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ABSTRACTS

extinct. Other teeth are tentatively identified as belonging to cf. *Eoviscaccia* that ranges from Early Oligocene to Early Miocene in Chile, Bolivia, and Argentina, but is absent from the middle Miocene in either Colombia or Bolivia.

NSF EAR 1338694 to PAB & RFK, National Geographic Society Young Explorer's Grant 9920-16 to WS, National Geographic Waitt Grant to RFK.

2D- and 3D-Micromorphological Cutmark Analyses

ARYSA GONZALEZ R.¹, CHRISTOPHER W. SCHMIDT¹ and BRIANA POBINER²

¹Anthropology, University of Indianapolis, ²Anthropology, Smithsonian Institution

Identifying tool types by analyzing cutmark profiles is a promising methodology for understanding cutmark variables. Previously, cutmark analyses relied on optical and SEM microscopy and were largely restricted to gross observations of magnified cutmark morphology. The application of a white-light confocal profiler (WLCP) allows for the creation of 2D and 3D surface reconstructions based on detailed topographic studies. Two- and three-dimensional parameters such as surface area (μm^2), volume (μm^3), depth (µm), slope, and angle can be used to distinguish cutmarks made with different types of tools. The current study seeks to refine recently established WLCP cutmark analysis methods by attempting to distinguish experimentally-created cutmarks. Cutmarks (n=51) were generated on deer long bones with worked flakes made from three different stone raw materials (basalt, chert, and obsidian) as well as steel knives. Emphasis was on 2D variables from profiles taken at or near cutmark midpoints. Cut width, depth, angle, and slope successfully distinguished steel and stone tools (ANOVA, p = < 0.001). Among the stone tools, discriminant function analysis determined that 94.1% of the cutmarks could be correctly classified as either stone or steel. Stone cutmarks were correctly classified 91.7% of the time as either basalt or chert/obsidian. The results support white-light confocal profilometry as a useful means of cutmark analysis. We anticipate that further refinement will generate methods that can be reliably applied to bones from archaeological contexts.

The evolution of human facial sexual dimorphism

TOMAS GONZALEZ¹, JULIE WHITE¹, ARSLAN ZAIDI², PETER CLAES³ and MARK D. SHRIVER¹

¹Anthropology, Pennsylvania State University, ²Department of Biology, Pennsylvania State University, ³ESAT/PSI, KU Leuven

Modern human facial variation is integral to social and ecological interactions and can yield important insights into recent human evolution. One important aspect of facial variation, critical to consider in terms of facial evolution, is sexual dimorphism. We tested whether human populations show differences in patterns of facial sexual dimorphism (FSD), that is, whether there are differences in the morphological regions that change as a product of sex. Such differences could indicate differential pressures of sexual selection across human populations. Briefly, we applied a geometric morphometrics approach utilizing a dense mesh of 6,790 guasi-landmarks (OLs) to 3D facial scans from 3.646 participants of various ancestries. Populations were defined by comparison to the 1000G Phase 3 reference using ~10,000 single nucleotide polymorphisms. We used Principal Component Analysis on the superimposed QLs to reduce the number of variables, and to summarize facial shape changes. We defined FSD as a vector estimated by the difference between female and male average PC coordinates. Moreover, we decomposed FSD into allometric and non-allometric components using height as proxy for size. Comparing patterns of FSD across populations, we found that African and East Asian populations show a similar pattern of FSD, while South Asian, Indigenous American, and European are similar to each other (significant p-values<0.05, 10,000 permutations). We discuss our findings in light of recent human evolution and admixture.

T.G. is funded by BecasChile

How epidemics devastated the indigenous people of the Americas

ROLANDO GONZALEZ-JOSE and VIRGINIA RAMALLO

Instituto Patagónico de Ciencias Sociales y Humanas, CENPAT-CONICET

There is growing consensus around the idea that much of our understanding on the causality of genetic plus environmentally based diseases and other complex phenotypes including susceptibility and/or resistance to pathogens is to be deciphered by exploring the fine-scale study of human genetic variation. When extrapolating this idea to the native populations, the challenge is greater due to the remarkable genetic variation that scientists have found within several regions of the Americas. After Columbus' landing in the Americas, the populations of the American continent experienced a precipitous decline. Even though the spread of pathogens of European origin across nonimmune Native American is suspected to be responsible for a great proportion of the post-contact mortality, the situation cannot be extrapolated straightforwardly to all the New World populations. In fact, the local genetic, environmental, and cultural particularities of the contact need to be considered in order to achieve a more sophisticated picture. Here I present some recurrent patterns regarding how epidemics devastated the indigenous people of the Americas. Specifically, I will focus on

pattern similarities among the population decline of the Chumash (California) and Fueguians (Patagonia). A statistical comparison indicates that decimation coincides with mission establishment. The concomitant increase in number of baptisms is almost-synchronically followed by a 15%/year of increasing in mortality each year, indicating a strong effect of density changes as a trigger to epidemic disease impact. Furthermore, I will discuss genetic and non-genetic factors that potentially generated deviations from the expected patterns of mortality due to infectious diseases.

A comparative growth study between children from the medieval Islamic and medieval late Christian Periods in Santarém, Portugal

ELLIE GOODERHAM¹, ANTONIO MATIAS², SARAH WALSHAW³, JOHN ALBANESE⁴ and HUGO F.V. CARDOSO¹

¹Archaeology and Centre for Forensic Research, Simon Fraser University, ²Câmara Municipal, Santarém, ³History, Simon Fraser University, ⁴Sociology, Anthropology, and Criminology, University of Windsor

Growth stunting and higher frequencies of skeletal indicators of stress in children are associated with disadvantaged or stressed populations. This study examines differences in long bone growth between two juvenile samples from Santarém, Portugal, from the 8th to 17th centuries AD. The earlier sample (n=24) spans the period of Islamic rule (8th-12th centuries AD) during which time, the Iberian Peninsula experienced occupation but also a period of enlightenment associated with the Golden Age of Islam. The later sample (n=17) spans the post-Islamic medieval Christian Period (13th-17th centuries AD) and was thought to have different secular and social practices, which could impact population health, through a variety of means, including diet, medicine, and hygiene. Long bone length-for-age plots were calculated for the humerus, radius, femur, and tibia and were compared with Maresh's reference data. Age specific z-scores for bone length were also calculated and the sample z-score means compared. The medieval Christian children were always smaller (mean z-score varied between -1.19 and -3.05) than the medieval Islamic children (mean z-score varied between -0.97 and -1.54) but the differences were not statistically significant. When examining both the Islamic and Christian samples in more detail by grouping the samples by historical context within a period, significant variation in z-score means were observed and seemed to reflect the internal dynamics of these two periods. This research indicates that analyzing each population as a whole might mask a more complex narrative when examining