Lipid metabolism and nutritive factors of the gut microbiota in human foragers

STEPHANIE L. SCHNORR[1,2], AMANDA G. HENRY[1] and ALYSSA N. CRITTENDEN[3]. [1]Plant Foods in Hominin Dietary Ecology Research Group, Max Planck Institute for Evolutionary Anthropology, [2]Department of Anthropology, University of Oklahoma, [3]Metabolism, Anthropometry, and Nutrition Laboratory, Department of Anthropology, University of Nevada, Las Vegas.

Lipid metabolism in bacteria is considered an important process both for energy production and cellular growth and maintenance. Lipids are rich in carbon and therefore are a rich sources of energy, which is especially critical to human forager nutrition. Significant focus on microbial metabolism of carbohydrates has earned us much insight to microbe-host mutualism. However, the role of lipid manufacture and processing in microbiota as it relates to host diet and health is by comparison less well understood. Here we contribute a focused analysis of the lipid metabolic profiles from gut microbiome communities in different human foragers, as well as other animals from different dietary niches. Shot-gun metagenomic sequences of the gut microbiome from two forager groups, the Hadza of Tanzania and the Matses from the Peruvian Amazon, were downloaded from public archives and compared to Western individuals from Europe and the US. A manually assembled database of protein families associated with lipid metabolism was used to target correspondent sequences among assembled microbial sequences. This conservative profiling of the lipid metabolic pathways illustrates interesting differences in gene abundance, especially for degradation pathways. This is suggestive of a dietary vector of influence, and we use other animal dietary specialists to make comparative models. Lipid pathways in human forager microbiota cluster more closely with that of herbivores, potentially due to a similar ability of the microbiota to harvest and convert phospholipids from fibrous plants that are passing into the colon. Importantly, this could supply nutritive fatty acids to the human host.

Brain function and Broca's Cap: A meta-analysis of fMRI studies

P. THOMAS SCHOENEMANN[1] and RALPH L. HOLLOWAY[2]. [1]Cognitive Science and Anthropology, Indiana University, [2]Anthropology, Columbia University.

The possibility of tracking the evolution of language using hominin fossil endocasts has long been of great interest. Because important aspects of language production are localized to the left hemisphere - in particular Broca's region - in most modern human brains, and because anatomical asymmetries favoring the left side have been documented for modern humans but not apes, there has been a keen interest in endocranial morphology overlying this region. Qualitative assessment of hominin fossil endocasts by Holloway et al. (2004) suggests a more pronounced Broca's Cap on the left side compared to the right in most specimens. However, Broca's Cap on an endocast overlays a brain region that is somewhat inferior to Broca's Region. This raises the question of whether asymmetry of Broca's Cap on endocasts is actually relevant to language.

The present study assesses the function of the cortex specifically underlying Broca's Cap on the endocranial surface (distinct from Broca's Region) using a meta-analysis of fMRI studies from neurosynth.org (11406 studies in total). A brain activation map summarizing the areas activated in studies for which the word "language" occurs in high frequency clearly includes cortical areas directly underlying Broca's Cap. In addition, 9 of the 13 (69%) of the top function words reported in studies with activation in the left Broca's Cap cortical region specifically refer to aspects of language, compared to only 1 of 6 (33%) for the right. These findings strongly suggest that Broca's Cap asymmetries are likely to be relevant to the evolution of language.

Variation in the $\delta^{18}O$ record of Allia Bay, Kenya hippopotamidae

MARGARET J. SCHOENINGER[1], MELANIE M. BEASLEY[1], IAN J. ORLAND[2] and JOHN W. VALLEY[2]. [1]Anthropology, University of California at San Diego, [2]Geoscience, University of Wisconsin, Madison.

The ecological niche exploited by early hominins is assumed to have played an essential role in the origins of our lineage and of bipedalism, a distinguishing characteristic. We focus on one aspect of the paleoenvironment at the early hominin site of Allia Bay, Kenya (3.97±0.03 Ma). This poster highlights variation in the oxygen isotope ratios of fossil faunal tooth enamel ($\delta^{18}O_{en}$) within one single family, the hippopotamidae. We reconstruct seasonal rainfall patterns using a secondary ion mass spectrometer (SIMS) to generate high-resolution $\delta^{18}O_{en}$ values.

The hippopotamidae, whose closest living relatives are the cetaceans, is composed of fossil and extant water-dependent species, such as today's common and pygmy hippopotamus. Similar to extant water-dependent species, we expect the $\delta^{18}O_{en}$ values in the Allia Bay hippopotamidae to track variation in precipitation patterns. The fossil enamel analyzed in this study dates to a fluvial phase of the Omo River within the Turkana Basin of northern Kenya. The river, which originates in the Ethiopian Highlands, provided the most important water source for the fossil fauna at Allia Bay. Intra-tooth variation is only 1.4‰, which indicates relatively little seasonal variation in rainfall amounts during the time of enamel deposition. There is, however, a 7.5‰ difference between individual animals. This large difference might be due to 1) two species of hippopotamidae with different adaptations (e.g., body water from food vs surface water) or 2) a change in the amount and/or pattern of rainfall during the time represented at the site (3.97±0.03 Ma).

Wenner Gren Foundation

Socializing Violence: Interpersonal Violence Recidivism at Abu Fatima (Sudan)

SARAH SCHRADER. Dept. of Anthropology, University of California, Santa Cruz.

Recent excavations at Abu Fatima, Sudan, have uncovered a Kerma Period cemetery that was in use from ~2,500-1,500 BCE. During this period the Kushite State, centered at the capital city of Kerma (5km from Abu Fatima), emerged as a major player in Near Eastern politics. A total of nine individuals were excavated during a pilot study (February-March, 2015). Of the seven adults in this sample, six display indicators of interpersonal violence (sharp force trauma, blunt force trauma, broken nasals, broken hands, stab wound to the sternum). Furthermore, four of these individuals have multiple injuries that appear to be at various stages of healing; we can infer that these individuals likely experienced several episodes of interpersonal conflict throughout their lifetimes.

This poster examines the diachronic trends of interpersonal recidivistic violence in this pilot sample. The prevalence of interpersonal violent injury in this small sample is marked and speaks to the possibility of a socially sanctioned form of interpersonal violence. Due to the low sample size, definitive conclusions cannot be made at this time. However, continued excavations (January-March 2016) will elucidate the interesting context of Abu Fatima.

This research was supported by the National Science Foundation, grants #BCS-1359210 and #BCS-1359496

A preliminary examination of genetic diversity in mantled howler monkeys (*Alouatta palliata)* in a fragmented forest in Costa Rica

AMY L. SCHREIER[1], MARIE-DOMINIQUE FRANCO[1], MATTHEW BARTON[1], NATHANIEL P. PRYOR[1] and NANCY L. BARRICKMAN[2]. [1]Department of Biology, Regis University, [2]Department of Biology, Salt Lake Community College.

Dispersal from one's natal group reduces inbreeding. Habitat fragmentation may limit primates' dispersal opportunities, however, which has implications for species survival. We examined the influence of fragmentation on genetic diversity in wild mantled howler monkeys (*Alouatta palliata*) at La Suerte, Costa Rica. The La Suerte region has seen increased