Mexican populations, in agreement with previous findings of IBD sharing between present-day Mayas and present-day indigenous groups from Central-East Mexico, like the Totonacs.

Integration of the hominoid spine, part I: Shoulder function and integration of the cervical and thoracic vertebrae

CATALINA I. VILLAMIL[1] and EMILY R. MIDDLETON[2]

[1]School of Chiropractic, Universidad Central del Caribe, [2]Dept. of Anthropology, University of Wisconsin-Milwaukee

Shoulder anatomy has evolved substantially in hominins relative to other hominoids, and these anatomical changes have been linked to the loss of locomotor function in the shoulder and to the increase in manipulative activities in hominins. Importantly, the evolution of modern human-like shoulder morphology likely enabled high speed, high accuracy throwing, which is used for hunting. Many of the muscles involved in shoulder function attach to the vertebral column, and shifts in shoulder anatomy and function would have inevitably impacted relationships between muscles and vertebrae, as well as the potential evolutionary trajectories of the cervical and thoracic vertebrae. This study aims to clarify how shoulder evolution may be linked to the evolution of the cervicothoracic regions by investigating integration of these regions in *Homo* (N=151), *Pan* (N=92), and *Hylobates* (N=77). Four variables were calculated for vertebrae C3 through T12 and their paired relationships: VE, mean integration, mean evolvability, and mean conditional evolvability. Results show that *Homo* tends to display the highest evolvability and conditional evolvability, while *Pan* is intermediate, and *Hylobates* is the lowest. *Hylobates* has greater integration between the lower cervicals and thoracics than the other taxa, and *Pan* is intermediate in overall integration between *Hylobates* and *Homo*. These results are consistent with the hypothesis that the locomotor function of the hominoid shoulder significantly constrains the evolution of the cervicothoracic region and suggest that shoulder morphologies associated with swinging and climbing may result in significantly more constraints in non-human hominoids and a *Pan*-like hominin ancestor than in *Homo*.

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ABO blood type variation in archaic humans: haplotype structure in Neanderthals and Denisovans

FERNANDO A. VILLANEA[1], KEOLU FOX[2] and EMILIA HUERTA-SÁNCHEZ[1]

[1]Center for Computational Molecular Biology, Brown University, [2]Department of Anthropology, UC San Diego

Genetic variation of the ABO gene is well characterized in modern humans, corresponding to phenotype variation observed globally in ABO blood types. However, little attention has been paid to ABO blood type variants in our archaic relatives: neanderthals and denisovans. Here, we analyze coding variation at the ABO locus from next-generation sequencing in ~2,500 individuals from 28 populations, including two neanderthal and one denisovan individuals. Our analysis validates previous estimates of ABO blood type frequencies in living populations. We then use the modern human haplotypes to impute ABO genotypes for the three archaic human genomes. We found that the Altai neanderthal is homozygous for a derived neanderthal variant of the O allele, while the Vindija neanderthal is an AO heterozygote, the A allele is a derived neanderthal variant, and the O allele is an ancestral variant shared with modern human populations. The denisovan individual is homozygous for an ancestral variant of the O allele, also shared widely with modern humans. Perhaps more surprisingly, the O allele variant found in the Altai neanderthal is also found at very low frequencies in modern European and Southeast Asian individuals, and our genetic distance analysis suggests this allele was introgressed through neanderthal-human gene flow. Our study explores the genetic variation of the ABO gene in two extinct archaic human populations, and highlights how neanderthal-specific ABO variants were inherited by modern humans, which are still retained in observable frequencies today.

New Pliocene hominin specimens from East Turkana are associated with extensive C_4 resources

AMELIA VILLASEÑOR[1], DAVID R. BRAUN[2], KEVIN UNO[3], ELDERT ADVOKAAT[4], MARION BAMFORD[5], ANNA K. BEHRENSMEYER[6], BOBE RENÉ[7], CARVALHO SUSANA[8], HAMMOND S. ASHLEY[9], KINYANJUI RAHAB[10], DAN V. PALCU[11], MARK SIER[12] and CAROL V. WARD[13]

[1]Department of Anthropology, University of Arkansas, [2]Center for the Advanced Study of Human Paleobiology, The George Washington University, [3]Lamont-Doherty Earth Observatory, Columbia University, [4]Department of Physical Geography, Utrecht University, [5]Evolutionary Studies Institute, University of the Witwatersrand, [6]Department of Paleobiology, National Museum of Natural History, [7]Gorongosa, Gorongosa National Park, [8]Institute for Cognitive and Evolutionary Anthropology, Oxford University, [9]Division of Anthropology, American Museum of Natural History, [10]Department of Earth Sciences, National Museums of Kenya, [11]Department of Physical Oceanography and Geochemistry, University of Sao Paulo, [12]Department of Earth Sciences, University of Oxford, [13]Department of Pathology and Anatomical Sciences, University of Missouri

The mid-Pliocene corresponds to a peak in hominin diversity. Two species, *Australopithecus afarensis* and *Kenyanthropus platyops*, are known from the Turkana Basin region after 3.44 million years ago (Ma). Here, we describe four hominin specimens, the first occurrences from East Turkana between 3.9 and 3.44 Ma, and the paleoecological evidence from the associated faunal community and paleovegetation proxies. Existing geochronology and paleomagnetic analysis of sediments constrain the age of these specimens from 3.55-3.44 Ma. Stable carbon isotopes from pedogenic carbonates (n=50) indicate that East Turkana was less wooded than concurrent habitats in the Nachukui and Hadar Formations, though there is no difference in mean ⊠ùõÕ^{13}C values. When converted to percent C_4 values, pedogenic carbonates suggest that C_4 abundance was less than 50% (median 28%). In contrast, stable carbon isotopes from leaf wax biomarkers (n=14) show C_4 abundance up to 97% (median 51%). Mammal abundance associated with the hominin fossils includes primarily alcelaphin bovids, as well as a greater proportion of small cercopithecine primates compared to the whole East Turkana region. Stable carbon isotopes from mammal enamel (n=45) show that many large herbivores had a mixed C_3/C_4 diet dominated by C_4 resources (median 60%). These data suggest that mid-Pliocene hominins in East Turkana were associated with environments that supported extensive C_4 resources and a diverse primate community. Our findings suggest that multiple paleoecological proxies are necessary to demonstrate a cohesive picture of the paleoecosystem at fossil sites.

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Testing repeatability in dental morphology: Interobserver error in a worldwide collection

TATIANA VLEMINCQ-MENDIETA[1], LAURA E. CIRILLO[1] and DOROTHY DECHANT[2]

[1]Anthropology, University of Nevada, Reno, [2]Center for Dental History and Craniofacial Study, AA Dugoni School of Dentistry, University of the Pacific

Despite the standardization of dental morphology (Turner et al., 1991; Edgar, 2017; Scott and Irish, 2017) and its broad use in biological anthropology, very few publications have evaluated the levels of interobserver error inherent in these data. This study identifies levels of error across several traits. Using the Arizona State University Dental Anthropology System definitions (Scott and Irish, 2017), three observers scored 17 traits on 20 skulls found in the Atkinson Collection housed at the University of the Pacific AA Dugoni School of