

associated with bioenergetics and the need to meet requisite oxygen demands is thought to contribute to variation in nasal development and patterns of sexual dimorphism in recent humans. To further our understanding of the influence of energetics on nasal variation, we examined the ontogeny of sexual dimorphism in nasal shape using coordinate landmark data from lateral cephalograms and body size data from $n=20$ males and $n=18$ females between 3.0 and 20.0+ years of age. We first tested whether there are sex differences in nasal shape related to ontogenetic increases in body size. Additionally, we examined whether there are male-female differences in patterns of non-allometric variation in nasal shape. Next, we tested whether there are sex differences in the strength of integration between the nasal region and other aspects of the craniomandibular skeleton. While our results indicate a number of similarities in the nasal region between males and females, relative to body size, the male nasal cavity exhibits a disproportionate increase in height that is not present in the female sample. Moreover, the male nasal region is less integrated with the surrounding facial skeleton when compared to the female sample. These results are consistent with the hypothesis that sex differences in nasal development are associated with male-female differences in energetically relevant variables and suggest that larger systemic factors influence variation in facial form.

Genetic analyses of pre- and post-contact North American *Mycobacterium tuberculosis* complex strains

TANVI P. HONAP¹, ÅSHILD VÅGENE², ALEXANDER HERBIG², MICHAEL S. ROSENBERG¹, JANE E. BUIKSTRA³, KIRSTEN I. BOS², JOHANNES KRAUSE² and ANNE C. STONE³. ¹School of Life Sciences, Arizona State University, Tempe, AZ, USA, ²Max Planck Institute for the Science of Human History, Jena, Germany, ³School of Human Evolution and Social Change, Arizona State University, Tempe, AZ, USA.

The origins of tuberculosis (TB) in the New World have long been a topic of debate. Ample skeletal evidence for TB is present in the pre-contact New World. Currently, New World TB is caused by *Mycobacterium tuberculosis* complex (MTBC) strains of European origin, suggesting that pre-existing MTBC strains were replaced following European contact. Previous research from our group led to the recovery of three 1000-year old MTBC genomes from skeletal TB cases from coastal Peru; these ancient Peruvian MTBC strains are closely related to MTBC strains found in pinnipeds. However, it remains unknown whether such pinniped-derived MTBC strains spread to the inland parts of South America as well as North America by human-to-human transmission. The present work focuses on skeletal TB cases ($n=13$) from pre-contact, protohistoric, and historic sites from Alaska. DNA was extracted using a silica-based method

and tested for presence of MTBC DNA using quantitative PCR (qPCR) assays. Eight DNA extracts tested positive for a region of the *rpoB* gene specific to the MTBC and nine extracts tested positive for the IS6110 repeat element. In-solution target enrichment and sequencing of MTBC-specific genes is underway for these samples, as well as for samples from other pre- and post-contact sites from the Americas. Such analyses will help determine coverage as well as authenticate the presence of ancient DNA. Additionally, samples that test positive are being enriched for the entire MTBC genome using an array-capture method and then sequenced. Analyses of these genomic data are currently ongoing.

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Human males have low reproductive skew compared to other mammals: An analysis of new data from small-scale human societies

PAUL L. HOOPER¹, CODY ROSS², SERGEY GAVRILETS³ and MONIQUE BORGERHOFF MULDER². ¹Anthropology, Emory University, ²Anthropology, University of California Davis, ³Ecology and Evolutionary Biology, University of Tennessee.

To what extent are human patterns of reproduction typical or atypical compared to other mammals? In this presentation, we give an answer to this question focusing on one aspect of reproduction: reproductive skew, or the degree of inequality in reproductive outcomes within a population. We draw on a new cross-cultural dataset to provide estimates of reproductive skew for each sex in small-scale human societies, including hunter-gatherers, horticulturalists, pastoralists, and agriculturalists prior to the demographic transition to low fertility. We compare these values to estimates of reproductive skew for a variety of non-human mammals. The results indicate that while reproductive skew among human females falls within the expected range for non-human mammals, reproductive skew among human males is substantially lower than expected compared to non-human mammals. We hypothesize that the remarkably low levels of skew among human men are due to the high frequency of monogamous pair-bonding and paternal investment observed small-scale human societies. This talk also introduces a new method for measuring skew that overcomes weaknesses of previous methods.

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Building ancient noses: a functional approach to paleogenomic data

KARA C. HOOVER.
Anthropology/Biochemistry & Molecular Biology, University of Alaska Fairbanks.

Taste and smell (chemosensing) are the first senses to evolve. Smell has an intricate and complex neuronal structure which reflects the dynamic interaction among genes, biology, environment, and perception. Olfactory science is emerging as a multi-disciplinary field aimed at understanding these interacting elements. A key area of interest is the link between genes that allow detection of odors (and create an olfactory repertoire) and how this might influence food choice. Taken in the broader evolutionary hominin context of human olfaction, our aim was to determine if novel variants in the paleogenomes of Altai Neandertal and Denisova resulted in distinct olfactory repertoires. Identifying variation in olfactory repertoires within a comparative evolutionary frame advances knowledge on hominin dietary evolution and evolutionary ecology. Traditional approaches to inferring gene function in extinct species have relied on computational methods. We introduce a transformative and novel approach that allows reconstruction of hominin olfactory receptors from paleogenomic data and experimental validation of their functional responses to odorants. Results include: 1) catalog of variants in paleogenomic sequence data using a custom bioinformatics pipeline; 2) creation of ancient hominin olfactory receptors using overlap extension PCR; 3) experimental validation of functional variant impact on odorant response in ancient hominin olfactory receptors.

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Polyspecific associations of red uakaris in northeastern Peru

ROSE M. HORES and SUSAN M. FORD.
Department of Anthropology, Southern Illinois University.

Red uakaris (*Cacajao calvus ucayalii*) remain one of the least studied Neotropical primates. They are restricted to northeastern Peru and have extremely large home and day ranges. They are known for their extremely fluid social system, able to change in size and composition nearly hourly. Red uakaris have been reported to form polyspecific associations (PSAs) with other primates.

As part of a larger project on primate community ecology within a mosaic landscape, we report data on the occurrence of PSAs as red uakaris navigate through varying habitat types. The study took place at the Tahuayo River Amazon Research Center (TRARC) in northeastern Peru (September 2012-February 2014). The mosaic landscape of the TRARC is home to 12 primate species, including the red uakari. We tested the hypothesis that red uakaris