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shows that variation in *A. afarensis* is lower than that seen in African apes. Most facial features of *A. afarensis* are variably documented across individuals of different size and sex. For example, the average-sized A.L. 822-1 individual shows an overall facial morphology documented in the classic female *A. afarensis* but it also has a robust masticatory apparatus similar to larger, male individuals. In this regard, geometric morphometric analysis ($n = 356$) reveals that facial shape in average-sized individuals is similar to what is seen in larger males when size differences are standardized. Thus, our results suggest that patterns of variation across sex and size range and how that relates to the distribution of ancestral versus derived facial traits deserve further investigation in the light of expanded sample size. In sum, our study offers a new insight into the taxonomic significance of facial features and degree of variation in early hominins which are relevant to our understanding of their phylogeny.

This project is funded by the Wenner-Gren Foundation and the Biological Sciences Division Office of Inclusion and Diversity, The University of Chicago.

An Examination of NAGPRA within the Illinois Medicolegal System

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This paper presents preliminary findings related to compliance with the Native American Graves Protection and Repatriation Act (NAGPRA) [1] within Illinois medicolegal offices. Under NAGPRA, Indigenous Ancestors must be repatriated by all "museums," which has only recently been realized to include medical examiner and coroner (MEC) offices [2]. Illinois enacted the Human Skeletal Remains Protection Act (HSRPA) in 1989 [3], which states that a coroner must be contacted should any human skeletal remains be discovered on land within the state, including private land. The coroner must then reposit the remains to the Illinois State Museum should they be determined non-forensic. However, the present study's findings show only two inadvertent discoveries in Illinois deemed Indigenous Ancestors have a NAGPRA public notice on file. Furthermore, the National NAGPRA databases showed no evidence of plans for repatriation of Indigenous Ancestors in Illinois MEC offices. Especially in considering Illinois burial laws and the recent realization of national MEC NAGPRA noncompletion, the number of unrepatriated Indigenous Ancestors inadvertently discovered in Illinois is expected to be greatly underrepresented. These findings are discussed considering factors that may have contributed to these potential trends: 1) Ancestors in holdings/collections are not being repatriated in a timely manner [4]; 2) new inadvertent discoveries are not being reposit properly by medicolegal personnel and/or 3) Ancestors already stored in

medicolegal offices not being reported and having no plans for NAGPRA compliance [3]. The paper concludes by discussing next steps in identifying paths forward for the repatriation of Ancestors by Illinois MEC offices.

Market integration alters sleep-wake patterns among Malaysian Orang Asli

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Industrialized societies are experiencing a global epidemic of sleep disorders, in which extended lack of sleep has been associated with a number of adverse health effects. Because circadian rhythms are entrained to environmental exposure, studying sleep quality and quantity in a cross-cultural framework across environmental gradients is vital for understanding the global sleep epidemic. As part of the Orang Asli Health and Lifeways Project (OAHLP), we hypothesized that small-scale societies undergoing market integration experience disruption of circadian rhythms and extended sleep loss due to increased exposure to artificial lighting at night-time and a constructed environment. We deployed wearable accelerometers among two groups of Orang Asli (the Indigenous peoples of Peninsular Malaysia) experiencing different levels of market integration: peri-urban Temuan ($N = 9$), who live in government-built stone houses with electricity, and rural-living Temiar horticulturalists ($N = 12$), who live in traditional thatch housing without electricity. Temuan individuals displayed a shorter sleep duration (5 ± 1.7 -h) compared to the Temiar (7 ± 3.2 -h). Both groups displayed similar waking times, while the Temuan had more flexible sleep-wake patterns with a later sleep onset. The Temiar experienced a higher frequency of brief awakenings lasting more than 5-min during sleep. Our data suggest that market integration alters sleep-wake patterns due to artificial lighting and permanent housing. These results are consistent with the *circadian entrainment hypothesis*, which suggests that changes in the sleep ecology of industrialized societies can be attributed to circadian disruption.

National Science Foundation BCS-2142091

Ecology, Group Size, and The Evolution of Aggression in *Pan*

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Our two closest living relatives, chimpanzees (*Pan troglodytes*) and bonobos (*Pan paniscus*), differ in their aggressive behavior, especially in between-sex interactions with higher female-to-male but lower male-to-female rates of aggression in bonobos compared to chimpanzees. Researchers have proposed that bigger party size and different environmental conditions such as higher food quality, lower patchiness, and lower seasonality in bonobos compared to chimpanzees might have driven these differences. However, these hypotheses are difficult to test without comparable behavioral and environmental data on multiple populations. Thus, we used an agent-based model, B3GET, to simulate a "protoPan" population, which shares morphological and behavioral similarities with real-world bonobos and chimpanzees. In total, we ran 18 simulations for 30 to 60 generations with different starting environmental conditions (i.e., food quality, seasonality, patchiness) and recorded group sizes and aggressive interactions from 713 individuals. We found that group size was the strongest predictor of male-male (model average parameter estimate (MAPs) = 0.33; 95% CI [0.32, 0.34]) and female-male (MAPs = 0.54; 95% CI [0.32, 0.75]) aggression, supporting that bigger party size in bonobos compared to chimpanzees might have driven differential aggression patterns. Patchiness was the strongest variable for predicting male-female aggression (MAPs = -2.16; 95% CI [-2.28, -2.04]) and the second-best variable affecting other types of aggression, supporting the idea that higher patchiness decreases the rate of aggression. These findings indicate that group size and environmental conditions, including patchiness, might be key to explaining the differences observed in *Pan's* aggressive behavior.

Identifying growth plate specific genes using the unusual ossification of the mammalian metatarsal and pisiform

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Primates vary in skeletal proportions, and humans have uniquely shorted pisiforms. Both are the result of regulation of growth plate patterning. Genes regulating differential growth are generally unknown. We utilize normal variation in mammalian skeletal ossification to identify genes specific to growth plate patterning. Third metatarsals (MT3) form only a single distally placed

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growth plate, and the pisiform (in non-human mammals) is the only carpal to form a growth plate. We compared gene expression in distal versus proximal MT3s and pisiform versus other carpals; tissue pairs that control for the effects of age, systemic growth factors, and biomechanical environment. Using RNA-seq in 4- and 9-days old mice we identify numerous differentially expressed genes (DEGs). Gene ontology (GO) analysis revealed MT3 DEGs are disproportionately associated with limb development/growth and factors associated with the Fzd8-Ror2-Wnt5a pathway. Significant pisiform-carpal GO terms include skeletal and cartilage development and abnormalities of the wrist. We identified a limited set of DEGs shared by both the MT3 and pisiform-carpal comparisons, including *Wnt5a*. *Wnt5a* is expressed in the perichondrium and columnar/hypertrophic cell boundary in both the distal and proximal MT3. However, the related *Wnt10a* gene is strongly expressed in the distal but not proximal MT3 bone collar. This conforms with previously identified roles for Wnt genes in regulating osteogenesis and cell polarity within the growth plate and provides potential genetic targets that may harbor regulatory adaptations associated with the evolution of primate limb proportions and human pisiform reduction.

This work is supported by grants from the NSF IOS-1656315 & BCS-1638812.

Characterization of color vision variation in a group of wild *Ateles belzebuth* in Amazonian Ecuador

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Color vision among primates is remarkably diverse. Catarrhines and howler monkeys have independently acquired routine trichromacy through duplication of the middle-to-long-wavelength-sensitive (M/LWS) opsin gene on the X-chromosome. Most platyrrhines and some strepsirrhines, however, possess polymorphic color vision due to allelic variation at a single M/LWS locus; heterozygous females are trichromats, while males and homozygous females are dichromats. This variation allows the correlates of different color vision phenotypes to be evaluated within a single population. Yet such investigations are rare, and the selective advantages of individual phenotypes remain unclear. Previous studies have found that spider monkeys- a genus of large-bodied frugivorous platyrrhines- have two

possible opsin alleles determined by a SNP site in exon 5; in reconstituted pigments they have absorption spectra with peaks at 553 and 538 nm, respectively. Using fecal-extracted DNA, we sequenced exon 5 for 43 members of one social group of white-bellied spider monkeys (*Ateles belzebuth*) that has been monitored at Tiputini Biodiversity Station since 2005. We identified 13 male dichromats (six P553, seven P538), 10 female dichromats (eight P553, two P538), and 20 female trichromats (P553/P538). We then compared foraging activity for dichromat versus trichromat adult and subadult females, but found no differences in observations of feeding on major food types. Preliminary analyses likewise revealed no difference between dichromat and trichromat adult females in interbirth interval or number of offspring produced. Future work may assess other aspects of foraging behavior and fitness to better understand the maintenance of multiple color vision phenotypes in this population.

Funded, in part, by NSF BCS-1638822, the Harry Frank Guggenheim Foundation, the National Geographic Society, and The University of Texas at Austin.

Physical Effects of Castration on the Male Skeleton

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Castration was practiced on individuals assigned male at birth by many societies over the last 10,000 years for varying cultural and religious reasons. Castration was frequently performed between the ages of 6-10, but could also be done while an individual underwent puberty or after they finished puberty. While many studies have assessed the social effects of castration, with some discussion of soft tissue changes, few have examined the skeletal effects of castration. This paper combines original research on castrate skeletons with published studies of castrates to define the effects of castration on the growth, development, and maintenance of male skeletons. The majority of these effects are caused by deficits in both androgens (more plentiful on the male end of the sex spectrum) and estrogens (more plentiful on the female end of the sex spectrum) in the bodies of castrates. Due to the lack of both sets of hormones, those castrated before puberty grow and develop skeletons that take on very intermediate characteristics. These effects occur not only along the male-female sex spectrum, but also along the child-adult developmental spectrum. Those castrated during or after puberty take on some of these characteristics, but to a lesser extent than those castrated prepubertally. Understanding the skeletal changes caused by castration is useful not only for gaining a more holistic understanding of past individuals, but for

anticipating similar effects in present-day individuals whose hormones may be low or changing due to exogenous or endogenous factors, such as those who are intersex or transgender.

Sex-biased gene regulation varies across human populations as a result of adaptive evolution

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Gender disparities in health and disease are widespread, but their molecular underpinnings remain poorly understood. One mechanism affecting gender-specific disease phenotypes is sex-biased gene expression. Prevalent throughout both the autosome and sex chromosomes, sex-biased expression is known to vary by tissue, developmental stage, and disease context. Using RNA-Seq data and whole genome sequences from hundreds of individuals, we test whether humans exhibit variation in sex-biased gene expression across eleven human populations from diverse environments and evolutionary backgrounds. We find that sex-biased gene expression in humans is highly variable, mostly population-specific, and demonstrates between-population reversals. Expression quantitative trait locus (eQTL) mapping reveals sex-specific regulatory variants that show evidence of recent positive natural selection, suggesting that human have acquired population-specific sex differences in gene regulation through adaptive evolution. Our results indicate that sex-biased gene expression is more flexible than previously thought and may be influenced by environmental variation and the unique evolutionary histories of different populations. In an era of increasingly personalized medicine, this study highlights the importance of understanding population-level adaptation in functionally-relevant molecular pathways underlying gender disparities in health and disease.

This work was supported by a New Mexico-INBRE Award from the National Institute of General Medical Sciences (5P20GM103451) and staff at the National Center for Genome Resources.

Sleep In the Time of COVID-19: College Students Internal and Social Times are Better Aligned under Stay-at-Home Mandates

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Late chronotype, or preference to wake up and sleep in late, is prevalent in university students, but it is at odds with their morning social obligations like work and school. This misalignment between