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## Migrating Genes: Using aDNA and Archaeological Data to Explain Migration in the Casas Grandes Region of Northern Mexico

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## Elemental evidence for birth in primate tooth enamel

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In 2013 we presented a model for identifying the initiation and cessation of nursing in primate teeth based on changes in the non-essential trace element barium. This drew upon on a study of human physiology; average barium values were seven times higher in colostrum than umbilical cord blood, indicating that barium is enriched in mother's milk relative to fetal supply. Consistent with this, we found that human deciduous teeth (n = 22/25) and macaque M1s (n = 4/4) showed a marked barium increase in close association with the neonatal line, a microscopic feature formed at birth and visible in sectioned enamel. Here we compare pre- and postnatal trends in barium, lead, lithium, strontium, and zinc, as they can each show developmental patterning in teeth. Barium remains the most consistent biomarker of milk: > 70% of M1 cusps (n = 24) show the expected increase from prenatal to postnatal enamel. Exceptions occurred in cusps that had been mineralizing for less than three weeks, showed heavy wear, and/or were derived from bottle-reared monkeys. Only a third of our sample showed postnatal increases in lead and zinc, also reported to be highly enriched in colostrum. In contrast, strontium decreased or remained steady across the neonatal line, as did lithium, suggested limited utility for tracking changes in milk consumption. Research is needed to parse out anthropogenic and natural bioavailable sources of these elements; this would help contextualize substantial variation in absolute values that characterize contemporary humans and nonhuman primates from captive and wild environments.

This work was funded by the Australian Academy of Science, Griffith University, Harvard University, and the Icahn School of Medicine at Mount Sinai.

# A comparison of diceCT and histology for determination of nasal epithelial type

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Diffusible iodine-based contrast-enhanced computed tomography (diceCT) is a potential tool for discriminating soft tissues in serial CT slices, which can then be used for three-dimensional analysis. With increasingly fine scan resolution, diceCT has the potential to supplant histology in some cases as a tool for identification of body tissues. Here, we studied the head of a fruit bat (Cynopterus sphinx) using micro-diceCT. Subsequently, we decalcified, serially sectioned and stained the same head. The diceCT volume was rotated so that the sectional plane of the slice series closely matched that of histological sections. One investigator (HC), blind to the histological sections, examined the diceCT slice series and annotated changes in thickness of epithelium lining the first ethmoturbinal and the roof the nasal fossa and nasal septum. Then, a second investigator (TS) annotated images of matching histological sections based on microscopic observation of epithelial type. Measurements of epithelial perimeter using ImageJ revealed a close match between methods. DiceCT conformed to a gradually increasing perimeter of thicker epithelium as the slice series progresses from rostral to caudal; matching histological sections confirm this to be olfactory epithelium. Only one patch of unusually thick non-olfactory epithelium was annotated in diceCT series. Our results demonstrate that diceCT is, as vet, only a match for histology at low magnifications. However, diceCT slices offer a valuable tool to annotate changes in epithelial thickness. In combination with histology from a representative specimen of the same species, diceCT is highly effective in identifying distribution of olfactory epithelium.

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### Climate change and health among Indigenous Siberians

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Arctic and subarctic regions are experiencing profound environmental shifts as the result of global climate change. This has led to long-term shifts in temperature, reductions in permafrost, and glacial and sea ice melting. The present paper systematically reviews the health effects of climate change on contemporary Indigenous Siberian populations, with particular attention to the effects of altered ecology, shifting access to traditional foods, and changes to the burden of infectious/parasitic diseases. Indigenous Siberian populations, like other northern populations, are extremely vulnerable to the effects of climate change as these populations are experiencing rapid economic development and the effects of marginalization and pollution. Furthermore, Indigenous Siberians show overall poor health compared to other Arctic populations, and also pronounced health disparities compared to non-native Russians. Key issues related to climate change in northern Russia include: shifts in weather patterns and ecological conditions; threats to coastal communities from higher sea level; altered access to traditional lands and foods;

disturbances to psychological well-being based on disruption of traditional lifeways; increases in infectious disease burden; and, northern range expansion of parasitic zoonoses. Results of this review indicate that climate change has already altered Indigenous Siberia lifeways and health. Indigenous Siberian populations are serving as bellwethers of global climate change.

### Using aDNA and Archaeological Data to Explain Migration in the Casas Grandes Region of Northern Mexico

MERADETH SNOW<sup>1</sup> and MICHAEL SEARCY<sup>2</sup> <sup>1</sup>Anthropology, University of Montana, <sup>2</sup>Anthropology, Brigham Young University

Migration as an archaeological topic has addressed huge distances, such as the colonization of the Americas, as well as smaller regions. such as the peopling of specific sites. The use of genetics as a medium to enhance our understanding of population movement can be an asset. There are potential pitfalls, however, such as the misrepresentation of DNA ranging across the landscape without human vectors or motivations. Genetic data must be interpreted through the lens of all available data from the site and surrounding region in order to understand how it fits into the potential for human migration. These ideas will be presented with mitogenome data accumulated from the site of Paguimé in Casas Grandes, Mexico, which has long been tied to hypotheses of migration from the south and north. How such migrations could be identified genetically and fit into the larger understanding of the site will be discussed, particularly in respect to the cultural transformation and fluorescence that marks the transition from the Viejo to Medio periods. While mitogenome data points to in situ population growth, our genetic evidence aligns with the archaeological record that individuals were migrating into the region from both the north and south. Our data points to the potential of individuals being brought to the site from elsewhere in what is now Mexico for sacrificial purposes, as well as regional migrants attracted to the site for reasons that may be associated with other cultural factors.

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### Strontium Isotope Analysis Indicates Restricted Mobility among Early Foragers in the High Andes

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Extreme high-altitude environments were some of the final frontiers of human habitation. Recent research shows that the Andean highlands were permanently inhabited beginning around 9000