may represent miniaturization in response to the Permo-Triassic extinction event.

Funding Sources Fulbright FLEX Global Scholar Award

Technical Session 15: Theropods (Saturday, November 5, 2022, 8:00 AM)

QUANTITATIVE TESTING OF EGGSHELL ORNAMENTATION CATEGORIES WITHIN A CLUTCH OF DINOSAUR EGGS (ELONGATOOLITHIDAE) FROM THE CEDAR MOUNTAIN FORMATION (CENOMANIAN) OF UTAH

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Quantitative measures of surface variation are commonly used to analyze dentition. More recently, their efficacy has been demonstrated in differentiating the topography of extant (emu) and extinct (oviraptorosaur) theropod eggshells. However, to date, quantitative metrics of eggshell ornamentation have not been widely applied, thus their potential for advancing studies on theropod reproductive ecology and more broadly, the field of ootaxonomy, remains largely unknown. Using a recently discovered clutch of elongatoolithid eggs from the Mussentuchit Member of the Cedar Mountain Formation in Utah, we tested the quantitative variation of external eggshell ornamentation across a single oviraptorosaur nest. We sampled and created high-resolution, three-dimensional models via μCT scans of current categorizations of elongatoolithid ornamentation types (e.g., dispersituberculate, lineartuberculate) from within the clutch. Scans were discretized into uniform, 5mm-radius, 8,000 triangle-face surfaces using Avizo, GeoMagic Studio, and MeshLab. We collected data on the variation in topographic complexity (Dirichlet Normal Energy) and relief (Slope) using the r package molaR, to test if grossly-observed differences between the current ornamentation types, and thus the differences in eggshell texture across a clutch, were borne out by the quantitative data. Our results demonstrate that DNE and Slope criteria can be used to distinguish between and within ornamentation types. DNE values for the most complex sagenotuberculate-type were an order of magnitude greater than those for the simplest dispersituberculate-type, and dispersituberculate-type values could vary by 300%. This is the first known study to quantitatively record ornamentation variation across a nest of fossil eggs. Applied with gross observation, these numeric criteria provide a new layer of descriptive granularity that could better interpret historically enigmatic ootaxa within Elongatoolithidae, with potential future use in ootaxonomic descriptions and diagnoses.

Funding Sources This material is based upon work supported by the National Science Foundation under Grant FRES-1925973

Colbert Prize Session

EARLY ORIGINS OF THE GENUS *HOMO*: TAXONOMIC AND PHYLOGENETIC ASSESSMENT OF KNM-ER 5431

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The scarcity of hominin fossils discovered in east Africa from 2.0–3.0 million years ago (Ma) is a significant barrier to the study of the origins of our genus, *Homo*. Despite this, resolving the evolution of our ancestors is not out of reach. Even very incomplete specimens for which comparable finds may be unavailable are potentially informative. This is especially so in cases where analytical methods were not sufficiently developed at the time of their discoveries.

This study reexamines the KNM-ER 5431 fossil from the Koobi Fora Formation of Kenya. It is a well-preserved set of associated but isolated teeth from 2.7–3.0 Ma. Originally it was categorized only as Homininidae sp. et. gen. indet.; thus, it has not been sufficiently considered despite being excavated decades ago.

By using geometric morphometric techniques together with cladistics analysis, the fossil is now taxonomically attributable at the genus level and can be coarsely situated phylogenetically amnog other archaic hominins. These results support the inclusion of KNM-ER 5431 within the *Homo* hypodigm.

Funding Sources Supported in part by the Angela Peterson Memorial Scholarship fund

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Regular Poster Session 4 (Saturday, November 5, 2022, 4:30 - 6:30 PM)

A COMPREHENSIVE META-PHYLOGENY OF ALL NON-MAMMALIAFORM SYNAPSIDS: NEW TOOL FOR STUDIES OF MACROEVOLUTION IN THE FORERUNNERS OF MAMMALS

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A large phylogenetic tree is a critical component of comparative analyses that examine broad macroevolutionary

patterns, such as the tempo and mode of evolution or morphological disparity through time. However, the sample of species included in published phylogenies rarely aligns with the species that researchers wish to examine in comparative analyses. For instance, early synapsid phylogenies often focus on specific subclades, such as pelycosaurs or anomodonts, rather than broadly encompassing all known synapsid lineages, thus hindering analyses that require detailed sampling across synapsid lineages. To address this issue, we generated a time-calibrated meta-phylogeny ('metatree') of synapsid species from the Carboniferous through the Eocene (305–34 Ma). The metatree approach uses source character matrices (rather than source trees) and generates complete sets of most parsimonious trees, combining them rather than generating a single consensus tree. We incorporated 269 published morphological character matrices, which includes every non-mammaliaform synapsid character matrix that has ever been published (as of July 2021) and 57 mammaliaform-focused matrices. Due to evolving ideas of relationships and frequent matrix reuse, each of the matrices was weighted according to its publication year and its dependence on 'parent' matrices using an established metatree procedure. The metatree approach relies on XML metadata files that reconcile taxon names to valid Paleobiology Database taxa (PBDB). Because the metatree approach utilizes PBDB taxonomy, we vetted the PBDB information and made approximately 500 additions and corrections to taxon information. The resulting metatree includes 2,128 synapsid species, making it one of the largest fossil phylogenies ever produced. Approximately 1600 species are non-mammaliaform synapsids, and the remaining ~525 species are mammaliaforms, including many of the known Mesozoic and early Cenozoic mammaliaforms. The massive taxonomic and temporal breadth of the metatree make it broadly applicable to studies on synapsid macroevolution. The past decade has witnessed a resurgence of research on non-mammaliaform synapsids, and our new, comprehensive metatree provides a rigorous foundation for continuing work on macroevolutionary patterns and processes among the forerunners of mammals.

Funding Sources NSF DEB-1754502, NSF DBI-1812126

Regular Poster Session 2 (Thursday, November 3, 2022, 4:30 - 6:30 PM)

A NEW LATE CARBONIFEROUS (GZHELIAN) ARAEOSCELIDIAN (REPTILIA, DIAPSIDA) FROM THE BIRTHDAY BONEBED, HALGAITO FORMATION, BEARS EARS NATIONAL MONUMENT, UTAH, USA

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Araeoscelidians are a clade of small, lightly built, diapsid reptiles known by only two taxa from the late Paleozoic of Europe and four from North America. All are terrestrial except for the aquatic *Spinoequalis schultzei* from the late Carboniferous (Gzhelian) of Kansas, USA. An undescribed genus and species of Gzhelian araeoscelidian is represented by numerous specimens, including an ontogenetic series, from the Halgaito Formation, Valley of the Gods, Bears Ears National Monument, southeastern Utah. The specimens occur in a multitaxic bonebed discovered in 1989 that was deposited as a discrete sedimentologic unit in the lower portion of the formation in a fluvial channel system during a flooding event. The Halgaito araeoscelidians inhabited the coastal plain on the southwestern border of the Paradox Basin in western Pangea during a relatively short wet interval when intermittent-to-perennial streams and rivers traversed it during an otherwise semi-arid to arid climate. The Halgaito araeoscelidian is an overwhelming component of the Birthday bonebed tetrapod fauna in comprising 55 percent of the five identified taxa.

To determine the relationship of the Halgaito taxon to other North American araeoscelidians (those from Europe are too poorly documented to include) and to early neodiapsids, a phylogenetic analysis was conducted using TNT. Results indicate the Halgaito araeoscelidian resolves within the monophyletic clade Araeoscelidia as the sister taxon to the early Permian (Artinskian–Kungurian) *Araeoscelis* from Texas, with the late Carboniferous (Kasimovian) *Petrolacosaurus kansensis* from Kansas and the early Permian (Asselian–Sakmarian) *Zarcasaurus tandyderus* from New Mexico forming successively more basal sister taxa relative to this clade. Unexpectedly, *Spinoequalis schultzei* resolves as a member of Neodiapsida, which is the sister clade to Araeoscelidia. Although the tree has high Consistency and Retention indices, the support for internal clades is low, except for Diapsida and Araeoscelidia, which are high and moderate, respectively. The Halgaito araeoscelidian is distinguished from the others by relative sizes of the maxillary teeth, a small contribution of the jugal to the ventral margin of the skull, and eight cervical vertebrae.

Technical Session 8: Evolutionary Developmental Biology (Thursday, November 3, 2022, 1:45 PM)

TESTING THE INHIBITORY CASCADE MODEL IN ELEPHANTS

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The Miocene-Pleistocene proboscidean trend towards larger, higher-crowned molars, with an increased number of more closely spaced plates, is a textbook example of adaptation to climatic change, reflecting increased grazing in a