferating cell nuclear antigen (PCNA) in chondrocytes of the NCC. Sixteen perinatal primates (7 lemurids; 2 bushbabies; 7 monkeys) were studied using histochemistry and immunohistochemistry following routine paraffin sectioning. The septal cartilage is completely unossified at birth in all primates studied except galagids, in which ossification of the mesethmoid center is commenced. All primates possess at least a partially intact and cartilaginous tectum ("roof") of the NCC, whereas most primates lack the most posterior end, or cupula. In most primates, the lateral nasal wall is highly fragmented, especially anteriorly; it is nearly completely resorbed or ossified in galagids, providing further evidence of an accelerated pace of NCC development in this clade. PCNA expression is most ubiquitous in septal cartilage and the tectum, whereas turbinals appear to have more specific, localized chondroblastic modeling (e.g., at convex surfaces). Results demonstrate regional differences in NCC fate, and support the highly specialized role of septal cartilage in primate facial growth.

Funded by NSF grant #s BCS-1830894 and BCS-1830919

Genetic anomaly or congenital syphilis? The anomalous crown morphology of a 1500-year-old isolated molar from Panamá

NICOLE E. SMITH-GUZMÁN

Center for Tropical Paleoecology and Archaeology, Smithsonian Tropical Research Institute

Molar teeth with abnormal supernumerary cusp morphologies have varied etiological explanations and have been described using numerous differing terminologies, complicating the identification, quantification, and understandings of their genetic and infectious causative components. Aberrant molars described in individuals with congenital syphilis appear phenotypically

identical to the bud-shaped molars attributed to several rare genetic diseases. This study presents the case of an isolated molar of this abnormal form recovered from a pre-Columbian context (129–588 cal CE) at the archaeological site of Cerro Juan Díaz (LS-3) in Los Santos, Panama. A cautious and thorough approach to differential diagnosis is taken, considering the possible causative factors through a regional survey of 267 individuals from pre-Columbian sites throughout Panama. Overall, this study found substantial evidence for both treponemal disease and developmental anomalies in the regional sample, but more evidence to support the notion of congenital syphilis in this case, while being unable to rule out the possibility for several genetic syndromes. The results of this study highlight the importance of the consideration of both infectious and non-infectious causes in differential diagnosis, and caution strongly against the assumption that any one lesion in isolation is unique to only one specific pathological condition.

Funding for this study was provided by the Smithsonian Tropical Research Institute and the Sistema Nacional de Investigación (SNI) of the Secretaria Nacional de Ciencia y Tecnología (SENACYT) of Panama.

Unraveling demographic history and complex trait architecture from 6,000 Mexican genomes

MASHAAL SOHAIL[1,2,3], AMANDA Y. CHONG[4], MARIA J. PALMA[1], CONSUELO D. QUINTO-CORTES[1], AARON RAGSDALE[1], SANTIAGO G. MEDINA[1], GUADALUPE DELGADO-SÁNCHEZ[5], LUIS P. CRUZ-HERVERT[5,6], LETICIA FERREYRA-REYES[5], HORTENSIA MORENO-MACÍAS[7,8], CARLOS A. AGUILAR-SALINAS[9], ADRIAN CORTES[10], SELENE L. FERNANDEZ-VALVERDE[1], VICTOR ACUÎA-ALONZO[11], GENEVIEVE WOJCIK[12], CHRISTOPHER R. GIGNOUX[13], CARLOS D. BUSTAMANTE[14], ADRIAN HILL[15,4], MARIA T. TUSIE[7,8], ALEXANDER J. MENTZER[10,4], JOHN NOVEMBRE[16,2], LOURDES GARCÍA-GARCÍA[5] and ANDRÉS MORENO-ESTRADA[1]

[1]Laboratorio Nacional de Genómica para la Biodiversidad (UGA-LANGEBIO), CINVESTAV, [2]Department of Human Genetics, University of Chicago, [3]Centro de Ciencias Genómicas (CCG), Universidad Nacional Autónoma de México (UNAM), [4]The Wellcome Centre for Human Genetics, University of Oxford, [5]Instituto Nacional de Salud Pública (INSP), [6]Facultad de Odontología, Universidad Nacional Autónoma de México (UNAM), [7]Unidad de Biología Molecular y Medicina Genómica, UNAM-INCMNSZ, [8]Universidad Autónoma Metropolitana, [9]Division de Nutrición, Instituto Nacional de Ciencias Médicas y Nutrición Salvador Zubirán, [10]Big Data Institute, University of Oxford, [11]Escuela Nacional de Antropología e Historia (ENAH), [12]Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, [13]Colorado Center for Personalized Medicine, University of Colorado Anschutz Medical Campus, [14]Department of Biomedical Data Science, Stanford University, [15]The Jenner Institute, University of Oxford, [16]Department of Ecology and Evolution, University of Chicago

We present the Mexican Biobank Project genotyping 6,059 individuals from 32 states at ~2 million SNPs with linked trait information. We call genetic ancestries and identity-by-descent tracts genome-wide to estimate ancestry-specific effective population size (Ne) for the last 300 generations, revealing elaborate fine-scale structure reflecting the different cultural histories of Mesoamerican regions. While the Gulf, Occident, Mayan region, and Oaxaca reach their peak Ne in the classical period, followed by a slow decline in the post-classical, the center of Mexico shows an increase in Ne in the post-classical period and into the colonial period. Later in the colonial and post-colonial periods, while the center decreases in Ne, the Mayan region and Oaxaca increase. European and African ancestries also present varying dynamics and strengths of founder effects. We further call runs of homozygosity (ROH) and find that they are positively correlated with native ancestry, with a larger genomic imprint of short ROH (< 8 Mb) moving southward and eastward, reflecting smaller long-term Ne due to higher native ancestry. We find that rare mutation burden is depleted in individuals with higher native ancestry, also likely due to their lower Ne. We model trait values using a set of predictors in a mixed model framework including genetic ancestry, ROH, socioeconomic and biogeographical variables and find strong effects of genetic ancestry and/or ROH for height, BMI, triglycerides, and glucose levels. Our work highlights that studying under-represented populations at fine-scale is warranted to uncover population substructure revealing lesser-known histories and generating findings of biomedical relevance.

This work was supported by a binational initiative (Mexico/UK) co-funded by CONACYT (FONCICYT/50/2016), Newton Fund, and Medical Research Council (MR/N028937/1). MS was also supported by a Chicago Fellows award.

Intralimb patterns of diaphyseal cross-sectional properties of the femur and calcaneus in vertical clinger and leapers

MEGAN P. SOLÍS and KRISTI L. LEWTON

Integrative Anatomical Sciences, University of Southern California

During leaping, primate vertical clinger and leapers encounter large substrate reaction forces relative to their body size. As a result, the hindlimb diaphyses of leapers are relatively more rigid than those of their forelimbs. However, variation in diaphyseal cross-sectional geometry among the bones of the hindlimb has not previously been examined and it is unknown whether distal limb elements in proximity to the substrate (such as the distally elongated calcaneus in galagids and tarsiers) exhibit increased strength or rigidity compared to proximal limb elements. We investigated intralimb patterns of diaphyseal rigidity and strength in primates that differ in the amount of leaping locomotion they use (i.e., high-frequency leapers versus low-frequency leapers). We derived estimates of torsional rigidity (J) and compressive strength (cortical area) from femora (from the literature) and calcanei (from micro-CT scans) in 56 individuals from 6 galagid and 1 tarsiid species. Diaphyseal cross-sectional properties were scaled by bone length to account for differences in body size. We tested the hypothesis that the ratios of femoral to calcaneal scaled J and cortical area relate to leaping frequency using Kruskal-Wallis tests and linear regression. We predicted that high-frequency leapers would have stronger and/or more rigid distal limb elements relative to proximal limb elements compared to low-frequency leapers. This prediction was not supported; instead, high-frequency leapers have stronger and more rigid femora relative to calcanei compared to low-frequency leapers. Future research incorporating tibial measures may help to clarify patterns of intralimb diaphyseal cross-sectional properties in leaping species.

Funding provided by the National Science Foundation (BCS-1944571).

The impact of physical contact during fur-rubbing behavior on urinary oxytocin in tufted capuchin monkeys

MEGHAN J. SOSNOWSKI[1,2], MARCELA E. BENÍTEZ[2,3], OLIVIA B. REILLY[1,2] and SARAH F. BROSNAN[1,2,4,5]

[1]Department of Psychology, Georgia State University, [2]Language Research Center, Georgia State University, [3]Department of Anthropology, Emory University, [4]Center for Behavioral Neuroscience, Georgia State University, [5]Neuroscience Institute, Georgia State University

In highly social species, like primates, oxytocin plays an important role in cooperation and the formation and maintenance of social relationships. In capuchin monkeys, we previously found that oxytocin increased after fur-rubbing, a behavior in which capuchins rub pungent materials on themselves and others. This species-specific behavior provides a novel method to increase endogenous oxytocin non-pharmacologically. It is unknown, however, whether it is the social nature of this behavior or physical touch that increases oxytocin. Here, we tested this in nine tufted capuchins (*Sapajus apella*) by inducing fur-rubbing in two contexts: social fur-rubbing, in which individuals fur-rubbed with social partners, and solo fur-rubbing, in which subjects were physically (but not visually) separated from their social group. As in previous research, fur-rubbing significantly increased urinary oxytocin (b = 0.16, SE = 0.06, t = 2.51, p = 0.01), as compared to a control condition (log-transformed OT: M = 1.64, SD = 0.31). Specifically, oxytocin increased after fur-rubbing both with (log-transformed OT:

M = 1.83, *SD* = 0.17) and without social partners (log-transformed OT: *M* = 1.74, *SD* = 0.28), though the increase with a social partner was significantly higher (*b* = 0.20, SE = 0.07, *t* = 2.75, *p* = 0.006). These results suggest that the action of fur-rubbing, presumably through touch, may increase oxytocin even in the absence of physical contact with conspecifics, suggesting that physical touch alone can affect oxytocin.

Putrid Meat in the African Paleolithic: It Wasn't Just for Eskimos

JOHN D. SPETH[1] and EUGÈNE MORIN[2]

[1]Department of Anthropology, University of Michigan, [2]Department of Anthropology, Trent University

The ethnohistoric record underscores the importance of putrid meat in the diets and foodways of arctic and subarctic foragers. Allowing meat to putrefy breaks down ("predigests") proteins and fats without cooking or using scarce fuel; inhibits pathogens by reducing the meat's pH; prevents lipid rancidity; and preserves vitamins. While acknowledging the viability of this practice in colder, northern latitudes, most scholars believe such foodways would be impossible in tropical latitudes where decay and invasion by dangerous pathogens would quickly render meat toxic. A search of the ethnohistoric record of traditional tropical latitude societies finds instead that rotten meat consumption was both widespread and safe. This paper (1) compiles a comparative database of documented 18th- and 19th-century cases of rotten meat consumption in tropical environments (e.g., putrid hippos, elephants, antelope, boars); (2) explores the traditional ways rotten meat was processed and prepared for consumption (e.g., roasting, stewing) in order to render it safe for use; and (3) examines the microbiology literature to determine how such simple, traditional forms of food preparation, under tropical conditions, successfully eliminated the potentially lethal effects of the neurotoxins produced by *Clostridium botulinum* (i.e., botulism). The paper concludes with thoughts about the potential role of rotten meat in the adaptations of pre-modern hominins living in sub-Saharan Africa and Southeast Asia prior to and after the introduction of fire.

The effect of clothing on decomposition and scavenging in Cape Town, South Africa

MAXIMILIAN J. SPIES[1], DEVIN A. FINAUGHTY[1,2], LOUISE J. FRIEDLING[1] and VICTORIA E. GIBBON[1]

[1]Department of Human Biology, Faculty of Health Sciences, University of Cape Town, Cape Town, South Africa, [2]School of Anthropology and Conservation, University of Kent, Canterbury, United Kingdom

Limited taphonomic research has been conducted in the Western Cape, South Africa where most forensic cases involve clothed individuals. We assessed the influence of common seasonally appropriate clothing on decomposition in a forensically significant habitat in Cape Town. Deployed over two consecutive summers and winters, ten ~60 kg domestic pig carcasses (6 clothed, 4 unclothed), were used as proxies for human decomposition. Clothing was chosen based on local forensic case files and tailored to fit the pigs, preventing unrealistic scavenger access. Daily weight loss was used to quantitatively track decomposition progression. Clothed carcasses took on average 22 days longer (475.92 more ADD) than unclothed carcasses to reach 68% mass loss. Double-layer clothing notably inhibited decay during the colder, wetter winters with a mean of 108 vs 71 days (1921.94 vs 1099.64 ADD) for clothed and unclothed carcasses, respectively, to reach 68% loss. Thinner clothing appeared comparatively negligible during the hotter, drier summers with a clothed mean of 19 vs 14 days for unclothed carcasses (424.93 vs 295.38 ADD) to reach 68% mass loss. Weight loss was closely linked with scavenging activity by the Cape grey mongoose (*Galerella pulverulenta*) which displaced clothing to feed on the abdomen. Scavenging was hindered by denim trousers, causing altered feeding patterns and preferential scavenging on unclothed carcasses. This research suggests forensically realistic season-specific appropriately tailored clothing is required in taphonomic research. We show it can delay decomposition affecting ADD and postmortem interval estimations substantially by modulating the effect of weather, season, and vertebrate scavenging behaviour.

The National Research Foundation of South Africa (Grant numbers: 123254 and 115357); the University of Cape Town, Department of Human Biology internal research grant.

Communication, Collaboration, and Transparency: An Exploration of the Ethical Challenges Associated with the Analysis and Curation of Human Remains when Working with Multiple Stakeholders at the Capuchin Catacombs of Palermo, Sicily

KIRSTY E. SQUIRES[1] and DARIO PIOMBINO-MASCALI[2]

[1]Department of Criminology, Policing and Forensics, Staffordshire University, [2]Department of Anatomy, Histology and Anthropology, Vilnius University

The Capuchin Catacombs of Palermo (Sicily) are an exceptional and culturally rich site and are home to the largest assemblage (n=1,284) of mummified remains in Europe. Since their inauguration (AD 1599), the catacombs have been open to visitors. The constant draw of the site to visitors holds significant ethical and logistical challenges in the curation and scientific analysis of the mummified individuals. These difficulties are further compounded by lack of investment in the site and the multiple stakeholders (e.g. descendants of the dead, Capuchin Friars, cultural heritage bodies, scientific community, and visitors), all with vested interests, involved in decision-making and the operation of the catacombs. In this paper, the ethical challenges of curating and analysing human remains at this cultural site will be explored. We will highlight that transparency, collaboration, and regular communication between all stakeholders is essential in the curation and analysis of the Capuchin mummies. It is evident that the absence of open dialogue and cooperation would ultimately mean the beliefs and wishes of the living and deceased are not respected, the mummies would experience further degradation, and scientific analysis would not be possible. In turn, this holds significant ramifications for bioarchaeology and public archaeology more broadly.

Geometric Morphometric Approach to Sexual Dimorphism in the Zygomatic Bone

MARY E. ST JOHN and JEFRY R. GARCIA-BERNABE

Department of Anthropology, Binghamton University

Three dimensional geometric morphometrics (3D GM) is a powerful tool to reveal shape differences in anatomical structures. This approach is being increasingly applied to the study of sexual dimorphism in the human cranium, replacing the more traditional and subjective scoring of features into ranked categories. The human zygomatic bone and process have been shown in previous 3D GM studies to exhibit sexual dimorphism. The present study placed a series of 43 landmarks and semi-landmarks on the zygomatic bone and process on 3D models of 20 individuals of known sex (10 males and 10 females) from the Terry Collection to assess the level of sexual dimorphism. Procrustes analysis and PCA revealed a clear separation between males and females along PC1, with males falling toward negative values and females toward positive values. Thus, our study confirms the results of previous studies in finding clear patterns of sexual dimorphism in the human zygomatic bone and process. In particular, sexual dimorphism was expressed at the zygomaticomaxillary suture. Our results reveal that the zygomaticomaxillary suture is positioned further forward in females. Additionally, along the posterior edge of the frontal process, the outward curve of the bone protrudes more in males while being more rounded in females, and in males, the inward curve along the frontal and temporal processes is more acute than in female individuals. Continued research into the use of 3D GM can revolutionize our ability to accurately sex individuals, and vastly reduce observor error.

Femoral cortical bone distribution in *Sahelanthropus tchadensis*

NINA J. ST. HILLAIRE[1,2], CARRIE MONGLE[3,4], CHRISTOPHER M. SMITH[5,6,7], ALEXANDRA C. IDSO[5,7], WILLIAM E.H. HARCOURT-SMITH[5,7,8,9] and ASHLEY S. HAMMOND[10,7]

[1]Department of Anthropology, University of Maryland, [2]Department of Biology, University of Maryland, [3]Department of Anthropology, Stony Brook University, [4]Turkana Basin Institute, Stony Brook University, [5]Department of Anthropology, The Graduate Center, CUNY, [6]Center for Anatomy and Functional Morphology, Icahn School of Medicine at Mount Sinai, [7]New York Consortium in Evolutionary Primatology, [8]Department of Anthropology, Lehman College, CUNY, [9]Division of Paleontology, American Museum of Natural History, [10]Division of Anthropology, American Museum of Natural History

Bipedalism incorporates skeletal adaptations that distinguish later hominins from other primates, including distinctive femoral cross-sectional properties, but it is unclear whether these features are present in the earliest hominins. Femoral cross-sectional images have recently been published online for a fragmentary femoral shaft, TM 266-01-063, attributed to early hominin *Sahelanthropus tchadensis*. Our study aims to evaluate whether the cross-sectional properties of TM 266-01-063 resemble those of extant primates or fossil hominins.

Our comparative sample includes *H. sapiens*, *Pan*, *Gorilla*, monkeys (*Brachyteles, Chiropotes, Pithecia*, *Papio, Mandrillus*), and fossil hominins. Some data (including TM 266-01-063) were gathered from published sources. Using ImageJ, cortical bone cross-sectional areas (CSA) were calculated from CT scan data at six different locations along the femoral shaft, from 45-80% of shaft length. Cortical bone thicknesses were measured at the same six locations, and the measurements were converted to ratios for comparisons (e.g., anterior to posterior cortical bone thickness). CSA and bone thicknesses were compared through the length of the shaft in TM 266-01-063 and the comparative sample.

TM 266-01-063 is most similar to chimpanzees in CSA throughout the shaft, perhaps simply reflecting similarities in size between chimpanzees and *Sahelanthropus*. However, the distribution of the cortical bone (as captured by the thickness ratios) reveals a pattern more similar to humans, especially proximally. Interestingly, TM 266-01-063 was unlike any of the comparative sample in the pattern of anterior to medial cortical bone thickness between 45-80% of the shaft. This preliminary study has implications for locomotor reconstructions in early hominins.

This project was supported by NSF Research Experiences for Undergraduates (REU) award #1950610.

Three transitions in Pleistocene human diets: a zooarchaeological perspective

MARY C. STINER

School of Anthropology, University of Arizona

The legacy of the human ecological footprint in Mediterranean Eurasia and its relation to the evolution of human social and energy networks is analyzed from the perspective of Paleolithic meat diets. The results are organized thematically in terms of predator-prey dynamics, transitions in energy acquisition, and labor allocation. Hominins emerged as big game hunters by at least half million years ago, but probably before this. By the Late Pleistocene, however, Paleolithic foragers were restructuring biotic communities to a significant degree, at least partly through feedback loops of increasing diet breadth and demographic robustness. This process had consequences for the scale at which cooperative and information networks could develop. Prior Middle Paleolithic populations lived at low densities and the top of the terrestrial food chain. Early Upper Paleolithic people were also big game hunters, but with expanded patterns of meat supplementation and increasingly diversified labor. The demographic advantage of the UP systems may have stemmed from wholesale strategies for evening-out or sharing risk both in internal and inter-group reciprocity systems, which also lowered (albeit slightly) humans' average position in the food web. These strategies ultimately may have contributed to the collapse of some large game populations towards the end of the Pleistocene, when a strategy of diversification in diet gave way as a direct trade-off between varied small game hunting to management of selected ungulate species under semi- or fully captive conditions.

Nonshivering thermogenesis, body temperature, and bone mass in a model of cold-dwelling humans

ALEXIS STOKEL, ARIELLA RICHMAN, MAISEY SCHULER, REBECCA TUTINO, MIRANDA N. COSMAN, RACHEL HURWITZ, ISABEL HERMSMEYER and MAUREEN J. DEVLIN

Anthropology, University of Michigan

Cold-dwelling humans are at risk for bone loss through sympathetic nervous system signaling to osteoblasts. Such bone loss might be mitigated by nonshivering thermogenesis in brown adipose tissue (BAT), in which uncoupling protein (UCP1) diverts cellular respiration to generate heat. This hypothesis is difficult to test in humans, so here we used the UCP1 knockout mouse (UCP1KO). We pair-housed male and female UCP1KO and wildtype C5BL/6J (B6) mice at 22˚C (cool) or 26˚C (thermoneutrality) from 3-12 weeks of age. The prediction was that cool housing would lead to lower body temperature and lower bone mass in UCP1KO compared to B6 mice. Dorsal body temperature was measured via infrared thermography (FLIR E-8, FLIR Systems), and trabecular bone morphology was measured via µCT (Scanco Systems). In WT mice housed at 22˚C vs. 26˚C, trabecular bone volume fraction (BV/TV, %) in the distal femur was significantly lower in females (-25.9%, p=0.006) but not in males (-15.6%, p=0.086). Surprisingly, in UCP1KO mice, BV/TV did not differ at 22˚C vs. 26˚C in either sex. Body temperature was 1˚C lower in UCP1KO females, but 1˚C higher in WT females at 22˚C vs. 26˚C (p<0.05 for both). There were no temperature differences in males. These results are contrary to our hypothesis, and challenge the notion that BAT protects against cold-induced bone loss. Alternatively, BAT may induce energetic tradeoffs between thermogenesis and skeletal acquisition, particularly in females. This hypothesis has implications for understanding skeletal variation in cold vs. temperate-dwelling populations.

Funding for this project was provided by NSF BCS-1638553 to MD.

A Dental Metric Biodistance Analysis of the Rong and the A'chik

MARY A. STOUGH

Department of Anthropology, University of Alaska Fairbanks

Little is known about the population history and genetic affinities of many of the tribal groups of northeastern India, including the Rong and the A'chik. This study employs tooth size allocation analysis to test hypotheses concerning their origins and the impact of sex-biased post-marital residence patterns. Due to matrilineality and matrilocality, A'chik females ought to express less variability than males and be more isolated phenetically from members of other groups. The opposite should be true for the Rong who are patrilineal and patrilocal. Despite patrilineality, Rong females should share some affinities to members of other groups due to the widespread practice of hypergamous marriages. Mesiodistal and buccolingual dimensions of the permanent teeth were measured among 166 A'chik and 185 Rong individuals. These data were compared to that obtained among 1151 members of seven ethnic groups from other regions of South Asia. Group centroids from canonical variates were plotted in three dimensions to assess similarities among samples. Canonical variates, from both sex-pooled and non-pooled analysis, identify the Rong and A'chik as possessing closer affinities to each other than to members of the other groups, thereby supporting the hypothesis that members of these two tribal groups share a population history different from that of ethnic groups of other regions of the subcontinent. The sex-pooled analysis indicated a closer relationship between the A'chik females and the Rong and a more

distant relationship between the Rong males and females than expected. This likely stems from a lack of comparative samples of other north-eastern groups.

DNA methylation as a mediator of the association between maternal exposure to climate extremes and child growth outcomes

BILINDA STRAIGHT[1], XI QIAO[2], DUY NGO[2], CHARLES E. HILTON[3], OLUNGAH OWUOR CHARLES[4], AMY NAUGLE[5], STEPHANIE MORGAN HAFT[5], CAROLINE SISINA KELEMPU[4], SAMAN LESEELA[1], DANIEL L. LESEELA[1], CELINA JESKA[1], CLAUDIA LALANCETTE[6] and BELINDA L. NEEDHAM[7]

[1]Gender & Women's Studies, Western Michigan University, [2]Statistics, Western Michigan University, [3]Anthropology, University of North Carolina at Chapel Hill, [4]Institute of Anthropology, Gender, and African Studies, University of Nairobi, [5]Psychology, Western Michigan University, [6]Epigenomics Core, University of Michigan, [7]School of Public Health, University of Michigan

There is broad consensus that the effects of climate change on human health will be most deeply felt in the world's lowest income countries and populations, given their already struggling health systems that are ill equipped to meet the burden created by an increased incidence of food and water insecurity, emotional stress, and both non-infectious and infectious diseases. Better understanding of the epigenetic mechanisms by which physiological and emotional stress translate into positive or negative whole health outcomes is important. DNA methylation (DNAm) is one of the molecular mechanisms that has received widespread attention because it is feasible to study even in field conditions and some DNAm modifications may be reversible. Here we report findings of our multi-disciplinary epigenome-wide association study comparing Samburu pastoralist children exposed to an extreme 2009 drought in their first trimester of gestation (N=104) to unexposed same-sex siblings (N=109). Additionally, as a further test of the impact of climate extremes, we report on differences between children in our study in a cooler (higher rainfall and altitude) versus hot (low rainfall and altitude) region. After quality control; corrections for batch, chip, and genomic inflation; covariate adjustment; and multiple testing correction were performed, 1 significant mediator of drought, and 17 mediators of region and child outcomes were found. We discuss the biological significance of the results based on effect sizes, proportion mediated, and what is currently known about the function of nearby genes. We conclude with a discussion of the implications of the results for embodied, lived experience.

This research was funded by National Science Foundation Award #1728743, "A Bio-Cultural Investigation of Intergenerational Epigenetic Mechanisms" (Bilinda Straight, PI) and Western Michigan University FRACAA.

Assessing the extent of covariation between the shapes of the mandibular corpus and second molar

JULIE STRAIN[1] and CHRIS ROBINSON[2,3,4]

[1]Department of Anthropology, Hunter College, CUNY, [2]Department of Biological Sciences, Bronx Community College, CUNY, [3]Doctoral Program in Anthropology, The Graduate Center, CUNY, [4]NYCEP, New York Consortium of Evolutionary Primatology

The mandible has been documented to have changed substantially in shape through time over the course of human evolution. Various factors have been proposed to influence these shape differences among hominin species including differences in the stresses placed on the mandible due to dietary variation, differences in the shape of the cranium, and differences in the size and shape of the dentition. In this preliminary study we test the extent to which the shape of the mandibular corpus co-varies with the shape of the crown and roots of the second molar. Virtual models were created from MicroCT scans of 32 great ape and human mandibles. Landmark and semi-landmark data were collected on these models along the mandibular corpus and molar crown outline and from the EDJ to the root tips of each specimen. These data were subjected to Procrustes superimposition and the Procrustes aligned coordinates were used in a two-block partial least squares analysis to assess the correlations between the shapes of the second molar crown and roots and the shape of the mandibular corpus. Results show low levels of co-variation between mandibular corpus shape and shapes of the molar crown outline and roots, with the roots generally exhibiting higher squared covariation percentages with the mandibular corpus. The only significant correlation was found in humans between the molar roots and mandibular corpus. These results suggest that the size and shape of the molar crown and roots are not a major influence on the shape of the mandibular corpus.

This research was funded by NSF BSC 1515053

Advances in Subadult Age Estimation: The Mixed Cumulative Probit (MCP) and the Subadult Virtual Anthropology Database (SVAD)

KYRA E. STULL[1], ELAINE Y. CHU[1], LOUISE K. CORRON[1], CHRISTOPHER A. WOLFE[1] and MICHAEL H. PRICE[2]

[1]Anthropology, University of Nevada, Reno, [2]Applied Complexity Fellow, Santa Fe Institute

Although subadult age estimation is assumed to be accurate, methodological and practical shortcomings like the lack of subadults in skeletal collections and the prevailing culture of restricted access to data and algorithms, persist. The Subadult Virtual Anthropology Database (SVAD) is a collection of skeletal and dental data, demographics, and derivatives of 4850 individuals ranging from birth to 20 years from eight different countries, freely accessible through a Zenodo Community. The collaborations with Angola, Brazil, Colombia, France, the Netherlands, South Africa, Taiwan, and the United States provided a unique opportunity to collect 63 age indicators: diaphyseal dimensions, epiphyseal fusion, and dental formation. The mixed cumulative probit (MCP) was designed to accommodate features associated with biological data, including heteroskedasticity, mixtures of ordinal and continuous variables, missing values, conditional dependence, and alternative specifications of the age-dependent mean response. Uniquely, these are incorporated into a single model to provide a maximum likelihood estimate with 95% confidence intervals. The MCP is available through KidStats, a free interface for user-friendly subadult age estimation, and "yada", an R package. The user can choose to employ a global model or population-specific models. The MCP in the "yada" R package can be employed and adapted for other research questions, broadening methodological possibilities for adult age estimation, paleodemography, human biology, and those beyond biological anthropology. The open-access nature of the SVAD and MCP overcome the identified shortcomings that previously impeded advancements in subadult (and adult) age estimation.

Funding sources: This research was funded by the National Institute of Justice (2015-DN-BX-K409 and NIJ 2017-DN-BX-K144).

Prevalence, Variation, and Transmission of Anti-Microbial Resistance Among Sympatric Wild Primates

REBECCA STUMPF[1,2,3], ABIGAIL ASANGBA[4], CHRIS IRUMBA[3], MARTIN AINEBYONA[3], HOWARD ONYUTH[3] and MICHAEL NUTE[5]

[1]Department of Anthropology, University of Illinois, [2]Institute for Advanced Study, Notre Dame, [3]Kanyanchu River Research Collaborative, Kibale National Park Uganda, [4]Center for Individualized Medicine, Mayo Clinic, [5]Department of Computer Science, Rice University

Antimicrobial resistance (AMR) is a growing global threat. Currently, we lack fundamental knowledge of the presence and dynamics of AMR in wild environments. This study investigates AMR presence and transmission among wild primate communities in West Uganda. The goals were to apply innovative phylogenetic forensic approaches to identify zoonotic reservoirs of AMR, assess whether AMR is species-speciÔ¨Åc, track transmission dynamics among hosts and ultimately to better understand the prevalence, origins, variation, and etiology of AMR. We extracted DNA from fecal samples of seven sympatric wild primate species (chimpanzees, baboons, mangabeys, black and white colobus, red colobus, red-tailed monkeys, and vervets). AMR genes macrolide (ermB), sulfonamide (sul1 and sul2), and tetracycline (tetC, tetO, tetW) were sequenced on Illumina Hiseq 2500 and phylogenetic trees were constructed based on the total sequences. Finally, we applied a novel data visualization tool to visually assess gene variants and predict likely pathways for transmission. AMR genes were found among all wild primates, though variation was observed among host species. Chimpanzees had the highest prevalence of AMR, particularly Sul and Tet, potentially due to their greater terrestriality and exposure to humans. However, comparisons within chimpanzees indicated greater Sul2 prevalence and strain variation among the unhabituated than the habituated chimpanzee community. TetC variants overlapped extensively among chimpanzees. Shared AMR variants on the same phylogenetic branch were also evident between chimpanzee communities, suggesting transmission. The use of microbial phylogenetics to understand the presence and variation in AMR provides an effective means of identifying, tracking, and ultimately mitigating AMR transmission.

Notre Dame Institute for Advanced Study, NSF BCS-1441409

A comparative analysis of ontogenetic changes in catarrhine and platyrrhine cranial base angle

SIOBHAN A. E. SUMMERS[1], MALEA K. NEESE[1], EMILY R. BRYSON[1], TARA A. PEBURN[2], TIMOTHY D. SMITH[3,4] and VALERIE B. DELEON[1]

[1]Department of Anthropology, University of Florida, [2]Department of Rehabilitation Sciences, Florida Gulf Coast University, [3]School of Physical Therapy, Slippery Rock University, [4]Department of Anthropology, University of Pittsburgh

The primate basicranium is integral to analyzing and understanding cranial morphology and its associated soft tissue structures. Previous research indicates a direct correlation between the degree of cranial base flexion and brain size in primates. This study examines cranial base development as it relates to cranial base angle (CBA) and tests phylogenetic effects on the ontogeny of CBA.

The study sample included computed tomography (CT) data from a growth series of six catarrhine and six platyrrhine species. For most species, adult, juvenile, and infant data were available. Landmark coordinate data were collected to quantify CBA and cranial capacity was estimated for each primate specimen. As expected, the adult sample showed significantly greater flexion of the CBA in catarrhines compared to platyrrhines ($p<0.001$). The juvenile and infant samples also showed significantly greater CBA flexion in catarrhines relative to platyrrhines ($p<0.001$ and $p=0.001$, respectively). Results suggest that catarrhines and platyrrhines display significantly different CBA development from infancy to adulthood. CBA remained stable through ontogenetic stages in platyrrhines. In contrast, catarrhines overall showed progressively less flexion through growth, although this was not true for all taxa. These results are consistent with a previous report of CBA extension through ontogeny in *Pan* and CBA flexion in *Homo*. More research is required to parse out the mechanisms that produce these divergent growth trajectories.

Funded in part by the National Science Foundation (BCS-1830894 and BCS-1830919).

Investigating the impact of childhood vitamin D deficiency on cross-sectional area and cortical bone porosity at the femoral midsection

KAREN R. SWAN, LOUISE T. HUMPHREY and RACHEL IVES

Centre for Human Evolution Research, Natural History Museum, London

The amount and distribution of cortical bone in weight-bearing bones changes during growth and is highly sensitive to hormonal and mechanical environments. Vitamin D deficiency rickets in children can be caused by lack of exposure to sunlight and/or insufficient dietary intake and can lead to inadequate bone mineralization and impairment of the structural composition of bone. The impact of these effects on the cross-sectional structure of cortical bone at different stages of locomotor development during childhood has not been fully investigated. Femoral cross-sectional area and cortical bone porosity was examined in CT scans of 137 children aged from birth to 8.5 years from post-medieval London. Macroscopic manifestations of skeletal rickets identified children with an active (N=16) or healed (N=32) condition. Cross-sections were extracted at 50% of the total intermetaphyseal length and periosteal and endosteal outlines were generated using EPmacroJ. Cross-sectional area measurements including total area and medullary area were computed and binarized images were used to quantify the proportion of cortical bone porosity. The results demonstrate differences in the distribution of cortical bone in children with rickets in comparison to those without. The proportion of cortical bone porosity was frequently higher in children with active rickets, likely reflecting delayed mineralisation of newly formed bone together with increased bone resorption due to secondary hyperparathyroidism. Total area and cortical bone area were higher in children with healed rickets suggesting consolidation of cortical bone and reorganization of bone cross-sectional structure following recovery.

This project was funded by the Calleva Foundation through the Natural History Museum, London.

Variation in market integration and health affect early childhood growth in Daasanach pastoralists living in northern Kenya

ZANE S. SWANSON[1], ROSEMARY NZUNZA[2], HILARY J. BETHANCOURT[3,4], EMMANUEL NDIEMA[5], DAVID R. BRAUN[6,7], ASHER Y. ROSINGER[3,8] and HERMAN PONTZER[1,9]

[1]Evolutionary Anthropology, Duke University, [2]Kenya Medical Research Institute, (KEMRI), [3]Department of Anthropology, Pennsylvania State University, [4]Department of Anthropology, Northwestern University, [5]Department of Earth Sciences, National Museums of Kenya, [6]Center for the Advanced Study of Human Paleobiology, Department of Anthropology, The George Washington University, [7]Department of Human Evolution, Max Planck Institute of Evolutionary Anthropology, [8]Department of Biobehavioral Health, Pennsylvania State University, [9]Global Health Institute, Duke University

Changes in environmental condition, like those that occur as a function of sedentarization and/or market integration, can have broad effects on life history. Growth is particularly sensitive to such variation. Results from investigations into the effects of lifestyle change on growth in small-scale populations remain mixed, however. Here we test the potential proximate causes of early childhood growth variation (n=99; ages=0-5 years) at the household level among Daasanach semi-nomadic pastoralists who are becoming increasingly sedentary. Anthropometric, demographic, and socioeconomic status (SES) data were collected from 166 households across 11 communities. Population-specific measures of early childhood growth – height-for-age (HFA), weight-for-age (WFA), and weight-for-height (WFH) – were then calculated for children in these households using growth models derived from a novel longitudinal anthropometric dataset (observations=4587; individuals=1753). Linear mixed effects models were used to test the relationships between household variation and early childhood growth. Household values of HFA were significantly positively correlated with household distance to nearest market center (β=0.916,

SE=0.276, p<0.001), while neither WFA, nor WFH, were significantly affected by market distance. No significant relationships were found between any measure of growth and household mobility or SES. However, household WFA (β=0.73, SE=0.291, p=0.02) and WFH (β=0.75, SE=0.285, p=0.01) were positively correlated with parental health. Additionally, WFH was significantly negatively correlated with the number of children (>7 years) living in the same household (β=-0.358, SE=0.134, p=0.01). These results demonstrate the heterogenous effects of lifestyle change on life history, with specific negative consequence for linear growth among Daasanach experiencing increased market integration.

NSF ARCH #1624398; NSF REU #1930719; This work was funded by the PSU SSRI Human Health and Environment Seed Grant, and the Triangle Center for Evolutionary Medicine (TriCEM) Graduate Research Grant.

Increased homozygosity due to endogamy results in fitness consequences in a human population

NATALIE A. SWINFORD[1], SEAN P. PRALL[2], BROOKE A. SCELZA[3] and BRENNA M. HENN[4]

[1]Department of Anthropology, University of California, Davis, [2]Department of Anthropology, University of Missouri, [3]Department of Anthropology, University of California, Los Angeles, [4]Department of Anthropology and the Genome Center, University of California, Davis

Previous work has found differences in mutation load among human populations, i.e. variation in the efficacy of selection at removing deleterious variants, but an understanding of whether differences in load effect evolutionary fitness is lacking. Recessive allele burden has been linked to several phenotypes, but does it alter reproductive success? To address this question, we are working with the Himba, a pro-natalist, endogamous population of northwestern Namibia, who practice natural fertility. Using a sample of 681 individuals, we show that the Himba have been recently bottlenecked and exhibit elevated levels of inbreeding, calculated as the fraction of the genome in runs of homozygosity (FROH). Many individuals contain multiple long segments of ROH in their genomes, indicating the influence of recent events. However, we did not find evidence for first-cousin consanguinity, despite reports of this preference among arranged marriages. Because deleterious alleles tend to be recessive, an estimate of FROH highlights recessive mutation load. In this study, we test whether increased mutation load results in observed fitness consequences using linear models to assess the effects of FROH on reproductive success in a cohort of post-reproductive women. We find that higher FROH is associated with significantly lower (p=0.007) reproductive success for women who are known to have been fertile (have had at least one child). This signal is attenuated when women who never bore children are included in the model (p=0.03). Our data suggest a multi-locus genetic effect on fitness driven by the expression of deleterious recessive alleles.

This work was funded in part by the NSF (BCS-1534682 to B.A.S.).

Body mass and trabecular structure in the human talus

ADAM D. SYLVESTER[1], DANIEL J. WESCOTT[2], DEBORAH L. CUNNINGHAM[2] and DEVORA S. GLEIBER[2]

[1]Center for Functional Anatomy and Evolution, The Johns Hopkins University School of Medicine, [2]Department of Anthropology, Texas State University

A tremendous body of research argues that bone tissue responds to changes in loading regime and bone strain. Here, we assess the affect of body mass, in particular body mass index (BMI), on the trabecular structure of the human talus. We test the expectation that individuals with higher BMI values should evince bone parameters consistent with great load magnitudes.

Forty human tali that are part of the Texas State University Donated Skeletal Collected were scanned using an NSI X5000 micro-computed tomography system housed in the Grady Early Forensic Anthropology Research Laboratory. Surface models were generated from segmented image stacks, and bone shape variation was quantified using weighted spherical harmonic analysis. Resulting shape analysis output was used to warp a template VOI set (n = 1000) to all tali. Standard trabecular bone parameters were extracted and subjected to dimension reduction via principal components analysis. Groups (sex, BMI) were compared using ANOVAs performed on principal component scores.

In all analyses, the first principal component described variation in parameter magnitude, while subsequent components described variation in bone pattern. Within sexes, individuals with higher BMI showed greater bone volume fraction values across the entire talus (PC1 male; p-value <0.001; PC1 female; p-value <0.01). Other trabecular bone parameters investigated, including trabecular thickness and trabecular spacing, did not show group differences. This was also true of subsequent components. As expected, bone volume fraction was consistent with higher loads through the ankle of individuals with higher BMI values.

This research was supported by the National Science Foundation (Award Number 1923044).

Sexual dimorphism in human midfacial growth patterns from newborn to 5 years old based on computed tomography

TAISIYA A. SYUTKINA[1] and ANDREJ A. EVTEEV[2]

[1]Institute of Ethnology and Anthropology, Russian Academy of Science, [2]Anuchin Research Institute and Museum of Anthropology, Lomonosov Moscow State University

Understanding the growth patterns of the human facial skeleton is essential for scientific, forensic, and medical purposes. However, there has been some controversy regarding the extent of sexual dimorphism in the facial skeleton in infancy and early childhood. This study aims to describe the developmental aspects of sexual dimorphism in human midfacial ontogeny.

The dataset included clinical CT scans of 247 male and 184 female non-adult individuals and 36 male and 33 female adult individuals as reference samples. 25 linear measurements describing the facial skeleton were obtained from 3D reconstructed skulls. Basic descriptive statistics, growth increments, smoothing spline models and correlation matrices were calculated for each age cohort (4 cohorts for infants up to 1 year, 5 yearly cohorts up to 5 years) of each sex. Ontogenetic changes until the age of 5 were also compared with a published forensic sample.

The study revealed stable differences between males and females in most variables from birth until maturity. However, while mean values in the male group are higher in absolute terms, females present higher percentages of attained adult size for most measurements until the age of 5. Correlation matrices among the age cohorts show moderate associations for males and weak associations for females, correlation patterns being different at all ages. Comparison with the forensic data revealed fairly consistent results only for 5 out of 10 variables.

The study shows that males and females differ substantially in craniofacial measurements during ontogeny while the growth trends seem to be similar at all ages.

MSU, "Heritage of the Society of Naturalists, Anthropologists and Ethnographers (OLEAE) at Moscow University: museum funds and documents"; IEA RAS, "Cross-cultural and Interdisciplinary studies of historic and modern societies"

Long and short of craniofacial development – how cranial base chondrocytes shape the face

HEATHER L. SZABO-ROGERS

Center for Craniofacial Regeneration, Department of Oral and Craniofacial Sciences, School of Dental Medicine, University of Pittsburgh, McGowan Institute of Regenerative Medicine, University of Pittsburgh, Department of Developmental Biology, School of Medicine, University of Pittsburgh

Human Robinow Syndrome (RS) is a rare genetic disease where the patients develop a characteristic wider face, and shorter stature. The embryological and biochemical etiology of RS is largely unknown. We use the *Prickle1Bj/Bj* to model human RS. Both the *Prickle1Bj/Bj* mice and patients with RS have causative mutations in core components of the Wnt/PCP (Wnt/Planar cell polarity) pathway. The Wnt/PCP pathway determines the plane of cell division, and the location of primary cilia in vertebrates. The *Prickle1Bj* allele is a single nucleotide missense allele that disrupts a protein-protein interaction domain, while leaving the remaining protein unchanged. The *Prickle1Bj/Bj* cranial base proliferating chondrocytes lose their stereotypical localization of Prickle1, Dvl2, and Dvl3 proteins. In addition, *Prickle1Bj/Bj* experience enhanced Dvl2 and Dvl3 membrane localization which causes increased Wnt/PCP signaling. We determined that the protein-protein interactions between Prickle1^{Bj} and Dvl2 and Dvl3 are significantly decreased contributing to the randomization of cranial base chondrocytes. *Prickle1Bj/+* and *Prickle1Bj/Bj* fetuses have wider cranial bases. Consistent with the mouse data, we identified an intragenic single nucleotide polymorphism (SNP) in Prickle1 in normal human populations associated with wider cranial bases. These analyses also uncovered a gene-by-gene interaction between Prickle1 and FOCAD1 that further widens the human cranial base. Consistent with the genetic findings, we observe that Prickle1 and FOCAD1 proteins colocalize in the division plane of murine cranial base chondrocytes, and this is lost in *Prickle1Bj/Bj*. In conclusion, Prickle1 intracellular localization contributes to chondrocyte polarity and cranial base width.

This work is supported by the Fellows Grant Award Program from the American Association of Anatomy, Momentum Funds from Pitt and support from the University of Pittsburgh School of Dental Medicine.

Does parent-offspring conflict across mammals result in differing offspring growth by placental morphology?

MAYA SZAFRANIEC, TIFFANY PAN and AMY M. BODDY

Anthropology, University of California Santa Barbara

Mammalian reproduction likely evolved under selective pressure for more efficient nutrient transfer to offspring. However, the benefits of internal gestation for offspring growth come at energetic and immunologic costs to the pregnant parent. This parent-offspring conflict is particularly salient at the placental interface. We examine the relationship between offspring *in utero* growth rate and placental morphologies in 396 mammal species. Importantly, we distinguish growth of an individual offspring from the growth of a litter because they index the conflicting fitness of an individual offspring and parent, respectively. We employ fetal (FGQ) and litter growth quotients (LGQ), calculated as relative measures of neonate body size for a given gestation length. Placental morphology is categorized into three levels of interdigitation (a measure of the surface area at the parent-fetal interface) and invasiveness (number of tissue layers separating parental and fetal blood). We predict greater placental intrusiveness is associated with faster growth, resulting in larger offspring for a given gestation duration (e.g., FGQ >1). Using two-way ANOVA, we find both FGQ and LGQ have statistically significant differences in invasiveness (p=0.0172, p=0.0253) and interdigitation (p=< 0.0001, p=< 0.0001). However, post hoc analyses suggest the pattern is non-linear. Overall, this indicates the role parent offspring conflict plays in fetal growth is more than just placental morphology and degree of resource exchange, including interactions between metabolism and immunology. Or, there are additional trade-offs between placental morphology and offspring growth, possibly involving energy-expensive tissues, such as the brain.

Greater clarity of obstetric sufficiency of the human pelvic inlet with control of body size

ROBERT G. TAGUE

Geography and Anthropology, Louisiana State University

Humans give birth to big babies. Whereas males are larger than females for nonpelvic bones, females have a larger pelvis than males due to selection for its obstetric sufficiency. Researchers infer a positive relationship between percentage sexual size dimorphism (SSD; female mean/male mean*100%) of the pelvis and intensity of selection pressure within and among species. Surprisingly, percentage SSD of human pelvic inlet circumference is low, 3%. A reason for this low SSD may be the absence of control of nonpelvic SSD. This study uses a sample of 221 females and 204 males (skeletonized adults from the United States) from which to identify a subsample of 25 females and 46 males matched for femoral and clavicular lengths, and femoral head diameter; these nonpelvic measures are proxies for stature, shoulder breadth, and body mass. Percentage SSD of inlet circumference of humans control of body size is compared with that of three species that are sexually monomorphic in body size: *Aotus azarae*, *Hylobates lar*, and *Saguinus geoffroyi*. These three species give birth to relatively larger newborns than do humans (percentage newborn body mass = newborn body mass/adult female body mass*100%): humans (5.9%), *A. azarae* (9.6%), *H. lar* (8.6%), and *S. geoffroyi* (7.8%). Nevertheless, humans control of body size have the highest percentage SSD of inlet circumference: humans (12.0%), *A. azarae* (8.2%), *H. lar* (5.4%), and *S. geoffroyi* (3.3%). The explanation of results is that human newborns are of larger body mass than predicted for our adult female body mass.

Genomics and cellular biology of primate pigmentation: lessons from other taxa

ELIZABETH TAPANES[1,2], TINA LASISI[3], JASON M. KAMILAR[4] and BRENDA J. BRADLEY[2]

[1]Department of Biological Sciences, University of California San Diego, [2]Department of Anthropology, Center for the Advanced Study of Human Paleobiology, The George Washington University, [3]Department of Anthropology, The Pennsylvania State University, [4]Graduate Program in Organismic and Evolutionary Biology, University of Massachusetts Amherst

This abstract is part of the symposium *Integumentary Anthropology: Examining the Exterior*. Research on primate pigmentation has been driven, in part, by an interest in understanding the evolutionary function of coloration—including camouflage, communication, and thermoregulation. Yet the genetic architecture of pigmentation has mainly been studied through experimental work on model taxa and studies on domesticates, where different pigmentation phenotypes are induced through selective breeding. Therefore, a central question remains: is the underlying genetic basis of pigmentation in these contexts the same as in natural populations?

Recent work across vertebrates indicates pigmentation in natural populations might be dissimilar from laboratory and domesticated animals. Particularly, pigmentation may be the product of many genes (often with pleiotropic and epistatic interactions) instead of just the few large-effect loci seen in non-natural contexts. We performed a survey of previously reported pigmentation genes across vertebrates (fish, birds, mice, primates) to assess allocation of research effort across distinct taxa, populations, and genes. We report the distribution of species, genes, and populations under study are skewed. Across non-human primates, research effort on pigmentation genetics accounts for <0.02% of the literature compared to other vertebrates, and of that, 65% of studies disproportionately target *MC1R* or *ASIP*.

Due to sampling biases, we do not have enough data to understand the genetic architecture of pigmentation in non-human primates. However, based on studies across other vertebrates, we present hypotheses on the genetic basis of primate pigmentation and highlight future avenues of research.

Frequencies and patterns of hybrid fibers in the superficial masseter and superficial anterior temporalis in anthropoid primates

ANDREA B. TAYLOR[1] and MEGAN A. HOLMES[2]

[1]Department of Basic Science, Touro University, [2]Family Medicine and Community Health, Duke University School of Medicine

Skeletal muscle fiber types are important determinants of the contractile properties of muscle fibers, such as fatigue resistance, shortening velocity and isometric tension. Recent work has shown that the superficial masseter and temporalis muscles in anthropoid primates express ~100% hybrid fibers in various combinations. We used immunohistochemistry to compare frequencies and patterns of hybrid fiber type expression in the anterior superficial masseter (ASM) and superficial anterior temporalis (SAT) in three species of *Cebus*, four species of papionins and three species of African apes. In the ASM of all three clades, slow+2 (MHC-1+MHC alpha-cardiac+MHC-2) and fast+alpha-cardiac (MHC alpha-cardiac+MHC-2+MHC-M) were the two most frequently expressed hybrid patterns, though they differed significantly ($p<0.05$) in frequency of expression. However, we observed clade-specific patterns of hybrid fiber-type expression for the SAT, with 53% of *Cebus* fibers expressing slow+2, 53% of papionin fibers expressing either fast+alpha-cardiac or alpha-cardiac+MHC-M, and 65% of African ape fibers expressing fast+alpha cardiac. Hybrid fiber contractile properties are intermediate between nearest neighbor pure myosin isoforms. Thus, the ~100% expression of hybrid fibers in various combinations suggests a degree of flexibility in the anthropoid primate masticatory apparatus that is not readily apparent from the bony anatomy. The temporalis has been suggested to be functionally constrained relative to the masseter for creating vertical occlusal forces during biting and chewing in primates. However, the variety of SAT hybrid patterns may also enhance the ability of this muscle region to generate power over a greater range of displacements, power stroke durations, and jaw-closing muscle shortening velocities.

This work was funded in part by grants from the National Science Foundation (BCS 1719743) and the Yerkes National Primate Research Center (Grant No. ORIP/OD P51OD011132).

Variation in growth and asymmetry of long bones in children of known ages

CATHERINE E. TAYLOR

Integrative Biology, University of California, Berkeley

Understanding variation is an integral part of biological anthropological studies. Bilateral asymmetry is an important aspect of variation, both within an individual and between individuals. Many studies on the ontogenetic development of skeletal asymmetry rely on archaeological samples or skeletal collections with incomplete age data for juvenile individuals. Here, medical CT scans of 60 children from the New Mexico Decedent Imaging Database (NMDID) are used to explore variation in long bone growth and the development of bilateral asymmetry in modern human children of known age. The NMDID provides age at death data measured in months, which allows for a higher resolution view than the year-by-year age groups that are often available with skeletal collections. Data analyzed in this study include diaphyseal length measurements and midshaft circumferential measurements of the clavicle, humerus, and femur. Of the six traits measured in this study, clavicular midshaft circumference shows the greatest overall bilateral asymmetry, followed by humeral midshaft circumference. Both femoral length and femoral midshaft circumference are the least asymmetrical. Between individuals, the clavicle exhibits the most variation in length and the femur exhibits the least. Humeral and clavicular midshaft circumference show similar amounts of inter-individual variation. Overall, younger individuals exhibit more asymmetry in bone length than older individuals, most markedly in the femur. This study provides a preliminary analysis of long bone growth in children of precise, known ages.

Funding provided by NSF DGE 1752814.

Interspecific and ontogenetic differences of hyoid body shape in tufted vs. untufted capuchins

PARKER M. TAYLOR[1], JANINE CHALK-WILAYTO[2], MARIANA D. FOGAÇA[3,4], MEGAN A. HOLMES[5], MYRA F. LAIRD[6] and CLAIRE E. TERHUNE[1]

[1]Department of Anthropology, University of Arkansas, [2]Department of Biomedical Sciences, Mercer University School of Medicine, [3]Department of Biomedical Sciences, Institute of Population Genetics, University of Veterinary Medicine Vienna, [4]Neotropical Primates Research Group – NeoPReGo, [5]Department of Family Medicine and Community Health, Duke University, [6]Department of Integrative Anatomical Sciences, University of Southern California

The hyoid bone is central to many critical functions such as swallowing, mastication, breathing, and vocalization. However, the link between these functions and the shape of the hyoid remains unclear. One previous study in macaques suggested that hyoid shape is tied to age-related changes in vocalization; others have examined broad shape differences in hyoid anatomy across large taxonomic groups of primates. However, none have looked at ontogenetic shape differences between closely related taxa with notable dietary differences. Here we document general shape differences across development in the hyoid body (i.e., basihyal) within and between tufted (*Sapajus* spp.) and untufted (*Cebus* spp.) capuchins. We examined microCT scans of 53 individuals (33 *Sapajus*, 20 *Cebus*); each was assigned an age rank according to dental eruption/wear. Results suggest adult *Sapajus* have a smooth, mostly flat basihyal with frequent fusion to the lesser cornua, while adult *Cebus* basihyals are generally separate from the cornua and tend to be dorsoventrally deeper, creating a more concave shape. The anterior surface of adult *Cebus* basihyals possesses more clearly defined muscle attachments for the suprahyoid musculature, which contributes to a deeper hyoid bulla. Furthermore, deepening of the hyoid occurs earlier in *Cebus*, where young *Cebus* possess more concave basihyals than *Sapajus* at similar life stages, suggesting differences in growth rate. These differences in hyoid shape may reflect age-related behavioral and ecological differences in dietary niche exploitation and/or vocalization. Future analyses will focus on using dietary and vocal data to explain basihyal shape differences between these two taxa.

Funding statement: This research was supported by grants from the National Science Foundation's Biological Anthropology directorate (NSF-BCS-1945771, NSF-BCS-1944915, NSF-BCS-1945283, NSF-BCS-1945767).

Dental evidence for early hominin diets

MARK F. TEAFORD[1] and PETER S. UNGAR[2]

[1]Department of Basic Science, Touro University, California, [2]Department of Anthropology, University of Arkansas

Dental evidence for early hominin diets has traditionally focused on the dental *capabilities* of past populations. However, those analyses have been based on the classic assumptions of evolutionary adaptation and, as a result, have never been able to document precisely what specific individuals ate in the past. Recent work (e.g., dental microwear and stable isotope analyses) has begun to alter that situation by shifting questions about early hominin diets into the realm of actual behaviors of past individuals. As a result, the focus has begun to shift from how teeth work to how they are used on a daily basis. In short, why might individuals with similar dental morphology have different diets? Food choice relates to many things, from masticatory/digestive capabilities to availability of resources to personal preference. New approaches to reconstructing diet are beginning to lead researchers in new directions -- to explore paleoecological questions heretofore inaccessible to paleoanthropologists.

The best studied example involves comparisons of the early hominins *Paranthropus robustus* and *P.boisei*, for whom dental microwear and stable isotope analyses have consistently indicated dietary differences despite similar craniodental functional morphologies. Comparable work on various extant taxa has moved interpretations into even finer-level resolution distinctions including evidence of niche breadth and partitioning, and habitat and resource differences, both within and

between taxa. Here we provide examples of how paleobiological inference has expanded beyond species-level diet and capabilities to food choice for individuals, with a cascade of implications for evolutionary interpretations.

Permanent and deciduous canine size in tufted vs. untufted capuchins

CLAIRE E. TERHUNE[1], PARKER M. TAYLOR[1], JANINE CHALK-WILAYTO[2], MARIANA DUTRA FOGAÇA[3,4], MEGAN A. HOLMES[5] and MYRA F. LAIRD[6]

[1]Department of Anthropology, University of Arkansas, [2]Department of Biomedical Sciences, Mercer University, [3]Department of Biomedical Sciences, University of Veterinary Medicine Vienna, [4]Neotropical Primates Research Group, [5]Department of Family Medicine and Community Health, Duke University, [6]Department of Integrative Anatomical Sciences, University of Southern California

Tufted capuchins (*Sapajus* spp.) feed on more resistant food items than untufted capuchins (*Cebus* spp.), which has resulted in selection for robust morphologies in *Sapajus*, including more advantageous jaw leverage. These differences in feeding behavior and corresponding differences in craniofacial morphology are well-documented. Prior analyses have also documented clear differences in adult canine size dimorphism between sexes within capuchin species and differences in adult canine dimensions between species, which are likely a result of a combination of sexual selection and feeding behavior. However, no analyses have examined how the deciduous canines mirror patterns observed in adults. Here we examine dimensions of both the permanent and deciduous canines in an ontogenetic sample of tufted (n=33) and untufted (n=20) capuchins. All data were collected from microCT scans, which allowed us to measure both fully erupted teeth and dentition that were still developing. We measured crown dimensions of both maxillary and mandibular teeth, and we compared our adult data to previous work. Results for the permanent canines are consistent with prior work, showing that *Sapajus* canines are both absolutely and relatively larger than *Cebus* in nearly all dimensions. We find the same pattern for the deciduous canines. However, while permanent canines show clear patterns of sexual dimorphism within species, results for the deciduous canines are inconclusive. Future analyses will focus on examining shape differences in the permanent and deciduous canines using geometric morphometrics and collating these data with analyses of craniofacial shape and jaw leverage.

This research was supported by grants from the National Science Foundation's Biological Anthropology directorate (NSF-BCS-1945771, NSF-BCS-1944915, NSF-BCS-1945283, NSF-BCS-1945767).

Sharing of CYP450 genes between archaic hominins and modern Africans

KOLONDJA D. THILLOT and FERNANDO A. VILLANEA

Department of Anthropology, University of Colorado-Boulder

Cytochrome P450 (CYP450) are a large family of liver enzymes that metabolize over 50% of xenobiotic drugs in the human bloodstream. These CYP450 genes are theorized to have had a similar function in archaic hominins who likely evolved variants of these genes to digest plant secondary metabolites. Some archaic hominins, Neanderthal and Denisovans, were found to have unique CYP450 variants in a recent study by Wroblewski and colleagues, that were then admixed into the modern gene pool, with many of these variants being deleterious. Current consensus is that natural selection then removed harmful archaic variants from the modern gene pool. Wroblewski and colleagues found archaic CYP450 variants among Eurasian, Papuan, and admixed American populations, but excluded African populations by using them as an outgroup. To investigate if archaic CYP450 variants are also shared with Africans, we build phylogenies for the 11 CYP450 genes from the Wroblewski and colleagues study. Phylogeny consists of sequences from three Neanderthal, one Denisovan, and all individuals in the 1000 Human Genome Project. We found incomplete lineage sorting for the majority of these 11 CYP450 genes. There was a unique sharing of an African CYP2E1 variant into the Altai Neanderthal's population, indicating an introgression event from ancient Africans into Neanderthals. The unique CYP2E1 phylogenetic tree questions the possibility of other shared CYP450 variants between African populations and archaic hominins, as a future research goal.

Kolondja Thillot was funded through the Biological Sciences Initiative at the University of Colorado-Boulder.

Ancient dog mitochondrial lineages indigenous to North America recovered from Jamestown Colony

ARIANE E. THOMAS[1], ALIDA DE FLAMINGH[2], KELSEY E. WITT[3], MATTHEW E. HILL, JR.[1], RIPAN S. MALHI[2] and ANDREW KITCHEN[1]

[1]Department of Anthropology, University of Iowa, [2]Department of Anthropology, University of Illinois at Urbana-Champaign, [3]Center for Computational and Molecular Biology, Brown University

Multiple studies have demonstrated that the colonization of the Americas led to the replacement of nearly all indigenous dog lineages with European ones sometime between 1492 and the present day. However, the timing and rate of this replacement are unknown and little attention has been given to this topic of research. To clarify the demographic change of dog populations in the Americas, we sequenced relatively high coverage ancient mitochondrial DNA from dogs at Jamestown Colony, Virginia, 1609-1619. Our analysis shows that the Jamestown dogs have maternal lineages most closely associated with the A1b haplotype, which has been previously reported in ancient dogs indigenous to the Americas. Furthermore, these maternal lineages cluster with dogs that derived from the earliest movement of dogs to the Americas and are not associated with the later introduction of Arctic dogs by humans. The recovery of dog lineages indigenous to North America from a European colonial site suggests that indigenous dogs were not isolated from colonial contexts. Our results complicate current hypotheses about the degree of human management of Indigenous and European dogs and indicate that the replacement of Indigenous dog lineages occurred later in time.

This work was supported by a Graduate and Professional Student Govenment research grant and the Graduate College Iowa Recuritment Fellowship from the University of Iowa.

Lemur catta growth and development: Evidence for a male juvenile growth spurt in captive populations

JULIE M. THOMAS, MICHELLE L. SAUTHER and STEVEN R. LEIGH

Department of Anthropology, University of Colorado - Boulder

Variation in growth and development drives evolution and species variation, with an organism's environment during its early life selecting for diverse life history and allometric traits. While important, the underlying mechanisms driving species' ontogeny are poorly understood. Previous strepsirrhine growth studies have been limited in scope due to small sample sizes and a paucity of longitudinal data. With the development of publicly accessible databases with detailed longitudinal growth data and recent advances in statistical analyses, it is now possible to produce high-resolution strepsirrhine growth models. This study focused on the normal variability in growth rates and duration in captive ring-tailed lemur (*Lemur catta*) populations housed in the Duke Lemur Center (n = 200, males = 99, females = 101) aged 0 to 5 years. We applied the SuperImpositon by Translation and Rotation (SITAR) model, a shape invariant model, to mixed longitudinal data to summarize individual growth curves. Results demonstrate that male *L. catta* experience a juvenile growth spurt in body mass whereas females do not. In other species, juvenile growth spurts are associated with peak gains in strength, power and maximal aerobic capacity being attained either during or immediately after the growth event. The presence of a male growth spurt raises the question of the selective role of non-dimorphic male-competition and migration within this energetically conservative, seasonally constrained and female-dominated species. These growth

and development data provide new and important insights towards answering critical questions regarding how this primate lineage evolved to survive in Madagascar's unique environment.

Graduate Student Funding Scholarship, University of Colorado-Boulder

Automated morphological phenotyping using learned shape descriptors and functional maps: A novel approach to geometric morphometrics

OSHANE O. THOMAS[1], HONGYU SHEN[2], RYAN L. RAAUM[3,4,5], WILLIAM E H. HARCOURT-SMITH[3,4,5,6], JOHN D. POLK[1,7] and MARK A. HASEGAWA-JOHNSON[2]

[1]Department of Anthropology, University of Illinois at Urbana Champaign, [2]Department of Electrical and Compute Engineering, University of Illinois at Urbana Champaign, [3]Department of Anthropology, Lehman College, [4]Department of Anthropology, CUNY Graduate Center, [5]NYCEP, New York Consortium in Evolutionary Primatology, [6]Department of Vertebrate Paleontology, American Museum of Natural History, [7]Department of Biomedical and Translational Sciences, University of Illinois at Urbana-Champaign

The methods of geometric morphometrics are commonly used to quantify morphology in a broad range of biological sciences. The application of these methods to large datasets is constrained by manual landmark placement limiting the number of landmarks and introducing observer bias. To move the field forward, we need to automate morphological phenotyping in ways that capture comprehensive representations of morphological variation with minimal observer bias. Here, we present Morphological Variation Quantifier (morphVQ), a shape analysis pipeline for quantifying, analyzing, and exploring shape variation in the functional domain. morphVQ uses descriptor learning to estimate the functional correspondence between whole triangular meshes in lieu of landmark configurations. With functional maps between pairs of specimens in a dataset, we can analyze and explore shape variation. morphVQ uses Consistent ZoomOut refinement to improve these functional maps and produce a new representation of shape variation, area-based and conformal (angular) latent shape space differences (LSSDs). We compare this new representation of shape variation to shape variables obtained via manual digitization and auto3DGM, an existing approach to automated morphological phenotyping. We find that LSSDs compare favorably to modern 3DGM and auto3DGM while being more computationally efficient. By characterizing whole surfaces, our method incorporates more morphological detail in shape analysis. We can classify known biological groupings, such as Genus affiliation with comparable accuracy. The shape spaces produced by our method are similar to those produced by modern 3DGM and to auto3DGM, and the distinctiveness functions derived from LSSDs show us how groups of shapes differ from each other.

A coupled humanitarian and biodiversity crisis: lemur hunting and consumption in Western Madagascar

KATHARINE E. THOMPSON[1], CORTNI BORGERSON[2], PATRICIA C. WRIGHT[1,3], JEANNE M. RANDRIAMANETSY[4], YVES M. ANDRIANANTENAINA[4], MAHEFA N. ANDRIAMAVOSOLOARISOA[5], THEOFRICO A. RAZAFINDRAHASY[4], RYAN S. ROTHMAN[1], CLAIRE SURKIS[3], RICHARD J. BANKOFF[6] and KATHERYN C. TWISS[1,3]

[1]The Interdepartmental Doctoral Program in Anthropological Sciences (IDPAS), Stony Brook Univerisity, [2]Department of Anthropology, Montclair State University, [3]Department of Anthropology, Stony Brook Univerisity, [4]NA, Madagascar Health and Environmental Research (MAHERY), [5]Zoology and Animal Biodiversity, University of Antananarivo, [6]NA, ComplexityNexus LLC

The unsustainable hunting and consumption of primates destabilizes both wildlife populations and the humans who depend upon them. This is especially pertinent in Madagascar — one of the world's poorest, least food secure, and most biodiverse countries. In western Madagascar, the people of Kirindy Mitea National Park have faced numerous famines during the prior decade. Despite being one of Madagascar's highest conservation priorities, interactions between food insecurity, dietary diversity, and lemurs and other wildlife hunting have not been studied here. To address this gap, and to provide foundational data for primate conservation as well as public health policy, we examined forest resource exploitation, nutrition, and food security in a village adjacent to the park (N = 89 households) over six months (September 2018 - March 2019). We observed high levels of food insecurity and malnutrition. One third of individuals ate a forest animal during the prior year. Of all taxa, lemurs, tenrecs, and bushpigs were hunted in the greatest numbers. While less-food-secure households were more likely to hunt non-threatened animals, such as tenrecs, lemurs comprised one third of all wildlife consumed; households ate an average of five lemurs during the prior year. Food insecurity significantly increased within-household lemur consumption, especially the Critically Endangered *Lepilemur ruficaudatus* and Vulnerable *Eulemur rufifrons*. Our results indicate that Kirindy Mitea is among the most heavily hunted national parks in Madagascar. Given the region's fragile environment and challenging living conditions for both its primate and human communities, the effects of hunting may be especially severe.

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.

The evolution of the ape trunk bauplan is not explained by small back muscles

NATHAN E. THOMPSON[1], BETTINA FAERBER[2] and JOHANNA NEUFUSS[3]

[1]Department of Anatomy, New York Institute of Technology College of Osteopathic Medicine, [2]Institute of Systematic Zoology and Evolutionary Biology, Friedrich-Schiller-University, [3]Locomotor Ecology and Biomechanics Lab, School of Biosciences, University of Birmingham

Apes exhibit a unique trunk bauplan among primates including a short lumbar region, tall iliac blades, and a wide thorax with dorsally positioned scapulae. This bauplan, often termed 'osteologically rigid' is generally linked with the evolution of climbing and suspensory behaviors. Some recent evolutionary hypotheses have suggested that 'osteological rigidity' was a direct consequence of reduced area for back musculature, following the dorsal positioning of the scapula. However, data on back muscle area in apes with which to test this hypothesis is extremely limited.

Here, we investigated back muscle cross-sectional area using CT scanning and histological imaging in 20 mammals, including all great apes and a siamang. Four muscle groups were investigated (sacrospinalis mm., transversospinalis mm., psoas mm., and quadratus lumborum m.) at each presacral level where possible in the lower thoracic and lumbar region. We used phylogenetic ANCOVA to investigate differences in cross-sectional area between apes and non-ape mammals, taking into account known or estimated body mass.

For most muscles, we found little-to-no difference in cross-sectional area between apes and non-apes. No differences were detected for the transversospinalis mm. and the quadrutus lumborum m. at any level. In the sacrospinalis mm., apes had muscle areas that were slightly below the non-ape regression, however this was only significant at the fifth presacral level. These results indicate that evolution of the apparent 'trunk rigidification' was not a consequence of reduced area for back musculature; there are no dramatic differences in cross sectional area of back muscles between apes and non-apes.

Funded by Friedrich-Schiller-University (Jena, Germany) and the Berufsgenossenschaft Nahrungsmittel und Gastgewerbe (Erfurt, Germany) to B. Faerber (née Hesse).

Towards a bioarchaeology of cremation

TIM J U. THOMPSON

Health & Life Sciences, Teesside University

This abstract is part of the symposium 'Biocultural Taphonomies: Teasing apart taphonomic filters in bioarchaeology'. This presentation introduces the factors which influence the response of bone to burning. Extensive recent research in both the archaeological and forensic arenas has expanded the boundaries of the study of burned bodies, supporting a more nuanced understanding of human behaviour. This presentation reviews the synergistic impacts of taphonomy and thermal alteration on the preservation of skeletal remains, and the ways in which these introduce complexities to anthropological interpretation.

The skeleton undergoes very specific changes during heating and burning, although recent research has demonstrated the intimate interaction between the soft and hard tissues. Changes occur within the physical, chemical and crystalline structure of the hydroxyapatite, which historically have confounded interpretation. Current research on burned or cremated remains highlights the significance of both intrinsic and extrinsic factors for understanding how heat-induced changes manifest.

Using examples from my research projects in Europe and South America that cover a range of time periods, I will demonstrate how the methods that we have developed have allowed us to study increasingly complex cremation contexts. I will show how we are now able to combine heat-induced changes in the skeleton to reinterpret our perceptions of how the dead are treated. The bioarchaeology of cremation is moving into an exciting period of discovery and one in which the potential of this previously neglected archaeological resource can become more fully realised.

Adaptive evolution of *Plasmodium*-associated genes in primates

KEVIN M. TILTON[1,2], AMBER E. TRUJILLO[3,4], REBECCA M. DECAMP[2,5,6], MARY E. BLAIR[7], LUCA POZZI[8], TODD R. DISOTELL[9], ANTHONY J. TOSI[10,11], ANDREW S. BURRELL[3] and CHRISTINA M. BERGEY[1,2,6]

[1]Department of Genetics, Rutgers University, [2]Center For Human Evolutionary Studies, Rutgers University, [3]Department of Anthropology, New York University, [4]New York Consortium in Evolutionary Primatology, [5]Department of Anthropology, Rutgers University, [6]Human Genetics Institute of New Jersey, Rutgers University, [7]Center of Biodiversity and Conservation, American Museum of Natural History, [8]Department of Anthropology, University of Texas - San Antonio, [9]Department of Anthropology, University of Massachusetts - Amherst, [10]Department of Anthropology, Kent State University, [11]School of Biomedical Sciences, Kent State University

Malaria and related parasites have been infecting vertebrates, including primates, for millions of years. The parasite has arguably caused the most intense selective pressure on humans, leading to well-known adaptations affecting genes encoding, *e.g.*, hemoglobin. However, less is known about how non-human primates have adapted to similar parasites. A recent study investigated the evolutionary relationship between malaria (and malaria-like parasites) and mammals in a broad comparative context. Here, we focus on an expanded dataset of published and novel primate genomes. We identify orthologous genes across primates and identify signatures of positive selection by calculating the ratio of nonsynonymous to synonymous basepair changes (*dN*/*dS*) in genes associated with malaria for 11 newly generated and 29 published primate genomes. The proportion of branches that were positively selected is roughly equal between malaria- and non-malaria-associated genes (p=0.787). There were 483 instances where a primate lineage malaria-associated gene had a significant signature of selection, representing 261 genes. Non-human primate genes with the strongest evidence for branch-based signatures of selection include: *CACNB4* in *Macaca nemestrina* (upregulated during *P. berghei* infection in mice); *PROS1* and *EPOR* in *Rhinopithecus bieti* (regulates blood coagulation and associated with severe malarial anemia, respectively); *AMPKA2* in *Pan paniscus* (linked to liver stage malaria); and *TMEM164* and *SRSF8* in *Pan paniscus* (possibly linked to anemia and hemoglobin levels, respectively). Our work identifying genes that have undergone selection in a comparative primate context provides insights into differential adaptation avenues that various primates have used throughout this arms-race.

Funding for work provided by National Science Foundation (BCS1640500/1640515, BCS1717188/1718715/1718339, and BCS1926105/1926215).

Socioeconomic development predicts a weaker contraceptive effect of breastfeeding

NICOLAS TODD[1] and MATHIAS LERCH[2]

[1]Centre Roland Mousnier, CNRS, [2]Urban Demography Laboratory, EPFL

The contraceptive effect of breastfeeding remains essential to controlling fertility in many developing regions of the world. The extent to which this negative effect of breastfeeding on ovarian activity is sensitive to ecological conditions, notably maternal energetic status, has remained controversial. We assess the relationship between breastfeeding duration and postpartum amenorrhea (the absence of menstruation following a birth) in 17 World Fertility Surveys and 284 Demographic Health Surveys conducted between 1975 and 2019 in 84 low- and middle-income countries. We then analyze the resumption of menses in women during unsupplemented lactation. We find that a sharp weakening of the breastfeeding– postpartum amenorrhea relationship has globally occurred over the time period analyzed. The slope of the breastfeeding–postpartum amenorrhea relationship is negatively associated with development: higher values of the Human Development Index, urbanization, access to electricity, easier access to water, and education are predictive of a weaker association between breastfeeding and post- partum amenorrhea. Low parity also predicts shorter postpartum amenorrhea. The association between exclusive breastfeeding and maintenance of amenorrhea in the early postpartum period is also found in rapid decline in Asia and in moderate decline in sub-Saharan Africa. These findings indicate that the effect of breastfeeding on ovarian function is partly mediated by external factors that likely include negative maternal energy balance and support the notion that prolonged breastfeeding significantly helps control fertility only under harsh environmental conditions.

Trabecular structure in the distal femur and patella of foraging and post-industrial groups from South Africa

KIMBERLEIGH A. TOMMY[1], LYNNE SCHEPARTZ[1], BERNHARD ZIPFEL[3] and KRISTIAN J. CARLSON[2,3]

[1]Human Variation and Identification Research Unit, School of Anatomical Sciences, University of the Witwatersrand, Johannesburg, South Africa, [2]Department of Integrative Anatomical Sciences, Keck School of Medicine, University of Southern California, Los Angeles, CA, USA, [3]Evolutionary Studies Institute, School of Geosciences, University of the Witwatersrand, Johannesburg, Gauteng, South Africa

Studies of cortical and trabecular structure in various skeletal elements across hominoid taxa, notably of the lower limb, support the hypothesis that humans have undergone postcranial gracilization since the Late Pleistocene. This trend was not linear, and variation has been observed among post-industrial and archaeological groups sampled.

Trabecular bone demonstrates high environmental plasticity and is ideal for studying locomotor and postural effects on bone modelling and remodelling. The patellofemoral joint component of the knee joint is important in facilitating bipedal locomotion, although its internal structure has not been studied in detail. We compared post-industrial individuals from South Africa with presumably highly active foragers from the Later Stone Age site of Matjes River Rock Shelter (9000-2000 BP) to test the hypothesis that trabecular structure in the patellofemoral joint of these two groups is not significantly different. High resolution microCT scan data from the femora (43-66µm) and patellae (23-38µm) of individuals were included (n=20 post-industrial; n=8 (patellae),15

(femora) forager). Patellae were subdivided into 9 volumes of interest (VOIs) and femora into 8 VOIs where selected trabecular parameters (bone volume fraction (BV/TV), trabecular spacing (Tb.Sp), trabecular thickness (Tb.Th), connectivity density (Conn.D) and degree of anisotropy (DA)) were then quantified using BoneJ. Preliminary results show significant differences in trabecular structure of the patella and femur between the two groups, with higher BV/TV, ConnD and Tb.Th values and lower Tb.Sp and DA in the foragers compared to post-industrial individuals. These observed differences may relate to their different activity levels and subsistence strategies.

Funding support received from National Research Foundation, Centre of Excellence in Palaeosciences, School of Anatomical Sciences Smieszek Fellowship, L'Oréal UNESCO For Women In Science South Africa National Young Talents Award.

A Quantification of the Effect of Regional Climate Change on the Prehistoric Foraging-Farming Transition in Midwestern North America

MELISSA G. TORQUATO and ERIK R. OTÁROLA-CASTILLO

Department of Anthropology, Purdue University

For over a century, anthropologists studying subsistence trends have investigated why humans transitioned from hunting and gathering economies to ones based on farming. One hypothesis is that climate change contributed to the emergence of plant and animal domestication and thus, the widespread adoption of farming economies. This hypothesis is particularly relevant in Midwestern North America, where scholars have identified climatic changes preceding the independent domestication of native plants approximately 4500-4000 years ago. Our previous research examined the effects of climate on the prehistoric foraging-farming transition in a small area of the Midwest. This study suggests that climate influenced subsistence behavior, leading to an increase in the use of cultivars. The present study moves our previous research forward by expanding the sample of archaeological components from Midwestern North American to provide a more complete representation of the region (n = 139). We evaluated the effect of climate change on subsistence by combing paleoenvironmental reconstructions with archaeological dietary data from the relevant prehistoric periods. A non-parametric multivariate regression revealed a statistically significant effect of mean intra-annual precipitation ($F = 1.7940$; $p = 0.0110$) on diet over time. Additional analyses using principal coordinate analysis and vector fitting allowed for visualizing the effects of dietary variables, dates, and mean intra-annual precipitation on diet. Our results show that an increase in mean intra-annual precipitation is associated with a plant-based diet, suggesting an increase in the use of cultivars during the foraging-farming transition.

Contributions by MGT were supported in part by the National Science Foundation Graduate Research Fellowship Program (Grant No. 106469).

Investigating adaptations to competing functions in the human pelvic floor

NICOLE TORRES-TAMAYO[1] and NICOLE D.S. GRUNSTRA[2,3,4]

[1]Department of Paleobiology, Museo Nacional de Ciencias Naturales, Madrid, Spain, [2]Konrad Lorenz Institute (KLI) for Evolution and Cognition Research, Klosterneuburg, Austria, [3]Department of Evolutionary Biology, University of Vienna, Vienna, Austria, [4]Mammal Collection, Natural History Museum Vienna, Vienna, Austria

The human pelvic floor has to withstand intra-abdominal pressure to maintain continence and prevent organ prolapse, facilitated by smaller pelvic floor dimensions. In females, however, these dimensions also dictate the size available for a fetus to pass through, predicting trade-offs in female pelvic floor morphology. We investigated a potential decoupling in the female human pelvic floor with regard to stature and thoracic and abdominal torso morphology, using 3D geometric morphometrics on a sample of CT-scanned articulated torsos (35 females, 12 males, 772 landmarks). Although pelvic floor size (CS) scaled negatively allometrically with stature in both females (slope = 0.60) and males (slope = 0.58), stature explained more variation in males ($R2 = 0.53$) compared to females ($R2 = 0.26$). Mediolateral breadth and anteroposterior length of the pelvic floor were both positively correlated with stature in males, whereas mediolateral breadth was decoupled from stature in females ($r = 0.044$, n.s.). We also investigated associations between pelvic floor shape and non-pelvic torso shape using 2B-PLS. Females showed consistently weaker associations between the two anatomical regions compared to males (both in terms of the total covariance and individual PLS correlations). Similarly, correlations among pelvic floor size (CS) and non-pelvic torso size were moderately strong in males ($0.50 < r < 0.83$), whereas they were often weak in females ($0.21 < r < 0.58$). These results suggest that pelvic floor shape has more strongly been influenced by body size-*unrelated* factors in females compared to males, consistent with a scenario of competing selection pressures.

This work was made possible by the Konrad Lorenz Institute (KLI) for Evolution and Cognition Research, Klosterneuburg, Austria (fellowships to both NTT and NDSG).

Nationwide anthropology engagement: Utilizing the 4-H Youth Development program for community outreach

SHARON A. TOTH[1,2] and ALICIA R. GROSSO[3]

[1]Department of Anthropology, University of Pittsburgh, [2]Virginia Cooperative Extension, Virginia Tech, [3]Department of Physical Therapy, Clarkson University

The United States Department of Agriculture (USDA) passed the Smith-Lever Act over 100 years ago, forming the cooperative extension system recognized today that serves communities throughout the country by means of non-formal programming. The Smith-Lever Act connected USDA to land-grant universities for delivering the most current research and education to communities. 4-H Youth Development is one branch of extension, and it is the largest youth development program in the country reaching over 6 million youths and active in over 80 other countries. Despite its size, it is well cited that many people are still unaware of the program or its extent, and I show here how anthropologists can utilize extension more by presenting previous successful 4-H anthropology workshops. Activities have included forensic analyses, archaeological interpretations, osteology puzzles, in addition to transferable skills for other STEM activities used in a nationwide military children's program. The average range of participants were 5-18 years old and compromised a wide range of disabilities, socioeconomic, racial, religious, and educational backgrounds, providing anthropology outreach to a diverse audience. I also present here how to get connected to local extension programs to encourage continued professional development, outside university teaching experiences, and potential career paths into extension from the biological anthropology field. 4-H programs are conducted in 3,150 counties and cities, serving rural, suburban, and urban populations, providing ample opportunity for anthropology students and faculty to engage with outreach initiatives. This further increases public scientific literacy, promotes anthropology in the community, and motivates under-represented groups in STEM.

Is atypical tooth wear described in fossil hominins caused by grit mastication? Potential evidence from a living primate population

IAN TOWLE[1,2], ANDREW J. J. MACINTOSH[3,4], MICHAEL BERTHAUME[1] and CAROLINA LOCH[2]

[1]Division Mechanical Engineering & Design, London South Bank University, [2]Sir John Walsh Research Institute, Faculty of Dentistry, University of Otago, [3]Primate Research Institute, Kyoto University, [4]Wildlife Research Center, Kyoto University

Atypical tooth wear is regarded as evidence of tool use and non-masticatory behaviour in fossil hominins. Atypical wear includes macroscopically visible striations on the labial surface of incisors

and root grooves (e.g., within interproximal or 'toothpick' grooves). Both types of dental tissue loss are often considered unique to the genus *Homo*. In this study, dentitions of provisioned wild Japanese macaques, from Koshima Island, was studied for tooth wear and pathology. The aim was to conduct a differential diagnosis of atypical wear found in all 32 individuals and to make direct comparisons with similar wear in fossil hominins. Large macroscopic striations were visible on many teeth, with sub-vertical striations prominent on the labial surfaces of incisors. Root grooves were found in half the individuals and were most noticeable on the lingual root surface of upper molars, but interproximal lesions on posterior teeth were also evident. Directional striations similar to those reported in 'toothpick' grooves in fossil hominins were visible within some of these grooves. There seems to be no behavioural evidence to suggest this wear was caused by tool use. The likely cause for both types of atypical wear is sand mastication and potentially also regularly eating marine molluscs. These individuals ate food several times a week directly from the sand surface, with grains masticated and swallowed, evidenced by behavioural observations. Directional macroscopic striations likely relate to the interaction of sand grains within the masticatory cycle, saliva flow, swallowing, and tongue movements. Implications for similar wear in fossil hominins is discussed.

An *in silico* method for modeling the nasal cycle in 3D: Implications for assessing human nasal form and function

BAONHU TRAN[1], LYNDEE A. WARD[2], ELIZABETH THAI[2] and SCOTT D. MADDUX[2]

[1]Department of Sociology and Anthropology, University of Texas at Arlington, [2]Center for Anatomical Sciences, University of North Texas Health Science Center

The inability to morphologically account for varying levels of mucosal congestion (e.g., the nasal cycle) has greatly limited evaluation of soft-tissue contributions to ecogeographic variation in human internal nasal anatomy. Accordingly, the goal of this study was to develop an *in silico* method for accurately modeling the three-dimensional anatomy of the nasal airways while controlling for mucosal congestion. To assess the efficacy of the developed modeling protocols, airway surface area-to-volume ratios (SA/V) were calculated for three anatomical models of differing congestion levels derived 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%). Following theoretical expectations, the decongested model exhibited a substantially lower SA/V ratio (0.57) than the mid-cycle (0.72) and asymmetrical (0.74) models. Importantly, the similar SA/V ratios of the latter two models suggest that, despite morphological asymmetry during the nasal cycle, the overall air-conditioning capacity of the nose likely remains relatively stable throughout the cycling process. Subsequent unilateral analyses also met anatomical expectations, with the highly congested left nasal passage of the asymmetrical model demonstrating a higher SA/V (1.06) compared to the same left passage in the mid-cycle (0.84) and decongested (0.60) models. Cumulatively, these results suggest that the 3D digital methods developed for this project permit reliable *in silico* modeling of the nasal soft-tissues, allowing future studies to control for mucosal congestion while investigating the role of nasal morphology on respiratory airflow (using computational fluid dynamics analysis, etc.).

Funding was provided by the American Association for Anatomy Innovations Program.

Diachronic analysis of the Lake St. Agnes Mound (16AV26) site: Evidence for dietary inequality among Late Woodland period burials

KENNETH G. TREMBLAY and REBECCA SAUNDERS

Geography and Anthropology, Louisiana State University

The transition to maize agriculture in the Lower Mississippi River Valley is not well understood. Maize may have become a major food crop in isolated pockets of inhabited areas at different times in Louisiana between the Coles Creek (700-1200 CE) and Mississippian (1200-1700 CE) periods. The current study explores whether one of those pockets might have been in central Louisiana, near the junction of the Red and Mississippi Rivers—two major waterways which would have facilitated travel and trade.

The Lake St. Agnes Mound (16AV26) site, in Avoyelles Parish, is a multicomponent single mound site with two burial components. The first, found at the base of the mound, dates to the early Coles Creek period (810 CE), and the later burials, found at the mound's apex, date to the Mississippian period (1410 CE). A diachronic analysis of these remains for characteristics of dietary change, including dental pathologies, porotic cranial lesions, and dental macro- and microwear, was performed to assess change over time.

Few statistically significant differences between the two burial samples were found. Both exhibit low levels of caries and linear enamel hypoplasias (~10%) but higher rates of periodontal disease and porotic cranial lesions. While a maize-based diet is unlikely, the results do suggest consistency in diet over time, but variability within both samples. Variability in dental micro- and macrowear patterns is interpreted as potentially due to seasonal differences in the types of food available, as well as differences in access, or preference towards certain types of foods.

A bioarchaeological analysis of the intersections of structural violence and healthcare provisioning at the Oneida State Custodial Asylum

LORI A. TREMBLAY[1] and ALECIA SCHRENK[2]

[1]Liberal Arts and Sciences, SUNY Delhi, [2]Department of Anthropology, University of Nevada, Las Vegas

Bioarchaeologists are beginning to explore the intersectional relationship between healthcare and structural violence. We expand this discussion by exploring the lived experiences of inmates at the Oneida State Custodial Asylum (OSCA), who were subjected to structural violence via healthcare provisioning at this state of the art Institution of Care in the late 19th and early 20th centuries. The inmates at the OSCA in Rome, NY were society's undesirables - the physically or mentally impaired. Human skeletal remains associated with the OSCA (N=46) were examined. Periosteal reactions (63%), linear enamel hypoplasias (13%), antemortem tooth loss (82.6%), dental caries (DMI mean rank of 70.6), and skeletal trauma (13%) were observed using anthroposcopic analysis and standard osteological methods. Statistical analyses indicate that while inmates at the OSCA experience high rates of general physiological stress in adulthood, they had lower rates of skeletal trauma (13%) and childhood stress. This suggests that inmates at the OSCA were protected from specific risks; however, they were not buffered from general suffering and physiological stressors. This research demonstrates that marginalized individuals were often still at risk for structural violence even when receiving healthcare provisioning.

The Alumni Grant for Graduate Research and Scholarship and the Coca-Cola Critical Difference for Women Grant for Research on Women, Gender, and Gender Equity, both via The Ohio State University.

Responses to the Human Infant's Extreme Neurological Immaturity and What That Really Looks Like: A *Consilience* of Integrative Research Validating Adolf Portmann's Prophetic Observations

WENDA R. TREVATHAN[1] and JAMES J. MCKENNA[2,3]

[1]Anthropology, New Mexico State University, [2]Anthropology, Santa Clara University, [3]Anthropology, University of Notre Dame

This abstract is part of the symposium *Building on the Legacy of Adolf Portmann: Interdisciplinary Approaches to Human Evolution and Development.* Among his numerous contributions to our understanding of human development, Portmann was among the first to argue for the significance of the human infant being born in a more helpless and dependent state than the young of most other primates. Multiple lines of recent evidence including anthropological (evolutionary, cross-cultural, cross species) and cross-disciplinary studies

in neurobiology, epidemiology, pediatric sleep medicine, and epigenetics all lend increasing support to Portmann's emphasis on the critical importance of and implications for implementing more optimal infant caregiving practices that will accommodate and respond to the extreme neurological immaturity of the human infant. Moreover, it would appear that within this research focus on better matching the human infant's needs with a more optimal cultural micro-environment, E.O Wilson's 1998 concept of *consilience* seems especially relevant. In his 1998 book *Unity of Knowledge* he predicts that discipline-specific research domains with no histories of serious contact with other fields will begin to yield complimentary, mutually supportive discoveries that, if integrated, will prove more valuable and be more applicable than any one line of discipline-based research could offer. Here we review the intersection and integration of specific findings from these diverse fields that support and respond to Portmann's theories and, specifically, how infant caregiving choices made by parents can significantly affect the type of brain a human baby will grow.

Taphonomic trajectories: Funerary taphonomy and preservation in a medieval, multi-faith Portuguese cemetery

TRENT M. TROMBLEY[1], SABRINA C. AGARWAL[1] and ANTÓNIO MATIAS[2]

[1]Anthropology, University of California, Berkeley, [2]Diretor de Arqueologia, Câmara Municipal de Santarém

Within archaeology, taphonomy has long been treated in a dichotomous matter, often characterized as the *non*cultural factors that affect preservation of particular artefactual or biological remains. Curiously, the paleontological origins of taphonomy made no such distinction, instead emphasizing all possible factors (biostratinomic and/or diagenetic) that could contribute to the preservation of a particular set of remains. The recent development of funerary taphonomy has sought to transcend this characterization, conjoining osteological and funerary archaeological methodologies, with an attention to both the natural and cultural processes that affect human skeletal remains. This paper presents taphonomic data from a multi-faith Portuguese cemetery. The presence of two faith communities — Islamic (n = 422) and Christian (n = 217) with differing funerary customs utilizing the same geographic and geological space offers a unique opportunity to examine the extent to which culturally-mediated funerary rites influence axes of preservation in human skeletal remains. A sub-sample of 363 individuals were analyzed for their degree of skeletal preservation, element representation, erosion, and weathering. Data were then analyzed with attention to funerary group, age, and sex to see the relationships between differing variables. Results of binomial logistic regressions show that faith group has the biggest effect on preservation, with Christians having a 240% higher odds of being well preserved compared to their Islamic counterparts ($p < 0.01$). These results are an important step in understanding the biocultural dimensions and taphonomic trajectories that funerary behaviors can have, especially in spaces where urban development and sub-surface construction are frequent risk factors.

This research was funded with the help of a 2019-2020 U.S. Fulbright student research grant (Public Law 87-256 Fulbright-Hays Act).

Gene expression response comparison of macaques (*Macaca mulatta*) to two malaria species

AMBER E. TRUJILLO[1,2] and CHRISTINA M. BERGEY[3,4,5]

[1]Department of Anthropology, New York University, [2]New York Consortium in Evolutionary Primatology, NYCEP, [3]Department of Genetics, Rutgers University, [4]Human Genetics Institute of New Jersey, Rutgers University, [5]Center for Human Evolutionary Studies, Rutgers University

Malaria imparts an immense selection pressure on primates that have had to cope with infections from various malaria parasite (*Plasmodium*) species. For example, when macaques are infected with *P. coatneyi*, which is most comparable to the human *P. falciparum* pathogen, they experience a ~35% mortality rate if antimalarial drug treatment is not given. However, when infected with *P. cynomolgi*, most comparable to the human *P. vivax* pathogen, they have a much milder reaction, which may include acute anemia and thrombocytopenia. We compare the transcriptomic response of rhesus macaques (*Macaca mulatta*) that have been experimentally infected with two *Plasmodium* species: *P. coatneyi* and *P. cynomolgi*. We find that both groups have overlapping up- and down-regulated genes (323 and 116, respectively), including *APOBEC3A* (*P. coatneyi* adj. P-value=0.0003; *P. cynomolgi* adj. P-value=0.0268) and *RHAG* (*P. coatneyi* adj. P-value=0.0129; *P. cynomolgi* adj. P-value=3.67×10^{-9}), which are associated with human red blood cell disorders and liver stage malaria, respectively. Overlapping up-regulated genes were associated with immune response (e.g. regulation of defense response GO:0031347; adj. P-value=4.975×10^{-12}), while overlapping down-regulated genes were associated with the MHC class II protein complex (GO:0042613; adj. P-value=3.399×10^{-5}). By identifying differentially expressed genes that respond to general malaria infection, we may elucidate the essential molecular mechanisms involved in this host-pathogen evolutionary arms-race.

Funding: NYU MacCracken (AET), NSF: BCS2118108

Locomotor variability in Sterkfontein Member 4: Analysis of the external shape and internal bone structure of the StW 562 and StW 595 first metatarsals

ZEWDI J. TSEGAI[1], PIERS GARDNER[2], BENJAMIN CHAMBERLAIN[3], JEREMY M. DESILVA[4], BERNHARD ZIPFEL[5], TRACY L. KIVELL[1,2,6] and MATTHEW M. SKINNER[1,2,6]

[1]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, [2]School of Anthropology and Conservation, University of Kent, [3]Centre for Anatomical and Human Sciences, Hull York Medical School, University of York, [4]Department of Anthropology, Dartmouth College, [5]Evolutionary Studies Institute, University of the Witwatersrand, [6]Centre for the Exploration of the Deep Human Journey, University of the Witwatersrand

Recent fossil discoveries have highlighted the diversity of foot morphology among fossil hominins. However, determining whether such morphological differences can be interpreted as a signal of substantively different gaits and/or contributions of arboreal locomotion to a species' behavioural repertoire is unclear. Here, we address this question of behavioural diversity in two fossil first metatarsals from Member 4 of Sterkfontein that differ in their external morphology: StW 562 and StW 595.

We analyse external shape using landmark based geometric morphometrics and the internal structure using cross sectional geometry and whole-bone analysis of cortical and trabecular bone structure in StW 562, StW 595, and a comparative sample of humans (N=7), chimpanzees (N=14), bonobos (N=9), gorillas (N=7) and orangutans (N=11). Results of the shape analysis support previous descriptions with both fossil metatarsals being intermediate in shape between humans and extant great apes, with StW 562 more similar to the human sample and StW 595 more similar to extant apes. Cross-sectional geometric analysis demonstrates that StW 562 shares a robust shaft with humans and African apes, whereas StW 595 has a low bending rigidity and cross-sectional area, similar to the less robust orangutans. The pattern of distribution of cortical and trabecular bone differs between these fossils, adding further evidence of morphological and perhaps functional diversity.

These results suggest two foot morphotypes may be present in specimens from Sterkfontein Member 4. Future work will further explore the potential biomechanical implications of these differing morphologies and the taxonomic affiliation of these two specimens.

This research received funding from the Max Planck Society and the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme (grant agreement No. 819960).

Inclusion ≠ Equity: Empowering Indigenous Genomic Data Sovereignty and Justice

KRYSTAL S. TSOSIE

Bioethics and Community Engagement, Native BioData Consortium

Indigenous people constitute the lowest represented minority and ethnic group in most genomic and precision health research studies. However, most efforts to increase engagement of Indigenous people have been problematized in terms of increasing recruitment, but without correcting past research practices deemed extractive by Indigenous communities. Also, structural barriers and lack of preventative healthcare contribute more proximally to gaps in health disparities and are unlikely to be addressed by indeterminate advances of precision medicine in Indigenous communities. Indigenous people have always expressed concern over broad informed consent models that they felt granted too much decision-making authority to researchers acting outside of tribal research regulatory framework–a concern that has renewed significance in the current Big Data Era that collectivizes Indigenous genomes in databases controlled by non-tribal entities. Merely increasing inclusion of Indigenous people in precision health research without also expanding decision-making agency and equity is effectively misusing "inclusivity" as a guise for continued extractive work. Empowering Indigenous-led biorepositories enables participation and tribal oversight, but still facilitates research under tribal oversight that is more culturally consistent with Indigenous models of consent. Change is needed to build trust and encourage tribal participation in precision health research. Empowering Indigenous genomic and data sovereignty is the path forward for truly increasing health equity.

Integrating biological anthropology in perinatal clinical care and postpartum support

KRISTIN P. TULLY and ALISON M. STUEBE

Obstetrics and Gynecology, University of North Carolina at Chapel Hill

Appreciation for developmental needs is critical to the structure and culture of healthcare. An evolutionary lens on infant biology and behavior provides insights for application to medical education, public health, and individual health guidance. Our program of work has built upon Portmann's concept of humans as "secondarily altricial." Framing caregivers as the infant's environment of evolutionary adaptedness draws attention to the need for their close, frequent contact. Yet, modern technology and expectations can create iatrogenic obstacles. For example, standard hospital bassinets have four high sides and are positioned adjacent to the maternal bed, impeding visual and physical contact for mother-infants. An evolutionary perspective draws attention to dyadic needs and informs accommodations to promote learning and responding to infant cues. We have integrated biological anthropology in our approach to establish safer, more comfortable perinatal care and this resulted in collaborative invention of the "Couplet Care Bassinet." This bassinet has lower side walls and can be positioned over a mother in bed. Additionally, we elevate that lactation and breast/chestfeeding is implicitly expected to be a part of daily activities accomplished on one's own, without support for the extensive time and emotional investments. Educating that the limited neurological development at birth was possible in our evolution only because parental and allo-parental care adapted to meet the high infant needs supports policy for paid leave, extended family, peer support, postpartum doulas, and other approaches to recapitulate the cooperative parenting "village" that seems to have been a foundational part of human reproductive success.

Sexual dimorphism in the ontogeny of rhesus macaque body size

CASSANDRA M. TURCOTTE[1,2], EVA H. J. MANN[3], MICHALA K. STOCK[4], CATALINA I. VILLAMIL[5], MICHAEL J. MONTAGUE[6], EDWIN DICKINSON[7], SAMUEL BAUMAN SURRATT[8], MELWEEN MARTINEZ[8], SCOTT A. WILLIAMS[1,2], SUSAN C. ANTÓN[1,2] and JAMES P. HIGHAM[1,2]

[1]Anthropology, New York University, [2]New York Consortium in Evolutionary Primatology, NYCEP, [3]Anthropology, Rutgers University, [4]Sociology and Anthropology, Metropolitan State University of Denver, [5]Health and Allied Sciences, Universidad Central del Caribe, [6]Neuroscience, University of Pennsylvania, [7]Anatomy, New York Institute of Technology College of Osteopathic Medicine, [8]Caribbean Primate Research Center, University of Puerto Rico

Making inferences about the social lives of extinct primates is possible only through study of the interplay between morphology, sexual selection pressures, and social behavior in extant species. Somatic sexual dimorphism is an important variable in primate evolution, in part because of the clear relationship between the strength and mechanisms of sexual selection and the degree of dimorphism. Here, we examine body size dimorphism across ontogeny in male and female rhesus macaques to assess whether it is primarily achieved via bimaturism as predicted by a polygynandrous mating system, faster male growth predicted by polygyny, or both. We measured body mass in a cross-sectional sample of 364 free-ranging rhesus macaques from Cayo Santiago, Puerto Rico to investigate: 1) body size dimorphism across the lifespan; and 2) size dimorphism as an outcome of sex-specific growth strategies, including: a) age of maturation, b) rate of growth, and c) duration of total growth, using regression models fit to sex-specific developmental curves. Significant body size dimorphism was observed in rhesus macaques by prime reproductive age (dimorphism ratio: 1.51). LOESS models showed that males reached a maximum body weight of 11.02 kg at age 9.13 years, 1.5 times larger than females, who reach a maximum weight of 7.14 kg by age 12.24 years. We demonstrate that the ontogeny of size dimorphism in rhesus macaques is achieved through a combination of bimaturism and a faster rate of male growth. Our results provide new insights into the development and complexities of primate dimorphism.

Funding from National Science Foundation BCS-1754024, NSF RAPID 1648676 NCE, and a Leakey Foundation award (to JPH, SCA, SAW). CPRC is supported by NIH's Office of Research Infrastructure Programs #P40-OD012217.

How environmental uncertainty and correlated payoffs drive the evolution of social learning

MATTHEW A. TURNER[1], CRISTINA MOYA[2,3], PAUL E. SMALDINO[4] and JAMES HOLLAND JONES[1]

[1]Department of Earth System Science, Stanford University, [2]Department of Life Sciences, Brunel University London, [3]Department of Anthropology, University of California, Davis, [4]Department of Cognitive and Information Sciences, University of California, Merced

Social learning—reliance on information gleaned from others rather than through direct engagement with the environment (individual learning)—is widespread among social species; none more so than humans. Current theoretical consensus suggests that social learning is adaptive in temporally uncertain environments like those faced by Pleistocene hominins. However, uncertainty can take many forms, and formal models do not always distinguish between them. Among other obstacles, uncertainty is challenging to formalize. Furthermore, most formal models treat individuals as identical agents, whereas in the real world behaviors have different, though correlated, payoffs for different individuals. We hypothesize that social learning outcompetes individual learning only when environments are sufficiently uncertain and the payoffs from adopting particular behaviors are sufficiently correlated among individuals. To investigate these hypotheses, we develop and analyze an agent-based model of the evolution of social learning with three forms of uncertainty. First, we find that there is a critical level of inter-individual correlation required for social learning to take hold in heterogeneous populations. Second, we find that social learning increases with the number of behaviors available to agents. Finally, we find that social learning is favored primarily when inter-individual payoff correlations are sufficiently stable—frequent environmental change can even make social learning harmful by promoting non-optimal behaviors. This work identifies and fills in a number of gaps in our

existing theoretical understanding of the evolution of social learning in uncertain environments, with implications for how societies will learn to adapt to the changing environments in our future.

Hominin Taxonomic Confidence and its Impact on our Understanding of Paleoenvironmental Associations

ALEXIS S. ULUUTKU[1], BERNARD A. WOOD[1] and DAVID B. PATTERSON[2]

[1]Center for the Advanced Study of Human Paleobiology, George Washington University, [2]Department of Biology, University of North Georgia

Placing hominin remains within a resolved paleoenvironmental setting is critical for understanding the differences and overlap in their fundamental and realized niches. To test whether taxonomic noise (i.e., confidence in specimen identification) obscures these reconstructions, our study classifies *Homo* and *Paranthropus* specimens from East Turkana as either Class A, their taxonomic classification is strongly supported by morphological evidence, Class B, medium support, or Class C, weak support. We then paired these data with resolved depositional environment information (i.e. fluvial versus lake margin assignment through sediment type) from the site at which they were recovered to attain environmental associations. Using only Class A specimens for both genera effectively eliminates uncertainty in taxonomic classification resulting in a higher signal-to-noise ratio with respect to their association with a particular depositional environment. We found differences in depositional environments between Class A and Classes B & C in both *Homo* and *Paranthropus* specimens, suggesting that including specimens of lower confidence can potentially skew conclusions made about paleoenvironmental associations in hominins. We suggest that researchers should incorporate an estimate of confidence in their taxonomic classifications into their methods and results. This does not just apply to hominin paleobiology, but should also be considered for paleontological studies focusing on non-hominin specimens.

Semicircular canal morphology of the Miocene small-bodied catarrhine *Pliobates cataloniae*: Phylogenetic implications

ALESSANDRO URCIUOLI[1], CLÉMENT ZANOLLI[2], FLORIAN BOUCHET[1], SERGIO ALMÉCIJA[3,4], SALVADOR MOYÀ-SOLÀ[5,6] and DAVID M. ALBA[1]

[1]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, [2]PACEA, UMR 5199 CNRS, MCC, Université de Bordeaux, [3]Division of Anthropology, American Museum of Natural History, [4]New York Consortium in Evolutionary Primatology, (NYCEP), [5]Institució Catalana de Recerca i Estudis Avançats, (ICREA), [6]Unitat d'Antropologia Biològica, Departament de Biologia Animal, Biologia Vegetal i Ecologia, Universitat Autònoma de Barcelona

Phylogenetic hypotheses about the Miocene small-bodied catarrhine *Pliobates cataloniae* (11.6 Ma, NE Iberian Peninsula) consider it a stem hominoid, a pliopithecoid, or a dendropithecid. Given the phylogenetic signal carried by semicircular canals, we compared their morphology in *Pliobates* with that of extant and fossil anthropoids using deformation-based 3D geometric morphometrics. We investigated patterns of shape variation using phylogenetically aligned component analysis, computed typicality probabilities of group membership (for platyrrhines, cercopithecoids, hylobatids, and hominids), and modeled semicircular canal evolution using a phylomorphospace approach. We also assessed the phylogenetic position of *Pliobates* against previously identified synapomorphies for anthropoid clades and used cladistic indices to test among several competing phylogenetic hypotheses. Our analyses indicate that *Pliobates* displays close morphological similarities to platyrrhines and pliopithecoids (*Epipliopithecus*). They further render the stem hominoid hypothesis much less parsimonious than considering *Pliobates* a stem catarrhine, thereby hinting at an independent acquisition of its ape-like locomotor adaptations. However, the shorter common crus of *Pliobates* supports a more derived status than that of pliopithecoids and older African catarrhines (*Aegyptopithecus* and *Saadanius*). This suggests that the ossified ectotympanic of *Saadanius* may be homoplastic relative to that of crown catarrhines and that *Pliobates* may belong to a stem catarrhine clade other than pliopithecoids. The latter hypothesis would be consistent with the dental similarities between *Pliobates* and African dendropithecids, which are frequently considered stem catarrhines but whose inner ear is unknown. The inclusion of semicircular canal characters in future cladistic analyses will hopefully help to clarify the phylogenetic relationships of *Pliobates*.

Funded by: MCIN/AEI (PID2020-116908GB-I00, PID2020-117289GB-I00), Generalitat de Catalunya (CERCA Programme and 2017 SGR 086 and 2017 SGR 116), MCIN (PRE2018-083299), French CNRS. Data: Morphosource, UMich, ESFR, AMIS-UMR5288, KNM.

Curricular Adaptation in Evolutionary Medicine Courses: A Covid-19 Selective Sweep

BETHANY M. USHER

Office of Provost/Department of Sociology and Anthropology, George Mason University

Evolutionary perspectives on health began to be introduced in college courses in the 1990s, using Nesse and Williams (1994) *Why We Get Sick*. Medical anthropologists have been taking a biocultural approach towards studying health since at least the 1960s and biological anthropologists formalized paleopathology as a field in 1973. The author designed a course on evolutionary medicine, paleopathology, diet, and demography in 2002 which has evolved into two courses: Humans, Disease, and Death (HDD) and Food and Human Evolution (FHE). These courses are offered at undergraduate and graduate levels, and serve students in anthropology, biology, public health, and nutrition programs. HDD considers the question *What is the evolutionary relationship between humans and disease?* Genetic, infectious, and chronic diseases are studied using the evolutionary medicine (Gluckman, Beedle, and Hanson, 2016), biocultural perspectives, and bioarchaeological evidence. In 2013, a descendent course, FHE, emerged to fill a niche, concentrating on the role that expanding dietary breadth and cooking have played in the evolution and health of modern humans.

The Coronavirus pandemic has influenced the content and format of both courses. FHE was redesigned as a synchronous online course in Fall 2020, using "food insecurity" in dietary adaptions as a relevant theme. HDD was redesigned for Fall 2021, using Covid-19 as a model of a disease emerging, becoming pandemic, and transitioning to endemic status. Both courses now emphasize the value of anthropological approaches to understanding how social inequality influences diet and health. This poster describes the evolution of the courses and student learning outcomes.

Negligible integration of neurocranial and labyrinthine morphology in a mouse model of Industrialized diet

ELSA M. VAN ANKUM[1], DEVIN L. WARD[2], MARY T. SILCOX[3], BENCE VIOLA[2] and JULIA C. BOUGHNER[1]

[1]Anatomy, Physiology, & Pharmacology, University of Saskatchewan, [2]Department of Anthropology, University of Toronto, [3]Department of Anthropology, University of Toronto Scarborough

The transition to a softer, vitamin D-deficient diet during Industrialization correlates with craniodental shape changes. Our earlier work showed that diet influenced bone remodelling & masticatory muscles, leading to increased bicondylar breadth in mice fed a soft, vitamin D-free diet. These changes may also affect the anatomically proximate temporomandibular joint (TMJ), basicranium & bony labyrinth. While recent human labyrinthine shape varies with subsistence strategy, here we use a mouse model to test whether diet texture & vitamin D level influence this variation. We hypothesized that bony labyrinth position & morphology is not integrated with the cranial base & TMJ such that diet will influence neurocranial shape but not labyrinthine form. C57BL/6J mice weaned at 7 weeks were raised on a soft or hard diet containing vitamin D (n=20; n=20), or a soft diet without vitamin D (n=20). Post-sacrifice, mice were micro-CT scanned, and basicrania & labyrinths were landmarked. Datasets underwent Principal Component (PC)

& 2-Block Partial Least Squares Analyses. The neurocrania of mice fed a hard diet + vitamin D were longer & narrower compared to those fed a soft diet + or - vitamin D. Diet accounted for 14.07% (PC1) of neurocranial shape variation. Diet did not influence labyrinthine shape. The labyrinth & neurocranium covaried independently of diet: mice with shorter, wider neurocrania had labyrinths rotated to span less distance medio-laterally. The labyrinth & basicranium were not integrated. While recent human labyrinthine variation correlates with subsistence strategy, dietary texture & vitamin D do not appear to influence this variation.

CFI grant (JCB); NSERC Discovery Grants (JCB & MTS); SSHRC Insight & Connaught New Researcher Grants (BV); NSERC Undergraduate Student Research Award & NSERC Canada Graduate Scholarship (EMV).

The Population Problem: A primary unit with no definition

ADAM P. VAN ARSDALE[1] and ROBIN G. NELSON[2]

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

In a two year span (2018-2020), more than one-third of the articles published in the *American Journal of Physical Anthropology* reference the term "population" within their abstract. The emphasis on "populations" as a primary unit of evolutionary study within Anthropology can be traced to Dobzahnsky (1937) via Washburn (1951). Dobzhansky, however, does not offer a clear definition of the term, but instead alternately moves between referencing populations as groups defined by patterns of phenotype, geography, and reproduction. In this paper, we begin to examine these constructions of the population concept, with particular attention to the challenges they present in typology, the conflation of place and organism, and tractability. In doing this, we will provide a comprehensive analysis of the use of "population" as a term within the *AJPA* 2018-2020. The uses of the term within contemporary biological anthropology reflect an even more expanded malleability, with large variation in the size of samples used to represent populations, the time period encompassing a population, and the biological characteristics used to identify a population, among many other varieties of usage. As in Dobzhansky's time, the term population is wielded as a concept of convenience. We argue this presents a two-fold problem: First, the lack of a coherent and consistent use of population as a framing construct inhibits the ability to integrate understandings of human and non-human primate evolution. Second, our inability to consistently demarcate populations feeds into public misunderstanding and misuse of the term in discussions of human biological diversity.

Respiratory survivorship before, during, and after the 1918 influenza pandemic in Newfoundland: Implications for populations in transition

TAYLOR P. VAN DOREN[1] and SAIGE KELMELIS[2]

[1]Anthropology, University of Missouri, [2]Anthropology & Sociology, University of South Dakota

Research on some severe pandemic events, like the Black Death, has shown that survivorship increased in the aftermath of the pandemic. Rarely is the 1918 influenza pandemic put into context with the epidemiologic and demographic conditions of the surrounding years to understand its long-term impacts. For the four regions of Newfoundland, we investigate changes in survivorship for influenza and pneumonia (P&I), tuberculosis (TB), bronchitis, measles, and whooping cough using Kaplan-Meier survival analyses during three periods: pre-pandemic (1909-1911), pandemic (1918-1919), and post-pandemic (1933-1935). These analyses are performed using individual-level early-20th century death records (n=8,242). These results are integrated with the historical record on public policy shifts, with specific emphasis on the two post-pandemic decades. Temporal trends in respiratory survivorship indicate general increases in population health after the 1918 pandemic. Aggregate survivorship was significantly different pre-pandemic (p=0.049), insignificant during the pandemic (p=0.32), and highly significantly different post-pandemic (p<0.001). Results examining trends in cause-specific mortality (p<0.0001) indicate that P&I was the only cause of death for which survivorship significantly increased after the pandemic; from pre- to post-pandemic periods, median age at death for P&I increased from 5 to 31.5 years of age. Increases in respiratory survivorship throughout the early-20th century in Newfoundland are evident, but post-pandemic increases were unequal among regions, suggesting sociocultural and/or underlying health inequalities. Additionally, selective effects during the 1918 influenza pandemic may have contributed to the observed patterns. We discuss the development of a more thorough perspective of pandemic events to better understand long-term shifts in population health.

This research has been funded by NSF DDRIG Biological & Cultural Programs, Award #1919515.

Differences in thumb mobility across primate taxa are associated with differences in joint anatomy and loading

TIMO VAN LEEUWEN, MARIE VANHOOF, MAARTEN VANNESTE and EVIE E. VEREECKE

Development & Regeneration, KU Leuven

In this study, we investigate the mobility and structural constraints of the trapeziometacarpal (TMC) joint in primates with a distinct locomotor behaviour but similar manipulative capacities. We hypothesize that differences in locomotor behaviour are reflected in differences in joint structure and function.

We have developed an innovative Python routine allowing quantification of 3D kinematics based on semi-dynamic CT scans of the thumb in a unique sample of 20 primate specimens (*Macaca mulatta*: n=7; gibbons (Hylobatidae): n=8, *Pan paniscus*: n=5). These analyses are further supported by detailed dissection of the surrounding ligaments. Data of one human specimen are included for comparison.

The data demonstrate distinct differences in TMC joint mobility between the primate taxa, with a wide range of motion in the gibbon TMC joint and most restricted movement in macaques. Bonobos fall somewhere in between. Differences between bonobos and humans can be explained by differences in ligament anatomy. The large mobility of the gibbon TMC joint is largely due to its ball-and-socket morphology and lack of ligament reinforcement. Macaques, being the most terrestrial among the included primate taxa, are characterized by a strongly restricted TMC joint. Here, thumb mobility largely originates from the more distal joints.

We conclude that the mobility of the TMC joint in macaques, gibbons, and bonobos is a result of skeletal as well as ligamentous features. The contribution of these anatomical features differs across primate taxa, as does the TMC joint mobility which differs significantly between highly arboreal and more terrestrial species.

Funding for this study was obtained from KU Leuven (C14/16/082).

Linking wrist mobility with ulnar styloid reduction across different primate taxa

MARIE JM. VANHOOF[1], ISABELLE DE GROOTE[2,3] and EVIE E. VEREECKE[1]

[1]Department of Development and Regeneration, KU Leuven, [2]Department of Archaeology, Ghent University, [3]Research Centre in Evolutionary Anthropology and Paleoecology, Liverpool John Moores University

In the hominoid lineage, there is a reduction of the ulnar styloid which has been linked to a greater ulnar deviation and/or pro-supination. Across primates, we lack a full insight in the relation between wrist mobility and ulnar/carpal morphology. In our study, we quantify wrist mobility during radioulnar deviation (RD/UD) and pro-supination (PRO/SUP) across primate taxa and link that to ulnar and carpal morphology. We CT-scanned the forearm of 23 primate cadavers (8 hylobatids, 7 macaques, and 8 humans). Each forearm was scanned in five standardized positions using a custom-designed rig (neutral, maximal RD/UD, and maximal PRO/SUP). For each specimen, we created 3D meshes of the

carpal bones, third metacarpal (MC3), ulna and radius. The range of motion (ROM) of MC3 relative to the radius or ulna is calculated as a measure of maximal RD/UD and PRO/SUP, respectively, using an in-house developed Python code. The ROM is highest in hylobatids for both RD/UD (57.0 ± 9.7˚) and PRO/SUP (219.8 ± 30.2˚). Humans have a low RD/UD ROM (29.1 ± 8.5˚), and both humans and macaques have a low PRO/SUP ROM (159.6 ± 26.4˚ and 155.4 ± 25,1˚, resp.). These results indicate that wrist mobility is not just a result of ulnar styloid reduction, as hylobatids show the highest ROM in RD/UD and PRO/SUP although their ulnar styloid is relatively longer compared to humans. Further research and a broader range of primate taxa are needed to elucidate the precise contribution of ulnar and carpal 3D geometry to overall wrist mobility.

Archived bodies: Death, dissection, and inequality in Depression-Era California (1930-1939)

WESLEY A. VANOSDALL

Department of Anthropology, University of Wyoming

I compare the death and postmortem treatments of different marginalized groups within the University of Iowa-Stanford Collection (UI-SC) of individuals from early-mid 20th century Santa Clara and neighboring counties in California. Initial data analysis for the UI-SC compares nominal data from the subset of documented individuals with death dates between 1930-1939 (n=162). The goal is to understand how subgroups within the UI-SC may or may not have experienced differences in death and postmortem treatment based on aspects of identity including institutionalization, socially-defined race, and nativity. Chi-square tests for independence of variables explore the relationships between several variables. While most of the variable pairings were not statistically significant, three pairings of variables had statistically significant results: place of death and length of residence (n=162, X^2=182.38, df=9, p<0.001); place of death and cause of death (n=132, X^2=15.69, df=6, p<0.05); and, socially-defined race and cranial and/or mandibular dissection (n=162, X^2=7.67, df=1, p<0.01). The data for the third significant variable pairing indicate that individuals identified as "White" were more likely to have skulls that exhibited dissection trauma. However, because the majority of individuals not coded as having cranial and/or mandibular dissection trauma had no skull to observe, it is not necessarily that people identified as "White" are more likely to exhibit dissection trauma, but that their skulls are more likely to be present at all. Overall, these results help to contextualize the practices that shaped the UI-SC and the death experiences in Santa Clara and neighboring counties.

This research was supported by funding from the Frison Institute at the University of Wyoming.

Female pelvic dimensions at different ages in parous and nulliparous individuals

CAROLINE VANSICKLE and PAIGE GRONDEL

Kirksville College of Osteopathic Medicine, A.T. Still University

The obstetrical dilemma hypothesizes that the human female pelvis evolved adaptations for birthing large-brained neonates, differentiating it from the male human pelvis and from fossil hominin pelves. This hypothesis depends on pelvis morphology being static throughout adulthood—that the skeletonized pelvis of a person who passed away at 86 is identical to their pelvis at age 24. However, this assumption has been challenged by research suggesting that the bony pelvis remodels throughout adulthood. These studies used samples representing different geographies and time periods, making it difficult to determine if observed differences were the result of age changes or an effect of the place and time in which the person lived. Here, we test the null hypothesis that there are no differences in female pelvis dimensions between age groups based on a sample from a limited geographic region and time period. We segmented the pelvis from 78 female CT scans from the New Mexico Decedent Information Database. Our sample included three age groups (each n = 26) each with an equal representation of parous and nulliparous individuals. We compared age groups for 10 pelvic measurements using a Student's T test. We found significant differences for some measurements between the old age group and the others. We repeated this test to compare parous and nulliparous individuals, finding that anteroposterior outlet diameter differed significantly with parity. This study demonstrates that pelvis shape is not static in adult human females and does need to be accounted for when comparing our anatomy with fossil species.

Zooarchaeology and Taphonomy of Small Mammal Remains from Liang Bua

ELIZABETH G. VEATCH[1,2], THOMAS SUTIKNA[3,4,5] and MATTHEW W. TOCHERI[2,3,6]

[1]Department of Anthropology, Emory University, [2]Human Origins Program, Smithsonian Institution, [3]Australian Research Council Centre of Excellence for Australian Biodiversity and Heritage, University of Wollongong, [4]School of Earth and Environmental Sciences, University of Wollongong, [5]Arkeologi, Pusat Penelitian Arkeologi Nasional, [6]Department of Anthropology, Lakehead University

Liang Bua, an archaeological cave site located on the Indonesian island of Flores, contains evidence for non-overlapping occupations by *Homo floresiensis* (~190 – 50 ka) and *Homo sapiens* (foragers ~46 – 3 ka, farmers <3 ka). Remains of murine rodents (i.e., rats) span the entire ~190 ka stratigraphic sequence (~78% of total vertebrates) and were potentially an important food resource for both *H. floresiensis* and *H. sapiens*. This study analyzed ~8,000 murine dental and skeletal elements using taphonomic and zooarchaeological methods, including skeletal part profiles, breakage and fragmentation patterns, and bone surface modifications, to determine if and how hominins at Liang Bua incorporated murines into their diet. Damage caused by avian digestion was also recorded to determine raptor contribution. Where possible, skeletal elements were classified into murine body size categories. Results indicate that *H. floresiensis* consumed murines of both size 5 (~3 kg) and size 2 (~300 g) categories that were from more open environments. Evidence for consuming murines from more closed environments by foraging *H. sapiens* was also identified and included murines from both size 5 and size 1 categories (~50 g). Between ~5 – 3 ka, modern humans expanded their diet breadth to include murines of all body size categories. After the onset of agriculture at the site ~3 ka, endemic murines continued to be part of the human diet in addition to domesticated resources.

Funding for this study was provided by the NSF Dissertation Improvement Grant (1830816); Wenner-Gren Fieldwork Improvement Grant; a PEO Women in Science Scholar Award; and SSHRC Insight Grant (435-2017-1234).

Femoral cross-sectional geometry of *Paranthropus boisei*

ALESSANDRA VECINO GAZABÓN[1,2], CARRIE S. MONGLE[3,4], NINA ST. HILLAIRE[5,6], JULIA ARAMENDI[7,8], MANUEL DOMÍNGUEZ-RODRIGO[7,9] and ASHLEY S. HAMMOND[1,2]

[1]Richard Gilder Graduate School, American Museum of Natural History, [2]New York Consortium in Evolutionary Primatology, (NYCEP), [3]Department of Anthropology, Stony Brook University, [4]Turkana Basin Institute, Stony Brook University, [5]Department of Anthropology, University of Maryland, [6]Department of Biology, University of Maryland, [7]Institute of Evolution in Africa (I.D.E.A.), University of Alcalá, [8]Department of Cartographic and Land Engineering, University of Salamanca, [9]Department of Anthropology, Rice University

Hominin femoral cross-sectional properties have been linked to locomotor behaviors but few femoral diaphyses are associated or attributed to *Paranthropus*. Here we examine the internal structure of OH 80, a 1.34 million-year-old femoral shaft from Olduvai Gorge attributed to *Paranthropus boisei*. Three cross-sectional properties were chosen for comparative analysis: cross-sectional area (CSA) to measure resistance to axial loads, maximum (Imax) and minimum (Imin) second moments of area to assess bending strength, and polar second moment of inertia (J) to gauge resistance to torsion. Data for OH 80 could be extracted for locations at approximately 60-80% of the diaphysis. Cross-sectional geometry of OH 80 was collected from microCT-scans using BoneJ in ImageJ. Comparative fossil data are from published data. Extant data (*Pan troglodytes*,

Gorilla gorilla, *Homo sapiens*) were collected from CT scans. Among extant taxa, CSA values for OH 80 fall between *Gorilla* and humans. OH 80 most closely approximates other hominins in this measurement (i.e., OH 28, KNM-ER 1472, KNM-ER 737, KNM-ER 1808), likely reflecting comparable femur sizes. J values were intermediate between humans and *Pan*, approximating the values of KNM-ER 1481a and KNM-ER 1472 for this shaft region. OH 80 is similar to *Paranthropus robustus* (SK 97, SK 82) in CSA and J values at 80% of the diaphysis. Bending strength (Imin/Imax) was low and displayed a decreasing trend from 60% to 80%, unlike the comparative sample. These preliminary results of the OH 80 diaphyseal cross-sectional properties may suggest distinct loading patterns in *Paranthropus boisei*.

Spanish Ministry of Culture; Richard Gilder Graduate School

Fermentation does not replicate the energetic benefits of cooking in a starch-rich tuber

EMILY MARIE. VENABLE[1], EMILY E. PUTNAM[2], BENJAMIN E. WOLFE[2], KATHERINE L. BRYANT[3], ERIN E. HECHT[1] and RACHEL N. CARMODY[1]

[1]Department of Human Evolutionary Biology, Harvard Universtiy, [2]Department of Biology, Tufts University, [3]Wellcome Centre for Integrative Neuroimaging, University of Oxford

Cooking increases net energy gains from starch-rich foods through physicochemical transformations that increase digestibility and reduce thermogenesis. Through these effects, cooking is thought to have contributed to anatomical and physiological changes in *Homo* consistent with a high-quality diet. However, whether other forms of food processing could have mimicked these effects prior to the hominin control of fire remains unclear. Here, we tested the hypothesis that food fermentation increases net energy gain and compared effects against those of cooking. We fed mice homogeneous diets of starch-rich sweet potato or starch-poor cabbage in raw, cooked, fermented, or fermented+cooked form (n=6 per diet, n=48 total), measuring changes in body mass and composition. Per gram of raw-equivalent diet consumed, mice fed fermented diets exhibited lower body mass (sweet potato: $p<0.001$, cabbage: $p<0.001$; two-way ANOVA), fat mass (sweet potato: $p<0.001$, cabbage: $p<0.0001$) and lean mass (sweet potato: $p<0.001$, cabbage: $p<0.0001$) versus mice fed unfermented diets. By contrast, mice fed cooked diets exhibited higher body mass (sweet potato: $p<0.001$, cabbage: $p=0.012$), lean mass (sweet potato: $p<0.001$, cabbage: $p=0.018$), and fat mass (sweet potato: $p=0.001$, cabbage: NS) versus mice fed raw diets. Our preliminary data indicate that, contrary to our predictions, fermentation decreases the net energetic value of food, perhaps due to microbes gaining primary access to macronutrients or xenobiotic compounds produced during fermentation. Although additional experiments are required, we propose that incorporation of fermented foods into the hominin diet may have been driven by improvements in food storage and pathogen exclusion, rather than implicit energy gains.

This study was supported by the William F. Milton Fund, Dean's Competitive Fund for Promising Scholarship, and the Department of Human Evolutionary Biology at Harvard University.

Exploring morphological variation of the shoulder girdle within and between extant non-human primates

MARIE VERGAMINI[1], LISA M. DAY[2], CHRISTINA MCGRATH[2], ERNESTO GAGARIN[2] and AMY L. RECTOR[3]

[1]Integrative Life Sciences, Virginia Commonwealth University, [2]Biology, Virginia Commonwealth University, [3]Anthropology, Virginia Commonwealth University

Variation in joint structures 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 distal humerus and the proximal ulna (Rector et al., 2018). More precise investigations of the morphological variation in the shoulder girdle can strengthen methods in identifying locomotor repertoires in extant and fossil Cercopithecidae. This study looks to improve the methodology by studying the shoulder joints throughout the Primate order.

Scapular outlines were collected from a sample of 300+ extant specimens using a MicroScribe point digitizer. Species were assigned a primary traveling locomotor category, including ground and/or branch quadrupeds, brachiators, leaping, and knuckle-walking. Variation in scapular shape was analyzed using MorphoJ 3D geometric morphometric PCAs, CVAs, PGLs, and phylogenetic ANOVAs. The analyses tested whether locomotive patterns can be established from the shape and variation of extant non-human primates' scapula.

Results suggest that morphology of the scapula can be determined throughout the Primate order and can differentiate further into shoulder joint differences in Colobinae and Cercopithecinae. This study contributes methodological and ecological information about anatomical variation, niche differentiation, resource competition, and community organization in living primates. Further exploration of locomotor variation within African and Asian Cercopithecidae, especially Colobines, could provide more information on the timing and context of Cercopithecid arboreal and terrestrial quadrupedal adaptations.

Modularity in the facial skeleton of *Homo* and *Pan*: support for functional modules with ontogenetic components

CATALINA I. VILLAMIL

School of Health and Allied Sciences, Universidad Central del Caribe

Previous works have shown that the face and basicranium are likely evolving independently in primates. However, patterns of integration and modularity within the facial skeleton, and the determinants of those patterns, are not yet well understood. I assessed two hypotheses of modularity in *Homo* (N=60) and *Pan* (N=40) using 18 3D landmarks on the face. I used the modularity test function on MorphoJ to test two hypotheses: 2 partitions based on general embryologic origin, and 3 partitions based on general function (oral, nasal, and orbital). Neither hypothesis was supported, but the functional hypothesis fell within the minimum 5% of all possible partitions in both taxa (*Homo*=0.049, *Pan*=0.002). *Homo* and *Pan* displayed different patterns of modularity with some shared components. Both taxa showed a consistent association of landmarks on structures that arise embryologically from the frontonasal process, as well as of landmarks on the nasal aperture. Nonetheless, even minimum RV values were relatively high in both taxa (0.2363-0.3581) indicating overall weak modularity in hominid faces. rPLS, effect size and covariance ratios were then calculated on R on both hypothesized modules and those identified by MorphoJ. These results also provide greater support for functional modules (CR=0.46-0.719, $p<0.05$) than embryological ones (CR=0.75-0.783, $p<0.05$), and suggest integration between at least some well-supported modules (rPLS=0.57-0.693, $p<0.05$). These results are consistent with those of other researchers who have focused on different taxa or used different methods, and have implications for understanding observed morphologies of the facial skeleton in hominids.

Margaret and Herman Sokol Travel/Research Award from New York University

Shared super-archaic ancestry between *Homo sapiens* and Neanderthals

FERNANDO A. VILLANEA[1] and KELSEY E. WITT[2]

[1]Department of Anthropology, University of Colorado Boulder, [2]CCMB, Brown University

The modern human genome includes segments inherited from archaic species such as Neanderthals and Denisovans, and to a smaller degree, archaic segments that map to neither of these two species. These segments tend to be more divergent relative to modern humans than Neanderthal and Denisovan genome segments, and have been dubbed "super-archaic", representing admixture with more distantly-related hominid species. A connection between these super-archaic genome segments to known

fossil morpho-species remains elusive. Here, we identify super-archaic genomic regions that are shared between modern Africans and three Neanderthals, and calculate their relative sequence divergence. We identified 13 such genome regions in the Vindija Neanderthal, 24 in the Chagyrskaya Neanderthal, and 21 in the Altai Neanderthal. For a handful of these regions, sequence divergence indicates that the African and Neanderthal super-archaic genome segments are most closely related to each other, and yet diverged much earlier from each other than the modern human-Neanderthal-Denisovan genomes. This pattern is best explained by the two super-archaic genome fragments originating from two separate but closely related species, one admixing into Africans and one into Neanderthals. Genomic regions of interest presenting this pattern include the gene CYP2B6, which codes for an enzyme responsible for metabolizing medically important plant compounds, including ketamine. Together, these results provide some clarity on the number and relationships of these super-archaic species.

Evaluating dental morphology on computed tomography (CT) scans from a contemporary U.S. sample

TATIANA VLEMINCQ-MENDIETA, LOUISE K. CORRON, G. RICHARD SCOTT and KYRA E. STULL

Department of Anthropology, University of Nevada, Reno

To improve methods, biological and forensic anthropologists are expanding the modalities of data collection and incorporating more 3D imaging in their research design. However, different modalities require a thorough evaluation of the ability to score dental morphology on computed tomography (CT scans) following the standardized definitions created on dry bone. Sixteen dental nonmetric traits were observed on a modern U.S. sample of 519 individuals identified as Black Americans, White Americans, White Hispanics, and Native Americans, queried from the Subadult Virtual Anthropology Database (SVAD). The definitions presented in Scott and Irish (2017) were followed with some modifications for virtual data. Trait frequencies were calculated for each group following the key teeth and breakpoints from Scott and Irish (2017), which allowed for comparisons to 24 worldwide population frequencies. The majority of traits exhibited frequencies comparable to the usual trends identified in dental morphology. Distal accessory ridge and *tuberculum dentale* on canines, metaconule, and Carabelli's trait were the exceptions. In the case of the first three traits, it could be because ridges and small cuspules are more difficult to identify on CT scans, even with high resolution. Further exploration of Carabelli's trait showed that it is difficult to score on virtual images if the grade is not 5 or superior (*i.e.*, cusp with free apex). Overall, this study confirms the feasibility of scoring dental traits on CT scans, which expands the potential of dental morphology to answer research questions in varying contexts. The protocols are freely available.

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

Integrated behavioral and metabolically flexible responses of wild orangutans to variation in nutritional intake

ERIN R. VOGEL[1,2], SHAUHIN E. ALAVI[3,4,5], DANIEL J. NAUMENKO[6,7], MALCOLM WATFORD[8], SRI SUCI UTAMI ATMOKO[9], BROOKE E. CROWLEY[10], REBECCA S.A. BRITTAIN[1,2], TIMOTHY D. BRANSFORD[11], MELISSA EMERY THOMPSON[12], ASTRI ZULFA[9], WILLIAM D. AGUADO[1,2], MARIA A. VAN NOORDWIJK[13], JESSICA M. ROTHMAN[14] and DAVID RAUBENHEIMER[15]

[1]Anthropology, Rutgers, The State University of New Jersey, [2]Center for Human Evolutionary Studies, Rutgers, The State University of New Jersey, [3]Ecology of Animal Societies, Max Planck Institute of Animal Behavior, [4]Centre for the Advanced Study of Collective Behaviour, University of Konstanz, [5]Department of Biology, University of Konstanz, [6]Department of Anthropology, University of Colorado Boulder, [7]Institute of Behavioral Science, University of Colorado Boulder, [8]Department of Nutritional Sciences, Rutgers, The State University of New Jersey, [9]Facultas Biologi, Universitas Nasional, [10]Department of Geology and Department of Anthropology, University of Cincinnati, [11]Animal Studies Discipline, Eckerd College, [12]Department of Anthropology, University of New Mexico, [13]Department of Anthropology, University of Zurich, [14]Department of Anthropology, Hunter College, [15]Charles Perkins Centre and School of Life and Environmental Sciences, The University of Sydney

Diet and nutrition are critical factors influencing energetics and health, and it is well known that animals modify their behavior in response to temporal and spatial variation of food resources. The shifts in energetic and nutrient intake have physiological consequences, and recent studies have demonstrated how model laboratory organisms exhibit metabolic flexibility when faced with such shifts. We integrate macronutrient regulation and metabolic flexibility to elucidate how wild orangutans (*Pongo pygmaeus wurmbii*) are buffered against ecological fluctuations by examining their behavioral and physiological responses to ecologically driven variation in macronutrient intake. Using Bayesian additive models and full-day focal follows (n=4873), we found that orangutans follow a model of protein prioritization, with the contribution of non-protein energy varying more than protein intake. Combining nutritional intakes with urinary biomarkers of energy and protein balance (Urea (n=540), C-peptides(n=629), ketones (n=1057), $\delta^{15}N$ (n=290)), we found that during episodes of fruit scarcity when lipid and digestible carbohydrate intakes decline, orangutans catabolize adipose tissue and concomitantly draw on endogenous gluconeogenic amino acids. Due to extreme variation in resource availability and subsequent nutrient intake, orangutans regularly switch between different exogenous and endogenous nutritional substrates. Ultimately for orangutans, fat and carbohydrate hyperphagia, positive energy balance, and adipogenesis are beneficial only in the context of alternating periods of caloric scarcity and abundance. Knowing how hominids respond to extreme variation in food resources could be critical for understanding how early hominins may have adapted to novel environments when faced with limited and unpredictable food availability.

This research was funded by USAID (APS-497-11-000001), L.S.B Leakey Foundation, A.H. Shultz Foundation, National Science Foundation (BCS-0643122), Rutgers University, Center for Human Evolutionary Studies

Screen time and poor cardiometabolic health: the potential role of circadian disruption

JANELLE M. WAGNILD and TESSA M. POLLARD

Department of Anthropology, Durham University

Sedentary time, which refers to time spent sitting or lying down during waking hours, has been linked to poor cardiometabolic health outcomes amongst adults in industrialized contexts. In industrialized populations, a substantial proportion of daily sedentary time is spent viewing screens, including television time, which takes place mainly in the evening. Television time has a particularly strong link with poor cardiometabolic outcomes. The main mechanism by which sedentary time is thought to affect health is muscular inactivity, as chair-sitting requires little-to-no muscular contraction, which alters carbohydrate and lipid metabolism. We suggest an additional mechanism that may be at play in relation to screen time is circadian disruption. There is evidence that time spent watching TV is associated with prolonged periods of sedentary time during the evening, and we have reported that prolonged sedentary time in the evening is associated with poor glucose metabolism. We have also conducted a systematic literature review to provide evidence for three other key pathways through which TV time may disrupt circadian rhythms: suppression of melatonin, delay of sleep, and co-occurrence with eating. Taken together, these findings suggest that, in addition to muscular inactivity, circadian disruption may be another mechanism by which screen time negatively impacts cardiometabolic health in industrialized contexts, reflecting another form of evolutionary 'mismatch.'

Bone Cross Sectional Geometry, Haversian Remodeling, and Age Estimation at Death in a Sample of Homo sapiens of Known Age, Sex, and Population of Origin

ROBERT A. WALKER

Anatomy Emeritus, Northeast College of Health Sciences, Adjunct Professor of Anthropology, University of Arkansas at Fayetteville

The human skeleton is known to be affected by numerous developmental and biologically degenerative processes throughout life. Biological anthropologists have long used such changes to estimate age at death in human skeletal material.

In this study, histological characteristics (complete and fragmentary secondary osteons), and cross sectional geometry (area moments of inertia, cross sectional areas) are examined in a series of both male and female human femurs, (n = 216, 117 males, and 99 females) ranging in age from 15 to 97 years.

All features bear a significant ($p < .05$) relationship with chronological age. Complete osteons have a Pearson correlation coefficient with age of 0.701, and fragmentary osteons correlate with age at 0.679. Total cross sectional area, cortical area, and endosteal area have a similar correlation with age. When separated by sexes, males demonstrate a slightly higher correlation between these variables and age. This is not surprising, as much previous research has shown that there is more variation in bone biology among females, especially in later ages, primarily due to variations in estrogen levels in later life. Cross sectional geometric properties (cortical, total, and endosteal areas; area and polar moments of inertia) show low yet significant correlations (r less than 0.3) with age.

As previous research has shown, correlations of Haversian structures with age are relatively strong across all ages, but the relationship is less so beyond 50. Haversian remodeling can be used to estimate age at death, but error becomes much greater beyond 50 years.

This research is supported in part by a grant from the Research Department at Northeast College of Health Sciences, Seneca Falls, New York.

Coping with Discrimination and Stress: Creative Activity and Health Among a Sample of Transgender and Gender Diverse people in the U.S

TIAN WALKER[1], KELSI KUEHN[1], ALICIA DELOUIZE[1], JAE A. PUCKETT[2], DEBRA HOPE[3], ROBERT-PAUL JUSTER[4], RICHARD MOCARSKI[5] and L. ZACHARY DUBOIS[1]

[1]Department of Anthropology, University of Oregon, [2]Department of Psychology, Michigan State University, [3]Department of Psychology, University of Nerbraska-Lincoln, [4]Department of Psychiatry and Addiction, University of Montreal, [5]Division of Research and Innovation, San Jose State University

Transgender and gender-diverse (TGD) people face a great deal of stigma and discrimination within the United States that lead to increased stress. This analysis sought to explore how creativity buffers the strain of stress on mental and physical health of TGD people. Creative engagement (CE) (defined as behaviors including creating, writing, or teaching art) as a form of coping has yet to be explored in relation to health outcomes among TGD people. This analysis is from baseline data of a larger, longitudinal study where TGD people in four US states participated in interviews, online surveys, and biomarker collection. The interview asked participants to describe activities that contributed to their resilience: 56 people talked about CE and 91 did not. We hypothesized better health outcomes among those who described CE. Multiple linear regressions controlling for income and age indicate a significant interaction such that anxiety increased at a steeper rate among those who described CE than those who did not in the face of higher chronic stress (b = .13, CI [0.03-.22], $p < .01$). The same is true with depression (b = .11, CI [.01-.21], $p < .05$). Regressions with C-reactive protein, BMI, cortisol, blood pressure, and self-report physical health measures were all non-significant. The increase in depression and anxiety as a result of stress is more prominent in people who reported CE. CE had no impact on physical health measures, thus we see divergent salubrious pathways whereby CE influences stress processes via other mechanisms or over different time courses.

The Endurance Loading Hypothesis: How the necessity of carrying babies shaped human locomotor morphology

CARA M. WALL-SCHEFFLER

Biology, Seattle Pacific University, Anthropology, University of Washington

This abstract is part of the symposium, *Building on the legacy of Adolf Portmann: Interdisciplinary approaches to human evolution and development*. Numerous human morphological characteristics seem to be particularly well suited for reducing the energy costs of walking, and these characters further differentiate *Homo sapiens* from other apes, and also from some other bipedal hominins. These characters include lumbar curvature; larger body size; short, broad ilium; and short, stiff toes. Physiological characters also differentiate *H. sapiens*, and include chemical signaling pathways related to endurance activity and excellent thermoregulatory abilities. Here I will present data that each of these characters specifically reduces the energetic cost of walking while carrying loads, particularly babies, further emphasizing that some of these cost reductions will be more evident at increased distances (i.e., endurance activities). Larger body size and *Homo sapiens*' body proportions (e.g., long lower limbs) decrease the cost of carrying by 15%, as compared to Australopithecines. Stiff feet can also decrease the metabolic cost of load carrying by about 3%, and the reduction of mass at the end of a limb (e.g., shorter toes and lighter feet) further saves 20% of the metabolic cost of carrying. A short, broad ilium reduces the cost of carrying by at least 16%, with further reductions by modulating position and speed. Human sweating, blood perfusion, and endorphin release augment the support of load carrying for long distances. Finally, though humans are not particularly fast, we carry loads for a lower metabolic cost than other endurance locomotors, including horses.

Effects of an energy balance transition on skeletal health among indigenous peoples of the southwestern United States

IAN J. WALLACE[1], CHRISTOPHER TOYA[2], MARIO ANTONIO PEÎA MUÎOZ[1], ALEXIS MARTINEZ[1], JANA VALESCA MEYER[1], JORDAN MARTINEZ[1], MARCUS MILLER-MOORE[1], TAYLOR BUSBY[1], ALEXANDRA R. HARRIS[1], ADAM Z. REYNOLDS[1] and CHRISTOPHER B. RUFF[3]

[1]Department of Anthropology, University of New Mexico, [2]Pueblo of Jemez, [3]Center for Functional Anatomy and Evolution, Johns Hopkins University School of Medicine

In recent generations, indigenous peoples of the southwestern United States have experienced an energy balance transition involving decreased physical activity and increased dietary energy intake. This transition has led to higher risk of multiple metabolic disorders, but the effects on skeletal health are unclear. Decreased physical activity would be expected to negatively affect bone health, yet increased energy availability could also enable greater investment in bone growth and maintenance. Here, we investigate the skeletal effects of the energy balance transition by comparing bone structure between contemporary indigenous adults in New Mexico (n=226) and adults from the pre/proto-historic archeological site of Pecos Pueblo (n=126). Contemporary and pre/proto-historic data were derived, respectively, from whole-body CT scans in the New Mexico Decedent Image Database and skeletal remains of people who lived between approximately 1200 and 1700 CE. We found that contemporary people were significantly taller than people in the past, but body breaths (bi-iliac widths) were similar between groups. Documented body weights of contemporary people were significantly heavier than would be predicted from their skeletal frame size (stature x bi-iliac width). Limb bone diaphyseal strength properties were significantly greater among contemporary people when scaled by skeletal frame size but significantly lower when scaled using documented body weights. These findings indicate that although the energy balance transition has led to increases in stature and absolute values of diaphyseal strength properties,

substantially greater increases in body weight among contemporary people have resulted in weaker diaphyses relative to the loads they sustain, potentially increasing fracture risk.

Funding provided by the Alfonso Ortiz Center for Intercultural Studies.

Age related changes of pelvic shape in adulthood

LUKAS WALTENBERGER[1,2], KATHARINA REBAY-SALISBURY[1] and PHILIPP MITTEROECKER[2]

[1]Austrian Archaeological Institute, Austrian Academy of Sciences, [2]Department of Evolutionary Biology, University of Vienna

The human pelvis undergoes shape changes in adulthood, but the exact processes and reasons for this change are still unknown. In this study, we analyzed pelvic shape changes by applying geometric morphometrics to a recent sample of 167 adults from the New Mexico Decedent Image Database (NMDID) with known age, sex, obstetrical records, and cause of death.Our results confirm that pelvic shape remodels during adulthood, showing a larger effect in females compared to males. In females, the pelvic shape changes occur in three distinct phases, which are consistent with the main reproductive period (from about 17 to 40 years), the period before menopause (40 to 50 years), and the postmenopausal phase (after 50 years). Males expressed two relatively similar periods of shape changes. These changes of adult pelvic shape presumably result from a combination of strain-induced bone remodeling and steroid hormone expression. Pregnancy-associated and estrogen-induced bone remodeling prevails in women during their reproductive period, whereas bone remodeling induced by mechanical factors seems to dominate pelvic shape changes in males and postmenopausal females. The widening of the birth canal during the reproductive period facilitates the birth process in humans. It is unlikely that this shape pattern specifically evolved as a novel obstetric adaption in humans. Estrogen-induced pelvic bone remodeling is highly conserved in mammals and was already present when the human brain size increased, although this conserved pathway may have been coopted in the human lineage.

This study was performed in the project "The value of mothers to society" and received funding from the European Research Council under the EU's Horizon 2020 program (grant agreement No. 676828).

Life history tradeoffs between growth and immune defense: risk for infectious disease among children in Kilimanjaro, Tanzania

KATHERINE WANDER[1], BRENDA N. KITALI[3,4], FEBRONIA SHIRIMA[2], NEEMA NG'UNDA[2], ZAWIA MASSAWE[2], BEATA KAVISHE[2], ROSE URONU[2], EVALINE MURO[2], THERESIA ASSENGA[2], NDETYA SAWE[2], IRENE HAULE[2], AMIN A. URONU[2], ALLUTU MASOKOTO[2], EMMANUEL SAMKY[2], ELINE NGOMU[2], HASHIMU URONU[2], IRENE MUSHI[2], JAZILA FERUZI[2], SALIM SEMVUA[2], IRASENI SWAI[2], RUNE PHILEMON[2,3], IREEN KIWELU[2,3] and BLANDINA MMBAGA[2,3]

[1]Anthropology, Binghamton University (SUNY), [2]No department, Kilimanjaro Clinical Research Institute, [3]No department, Kilimanjaro Christian Medical Centre, [4]No department, Kilimanjaro Christian Medical University College

Life history theory posits trade-offs across three domains (reproduction, growth, and maintenance) such that, among children, energy consumed by immune defense against infectious disease (maintenance) necessarily limits energy available for growth. This prediction is supported by several lines of evidence showing that children's growth can be compromised by infectious diseases and immune defense against them. The converse, compromised immune defense when more energy is devoted to growth, is also possible. However, as compromised immune defense seems more likely than slowed growth to lead to immediate death, we might expect regulatory mechanisms to prioritize energy availability for immune activity over energy devoted to growth. We tested the hypothesis that growth (captured in height-for-age Z-score, HAZ, and growth rate) increases risk for infectious disease among children participating in an on-going longitudinal study in Kilimanjaro, Tanzania. Among 270 children for whom baseline HAZ was available, taller children had higher risk for respiratory infection (HR: 1.30, 95% CI: 1.02, 1.64), controlling for age, sex, and adiposity. Among 177 children with complete height information for the first two months of monitoring, the rate of growth was also positively associated with risk for respiratory infection among female children (HR: 3.76; 95% CI: 0.98, 14.4), but not among male children (HR: 0.18; 95% CI: 0.01, 4.83), controlling for age. If these patterns hold as more growth data become available, it will be important to consider whether, and under what circumstances, children might benefit from investing energy in growth, even at the expense of increased infectious disease risk.

This project was funded by the US National Science Foundation (Biological Anthropology Program award #1825534).

The Mitochondrial Genome and Epigenome of the Golden Lion Tamarin from Fecal DNA using Nanopore Adaptive Sequencing

NICOLE M. WANNER[1], PETER A. LARSEN[1], ADAM MCLAIN[2] and CHRISTOPHER FAULK[3]

[1]Department of Veterinary and Biomedical Sciences, University of Minnesota, [2]Department of Biology and Chemistry, SUNY Polytechnic Institute, [3]Department of Animal Science, University of Minnesota

The golden lion tamarin (*Leontopithecus rosalia*) is an endangered Platyrrhine primate endemic to the Atlantic coastal forests of Brazil. Genetic data on this species remains scarce despite ongoing conservation efforts; complicating factors include limitations on sample collection and a lack of high-quality reference sequences. Here, we used nanopore adaptive sampling to resequence the *L. rosalia* mitogenome from feces, a sample which can be collected non-invasively. Adaptive sampling doubled the fraction of host-derived and mitochondrial sequences compared to non-enriched sequencing. 258x coverage of the *L. rosalia* mitogenome was reached in a single flow cell by targeting the unfinished genome of the distantly related emperor tamarin (*Saguinus imperator*) and the mitogenome of the closely related black lion tamarin (*Leontopithecus chrysopygus*). The *L. rosalia* mitogenome has a length of 16,597 bp and shares 99.68% sequence identity with the *L. chrysopygus* mitogenome. A total of 38 SNPs between them were identified, with the majority being found in the non-coding D-loop region. DNA methylation and hydroxymethylation were directly detected by applying a neural network model to the raw signal from the MinION sequencer. In contrast to previous reports, DNA methylation was negligible in mitochondria in both CpG and non-CpG contexts. Surprisingly, a quarter of the 642 CpG sites exhibited DNA hydroxymethylation greater than 1% and 44 sites were above 5%, with concentration in the 3' side of several coding regions. Overall, we report a robust new mitogenome assembly for *L. rosalia* and direct detection of cytosine base modifications in all contexts.

This work was supported by USDA AES Project. No. MIN-16-129, the UM Informatics Institute, and the SUNY Polytechnic Institute Research Foundation.

Locomotor and taxonomic diversity in Pleistocene hominins from Koobi Fora, Kenya

CAROL V. WARD[1], ASHLEY S. HAMMOND[2], CARRIE S. MONGLE[3], FREDERICK E. GRINE[3], JULIE LAWRENCE[4] and WILLIAM H. KIMBEL[4]

[1]Department of Pathology and Anatomical Sciences, University of Missouri, [2]Department of Anthropology, American Museum of Natural History, [3]Department of Anthropology, Stony Brook University, [4]Institute of Human Origins, Arizona State University

For decades, the hominin sample from Koobi Fora has been central to our understanding of Plio-Pleistocene hominin diversity and evolution. Craniodental fossils from Koobi Fora represent at least four distinct taxa: *Paranthropus (Australopithecus) boisei, Homo erectus, H. habilis* and *H. rudolfensis*. These fossils have revealed taxonomic variation in dietary specializations, brain size, and more. However, few postcranial fossils are clearly associated with diagnostic craniodental remains, confounding our ability to attribute most

of the postcrania to particular taxa. Christopher Ruff's work has provided important insights into morphological variation in eastern African hominins, revealing previously unappreciated diversity in limb structure that suggests proportional and functional differences among taxa. Here, we review the current understanding of the taxonomic status of the Koobi Fora postcranial fossils. Recent fossil discoveries from eastern Africa clarify attributions for some of the partial skeletons that have been associated with questionably diagnostic craniodental remains (KNM-ER 1500, KNM-ER 803). In the case of KNM-ER 1500, the prior attribution to *P. (A.) boisei* is strengthened by comparative data on mandibles and radii. Even the attribution of KNM-ER 803 to *H. erectus* is less certain than it was originally. Further, recently recovered fossils lacking association with craniodental material seem to reflect substantive taxonomic and functional differences among taxa from Koobi Fora (e.g., KNM-ER 5881, KNM-ER 47000). We summarize current understanding about postcranial similarities and differences among the Koobi Fora hominins, and what inferences can, and cannot, be made about taxonomic, behavioral and functional variation within the sample.

Leakey Foundation, Wenner Gren Foundation

Acceptance of evolution among South African Matric (final year high school) learners

KERRYN A. WARREN[1,2], CORNELIUS T. MUSHANGWE[2], LINDSAY K. HUNTER[1] and REBECCA R. ACKERMANN[1,2]

[1]Human Evolution Research Institute, University of Cape Town, [2]Archaeology, University of Cape Town

South Africa has included evolution as a part of its Matric Life Sciences curriculum since 2006. Because of the country's incredible fossil heritage, this change has been praised by biological scientists worldwide. However, the initial introduction of the revised curriculum was met with a backlash from parents and teachers alike, reflecting a potentially low acceptance of evolution within South African society. In a study evaluating the acceptance of evolution among South African Matric learners during a workshop of the curriculum (N = 80, using the I-SEA instrument), acceptance is above average to strong among learners for three dimensions: macroevolution (mean = 3.8, SD = 0.67), microevolution (mean = 3.8, SD = 0.58) and human evolution (mean = 3.4, SD = 0.57). Similarly, significant differences exist among learners from different schools and racial groups. However, for microevolution and human evolution, previous learning of evolution or natural selection were significantly associated with an increase in acceptance. Furthermore, acceptance did not necessarily align with qualitative responses regarding enjoyment of the workshop, nor did acceptance metrics change over the course of the workshop. Together, this indicates that enjoyment, acceptance and prior learning play a complex role in the overall learners perception of evolution broadly, and microevolution and human evolution specifically. Using this, we argue for a more holistic understanding of the South African learner when attempting interventions regarding evolution education. These interventions should arguably stem from more foundational pedagogical theories than those that are rooted in North American or European evolution education research.

This research has been funded by the South African NRF Centre of Excellence in Palaeosciences (CoE-Pal).

An overlooked island in the Irish Sea: palaeodietary reconstruction at a medieval Viking Abbey (AD1134-1540), Isle of Man

MARIE C. WEALE[1], DR. PETER DAVEY[2], DR. PHILIPPA TOMLINSON[3] and ALLISON FOX[4]

[1]School of Archaeological and Forensic Sciences, University of Bradford, [2]Department of Archaeology, Classics and Egyptology, University of Liverpool, [3]Curragh Environmental Consultancy, [4]The Manx Museum, Manx National Heritage

The Isle of Man is a British Crown Dependency, almost equidistant from Belfast and Liverpool, in the Irish Sea. The island has a rich archaeological record, spanning over 10,000 years but has often been overlooked within academic literature.

Rushen Abbey, located in the parish of Malew, was founded in AD1134 and dissolved in AD1540. Archaeological excavations and ^{14}C dating have shown evidence of a burial sequence spanning almost 1000 years, from the 5th to 15th century. As part of an on-going project, the human remains have been subject to osteological analysis with the aim of understanding more about the people and past lifeways on the Isle of Man.

Given the length of occupation, the samples were split into two sub-populations: early medieval (5th-10th century) and late medieval (11-15th century). This multi-method analysis has incorporated bulk collagen analysis (^{13}C and ^{15}N) of 24 human and 19 faunal samples, along with archaeozoological assessments and archaeobotanical evidence from each period.

The early medieval samples suggest that the diet was based on terrestrial protein, despite easy access to aquatic resources which were not a stable part of the diet. However, after the foundation of the Abbey, a dietary shift can be seen with a decrease in ^{13}C values and increase in ^{15}N, thought to be evidence of marine protein consumption. This analysis is the first of its kind to be carried out on Manx archaeological material with an aim of raising awareness of the Isle of Man and laying the foundation for future research.

This research was possible due to support from Manx National Heritage and financial grants from Culture Vannin and the Isle of Man Natural History and Antiquarian Society.

Comparing two episodes of divergence in hominins: Between Neandertals and humans and between *Paranthropus* and early *Homo*

TIMOTHY D. WEAVER[1], SARAH E. FREIDLINE[2] and PHILIPP GUNZ[3]

[1]Department of Anthropology, University of California, Davis, [2]Department of Anthropology, University of Central Florida, [3]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology

Two of the best documented episodes of divergence in hominins are the evolution of Neandertals and humans from a last common ancestor in the Middle Pleistocene and the evolution of *Paranthropus* and early *Homo* from an *Australopithecus* ancestor. In both cases, the divergence led to readily identifiable cranial differences, but these episodes differed in multiple ways, such as when they occurred, whether there was geographic isolation, and the explanations that have been proposed for the cranial differences.

Here we compare these two cases, and to provide context, we also compare them to the divergences among great apes and humans. We use methods introduced recently by Weaver and Gunz (2018), which combine theory from evolutionary quantitative genetics with geometric morphometric visualizations and comparisons. We investigate whether adaptive (natural selection) or neutral (genetic drift, mutation) evolutionary processes produced the cranial differences, and in situations for which selection is implicated, which regions of the cranium were the targets of selection.

Our analyses are based on three cranial datasets comprised of 247 Neandertals and humans; 352 early hominins, great apes, and humans; and 260 great apes and humans. The data are hundreds of landmarks and semilandmarks, after the semilandmarks have been slid on curves and surfaces. The results suggest more power to detect deviations from neutrality when morphological differences are characterized in the detail possible with landmarks and semilandmarks than when they are characterized by traditional linear measurements; and that both neutral and adaptive processes were important in producing cranial differences in hominin evolution.

The Max Planck Society supported this research.

Does adaptive variability in maternal skeletal dimensions shape gestation length?

JONATHAN C. WELLS

Population Policy and Practice Research and Teaching Department, UCL Great Ormond Street Institute of Child Health

This abstract is part of the symposium *Building on the legacy of Adolf Portmann*. This presentation considers how the phenotype of individual

mothers may modulate broader associations of pregnancy duration with cognitive development of the offspring. Portman observed that human infants preserve fetal rates of physical growth and neurological development in the year after birth. He coined the term 'secondary altriciality' to describe the relative immaturity of the human neonate. Subsequently, Washburn argued that these traits were linked with generic constraints on dimensions of the maternal pelvis. His 'obstetrical dilemma' hypothesis assumed that while larger dimensions of the birth canal would facilitate delivery of large-brained neonates, the obstetric pelvis was constrained by the requirements of bipedal locomotion, reducing fetal growth potential. Beyond their relevance to long-term human evolution, these insights may help understand contemporary human phenotypic variability. Maternal stature is an established determinant of birth weight. Taller mothers might produce larger neonates either by accelerating fetal growth per unit time, or by prolonging gestation. I review empirical evidence on the association of maternal stature with gestation length. The evidence robustly supports the hypothesis that on average, taller mothers have longer gestations, potentially mediated by larger birth canals. Beyond promoting neonatal survival and fitness, there are specific neurocognitive benefits, as gestation length is inversely associated with the risk of neurodevelopmental problems. Thus, although humans deliver offspring with relatively limited levels of brain development compared to other primates, taller mothers can help optimise long-term cognitive abilities of their offspring by lengthening pregnancy.

Tough at the top: competition in the East African large carnivore guild, Pliocene-present

LARS WERDELIN[1] and PHILIP J. HOPLEY[2]

[1]Department of Palaeobiology, Swedish Museum of Natural History, [2]Department of Earth and Planetary Sciences, Birkbeck, University of London

In the course of its long path from its largely frugivorous/herbivorous past to its omnivirous present with a significant animal protein component in its diet, the human lineage came into contact and conflict with a large carnivore guild that was fundamentally different from that of today. At its peak some 3 million years ago, that guild comprised 14 species larger than 21 kg body mass, as compared with 6 such species today. Leaving aside the effects on the human lineage of this plethora of species, the increasing encroachment of the human lineage on the ecospace of the large carnivore guild also had consequences for the carnivores. I have previously argued that the loss of species among large carnivores was a result of increasing hominin cognitive ability. If so, we must ask what specific factors could have led to this decrease. One such aspect is competition between large carnivores for prey. Preliminary data from δ13C values in carnivore tooth enamel from a range of sites in the Omo-Turkana Basin, Kenya indicates that, contrary to expectation, all carnivores had a similar grazer/mixed feeder dietary mix around 4-2 Ma. Coupled with the greater species richness, this indicates greater competition in the large carnivore guild than at present and that addition of another competitor may have destabilized the guild with species loss as a consequence.

This research was in part funded by the Swedish Research Council (2015-04587) and by the Palaeontological Assiciation.

Quantifying food resource availability: how to use consumer data to move beyond measuring abundance using examples from bonobo (*Pan paniscus*) feeding ecology

ERIN G. WESSLING[1], LIRAN SAMUNI[1,2], ROGER MUNDRY[3,4,5,6], MIGUEL ADAN PASCUAL[7], STEFANO LUCCHESI[1,2], BIENFAIT KAMBALE[8] and MARTIN SURBECK[1]

[1]Department of Human Evolutionary Biology, Harvard University, [2]Max Planck Institute for Evolutionary Anthropology, [3]Platform Bioinformatics and Biostatistics, VetMedUni, [4]German Primate Center, Leibniz Institute for Primate Research, [5]Department for Primate Cognition, Georg-August-University Göttingen, [6]Leibniz Science Campus Primate Cognition, [7]Kokolopori Bonobo Research Project, [8]Centre de Surveillance de la Biodiversité, l'Université de Kisangani

As food is an integral part of an organism's life, collecting data on aspects of food availability and distribution are crucial components of wild primatological research. Yet frequently, primatologists must collect data on food availability additionally to observational data collection which represent significant costs in time and resources. To evaluate food availability researchers typically use traditional ecological methods, e.g., quadrats or vegetation plots, which measure the environment in a manner that is intentionally independent from the consumer. While consumers are selective in resource consumption, traditional ecological measures by design do not incorporate components of resource selection and therefore only measure potential abundance but not the intended measure of availability of selectable resources to consumers. Here, we describe a method that uses bonobo observational data for evaluating resource availability (i.e., abundance, dispersion, and distribution of food). Over a dataset of 3+ years, we demonstrate how the aggregation of feeding location data can be used to measure food availability while simultaneously accounting for resource selectivity. We demonstrate that bonobos are selective about which resources they consume, ignoring approximately 20% of otherwise palatable species in the landscape based on size minima alone. We further demonstrate that resource density based on observational data reach adequate saturation and stability around 600 days, and correspond moderately well (r_{mean}=0.54, r_{max}=0.70) with estimates from traditional plot sampling. We therefore argue that researchers should consider the interplay between resource availability and consumer selectivity in their measurements and offer a potentially time-saving avenue for future ecological measurement in primatological research.

Historic dental calculus reveals geographic-specific shifts in oral microbiota during the Industrial Revolution

LAURA S. WEYRICH[1], STERLING WRIGHT[1] and EMILY SKELLY[2]

[1]Department of Anthropology, Pennsylvania State University, [2]School of Biological Sciences, University of Adelaide

Industrialisation irrefutably altered human health, as evident by the rapid rise of non-communicable diseases, such as obesity, Type II diabetes, and heart disease, but the causal mechanisms behind this remain poorly understood. While recent research suggests that key changes in the human microbiome—the collection of commensal microorganisms in the human body – are to blame, little research has investigated the specific shifts that occurred in the ancestors of Industrial populations. Here, we sequenced ancient DNA from calcified dental plaque (calculus) to examine potential shifts in oral microbiomes during the adoption of Industrialization in three European countries and a British Colony. Taxonomic and functional reconstructions of 128 oral microbiota from individuals from the 1400s to the present) identified significant shifts in oral microbiome composition and function during the Industrial Revolution (IR; post-1800s). However, geographic-specific signatures were still evident, suggesting that site-specific adaptations occurred. We also identified fewer shifts associated with rural lifestyles in an English colony in Adelaide, Australia, further suggesting unique microbial responses during this time period. Lastly, historic oral microbiota reconstructed from dental calculus with attention to oral geography and contamination began to overlap with diversity and composition of people living today in these areas, highlighting the importance of addressing technical details in calculus research. Together, this approach provides a framework to translate ancient and historic microbiota data in the context of modern health and disease and is the first to substantiate the oral human microbiome alterations before, during, and after the Industrial Revolution in different geographical contexts.

This work was funded by a Future Fellowship (FT180100407) awarded to LSW.

Functional Analysis of Anterior Tooth Root Surface Area in Tree-Gouging Primates

VICTORIA A. WHICHARD, ASHLEY R. DEUTSCH and ADAM HARTSTONE-ROSE

Department of Biological Sciences, North Carolina State University

Many primates consume tree exudates (gum and saps) as a part of their diet. In these species, anterior dentition is usually used to gouge or scrape tree bark to access this resource. Although gouging likely produces a unique dental loading, anatomical signals have largely been undetected in previous literature; however, finding such a signal would help us understand how exudates are accessed and, potentially, the role of exudates in the diets of fossil primates. As teeth with greater root surface areas (TRSA) are better able to resist displacement, anterior TRSA may reflect gouging adaptations. In the current study, we measured anterior TRSA relative to body mass of 17 species of gouging and non-gouging callitrichids and lorisids. Comparing gouging and non-gouging species within each lineage using ANOVA and Tukey post-hoc tests, we found that the relative TRSA of gouging callitrichids was larger, on average, in both mandibular incisors than in those of non-gouging callitrichids (significantly so for mandibular I2). Contrary to expectation, relative maxillary canine and mandibular I2 TRSA was, on average, larger in non-gouging lorisids than in their gouging confamilials, though not significantly so, in this taxonomically constrained group. Although the differences between TRSA of gouging and non-gouging species within these primate lineages are subtle and only some reach statistical significance in these taxonomically constrained groups (especially when phylogenetic correction is considered), these preliminary findings suggest some utility in anterior dentition TRSA analysis to help elucidate this functional adaptation in both extant and extinct primate taxa.

Funding was provided by the National Sciences Foundation IOS-15-57125.

Cross-sectional Study of Long Bone Growth in Medieval England

SINA D. WHITE[1], SOPHIE L. NEWMAN[2,4], CHARLOTTE PRIMEAU[3], PATRICK MAHONEY[1] and CHRIS A. DETER[1]

[1]School of Anthropology and Conservation, Skeletal Biology Research Centre, University of Kent, [2]Department of Archaeology, The University of Sheffield, [3]Department of Archaeology, University of York, [4]School of History, Classics and Archaeology, The University of Edinburgh

Living conditions during the 11th to 15th century AD in England influenced infectious and nutritional diseases which may have affected growth during childhood. Most medieval English studies on long bone growth focus on socioeconomic status, pathological conditions, and rural vs urban areas. Little is known about regional variation of bone growth in medieval England. The aim of this study is to compare long bone growth profiles of medieval children from the north and south of England. Standard dental estimation methods were used to reconstruct age-at-death for individuals recovered from St. Gregory's Priory (n=93) and Raunds Furnells (n=51) in the south and Black Gate (n=61) and York Barbican (n=25) in the north. Maximum diaphyseal lengths of tibiae and femurs were analyzed because they are directly linked to stature and potentially more likely to become disturbed by physiological stress during development. Growth patterns were identified from quadratic polynomial growth curves, and ANCOVA tests were used to assess differences between individuals from the north and south. The ANCOVA results for the femurs ($p < 0.001$) and tibiae ($p = 0.002$) reveal significant differences between sites from the north and south. Growth curves indicate individuals from the north and south had accelerated growth from 1 to 3 and 9 to 13 years of age; however, those in the south were more advanced at these ages. These results suggest medieval children from the north and south of England had different growth trajectories. Findings are explored within the context of resource availability, regional economies, and settlement patterns.

Dental hygiene, occupational activity and behavioural habits: investigating non-masticatory dental wear through time in the Fourth Cataract, Sudan

REBECCA J. WHITING[1], DANIEL ANTOINE[1] and SIMON HILLSON[2]

[1]Department of Egypt and Sudan, The British Museum, [2]Institute of Archaeology, University College London

The investigation of non-masticatory dental wear can offer direct insights into past dental hygiene and occupational practices that make use of the mouth, as well as cultural and behavioural habits. This study examined eight skeletal collections from the Fourth Cataract, Sudan, dating from between the Kerma (2500-1500 BC) to Medieval (AD c.550-1500) periods, all curated at The British Museum. The examination of 285 individuals revealed changing prevalence rates of non-masticatory wear through time and between cultural groups. The location and appearance of wear were recorded both macroscopically and via scanning electron microscopy. Seven out of the eight collections exhibited evidence of non-masticatory wear, and prevalence ranged from 5.8% to 27% of individuals. The prevalence appears to decrease through time, a pattern that may be connected to a move away from using teeth as a tool. In Medieval individuals, non-masticatory wear may have been connected to habitual and therapeutic dental hygiene, including tooth-picking and brushing. This study presents the first examples of Lingual Surface Attrition of the Maxillary Anterior Teeth and buccal grooving from the Middle Nile Valley. In some groups, the prevalence of non-masticatory wear also differed between males and females, with females having a statistically significantly higher prevalence (7.4%) at the Meroitic/Post-Meroitic site 3-Q-33 than males (0.7%). This study highlights the use of teeth as part of the proverbial 'tool kit' or as a third hand and gives evidence of habitual dental hygiene practices and how they changed and differed over time.

Research supported by an Arts and Humanities Research Council funded collaborative doctoral award.

Associations between ecological attributes and the gut microbiome of mantled howler monkeys in Los Tuxtlas, Mexico

TABOR L. WHITNEY[1], KATHERINE R. AMATO[1] and PEDRO AMERICO DUARTE DIAS[2,3]

[1]Department of Anthropology, Northwestern University, [2]Primate Behavioral Ecology Lab, Universidad Veracruzana, [3]Institute of Neurology, Universidad Veracruzana

The continuous conversion of natural habitats to agricultural fields and pasturelands creates fragments and patches that isolate animals. This isolation forces animals to adjust to a new environment with different resources resulting in altered health outcomes. This project provides a model by which the gut microbiome can be used as a conservationist tool to understand what aspects of habitat fragmentation are most detrimental to the wellbeing of threatened species. The gut microbiome is essential to host health and immune function and has been shown to differ across howler monkeys residing in different habitats. Nevertheless, previous studies have not quantified what aspects of habitat fragmentation drive differences in the gut microbiome. Here we study the effect of habitat fragmentation on the gut microbiome of 35 mantled howler monkeys (*Alouatta palliata*) in Los Tuxtlas, Mexico. We quantified the habitat structure of eight forest fragments to assess whether different ecological attributes are associated with differences in the mantled howler monkey gut microbiome. For ecological attributes, we measured plant community density, composition, and richness, forest fragment size, howler monkey population densities, dominant land use types in areas surrounding the fragments, and human prevalence within the fragment. The gut microbiome was characterized by sequencing the 16s rRNA hypervariable V-4 region. Using mixed modeling approaches we found that a combination of these ecological attributes influences the diversity and composition of their gut microbiome. Future work will focus on understanding the health impact this variation in the gut microbiome has on individuals residing between different habitats.

The Effect of Food Insecurity on Oral Health

PAMELA S. WHYMS[1], AFSAR NAQVI[2], DERIC TRUSKOSKI[3], ARACELI VALVERDE ESTEPA[2], SAHAR ALRAYYES[3], SLOAN WILLIAMS[1], CHAD SILVER[3], SARIA AWADALLA[4] and CHRISTINA NICHOLAS[1,5]

[1]Anthropology, University of Illinois at Chicago, [2]Periodontics, University of Illinois at Chicago, [3]Pediatric Dentistry, University of Illinois at Chicago, [4]Epidemiology and Biostatistics, University of Illinois at Chicago, [5]Orthodontics, University of Illinois at Chicago

Food insecurity, a lack of consistent access to sources of nutrition, is a complex public health problem which has many negative outcomes (e.g., obesity, malnutrition, depression and anxiety). The prevalence of food insecurity is often compounded by factors like race/ethnicity, income, education, whether a household has children, and neighborhood safety. Recent studies of food security in Chicago show that there are large racial disparities in household access to healthy food, with food insecurity highest among non-Hispanic Black households (41%) and lowest (14%) among non-Hispanic White households. Households which are food insecure are more likely to have diets higher in carbohydrates, sugar, and fat due to a lack of consistent access to fruits, vegetables, lean meats and healthy grains, which in turn may also have a negative impact on oral health. This project aims to examine the association between food insecurity and oral health measures (plaque and gingival bleeding during dental treatment). We recruited a diverse group of participants (n=31; aged 10-12) from a US urban setting through UIC's Pediatric Dentistry Clinic in Chicago, collecting demographic information, detailed dietary data, height, weight, and oral health measures. We found that 29.03% of subjects indicated they had food insecurity. Food insecurity was not associated with gingival bleeding ($p = 0.917$) but was significantly positively associated with plaque ($p = 0.037$). Increased plaque in subjects with food insecurity may reflect oral hygiene habits. Future work with larger sample sizes and oral hygiene habit data will be necessary to further elucidate this relationship.

Center for Clinical and Translational Sciences Pilot Grant, University of Illinois at Chicago; Biomedical Research Award American Association of Orthodontists Foundation

Wisdom from Teeth: Developing a new method of MNI estimation

NIKKI ANNE. WILCOX[1], LEXI CUTSHALL[2], CYDNIE O'BRIEN[3], MACKENZIE ANDERSON[4], AUTUMN HARRISON[5], NIX WILSON[6], ARMANDO ANZELLINI[10,7], NYÁRÁDI ZSOLT[8] and ANDRE GONCIAR[9]

[1]Department of Sociology & Anthropology, University of Mississippi, [2]Department of Anthropology, Drew University, [3]University of Northern Colorado, Department of Anthropology, [4]Indiana University of Pennsylvania, Department of Sociology, [5]North Carolina State University, Department of Anthropology, [6]University of California Sana Barbara, Department of Anthropology, [7]University of Tennessee, Knoxville, Department of Anthropology, [8]Haás Reszö Museum, Romania, [9]ArchaeoTek, BioArch Canada, [10]Middle Tennessee State University, Department of Sociology and Anthropology

Teeth are one of the most resilient parts of the human skeleton. Often at excavations, teeth may be the most well-preserved, or even the only, remains found. This is especially true of commingled contexts, where many, if not most, of the skeletal elements may be fragmented. This destruction makes the recording of an accurate MNI (minimum number of individuals) count challenging. At the site of Patakfalva-Papdomb, in Transylvania, Romania an ossuary was found in 2018 and is in the process of being excavated. Because of the extreme commingling, as well as taphonomic damage, there has been difficulty in calculating an accurate MNI from this context using the remains found in level 2 of the excavation. However, teeth were consistently found and identified in relatively good condition. As a result of their preservation, an MNI count was attempted through tooth identification and analysis. This process was conducted in a four-step process of sorting in which teeth were classified by adult or deciduous, type of tooth, maxillary or mandibular as well as side. Next, the teeth were evaluated for age estimation by root closure and finally MNI was assessed through an equation developed for this method. From this methodology, an MNI of 30 individuals over the age 15 (+/- 2 yrs), and 11 individuals under the age of 9 were recorded, which correlates with the MNI calculated from postcranial elements. We hope that this research will guide future attempts to estimate MNI from dental remains

Inferring the diet of La Quina 5 using dental microwear texture analysis and plant microremains from dental calculus

FRANK L. WILLIAMS[1], CHRISTOPHER W. SCHMIDT[2], AMANDA G. HENRY[3], JESSICA L. DROKE[4], GAEL BECAM[5] and MARIE-ANTOINETTE DE LUMLEY[6]

[1]Anthropology, Georgia State University, [2]Anthropology, University of Indianapolis, [3]Archaeological Sciences, Leiden University, [4]Anthropology, University of Wyoming, [5]History of Art and Archaeology, Université de Perpignan, [6]Paléontologie, Institut de Paléontologie Humaine

Neandertals are characterized as highly carnivorous from nitrogen isotopes and fauna remains. However, it has become increasingly clear that plants also were included in their diets, even during challenging environmental conditions. Southwest France during late Marine Isotope Stage (MIS) 4 and early MIS 3 was a particularly cold and arid time interval associated with open steppe habitat dominated by reindeer, which were hunted by the Neandertals of La Quina cave. One of these individuals, La Quina 5, is examined using dental microwear texture analysis (DMTA) and plant microremain analysis to reconstruct the diet. Reference samples for the DMTA include Hortus (n = 5), Krapina (n = 19), Malarnaud, Spy I, Vindija (n = 4), as well as Holocene *Homo sapiens* having various subsistence strategies (n = 150). For the plant microremain analysis, we compared La Quina 5 to Spy I and II, Shanidar III, La Ferrassie and a modern reference sample. La Quina 5 may have relied significantly on hunted resources in the cold glacial interval of Heinrich Stadial 6 or 5, indicated by a low complexity value that suggests limited hard food consumption. Plant microremains, such as starch grains from grass seeds and plant underground storage organs, are evidenced in the dental calculus. These coarse and poorly processed plant foods were masticated using varied movements of the jaws compared to most other Neandertals, reflected in the low anisotropy of La Quina 5. These findings emphasize the consumption of plant foods in Neandertal diets even during Ice Age climate extremes.

Fulbright-Belgium and the National Science Foundation (BCS 0922930) supported this research.

A new method to quantify vertebral wedging using 3D models

SCOTT A. WILLIAMS[1,2], IRIS ZENG[3], SAUL SHUKMAN[1], JORDAN S. GUERRA[1,2] and MARC R. MEYER[4]

[1]Center for the Study of Human Origins, Department of Anthropology, New York University, [2]New York Consortium in Evolutionary Primatology, [3]Department of Architecture, Massachusetts Institute of Technology, [4]Department of Anthropology, Chaffey College

Lumbar lordosis evolved in the hominin lineage to place the center of mass of the upper body over the pelvis during bipedal posture and locomotion. Sagittal curvatures of the vertebral column are achieved in part through wedging of the vertebral bodies and additionally through other bony and soft tissue morphologies like the shape of the intervertebral discs. Current techniques for quantifying the wedging of vertebral bodies are limited in utility. Lateral radiographs are typically used in clinical settings, but the static image of each vertebra is immobile and the whole vertebra cannot be visualized when the measurement is taken. Wedging angles can also be calculated from linear measurements taken with calipers or 3D landmarks, but the vertebra must preserve all midline landmarks, which must fully represent the distribution of bone ventrally, dorsally, cranially, and caudally. Here, we introduce a 3D method to quantify vertebral body wedging that yields the angle between two "best fit" planes in the software GeoMagic Wrap (3D Systems). The method

is similar to the "direct" method of measuring the angle from lateral images, and it produces statistically indistinct results from the calculated wedging angle method (paired t-test: t=-1.502, p=0.134), with which it produces a high, significant correlation on a large sample (N=320) of well-preserved specimens (r^2=0.978; p<0.001). One major advantage of the 3D method is that it allows specimens with nonrepresentative or missing midline landmarks to be quantified accurately. It is therefore preferred for archaeological and fossil material, which is frequently incomplete.

We thank the Leakey Foundation for supporting this work.

Isotopic investigations of mobility and their implications for mortuary ritual in Middle and Late Woodland period Florida

KYLIE A. WILLIAMSON[1], GEORGE D. KAMENOV[2], NEILL J. WALLIS[3] and JOHN KRIGBAUM[1]

[1]Anthropology, University of Florida, [2]Geological Sciences, University of Florida, [3]Florida Museum of Natural History, University of Florida

The Weeden Island archaeological culture in the Southeast United States is defined by the use of elaborate mortuary ceramics, secondary bundle burials, and highly patterned burial mound construction. Beginning in the late Middle Woodland period (ca. 500s CE), many Weeden Island artifact assemblages include high percentages of non-local ceramics and other artifacts demonstrating extensive extra-local connections that extend regionally across the Southeast. To clarify the spread and maintenance of distinctive Weeden Island mortuary rituals, this research employs isotope analyses of strontium ($^{87}Sr/^{86}Sr$) and oxygen ($\delta^{18}O$) from human enamel samples from three sites along the Gulf Coast of Florida: Crystal River (8CI1), Bayshore Homes (8PI41), and Pillsbury Mound (8MA31). Across the three sites, over 500 individuals were examined, and tooth enamel was sampled for 104 individuals in total. When possible, both a first and third molar were sampled in order to track chronological life history changes in mobility. The mean $^{87}Sr/^{86}Sr$ value from Crystal River (n=56) was 0.70901 (±0.00016), 0.70915 (±0.00007) for Bayshore Homes (n=54), and 0.70910 (±0.00018) for Pillsbury Mound (n=52). The mean $\delta^{18}O$ for Crystal River was -3.1‰ (±0.77), -3.2 ‰ (±0.64) for Bayshore Homes, and -3.0‰ (±0.93) for Pillsbury Mound. Several non-local individuals have been identified from each site based on their isotope signature. Results of this study are consistent with findings at other Weeden Island sites with reported non-local 'outlier' individuals. Detailed characteristics and context of these non-local individuals will be critical in understanding the spread and maintenance of mortuary practices across large geographic regions.

This research was made possible by generous funding by the National Science Foundataion, Award #1356961.

Binary Gender and Sexuality Assumptions in Biological Anthropology

MEREDITH WILSON

Department of Anthropology, University of Illinois, Urbana-Champaign

This abstract is part of the symposium *Advances and Challenges in the Identification of Sex and Gender in Human Osteological Contexts*. A prevailing naturalistic fallacy in the sciences is that being cisgender and heterosexual are the dominant, normative experiences. For example, sex is often categorized as binary and these categories can be ascribed gendered meaning in studies of human biology and behavior. This presentation examines issues of AJPA and AJHB from January 2020 to May 2021 and identifies original research articles that re/producing cis/heteronormativity in their research. I selected articles based on titles that might be engaging with cis and heteronormativity, namely ones which attempted to identify sex and/gender differences from osteological remains or which had reproduction in the title. I next read abstracts for each to better identify whether and how the article was re/producing these. I choose articles that most obviously identified/reified gender/sex difference, paired sex and gender in ways that are reductive, or that emphasized reproduction and heteronormative coupling. I identified 15 articles from AJPA and 14 articles from AJHB that engage with or reproduce cis/heteronomativity. This is not an exhaustive review and instead is bound by the last 2 years so that research is current. I utilize feminist and queer frameworks to critically engage with these assumptions and to identify ways in which we as biological anthropologists can more carefully consider questions, variables and interpretations beyond a gender and sex binary.

Comparing Diaphyseal Length to Dental Calcification Age of Subadults from Elmbank Cemetery

SARA WILSON[1,2] and J. CHRISTOPHER DUDAR[1]

[1]Department of Anthropology, Smithsonian Institution, National Museum of Natural History, [2]Department of Anthropology, Davidson College

Long bone growth is vulnerable to diet and disease and is a useful measure when studying individuals from a skeletal series. The goal of this preliminary research is to better understand the growth pattern of subadults buried at the historic Elmbank Roman Catholic Cemetery, primarily serving an Irish immigrant community in Upper Canada from 1833-1939. The predominantly middle-class St. Thomas' Anglican Church Cemetery (1821-1874) also from Upper Canada, was included for comparison (Saunders et al. 2002). Dental calcification, diaphyseal length, and presence of pathological conditions were recorded for 154 Elmbank subadults based on cemetery relocation field notes from 2001. Diaphyseal length was plotted with calcification age, serving as a proxy for chronical age. Included as a reference standard are Hoffman's (1979) growth curves of expected diaphyseal length and chronological age. R-Project was used to plot split regression and LOWESS curves to statistically compare the pattern of each long bone diaphysis length at Elmbank and St. Thomas'. Elmbank subadults tended to display reduced diaphyseal lengths, suggesting Elmbank children experienced chronic stress episodes such as disease and/or nutritional deficiency. This conclusion is further supported by the high rate of paleopathological stress indicators. Considering St. Thomas' children tended to have reached expected growth at the time of death, it is more likely they died from acute conditions, whereas many Elmbank children survived periods of disease and/or nutritional stress that caused delayed growth but no opportunity for catch up growth at the time of their death.

Thank you to National Science Foundation (NSF) (REU Site, OCE-1560088) for providing support through the National History Research Experience (NHRE) Program.

Sex-based survival differences during the 1918 influenza pandemic

AMANDA WISSLER

Department of Anthropology, University of South Carolina, Physical Anthropology, Cleveland Museum of Natural History

The ongoing Covid-19 pandemic has highlighted how social, cultural, and biological variation shape an individual's disease experience and the probability of death and disability. For example, in 2020, it was reported that males were among those with the greatest risk of severe outcomes due to Covid-19, along with the obese and those with heart problems. Many studies of the 1918 pandemic found that males also suffered greater influenza mortality during this event compared to females. More recent investigations of the 1918 pandemic, however, have found greater female mortality, while some scholars have found no significant difference between sexes. This study contributes to this dialogue by investigating differences in male versus female survival and risk of death during the 1918 influenza pandemic in the United States. Records data on age-at-death and sex were collected from a sample of individuals (n=497) from the Hamann-Todd documented skeletal collection and analyzed using Kaplan-Meier Survivorship analysis and Cox proportional hazards analysis. Results demonstrate that prior to 1918, females experienced only slightly greater risk of mortality compared to males. During the influenza pandemic, however, females were over 2.5 times more likely to die than males. These results shed light on sex- and gender-based health inequalities in the past and inform our understanding of how current day social and biological differences contribute to health inequality.

Interpreted via an anthropological perspective, these findings broaden our understanding of how social roles and expectations impact health and mortality.

Financial support was provided by a Wenner-Gren Dissertation Fieldwork Grant and an American Fellowship from the American Association of University Women.

Pharmacogenetic variation in archaic and modern humans

KELSEY E. WITT[1,2], TADEUSZ H. WROBLEWSKI[3], SEUNG-BEEN LEE[4], RIPAN S. MALHI[5,6], EMILIA HUERTA-SANCHEZ[1,2], FERNANDO VILLANEA[7] and KATRINA G. CLAW[3]

[1]Center for Computational and Molecular Biology, Brown University, [2]Ecology and Evolutionary Biology, Brown University, [3]Division of Biomedical Informatics and Personalized Medicine, Colorado Center for Personalized Medicine, University of Colorado Anschutz Medical Campus, [4]Precision Medicine Institute, Macrogen Inc., [5]Department of Anthropology, University of Illinois at Urbana-Champaign, [6]Carl R Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, [7]Anthropology, University of Colorado Boulder

Pharmacogenes, such as the *cytochrome P450* (*CYP450*) genes, encode enzymes that metabolize a variety of exogenous substances including plant compounds, medications, and pollutants. Evidence suggests that some pharmacogenetic variants have helped human populations adapt to new environments or lifestyles. Gene flow with archaic humans (Neanderthals and Denisovans) has introduced several gene variants that have helped modern humans adapt to novel environments, in a process known as adaptive introgression. While the process may have also occurred for pharmacogenetic variants, gene variation in archaic humans has not been explored in detail. Here, we characterize pharmacogenetic variation in 11 *CYP450* genes for all four high-coverage archaic human genomes and compare it to the *CYP450* variation in modern humans, represented by publicly available genomes from the 1000 Genomes and Simons Genome Diversity Projects. We find that Neanderthals and Denisovans have multiple CYP450 haplotypes with faster or slower metabolic function compared to the reference human CYP450 haplotypes. While over 150 *CYP450* single nucleotide variants (SNVs) found in archaic humans are shared with modern humans, few of the deleterious SNVs in archaic humans are shared with modern humans. Additionally, some archaic haplotypes are found exclusively in non-African human populations, suggesting that they may have been introduced via gene flow. We also identify one unique *CYP450* haplotype shared between a Neanderthal and Africans that may represent gene flow from another, older archaic population. Further interrogation of these variants can help determine if any of these archaic variants in modern humans represent adaptive introgression.

Advances in Subadult Age Estimation: Using Information Theory to explore the relationship between growth indicators and age

CHRISTOPHER A. WOLFE[1], ELAINE Y. CHU[1], LOUISE K. CORRON[1], MICHAEL H. PRICE[2] and KYRA E. STULL[1]

[1]Anthropology, University of Nevada, Reno, [2]Applied Complexity Fellow, Santa Fe Institute

Idiosyncratically choosing among a set of variables to base a final age estimation is something that has plagued subadult (and adult) age estimation. Information theory provides a framework to quantify the information content of complex biological data though it remains underutilized in biological anthropology. Mutual information (MI), an information theoretic method, provides a measure of how much information one can gain about one random variable by observing another. This research quantifies the MI of 63 growth traits with age after conditioning on a baseline age 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 calculate MI, each trait is modeled probabilistically using the novel mixed cumulative probit (MCP) algorithm. Results show that MI can vary substantially as a function of age, which proves individual traits provide varying levels of information throughout ontogeny. This demonstrates that (1) the predictive ability of growth traits changes with age and (2) calls into question the ability for any one trait to fully inform on an individual's age or growth stage. Importantly, the MI provides empirical evidence against the concept that there could be a 'best' indicator throughout all of ontogeny. Instead, differential developmental trajectories and unique relationships with age result in varying relationships. Information theoretic methods allow quantification of the utility of markers as a function of age and provide a means to disentangle complex ontogenetic relationships.

This research was funded by two federal grants (NIJ 2015-DN-BX-K409 and NIJ 2017-DN-BX-K144).

Tibial subperiosteal new bone formation: a comparative analysis of two western New York State poorhouses

KATHARINE C. WOOLLEN[1], JENNIFER F. BYRNES[1], KATHERINE GADDIS[1], JORDAN PHILLIPS[1] and JOYCE SIRIANNI[2]

[1]Department of Anthropology, University of Nevada, Las Vegas, [2]Department of Anthropology, The State University of New York at Buffalo

Poorhouse institutions often fostered environments that directly affected the health and well-being of those most impoverished and at-risk. This study compares the prevalence and severity of tibial subperiosteal new bone formation (SNBF) from the Erie County Poorhouse (ECPH) (1851-1913) and Monroe County Almshouse (MCA) (1826-1863) cemetery skeletal assemblages. The goal of this analysis was to determine if adults from these institutions suffered systemic-induced infections at similar frequencies. A subsample of 231 adults from ECPH and 194 from MCA were analyzed. Presence or absence of tibial SNBF was recorded, and the severity of the SNBF reaction subsequently scored. Of the 231 individuals from the ECPH subsample, 120 (52.0%) displayed tibial SNBF; only 75/194 (38.7%) individuals from the MCA were affected. Within the ECPH subsample, 27/48 females (56.3%) and 50/98 males (51.0%) displayed tibial SNBF compared to the MCA sample where 26/92 females (28.3%) and 43/90 males (47.8%) displayed SNBF. There was no statistical significance between sexes (ECPH p=0.552; MCA p=0.450), and neither sample displayed significant differences between sex and SNBF severity (ECPH p=0.584; MCA p=0.397). Prevalence of tibial SNBF was statistically significant between samples (p=0.006); the ECPH sample had a significantly higher mean SNBF severity score than the MCA sample (p=0.001). Differences in tibial SNBF severity between the ECPH and MCA samples suggest that adults from ECPH suffered a greater frequency of systemic-induced infections.

The influence of food geometry and material properties on feeding posture in bearded capuchin monkeys (*Sapajus libidinosus*)

KRISTIN A. WRIGHT[1], ZEENIA PUNJANI[2], RACHEL R. OSHAY[2], BARTH W. WRIGHT[3], MARIANNA DUTRA FOGAÇA[4,5], ADAM VAN CASTEREN[6], PATRÍCIA IZAR[7], ELISABETTA VISALBERGHI[8], DOROTHY FRAGASZY[9], DAVID S. STRAIT[10,11], CALLUM F. ROSS[12] and MYRA F. LAIRD[2]

[1]Department of Biomedical Sciences, University of Missouri-Kansas City, Kansas City, MO, [2]Department of Integrative Anatomical Sciences, University of Southern California, Los Angeles, CA, [3]Department of Anatomy, Kansas City University of Medicine and Biosciences, Kansas City, MO, [4]Department of Biomedical Sciences, Institute of Population Genetics, University of Veterinary Medicine, Vienna, Austria, [5]Neotropical Primates Research Group - NeoPRego, São Paulo, Brazil, [6]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, [7]Department of Experimental Psychology, University of São Paulo, São Paulo, Brazil, [8]Institute of Cognitive Sciences and Technologies, National Research Council, Rome, Italy, [9]Department of Psychology, University of Georgia, Athens, GA, [10]Department of Anthropology, Washington University in St. Louis, St. Louis, MO, [11]Paleo-Research Institute, University of Johannesburg, South Africa, [12]Department of Organismal Biology and Anatomy, University of Chicago, Chicago, IL

Primate feeding behavior and craniodental morphology has been associated with food geometric and material properties. However, the influence of food properties on positional behaviors during feeding is not well understood. Here, we examine differences in feeding postural behaviors in relation to the feeding event, substrate type and size, and food geometric and material properties in a population of wild bearded capuchins (*Sapajus libidinosus*) at Fazenda Boa Vista in Gilbués, Piauí, Brazil. We analyzed video data from over 1400 co-occurring postural and feeding behaviors and their durations. Food size, substrate type, and substrate size were coded from the videos, and food material properties were measured from foods collected at the time of the video recordings.

Our results suggest significant variation in feeding postures across the feeding sequence, with substrate size (x^2 = 419.57, p<0.01) and with food material properties (toughness, x^2 = 68.04, p<.01; Young's modulus, x^2 = 135.96, p < 0.01) in bearded capuchins. Large-sized and mechanically challenging foods were associated with reduced variation in feeding postures. Substrate had a significant effect on feeding postures. Large foods doubled as a substrate and were associated with suspended postures, whereas small foods were associated with sitting and squatting. We found that food geometric and material properties had a significant influence on feeding postural behaviors in bearded capuchins. We posit that reduced postural variation is associated with improving the animal's limb forces and body positioning during food processing and ingestion for large, mechanically challenging foods.

This research was supported by grants from the National Science Foundation's Biological Anthropology directorate (NSF-BCS-1440516, NSF-BCS-1440541, NSF-BCS-1440542, NSF-BCS-1440545, NSF-BCS-1627206).

Relative hindlimb length and hindlimb segmental proportions as indicators of locomotor category in primates, rodents, and tree shrews

GABRIEL S. YAPUNCICH[1], EMI HEGARTY[2], MADISON BRADLEY-CRONKWRIGHT[2], GRÉGOIRE BOULINGUEZ-AMBROISE[3], NOAH T. DUNHAM[4], ANGEL ZEININGER[2], DANIEL SCHMITT[2], JESSE W. YOUNG[3] and DOUG M. BOYER[2]

[1]Medical Education Administration, Duke University School of Medicine, [2]Evolutionary Anthropology, Duke University, [3]Department of Anatomy and Neurobiology, Northeast Ohio Medical University, [4]Conservation and Science, Cleveland Metroparks Zoo

Leaping is an important locomotor behavior for arboreal taxa such as primates, providing means to cross discontinuous substrates, escape predation, and/or capture prey. Primates that leap frequently have relatively longer hindlimbs than those taxa that leap less often. However, it is unknown if this pattern holds across a broader phylogenetic sample that includes non-primate arboreal taxa and non-primate specialized leapers. Here, we examine if relative hindlimb length and segmental proportions correlate with locomotor category across a sample of small-bodied (<800g) mammals. Lengths of six hindlimb elements (summing to total hindlimb length) were measured on micro-computed tomography scans. Total hindlimb length was regressed against body mass to calculate relative hindlimb length. Segmental proportions were calculated as the ratio of femoral, tibial, and pedal (the sum of calcaneal, cuboidal, metatarsal, and phalangeal lengths) lengths to total hindlimb length. We found that while three arboreal/scansorial taxa (common marmosets, greater dwarf lemurs, and palm squirrels) exhibit short hindlimbs relative to their body mass, all other arboreal and scansorial taxa have relatively long hindlimbs. Most arboreal, scansorial, terrestrial, and fossorial taxa distribute length evenly across segments (femur, tibia, and pes each comprise ~33% of total hindlimb length). Saltatorialists (*e.g.,* jerboas and kangaroo rats) were the only locomotor group with exceptional proportions, with pedal segments contributing ~38% of total hindlimb length. These results suggest to us that segmental proportions may distinguish specialized ricochetal hoppers from taxa that leap sporadically, while relative hindlimb length may predict general leaping ability across mammals.

This research was supported by NSF BCS 2020434 and BCS 2020515.

Anatomical and Shape Variation of the Endocranial Cavity in 6.0–8.0 Year-Old Humans

SAMANTHA E. YAWITZ[1], JENNIFER TACHIBANA[2], MEGAN LUI[2], CHLOE PHELY-BOBIN[3], CHRISTINA KAN[2], JESSICA M. CRONIN[4], ANNABEL T. DAVIS[2], EMIELYN DAS[2], REBECCA S. JABBOUR[5] and GARY D. RICHARDS[6]

[1]Molecular and Cell Biology, University of California, Berkeley, [2]Cognitive Sciences, University of California, Berkeley, [3]Political Sciences, University of California, Berkeley, [4]Integrative Biology, University of California, Berkeley, [5]Biology, St. Mary's College of California, [6]Biomedical Sciences, AA Dugoni School of Dentistry, University of the Pacific

Assessing brain evolution in fossil/modern skeletal remains relies on reconstructions of the endocranium. Whereas adults are relatively well documented, sufficient material to delineate the range of anatomical and shape variation in subadults is less well documented. This is particularly the case for late-stage children/adolescents, who are less well represented in skeletal samples. To address this issue, we provide an overview of the major anatomical differences and shape variations in 6-8.0 year olds.

We CT-scanned 43 crania (5.8-7.9 years of age; helical mode, standard kernel, 0.3 mm isotropic voxels). The degree of crown/root calcification for each tooth was compared to Schour and Massler's standards to determine developmental age. Shape variation was assessed via Principal Components Analysis, on Procrustes-aligned shape variables, in Morphologika. We use 34 (of 43) endocranial landmarks in the geometric morphometric assessment. Observations of brain anatomy relied on size-matched (geometric mean) virtual reconstructions.

PC1 explains 14.8% of the variance, with positive values representing height increase in the parieto-occipital region and depression of Broca's region and the temporal lobes. PC2 (10.5%) reflects the amount of flattening of the frontal-parietal-occipital lobes, but little change in basal structures. Changes along PC3 (7.6%) result from occipital flattening, with a rise/widening at asterion that is accompanied by frontal lobe rotation and anterior base depression.

Documenting anatomical and shape variation in the endocranium of modern children/adolescents allows greater insights into the evolution of brain structures and allows insights into potential developmental rate differences underlying cranial shape divergence in paleodemes and closely related species.

The AABA Education Committee: Where it has been, where it is going, how we hope to get there

KATRINA E. YEZZI-WOODLEY[1], ROBERT C. O'MALLEY[2], CAITLIN SCHREIN[3], KATE MCGRATH[4], NINA LOPERGOLO[5], AMANDA C. OWINGS[6] and BRIANA POBINER[7]

[1]Anthropology, University of Minnesota, [2]Dialogue on Science, Ethics, and Religion Program, American Association for the Advancement of Science (AAAS), [3]N/A, Independent Researcher, [4]Anthropology, SUNY Oneonta, [5]Anthropology, George Washington University, [6]Biology, University of Iowa, [7]Anthropology, Smithsonian Institution

The AABA Education Committee was established to "facilitate the engagement of K-12 students, teachers, and broader audiences with biological anthropology." Initially, the committee organized teacher workshops at AABA annual meetings and facilitated a program for hominin and other primate casts to remain in each meeting's host city for one year for use in local classrooms. Activities then expanded to creating lesson plans incorporating the casts (2016), visiting K-12 classrooms (2016), and conducting museum visitor outreach and educator training (2019). Committee activities have been well-received and impactful for audiences and committee volunteers; however, the shifting US sociopolitical climate, the challenges of the COVID-19 pandemic, and increasingly contentious public discourse on many science-and-society issues

related to biological anthropology (e.g., ethics of the study/curation of human remains, genetics, human diversity, racism, conservation, environmental justice, and public health) suggest an urgent need for greater professional support for public engagement by biological anthropologists.

To meet this need, in 2020, the committee began expanding its activities and scope. To date, this includes offering an online teacher workshop, curating >30 free, grade-targeted, NGSS-aligned K-12 lesson plans related to biological anthropology, and creating a resource hub for the AABA website to support impactful public engagement by association members. Planned future directions include opportunities for AABA members to share their engagement experiences and ideas, connect with engagement activities and funding sources, and align their science communication strategies with recognized best practices for centering "inclusion, equity, and intersectionality," as highlighted by Canfield et al. (2020).

Variation in ontogenetic trajectories of limb dimensions is the result of multiple evolutionary forces

AN-DI YIM[1,2], LIBBY COWGILL[3], DAVID C. KATZ[4] and CHARLES C. ROSEMAN[5]

[1]Department of Health and Exercise Sciences, Truman State University, [2]Department of Biology, Truman State University, [3]Department of Anthropology, University of Missouri, [4]Department of Cell Biology and Anatomy, University of Calgary, [5]Department of Evolution, Ecology, and Behavior, University of Illinois at Urbana-Champaign

The selective and neutral evolutionary forces (random genetic drift, mutation and gene flow) responsible for diversity in the limb dimensions and proportions of recent humans have been studies primarily for adult morphology. This study examines the effects of different evolutionary forces on the variation in ontogenetic trajectories of limb dimensions. We used a multivariate mixed effects model approach to quantify the effects of climatic adaptation and population structure (genetic relationships among groups) resulted from neutral evolution on subadult long bone (humerus, radius, femur, and tibia) linear measurements in a global sample (n = 4,193 from seven archeological groups and six contemporary groups). For all limb elements, models that take population structure into account generally outperform models without a population structure random term. After accounting for the effects of neutral evolution, and holding all other effects constant, extreme temperatures have weak, positive associations with diaphyseal length and breadth measurements, while mean temperature shows negative associations with diaphyseal dimensions. The association with extreme temperatures fits the expectations of ecogeographic rules, while the association with mean temperature may explain the observed among-group variation in intralimb indices. This study shows that neutral evolution, allometric effects associated with change in size, and directional effects from climate all contributed to the variation in ontogenetic trajectories of long bone dimensions in modern humans. All of these factors should be considered when interpreting postcranial skeletal morphology, even in subadults.

Funding provided by the National Science Foundation (NSF BSC 1945797) and the Wenner-Gren Foundation for Anthropological Research (Dissertation Fieldwork Grant 9868).

A survey of the inferior alveolar nerve and its corresponding bony canal and foramina in primates

CAITLIN B. YOAKUM and CLAIRE E. TERHUNE

Anthropology, University of Arkansas

The inferior alveolar nerve (IAN) enters the mandible via the mental foramen, supplies nervous sensation to the mandibular teeth as it travels through the mandibular canal, and exits the mandibular foramen to send information to the brain to maintain chewing cycles and protect the teeth from damage. Although bony canals and foramina have been shown to form around soft-tissue structures, there are some examples (e.g., the hypoglossal nerve/canal) where the nervous structures do not comprise most of the canal/foramina space. This study aims to assess variation in the IAN and its corresponding bony structures in 68 primate species (n = 273, 131 females, 134 males, 8 unknown) to determine how much space in the canal the IAN occupies. Ratios for these variables, created by dividing the cross-sectional area (CSA) of the IAN by the corresponding bony structures, showed that the nerve occupies 23.84% of the mandibular foramen, 22.35% of the mental foramen, 25.86% of the canal beneath M_1, and 19.72% of the canal beneath P_4. Additionally, the total volume of the IAN occupied 21.64% of the mandibular canal volume. Phylogenetic ANOVAs found no significant differences between primate families for these ratios at the mandibular foramen ($p = 0.993$), mental foramen ($p = 0.789$), canal beneath M_1 ($p = 0.863$), canal beneath P_4 ($p = 0.743$), or canal volume ($p = 0.951$). These results show that the IAN does not occupy most of the mandibular canal at any point in its CSA or total volume.

This work was funded by NSF DDRIG grant #1944642.

Dental morphology identifies significant admixture among 13th century Ancestral Puebloan communities in east-central Arizona

AARON J. YOUNG[1,2] and JAMES T. WATSON[1,2]

[1]School of Anthropology, University of Arizona, [2]Arizona State Museum, University of Arizona

Biological distance analysis is used in this presentation to measure the biological relationship of individuals from Slade Ruin (AZ Q:15:1) to other ancestral groups in the American Southwest. Slade Ruin is located in the Zuni/Cibola region and was occupied during the Pueblo III period (1150-1350 AD). Prior to 1000 AD, well-defined social and political communities did not exist, and by 1200 AD, settlement clusters appeared but were occupied for less than a single generation. A region with a high degree of mobility brings to question who individuals from Slade Ruin are more closely related to. The authors hypothesize that dental morphological trait frequencies measured from Slade Ruin would indicate closer relationships to individuals from nearby sites like Hawikuh, Pueblo Bonito, and Western Anasazi (Ancestral Pueblo). Nineteen dental nonmetric traits were recorded from 19 individuals from Slade Ruin using the ASUDAS scoring system. Slade Ruin trait frequencies are compared to frequencies collected from 19 Southwestern archaeological sites using Mean Measure of Divergence (MMD) to estimate biodistance, with smaller distances reflecting closer affinity. The distance statistics grouped sites into two clusters, with three outliers (Slade Ruin, Grasshopper Pueblo, and Hawikuh), and identified that Slade Ruin had the shortest distance to Grasshopper Pueblo. The similarity between these sites as outliers is suggestive of greater admixture due to significant population movement in and out of these areas. The results reflect broader social processes during the 13th century, including significant levels of migration and community aggregation.

Morphology of the Platyrrhine talus reflects differences in ankle mobility associated with positional behavior

LIAM M. ZACHARY

Anthropology, University of Arkansas

The talus forms the mechanical connection between the leg and the foot, and as such it can enable mobility or provide stability during a locomotor progression. Platyrrhines exhibit a range of locomotor behaviors, from the tiny callitrichines, which climb vertical substrates, to atelines, which suspend below branches. This locomotor diversity makes platyrrhines an ideal sample to study the functional morphology of the talus. Using three-dimensional geometric morphometric data, relationships between talus shape and locomotor patterns were assessed in a phylogenetically diverse sample of platyrrhines (n=298). Thirty 3D landmarks on the talus were collected from the platyrrhine sample as a series of Cartesian coordinate data. Principal components analysis and permutation tests indicate significant shape differences in the platyrrhine sample at the level of family, subfamily, and genus. The results suggest that talar shape is influenced by locomotor behavior. Suspensory

and climber/clamberer Atelids exhibit morphologies that suggest more ankle mobility, and more variable foot postures. The taxa (callitrichines and *Pithecia*) that leap the most (both VCL and quadrupedal leaping) have talar morphologies that indicate more ankle stability, particularly at the talocrural and subtalar joint, and less variable foot postures. Taxa (cebines) that are predominantly arboreal quadrupeds that employ relatively lesser amounts of leaping and climbing, exhibit morphology suggesting an intermediate degree of ankle mobility and foot orientations. These results suggest that talar morphology can serve as an excellent proxy for reconstructing ankle stability and mobility in fossil primates, particularly since the talus is well represented in the platyrrhine fossil record.

Association between age-related bone loss and vitamin D receptor polymorphisms in past populations living in north-central Poland from the Neolithic to early modern times

ELZBIETA ZADZINSKA[1], PAULINA BOROWKA[1], DOMINIK STRAPAGIEL[2], JOANNA MIETLINSKA[1], JUSTYNA KARKUS[1], EWA SEWERYNEK[3], MICHAL STUSS[3], DAMIAN PLAZUK[4] and WIESLAW LORKIEWICZ[1]

[1]Department of Anthropology, University of Lodz, [2]Department of Molecular Biophysics, University of Lodz, [3]Department of Endocrine Disorders and bone Metabolism, Medical University of Lodz, [4]Department of Organic Chemistry, University of Lodz

Osteoporosis is one of the most frequently diagnosed civilisation diseases in the ageing societies. Information about the direction of changes of bone loss of the skeleton in the past and information about the changes of the genetic basis of this process is crucial for a better understanding of the increasing frequency of diagnosis of osteoporosis in ever younger people.

This study analysed bone mass density (DEXA), bone fractures (including osteoporotic fractures) and variability of three vitamin D receptor (VDR) gene polymorphisms: FokI (rs 2228570), ApaI (rs 7975232) and TaqI (rs 731236) in 226 skeletons (116 males and 108 females) representing prehistoric (Neolithic) and historical (early Middle Ages to early modern times) populations from Kujawy.

The frequency of the variants of the analysed VDR polymorphisms did not differ significantly depending on the skeletal series and did not correlate with bone mass density. Generalised linear models (GLM) showed a significant relationship between the bone mass density and the individual age of the subject and the series it come from. Older men and women are characterised with lower BMD in all series. Neolithic men and women showed a significantly higher bone mass density and are characterised with absent osteoporotic fractures as compared to the historical samples. A major transition in bone maintenance patterns occurred between the Neolithic and the Early Middle Ages. Our research seems to confirm that current prevalence of osteoporosis is rather a side effect of civilisational changes of human populations than a consequence of changes in their genetic structure.

This research was funded by National Science Centre, Poland, grant no. 2016/23/B/NZ8/03145 (OPUS 12).

Dissecting the genetic and environmental variation between populations with skin pigmentation as a case study

ARSLAN A. ZAIDI[1], JINGUO HUANG[2] and MARK SHRIVER[2]

[1]Genetics, University of Pennsylvania, [2]Anthropology, Penn State University

It is difficult to estimate the degree to which genetic differences contribute to phenotypic differences between populations. This is because genetic and environmental variation between populations is often confounded. One way to get around this problem is through common-garden experiments, which are only possible in organisms that are amenable to manipulation in the laboratory or field. This is, of course, not possible in humans, for practical and ethical reasons. We show how one can leverage recent admixture in humans to reliably estimate the genetic variance between the source populations and thereby estimate the proportion of phenotypic variation between populations due to genetic effects (i.e. the heritability between populations). We present theoretical justification and proof of concept of this approach through simulations. We also demonstrate how the demographic history of the admixed population and the genetic architecture of the trait under study can complicate inference. Finally, we use this approach to estimate the heritability underlying skin pigmentation variation between West Africans and Europeans and compare these to independent estimates made using genome-wide association studies. We discuss the implications of these results for testing for divergent selection on skin pigmentation in humans.

Pelvic variance: Testing for evidence of stabilizing obstetric selection

SARAH M. ZALESKI and LEAH HARRELL

Anthropology, University of Florida

Researchers have proposed that stabilizing obstetric selection should manifest with less pelvic shape and size variance in females compared to that in males. Not all studies have produced these results, however. Previous research has shown that female pelves undergo shape change with aging, and a recent review suggests that failing to account for this change may preclude consistent findings that provide evidence for stabilizing obstetric selection. With an aim to account for potential increased female pelvic variability associated with aging, the current study tests for sex differences in pelvic variance separately in 19-25 year-olds, 26-40 year-olds, and 41-90 year-olds using re-articulated pelves from the Bass, Terry, and Hamann-Todd collections as well as a sample from medieval Kulubnarti in Nubia (n=157). Separate generalized Procrustes analyses aligned three-dimensional landmark coordinate data representing whole pelvic and pelvic canal shape in R geomorph. Morphological disparity analyses compared Procrustes variances between sexes in each age group for the whole pelvis landmark configuration and then the pelvic canal landmark set. Resampling tests assessed differences in canal centroid size variances. Results for all three age groups do not indicate any significant sex differences in variances of whole pelvic shape, pelvic canal shape, nor canal centroid size. These results do not provide evidence for stabilizing obstetric selection.

Funding: Lambda Alpha National Anthropology Honor Society Graduate Research Grant, University of Florida Graduate School Doctoral Research Travel Award, John M. Goggin Award (University of Florida Anthropology Department)

The phylogenetic signal of the enamel-dentine junction of primate molars

CLÉMENT ZANOLLI[1], ALESSANDRO URCIUOLI[2], MIGUEL DELGADO[3], THOMAS W. DAVIES[4], FLORIAN BOUCHET[2], JOSEP FORTUNY[2], AMÉLIE BEAUDET[2,5,6], DAVID M. ALBA[2], OTTMAR KULLMER[7,8] and MATTHEW M. SKINNER[4,9]

[1]PACEA, UMR 5199 CNRS, MCC, Université de Bordeaux, [2]Institut Català de Paleontologia Miquel Crusafont, Universitat Autònoma de Barcelona, [3]CONICET, Universidad Nacional de La Plata, [4]Department of Human Evolution, Max Planck Institute for Evolutionary Anthropology, [5]Department of Archaeology, University of Cambridge, [6]School of Geography, Archaeology and Environmental Studies, University of the Witwatersrand, [7]Department of Paleobiology and Environment, Institute of Ecology, Evolution, and Diversity, Goethe University, [8]Department of Palaeoanthropology, Senckenberg Research Institute and Natural History Museum Frankfurt, [9]School of Anthropology and Conservation, University of Kent

Tooth crown morphology plays a critical role in primate systematics, notably to make taxonomic assessments and to reconstruct the evolutionary history of hominids and hominins in particular. Compared with the outer enamel surface, which can be affected by wear and various taphonomic processes, the enamel-dentine junction (EDJ) is generally better preserved in fossil specimens. EDJ morphology is also considered to be less sensitive to dietary function and adaptation, and hypothesized to be a reliable phylogenetic proxy. However, no comprehensive and quantitative study across extant primates has been conducted yet to test these hypotheses. In this study, we test

and quantify the phylogenetic signal embedded in the shape of the EDJ of 248 lower first molars of 25 extant anthropoid genera (monkeys, apes and humans) and of four fossil specimens belonging to *Dryopithecus fontani* and Neanderthals. Following a deformation-based 3D geometric morphometric analysis, the phylogenetic signal was investigated in the raw data, PCA and bgPCA scores. Univariate and multivariate Blomberg's K and Pagel's λ reveal a significant and strong phylogenetic signal in the raw data, first two PCs and first three bgPCs (despite the presence of some degree of homoplasy in bgPC2). Our results show that the first PCs and bgPCs completely discriminate hominids, hylobatids and platyrrhines from cercopithecoids, while the different genera are partially to completely distinguished. Posterior probabilities for *Dryopithecus* and Neanderthal EDJs indicate closest affinities with *Pongo* and *Homo*, respectively. Our results confirm the relevance of the EDJ morphology for addressing the phylogenetic relationships of fossil primates.

IdEx Université de Bordeaux/GPR Human Past, CNRS, European Union's Horizon 2020 research and innovation programme (No. 819960), Max Planck Society, AEI (PID2020-116908GB-I00, PID2020-117289GB-I00, PID2020-117118GB-I00), Generalitat de Catalunya/ CERCA Programme, MICINN (PRE2018-083299).

Predicting the presence of the yellow-tailed woolly monkey (*Lagothrix flavicauda*) using habitat suitability models and newly confirmed localities in Junín, Peru

MELISSA A. ZARATE[1], ELVIS CHARPENTIER[2], SAM SHANEE[2] and CHRISTOPHER A. SCHMITT[1]

[1]Department of Anthropology, Boston University, [2]Peru Branch, Neotropical Primate Conservation

The Critically Endangered yellow-tailed woolly monkey (*L. flavicauda*) is nearing extinction due to the rapid deforestation and degradation of its habitat in the Peruvian Andes. Sightings of the species had not occurred further south than the region Huánuco until recent observations found *L. flavicauda* populations in the region of Junín, over 200 kilometers south of the previously observed range limited to the Marañon-Huallaga landscape. This study presents the results of further survey efforts in Junín and their inclusion in habitat suitability models that reveal predictions of where populations of *L. flavicauda* may reside between the previously known range and the new southern populations. We fit models using generalized linear modeling and MaxEnt software to determine the most tightly correlated variables with *L. flavicauda* presence. In both models, predictor variables comprised of various openly available environmental data. The MaxEnt model was the most accurate, and both models agreed that precipitation seasonality was the most influential environmental variable to predict species presence. Suitability maps allowed us to predict where along the Peruvian Andes the species is likely found, and to compare those locations to present protected areas. The results of our surveys and models give insight into the differential habitation patterns in the southern *L. flavicauda* range and elucidate the possible competitive exclusion with closely related species. With this information, we can better understand how the species is responding to its environment, find potential corridors they are utilizing, and recommend enhanced protection of these corridors.

Fiber digestibility in wild Bornean orangutans: Age-sex class differences and implications for slow juvenile growth

VICTORIA R. ZDANOWICZ[1], ERIN KANE[1], TRI WAHYU SUSANTO[2] and CHERYL D. KNOTT[1,3]

[1]Department of Anthropology, Boston University, [2]Department of Biology, Universitas Nasional, [3]Department of Biology, Boston University

Bornean orangutans (*Pongo pygmaeus wurmbii*), with their long lifespans and inter-birth intervals, and late age at first birth, have the most extended life history of all primates. According to the Ecological Risk Aversion Hypothesis, slow growth is a strategy to avoid starvation in unpredictable environments. When fruits are unavailable, bark and leaves, high in indigestible fiber, dominate orangutan diets. Orangutan hindgut fermentation is critical in the extraction of nutrients from fibrous fallback foods. However, body size and gut passage times are predicted to influence digestive efficiency. We investigated age-sex class differences in fiber digestibility in response to fluctuations in fiber intake. Researchers at Gunung Palung National Park, Indonesia, collected fecal samples during focal follows from 2016-2019 which were dried and then analyzed at Boston University's Primate Ecology Lab. Samples (N=143) were weighed before grinding in a Wiley Mill. Seeds separated from the fecal matter were counted, measured, photographed and identified using our reference database. Dry matter and percent organic matter were determined through drying, ashing, and hot weighing. We used an ANKOM 200 Fiber Analyzer to determine NDF and compared the percent fiber excreted by mother/ offspring pairs with feeding data. While adult female and juvenile diets showed similar percentages of fiber intake, juveniles excreted 50% more fiber than their mothers. Our results highlight the influence of body size, with smaller individuals demonstrating a lower capacity for fiber digestion. Juvenile digestive efficiency likely constrains growth, development, and survivorship during periods of low food availability when orangutan diets are high in fiber.

National Science Foundation BCS-1638823, US Fish and Wildlife Service F18AP00898 and F19AP00798, Conservation Food and Health Foundation, Disney Conservation Fund, Sea World Busch Gardens, Ocean Park Conservation Fund

The effect of grip type and tail placement on whole body mechanics during arm-swinging in *Ateles* and *Lagothrix*

ANGEL ZEININGER and DANIEL SCHMITT

Evolutionary Anthropology, Duke University

Tailless small-bodied apes, gibbons and siamangs, use a specialized form of arm-swinging, brachiation, in which the center of mass (COM) swings through a large pendular arc, resulting in minimal collisional energy loss (changes in the COM direction) and high energy recovery. In contrast, New World monkeys use a prehensile tail-assisted form of arm-swinging that differs between species based, in part, on body proportions. The slender and long-limbed *Ateles* uses its tail with every other handhold and is thought to use a fore-aft pendular swing, similar to small-bodied apes. *Lagothrix* is shorter-limbed, uses its tail with every handhold, and has more lateral body sway. The mechanism by which these COM movements (fore-aft or side-to-side) are achieved has not been explored. We test the hypothesis that the orientation of the hand and tail during a swing influence COM movements and energy recovery. Lateral, fore-aft, and overhead video-recordings of *Ateles* and *Lagothrix* arm-swinging were analyzed. *Ateles* most frequently used grips in which the hand in contact with the suprastrate was palm-in and, if in contact, the tail was relatively close to the hand, resulting in relatively high (>60%) energy recovery. *Lagothrix* also used palm-in grips but more frequently used palm-out grips and placed the tail significantly farther from the hand, resulting in a more side-to-side COM sway and lower energy recovery (<60%). These data suggest that the grip of both the hand and tail contribute to the different whole body mechanics observed in ateline arm-swinging.

Birth parameters and biomarkers of biological aging in men

AGNIESZKA ŻELAŹNIEWICZ, JUDYTA NOWAK-KORNICKA and BOGUSŁAW PAWŁOWSKI

Department of Human Biology, University of Wrocław

Previous studies showed that intrauterine growth restrictions, resulting in low body weight at birth, is associated with the risk of age-related diseases in adult life. As such it has been suggested that prenatal development predicts aging trajectories in humans. However there is little empirical evidence that intrauterine growth predicts the pace of biological aging in adults. The aim of this study was to verify if body size at birth is related with biological age in adult men. 160 healthy, non-smoking, born in term men (35.31±3.45 years) participated in the study. Information on birth parameters (birth weight, length, pregnancy age at birth) were taken from medical records and ponderal index at birth was calculated. Biological age was evaluated based on serum levels of

s-klotho, markers of oxidative stress, inflammation markers (Il-6, hsCRP), DHEA/S and mean blood pressure (MBP). Chronological age, BMI, socioeconomic status, serum levels of testosterone and cortisol were controlled in the analysis. The results showed no linear relationship between birth size and s-klotho level, oxidative stress, inflammation markers, DHEA/S or MBP (p>0.10). Comparison of mean levels of markers of biological aging in men born as small-for-gestational age (N=54) and men born as normal-for-gestational age (N=116) revealed the only difference in hsCRP level (t(158)=-1.99, *p*=0.02) and SGA men exhibited higher levels of hsCRP. The results were similar when controlled for chronological age, BMI, testosterone or cortisol level. The results suggest that there is no relationship between intrauterine growth and biomarkers of aging in men aged 30-45 years from affluent population.

Narodowe Centrum Nauki - grant no 2017/27/B/NZ8/00500

MaLAdapt reveals novel targets of adaptive introgression in worldwide human populations

XINJUN ZHANG[1], ARMAAN SINGH[4], ARUN DURVASULA[5], BERNARD KIM[3] and KIRK LOHMUELLER[1,2]

[1]Ecology and Evolutionary Biology, University of California, Los Angeles, [2]Human Genetics, David Geffen School of Medicine, University of California, Los Angeles, [3]Biology, Stanford University, [4]Computer Science, University of California, Los Angeles, [5]Genetics, Harvard Medical School

Adaptive introgression from archaic humans plays an important role in facilitating local adaptation in modern humans. Most state-of-the-art methods to detect adaptive introgression either rely on identifying outliers of a few summary statistics that may not be specific to AI signatures, or intersecting scans for positive selection with putatively introgressed genomic regions. Although widely used, these outlier-based approaches are vulnerable to a high false-negative rate, as the power of different methods and summary statistics can vary. Moreover, alternative evolutionary processes unrelated to introgression or positive selection, such as background selection, may create similar genomic signals as adaptive introgression, compromising the reliability of existing inference methods. In recent years, machine learning (ML) methods have been increasingly applied to human genomics studies, while ML to distinguish adaptive introgression is still in the early stages. In this study, we present a likelihood-free ML-based method called *MaLAdapt* for identifying candidate adaptive introgression loci in worldwide human populations. Using an decision tree-based algorithm, our method combines information from a large number of population genetic summary statistics, and powerfully captures the signature of adaptive introgression in 50kb-sliding windows across the genome. In contrast to existing methods, *MaLAdapt* is especially powerful at detecting introgressed loci with mild beneficial effects, including selection on standing archaic variation, and is robust to non-introgressed selection sweeps and non-adaptive population genetic processes. We apply *MaLAdapt* to the 1000 Genomes Project human genomic data, and discover novel candidate regions for adaptive introgression in all non-African populations.

This work was supported by NIH Grant 1K99GM143466 to Xinjun Zhang and NIH Grant R35GM119856 to Kirk Lohmueller at University of California, Los Angeles (UCLA).

Genomic features underlying the Andean pattern of high-altitude adaptations

KIMBERLY T. ZHU[1], MELISA KIYAMU[2], GIANPIETRO ELÍAS[3], JENNA ISHERWOOD[4], OBED GARCIA[5], FRANK S. LEE[6], MARIA RIVERA-CHIRA[2], FABIOLA LEON-VELARDE[2], TOM D. BRUTSAERT[3] and ABIGAIL 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, Ann Arbor, [5]Department of Biomedical Data Science, Stanford University, [6]Department of Pathology and Laboratory Medicine, University of Pennsylvania

Humans have inhabited the Andean Altiplano for over 11,000 years, where the partial pressure of oxygen is 35% lower than at sea level. Andeans who thrive in this hypoxic environment display a suite of adaptive phenotypes including elevated hemoglobin (Hb) concentration. Nevertheless, the genetic architecture underlying this adaptive phenotype is currently unknown. To identify genomic regions contributing to the elevated hemoglobin (Hb) phenotype among Peruvian Andeans, we first identified 31,932 single nucleotide polymorphisms (SNPs) that display signatures of past natural selection using two tests of positive selection, Locus Specific Branch Length (LSBL) and XP-nSL. We then performed a genome-wide association study (GWAS) for elevated Hb, restricting our analysis to those 31,932 SNPs showing evidence of past natural selection. We identified two polymorphisms located on chromosomes 4 and 8 that are significantly associated with Hb concentration. As GWAS nominated SNPs often have small effect sizes and represent a small portion of all associated SNPs, we aggregated SNP effects across the genome by creating a phenotype prediction model using Elastic Net regression. By investigating elevated hemoglobin concentration from a genomic perspective, this study contributes novel insights into the genetic basis of adaptive evolution among Peruvian Andeans and the role of positive selection in shaping trait variation.

This work was supported by the National Science Foundation and the University of California, Los Angeles.

Taphonomic and sharp-force trauma analysis of a non-identified anatomical teaching skeletal assemblage from Reykjavík, Iceland

ADAM NETZER ZIMMER

Anthropology, University of Massachusetts Amherst

Many anatomical skeletal assemblages used for teaching purposes in both bioarchaeology and forensic anthropology come from identified cadavers. Previous research on such collections demonstrate that a significant number of these collections are comprised predominantly of individuals from racial or religious minorities, or the unclaimed poor. Other analyses have demonstrated how such collections played a role in the construction of race-based science and medicine in the United States and western Europe.

An unprovenienced anatomical skeletal collection from the Læknagarður medical school in Reykjavík, Iceland demonstrates a potential departure from such "typical" sources. Taphonomic analysis of elements demonstrate a diverse array of skeletal element origin, including likely opportunistic archaeological finds, teaching specimens purchased in other Nordic nations, and many sourced from unknown cadaveric origin. Sharp-force trauma analyses at muscle origin and insertion sites demonstrate that few elements were used in anatomical dissection, counter to what is seen in similar skeletal assemblages in the United States and western Europe.

Iceland's place in the global cadaver trade between Western nations and their colonies during the late 1800s, with an emphasis on the construction of imagined anatomical racial hierarchies, is discussed as a potential explanatory factor for the greater diversity of skeletal element sources at Læknagarður.

This material is based upon work supported by the National Science Foundation with Fulbright Iceland under the Fulbright-National Science Foundation Arctic Research Grant Initiative.

A comprehensive single-cell atlas of the adult rhesus macaque brain

TRISHA M. ZINTEL[1], KENNETH L. CHIOU[1], CAILYN H. SPURRELL[3], AISHWARYA A. GOGATE[3,4], DIANA R. O'DAY[3], GABRIELLE DUGAN[5], LEA M. STARITA[3,6], HANNAH A. PLINER[3], SAMUEL E. BAUMAN[7], NICOLE R. COMPO[7], MELWEEN I. MARTINEZ[7], LAUREN J. BRENT[8], CHRISTOPHER S. WALKER[9], OLGA GONZALEZ[10], JACK STYLLI[11], ALEX R. DECASIEN[12,13,14], MARTIN O. BOHLEN[15], JAMES P. HIGHAM[12,13], MICHAEL J. MONTAGUE[11], MICHAEL L. PLATT[11,16,17], JAY SHENDURE[18,19,3,6] and NOAH SNYDER-MACKLER[1,2]

[1]Center for Evolution and Medicine, Arizona State University, [2]School of Life Sciences, Arizona State University, [3]Brotman Baty Institute for Precision Medicine, Brotman Baty Institute for Precision Medicine, [4]Seattle Children's Research Institute,

Seattle Children's Research Institute, [5]College of Engineering, Virginia Polytechnic Institute and State University, [6]Department of Genome Sciences, University of Washington, [7]Caribbean Primate Research Center, University of Puerto Rico, [8]Centre for Research in Animal Behaviour, University of Exeter, [9]Department of Molecular Biomedical Sciences, College of Veterinary Medicine, North Carolina State University, [10]Southwest National Primate Research Center, Texas Biomedical Research Institute, [11]Department of Neuroscience, University of Pennsylvania, [12]Department of Anthropology, New York University, [13]New York Consortium in Evolutionary Primatology, New York Consortium in Evolutionary Primatology, [14]Section on Developmental Neurogenomics, National Institute of Mental Health, [15]Neurobiology, Duke University School of Medicine, [16]Department of Psychology, University of Pennsylvania, [17]Department of Marketing, University of Pennsylvania, [18]Howard Hughes Medical Institute, Howard Hughes Medical Institute, [19]Allen Discovery Center for Cell Lineage Tracing, Allen Discovery Center for Cell Lineage Tracing

We are only beginning to resolve the cellular complexity of primate brains and to link the patterning and functions of molecularly distinct cell types to neurological phenotypes across different brain regions. Resolving this complexity will involve the development of molecular atlases across the brains of key nonhuman primate species and models. To this end, we developed a molecular atlas of the rhesus macaque brain–a cercopithecoid monkey with social and neurological features similar to humans. Our atlas consists of single-cell RNA-sequencing data collected from one male and one female macaque across 28 brain regions using sci-RNA-seq3, and represents the most comprehensive primate molecular atlas to date. Sampling spanned the four lobes of the cortex, subcortex, cerebellum, and brain stem. Preliminary characterization of transcriptional profiles of 979,189 nuclei demonstrates our ability to resolve major brain cell types, including inhibitory and excitatory neurons, astrocytes, oligodendrocytes, and microglia. We identified extensive heterogeneity in excitatory neurons from cortical regions, while neurons derived from non-cortical brain regions were more homogeneous. Additionally, we found considerable heterogeneity within astrocytes, including region-specific subtypes in the thalamus and cerebellum. We are currently further characterizing subtypes of major brain cell types to compare regional cellular distributions to those seen in humans, which may shed light on the evolution of uniquely human traits. Future analyses include exploring cell type-specific age-related changes in expression and a comparison to molecular atlases of humans and mice to determine interspecies differences in cell type abundance and gene expression that are evolutionarily and biomedically relevant.

This work is funded by the following grants: NIMH U01-MH121260, ORIP P40- OD012217, NIA R00-AG051764, NIA R01-AG060931, NIMH R01-MH096875, NIMH R01-MH089484, NIMH R01- MH118203.

When did the C677T mutation reach its high frequencies in Europe? A pilot study using ancient DNA samples

JAMIE ZOLIK[1,3], XIAOMING LIU[2] and LORENA MADRIGAL[3]

[1]Anthropology, University of Minnesota, [2]Public Health, University of South Florida, [3]Anthropology, University of South Florida

The MTHFR gene C677T polymorphism causes a reduction in 5, 10- Methylenetetrahydrofolate reductase (MTHFR) enzymatic activity and thus a diminished folate metabolism. While the T-mutation in its homozygous state is associated with numerous health problems, it is highly frequent in several populations through the world, thus suggesting a balanced polymorphism.

New ancient DNA (aDNA) work with European Neolithic samples indicates that light skin and lactase persistence in Europe evolved upon the adoption of agriculture as genetic adaptations to a diet lower in vitamin D (Olalde et al., 2014). Since solar radiation depletes folate, it is of interest to determine if the frequency of the T allele in European populations also changed in frequency upon the Neolithic. This project's purpose is to determine the presence and frequency of the C677T mutation in Western Europe before, during and after the Neolithic, using the aDNA of 341 individuals from 73 populations obtained from published sources.

The T allele has a low frequency in European hunters and gatherers (8001-1000 BC) regardless of location (,ÇÎ= 0.057, n=41). Early and middle Neolithic samples demonstrate an increase in frequency (,ÇÎ=0.17, n=71) while late Neolithic and fully committed agriculturalists have a mean frequency of ,ÇÎ = 0.17 n=229. We suggest that the selective force responsible for the increase for this allele manifested itself after the adoption of agriculture. We are not able to propose if the selective force is directly associated with UV radiation or to the change in diet that followed the Neolithic.

Biocultural perspectives on bioarchaeological and paleopathological evidence of past pandemics

MOLLY K. ZUCKERMAN[1,2], A G. TRIBBLE[3], RITA M. AUSTIN[4], TAYLOR EMERY[1] and CASSANDRA DEGAGLIA[1]

[1]Department of Anthropology and Middle Eastern Cultures, Mississippi State University, [2]Cobb Institute of Archaeology, Mississippi State University, [3]Department of Anthropology, Emory University, [4]Frontiers in Evolutionary Zoology Research Group, Natural History Museum, University of Oslo

While pandemics have exerted a tremendous influence on past and present-day societies, they have not yet constituted a major research focus within bioarchaeology and paleopathology, especially within explicitly biocultural analyses. Here, we survey relevant literature on pandemics in bioarchaeological and paleopathological literature, as well as historical demographic scholarship that employs biocultural approaches, sometimes integrated with intersectionality, ecosocial theory, and syndemic theory, in order to unpack relationships between social inequality and pandemics in the past. We conclude with a brief case study assessing the 1918 influenza pandemic's impacts on mortality within a socially vulnerable population: Patients at the Mississippi State Asylum (MSA), Jackson, MS (AD 1855-1935). Specifically, we analyze differential mortality from influenza relative to patient sex and social race amongst total patient deaths (N=3,697) in the MSA between 1912-1925. Preliminary findings show that influenza mortality rates were significantly elevated amongst young adults (20-39) in 1918-1919, as well as for male and Black patients relative to female and White patients. While the age- and sex-based patterns are broadly consistent with national and state-level trends, elevated mortality amongst Black patients likely reflects intersections between institutionalization, disability, racism, and race-based structural violence in the Jim Crow-era American South. As we demonstrate, future bioarchaeological, paleopathological, and historical demographic work on pandemics would benefit from explicit incorporation of biocultural frameworks, intersectionality, and ecosocial and syndemic theories. Such approaches enable holistic analyses of bidirectional interactions between social inequality and pandemics, with findings that can directly inform public health interventions and pandemic preparedness.