MEETING PROGRAM & ABSTRACTS

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The Megin Mammoth specimen represents the first and almost complete skeleton of a mammoth discovered in eastern Siberia. It was found in 2015 in the Suola River bank (Lena River Basin) deposits in the vicinity of Nizhniy Bestyakh, Yakutian Republic. The site deposits were accumulated during the Sartanian (~29,000–14,000 cal BP) glacial. Here, we characterize the morphological features of the Megin mammoth to explore its taxonomy, age, size and sex. We generate a radiocarbon date and extract ancient DNA from a small sample of tooth root to infer its relationship to other mammoths. The Megin mammoth is excellently preserved and nearly complete, allowing inference of its age and sex. The remaining last molars (M3) are preserved in all jaw quadrangles, show moderate wear and are positioned in closed alveoli. The mandibular foramina are also enclosed by grown-in bone. The tooth wear corresponds to that of a 58–62 year old Asian elephant, a very old age that is also supported by complete obliteration of fusion lines on all limb bones and vertebrae discs. The tusks are larger and heavier than those of the old male Lena Mammoth and fall near the upper limit of woolly mammoth tusk sizes, indicating that the Megin Mammoth was a male. This conclusion is supported by the large size of the other skeletal elements: the estimated height to the shoulders is 283–295 cm (taller than the Taymyr Mammoth but shorter than the Lena Mammoth), corresponding to a 304–308 cm tall animal. With respect to the taxonomic identification of the Megin mammoth, AMS radiocarbon dating provided an age of 17,820–17,330 cal BP, suggesting that it is probably a woolly mammoth, *M. primigenius*. In addition, we generated a high-coverage, complete mitochondrial genome, which placed the Megin mammoth within woolly mammoth clade I, the basal clade to the species. However, several morphological features appear to be too archaic to ascribe the specimen to *M. primigenius*. For example, the dental characteristics (relatively short M3, 14–15 plates on the upper M3 and 15–16 plates on the lower M3, relatively low plate frequencies [5.5–8.0], and high enamel thickness [2.9 mm]), the size and low torsion of the tusks, and the massive-sized limb bones are characteristic of the steppe mammoth, *M. trogontherii*. Because reconciliation of the morphological and mDNA data remains problematic, the specimen is temporarily identified as *Mammuthus* sp., as work continues to generate nuclear genomic data.

Technical Session XVII (Saturday, October 29, 2016, 9:45 AM)

THE RETURN OF *PROTOICHTHYOSAURUS*: A VALID SISTER TAXON OF *ICHTHYOSAURUS* (REPTILIA, ICHTHYOSAURIA)

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The genus *Protoichthyosaurus* was proposed in the late 1970s, but it was synonymized with the genus *Ichthyosaurus*, with which it shares several features including a wide forefin with at least five primary digits, an anterior digital bifurcation, a humerus that is slightly wider distally than proximally, and a coracoid with well-developed anterior and posterior notches. However, a closer examination has determined that the two genera are distinct, and can be distinguished on the basis of skull, forefin, and coracoid morphologies. The maxilla of *Protoichthyosaurus* is large, high, and triangular, separated from the external naris by a sliver of bone, if at all; whereas the maxilla of *Ichthyosaurus* is lower, and separated from the external naris by a fairly broad contact of the lacrimal and premaxilla. Differences also exist in the shapes and sizes of the postfrontal, prefrontal, lacrimal, and postorbital. In the forefin, the difference is most evident in the mesopodium, as was noted in the original diagnosis. *Protoichthyosaurus* has three elements in the distal carpal row rather than four as in *Ichthyosaurus*. Metacarpal 5 does not contact the ulnare in *Protoichthyosaurus*, as it does in *Ichthyosaurus*. Phylogenetic analysis confirms that *Protoichthyosaurus* is sufficiently different from *Ichthyosaurus* to be considered a valid genus. Thus there are two genera of wide-finned ichthyosaurs in the Lower Jurassic of the U.K. Recognized specimens of *Protoichthyosaurus* are in historic collections, and so the stratigraphic range is poorly known, although it is probably from the earliest Hettangian to early Sinemurian. The resurrection of this genus increases the diversity of ichthyosaurs in the lowest Jurassic and further supports the hypothesis of very rapid diversification of ichthyosaurs immediately after the Triassic extinction.

Poster Symposium II (Friday–Saturday, October 28–29, 2016, 4:32 PM)

LATE JURASSIC OF MORRISON FORMATION AND PORTUGAL TETRAPODS COMPARED: A MODEL TO EXPLAIN FAUNAL EXCHANGE AND SIMILARITY

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The precursor of the North Atlantic existed between the North American and Iberian blocks from the earliest Jurassic Hettangian and has been ever expanding since. By the Kimmeridgian and Tithonian, when much of the Morrison Fm rocks were deposited, the proto-Atlantic was more than 300 km wide at 27° paleolatitude between North America and Iberia. Macrovertebrate paleontology reveals a unique story to the isolation of Iberia and instead suggest a paleogeographic land connection between North American and Iberia. *Torvosaurus*, *Allosaurus*, *Ceratosaurus*, *Stegosaurus*, *Supersaurus* and others have a distribution restricted to Morrison Formation in North America and Lourinhã Formation in Portugal.

A novel paleogeographic model is here suggested: (1) around the Middle–Late Jurassic transition there is a major palaeoceanographic and palaeoclimatic reorganization, coincidental to a major eustatic sea-level drop and uplift associated with the Callovian–Oxfordian Atlantic Regressive Event; (2) creating an ephemeral land bridge presenting a temporary opportunity for terrestrial gateways likely across the Flemish Cap and Galician Bank land masses, allowing large dinosaurian taxa to cross the northern proto-Atlantic in both directions; (3) finally, a Callovian–Oxfordian faunal exchange around the 163 Ma, through latest Kimmeridgian at 152 Ma (the age of equivalent genera in both Morrison and Portugal), is was an interval that allowed speciation, but retaining generic similarity of vertebrates. This model is consistent with the chronology and taxonomy required for speciation of the Iberian and American forms, exemplified by the coeval sister-taxa pairs *Torvosaurus tanneri* and *T. gurneyi*, *Allosaurus fragilis* and *A. europaeus*, or *Supersaurus vivianae* and *S. lourinhanensis*.

While some of the smaller animals in the fauna show Morrison/Portugal affinities, most from Iberia have European or even Asian affinities. The larger-bodied fauna are more closely related to Morrison than to mainland Europe (except for dacentrurine stegosaurs). The body size differences and affinities of taxa across paleogeography is comparable to what is observed today across the Wallace Line.

Migration may have also occurred in both directions. The closest relative of *Torvosaurus* is likely the European Bathonian *Megalosaurus*, thus the presence of the genus in North America represents a European migration. On other hand, *Allosaurus* and *Supersaurus* origins are consistent with a North American origin, representing an west-to-east migration.

Colbert Prize (Wednesday–Saturday, October 26–29, 20164:15–6:15 PM)

RE-EXAMINATION OF DESMOSTYLIAN PHYLOGENETIC RELATIONSHIPS

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The order Desmostylia, belonging to Tethytheria or Perissodactyla, is an extinct clade of marine mammals of which remains are found from shallow marine strata of the uppermost Eocene to lowest upper Miocene in the North Pacific Rim. Traditionally, Desmostylia has been divided into two families, Desmostylidae and Paleoparadoxidae, on the basis of dental morphology. With recent establishment of two new genera, *Ounalashkastylus* and *Seuku*, Desmostylia now includes two families and 10 or 11 genera with 13 species, with the two genera *Seuku* and *Behemotops* with indeterminate familial affinities.

The phylogenetic relationships within Desmostylia have been debated. Two alternative hypotheses have been proposed on the relationship between the two families. Both Desmostylidae and Paleoparadoxidae are considered as monophyletic groups in one hypothesis, whereas Paleoparadoxidae is regarded as comprising paraphyletic, successive outgroups for monophyletic Desmostylidae in the other. One factor contributing to such different hypotheses has been the lack of well-preserved specimens that can be used as suitable outgroups for phylogenetic analyses. Another factor is the small size of data matrices used in previous studies unsuitable for analyses including all desmostylian taxa.

In this study, the desmostylian inter-relationship was assessed by rectifying the shortcomings of the previous studies. First, based on the recent description of a well-preserved skull of *Anthracobne*, this taxon was used as the outgroup. Second, previously published datasets were combined and revised to produce one large matrix including 13 species of Desmostylia based on both cranial and postcranial characters. Phylogenetic analyses were conducted with equally weighted parsimony using TNT v. 1.1. As a result, Paleoparadoxidae with the traditional taxonomic content was found as paraphyletic, successive outgroups for the monophyletic Desmostylidae. Furthermore, the systematic positions of new genera were resolved. *Seuku* was found to be a sister taxon of *Behemotops*, whereas *Neoparadoxia* was a sister taxon of the clade consisting of *Paleoparadoxia* and *Archaeoparadoxia*. *Ounalashastylus* was placed between *Desmostylus* and *Cornwalius*. This result provides a phylogenetic framework for discussing various aspects of Desmostylian evolution. In addition, it indicates that the classification of Desmostylia, especially at the family level, needs to be revised.

Poster Symposium I (Wednesday–Thursday, October 26–27, 2016, 4:15–6:15 PM)

A NEW CARPOLESTID FROM SOUTHWESTERN WYOMING AND ITS PHYLOGENETIC IMPLICATIONS

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Carpolestids are a family of plesiadapiform mammals that flourished during the Paleocene of western North America. They are particularly diagnostic in possessing a large plagiaulacoid lower fourth premolar, the size and shape of which serves as an important basis for determining evolutionary relationships within the clade. *Carpolestes,* with its hypertrophied and highly polycuspidate p4, is the youngest and most derived carpolestid genus. Older carpolestid species currently classified in either *Carpodaptes* or *Carpomegodon* retain a more primitive p4 morphology with fewer apical cusps, and these species are widely regarded as comprising a paraphyletic grade with respect to *Carpolestes*. However, identifying which of these earlier carpolestid species is most closely related to *Carpolestes* remains contentious. Fundamentally, this decision entails a longstanding debate over size versus shape in evolution, because p4 in species of *Carpodaptes* and *Carpomegodon* varies markedly with respect to these parameters. Here, we report the discovery of new late Tiffanian (Ti5) mammal fauna from the eastern flank of the Rock Springs Uplift in Sweetwater County, Wyoming. Carpolestid specimens from the new Twelvemile Bonanza local fauna document a new species of *Carpolestes* that illuminates the final stages in the transformation of carpolestid p4 blades. Morphometric analysis of the new *Carpolestes* from Twelvemile Bonanza shows that its p4 closely resembles that of *Carpodaptes hobackensis* in terms of shape, although the latter taxon differs significantly from species of *Carpolestes* and *Carpomegodon jepseni* in terms of size. A phylogenetic analysis based on dental characters that incorporates the new species of *Carpolestes* from Twelvemile Bonanza conflicts with previous interpretations of carpolestid phylogeny in reconstructing *Carpodaptes hobackensis* as the sister group of *Carpolestes*. Taken together, these results indicate that shape trumped size during the evolutionary transformation of the iconic p4 blade of carpolestids.

Poster Session I (Wednesday, October 26, 2016, 4:15–6:15 PM)

HERE AND GONE: EXPLANATIONS FOR THE VARIABLE ABSENCE OF THE ENTEPICONDYLAR FORAMEN IN SLOTHS (MAMMALIA, PILOSA)

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