QUANTIFYING BONE WEATHERING STAGES USING RA, A SURFACE ROUGHNESS PARAMETER MEASURED FROM 3D DATA

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Bone surface texture is known to degrade in a predicable fashion due to subaerial exposure, and can thus act as a relative proxy for estimating post-death/ pre-burial temporal intervals, which is relevant information for assessing time-averaging. To date, the majority of bone weathering data is collected on an ordinal scale based on observation. While this qualitative classification of weathering data is well established and quite successful, 3D surface analyses may provide means to quantify weathering stages. Here I test if different weathering stages are characterized by statistically distinct surface textures. Results indicate that the surface roughness parameter Ra, which is the average distance of valleys and peaks from the mean line of surface profiles measured from 3D scans, can quantitatively distinguish bone weathering stages from rib surfaces. I first determined the natural variation of fresh rib surface textures by measuring the Ra from several locations on 80 unweathered ribs belonging to 4 mammal groups that weigh over 20kg (Equidae, Camelidae, Suidae, Cervidae). I found that all ribs are statistically similar when compared using paired Student's t-test at a 0.05 significance threshold (Ra = 2.7 µm ± 0.08 µm). The dorsal and ventral portion of the rib are statistically different from the rest of the rib bone (Ra= 4.30 ± 0.22 µm) likely due to a more rugose bone texture related to tissue connectivity. After establishing natural bone texture variation, I measured Ra values from 30 weathered ribs, excluding rib heads and terminations. These same elements were also assigned a qualitative weathering stage. Paired Student's t-tests at a 0.05 confidence level indicate that each ordinal weathering stage is statistically distinguishable. Mean Ra values for each weathering stage are as follows: Stage 1= 4.47µm ± 0.76µm, Stage 2= 6.82µm ± 0.76µm, Stage 3=13.78µm ± 0.88µm, and Stage 4=22.26µm ± 0.9µm. To date, this has only been applied to large mammal ribs; however, investigations are underway to determine fresh surface texture variance of other bone types and other vertebrate groups, and the plan is to expand this work by analyzing additional weathered bones previously classified using the ordinal scale with this new technique. In conclusion, my results indicate that rib surface texture is similar across large mammal taxa and can thus be used for comparative bone weathering analyses. Using Ra to measure bone weathering characteristics may enable more reliable comparative taphonomic analyses by reducing inter-observer variations and by providing numerical data compatible for use in multivariate statistics.

A TALE OF TWO BASINS: COMMUNITY STRUCTURE DYNAMICS THROUGH SPACE AND TIME IN THE HADAR AND TURKANA BASINS, ETHIOPIA AND KENYA

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Australopithecus afarensis has a dense and geographically widespread fossil record that spans nearly 700,000 years. This taxon has been found in heterogeneous environments and generally does not show a preference for any habitat type (open grassland, woodlands, bushlands etc.). Analyses of dental microwear suggest that during its history the material properties of the foods eaten by *A. afarensis* did not change. To understand the context in which *A. afarensis* successfully avoided major adaptive change through time, this project explores the question of stability in the community structure within *A. afarensis* localities through time and space. To reconstruct these communities, guild structure was compared in localities where *A. afarensis* has been recovered. Mammalian genera (>1 kg) were categorized into guilds based on broad dietary, locomotor, and size classes (defined in the Evolution of Terrestrial Ecosystems Database). To compare guild structure across space, the proportion of guilds from the Sidi Hakoma Member in the Hadar Formation, Ethiopia (n=62 genera) were compared to the proportion of guilds in the Tulu Bor Member of the Koobi Fora Formation (n=19 genera) in East Turkana, Kenya, both dated to ~3.4 Ma. Guild structure was compared between all geological members of the Hadar Formation (the Basal (n=31), Sidi Hakoma (n=94), Denen Dora (n=105) and Kada Hadar Members (n=83)) to examine change through time (3.4–2.95 Ma). A chi-squared test was used to determine whether guild structure was significantly different between pairs of geological members. No differences exist between geological members through time at Hadar, despite a trend toward the environment becoming more arid and seasonal. Significant differences were found across space, however, in that the lower Sidi Hakoma Member was significantly different in guild structure from the lower Tulu Bor Member (0.02 > *p* > 0.01). This study differs from other paleoecological studies by focusing on community dynamics rather than habitat reconstruction. The results of this study highlight the fact that *A. afarensis* is found preferentially within the Hadar Formation as contrasted to the Koobi Fora Formation, possibly due to the environments that were present within the Hadar Formation. Further, these findings suggest that community structure within the Hadar Formation remained stable through time despite environmental change, suggesting a long period of coordinated stasis throughout the Hadar Formation. Future studies will seek to evaluate the mechanisms that allowed this ecological stability within the Afar basin, as well as where *A. afarensis* may have fit within the guild structure.

USING STABLE ISOTOPES AND TOOTH MORPHOLOGY TO RECONSTRUCT PALEOECOLOGY: A PILOT STUDY USING *MICROTUSCALIFORNICUS*

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The California vole, *Microtus californicus*, has a broad geographic range from southern Oregon to Baja California and a fossil record dating to the early Pleistocene. A change in tooth morphology of the lower first molar (m1) is observed throughout the geographical range of the species: individuals have a more gracile and curved m1 in cooler, moister habitats typical of northern populations while those in warmer, drier habitats typical in the southern portions of its range have a more robust and straight m1. A change in morphology has also been documented through time with a loss in the robust straight morphology from cooler, moister Pleistocene times until today. These findings imply that spatial variability in precipitation and associated changes in vegetation and diet could drive the variation in tooth morphology observed in the California vole. Since the m1 is the most abundant fossil of *M. californicus* in the Pleistocene and Holocene record, the correlation between morphology and differences in precipitation and diet could be a potential metric for shifting functional morphological traits during times of shifting climate. In order to test the possible influence of environmental differences on the tooth morphology of *M. californicus* we used stable isotope analyses of fur in individuals from extant populations collected along the latitudinal range of the California vole. We collected samples of 35 individuals from the Museum of Vertebrate Zoology at UC Berkeley: 27 from the northern portion of the geographic range, and 8 from the southern part. Specifically we analyzed the oxygen isotope ratio to test for a correlation between morphology and precipitation. On a broad geographic scale comparing the northern population to the southern population, we find no difference between oxygen isotope values. However, when we looked at the southern specimens and analyzed the difference between individuals from different environments, we do find a significant correlation between oxygen isotope values and habitat type (t-Test; p=0.009) of populations with different m1 morphologies. This suggests precipitation is influencing morphological variation at a local scale. Analyses of carbon, nitrogen and sulfur isotopes were undertaken to detect signs that the morphological variation is due to dietary differences that result from differing vegetation. This study helps determine the extent to which isotope data can be employed to understand the causes of fine-scale morphological changes.

A NEW MARINE TURTLE FROM THE MAASTRICHTIAN OF ANGOLA

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Well preserved skull, jaw and associated postcranial material of a new marine turtle was recovered from the mid Maastrichtian (Late Cretaceous) Mucuio Formation, Bentiaba, Angola, during the 2010 Project PaleoAngola expedition. Preliminary analysis was performed showing that the new material represents a sister-taxon of *Euclastes* based on synapomorphies such as extensive secondary palate, shovel-like mandible, low tomial ridge, and broad skull, and places the new Angolan specimen as the most basal *Euclastes.* This new taxon, plus *Angolachelys mbaxi*, and at least two other distinct taxa show a diversity of marine turtles previously unknown in the Cretaceous of Africa.

VARIATION IN COMPLEX SYSTEMATIC PROBLEMS: A CASE STUDY

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Levels of variation in one population that exceed interspecific levels known to be expressed between sister species can make specimen identification within a clade problematic. The situation is particularly difficult for the fossil record, where levels of variation within many species remain poorly understood. Box turtles of the extant genus *Terrapene* exemplify this problem. The clade is currently split into six species and ten subspecies. Morphological variation has been noted in many of those taxa, but remains poorly characterized. The situation presents a circular problem; characterizing variation across the temporal and geographic range of the clade remains intractable until lineages can be separated and studied individually, but lineages remain unidentifiable, especially in the fossil record, due to a lack of understanding of variation. In systematics, this problem can translate into poor understanding of apomorphies and a lack of resolution in phylogenetic analyses.

We used Pleistocene and recent specimens of *Terrapene* as a test case to approach the problem of variation and systematic resolution in phylogenetic analyses that include fossils. We used specimen-level phylogenetic analyses to explore whether variation between specimen-level terminals still allowed for species-level resolution. We scored multiple specimens of extant species of *Terrapene* as well as multiple fossils from several localities. We hypothesized that specimens would cluster in polytomic assemblages by species, if variation had a minimal effect on resolution. However, in our analysis not all specimens clustered together into species assemblages. Examination of character distribution indicated that coding specimen-level, as opposed to species-level, terminals caused signal from