

which was poorly documented in this area in the past. The fish remains consist mostly of ganoid scales, teeth, and dentitions, and represent taxa that are typical from Mesozoic continental environments. They mainly include: 1) euselachian chondrichthyans assessed to the order Hybodontiformes, and 2) neopterygian actinopterygians assessed to three orders: Semionotiformes, Pycnodontiformes and Amiiformes. More than two thirds of the specimens are ganoid scales assessed to the Semionotiformes. Among the rest, pycnodont and Hybodontiformes teeth are the most abundant. No teleost remains have been identified so far, but this is probably due to an ecomorphologic and taphonomic bias rather than to real absence in the original communities. Most taxa collected are identified for the first time in these basins. There are remarkable differences between both basins in the number of Berriasian-Aptian localities that have provided fish remains. In the Basque-Cantabrian Basin they have been found, to date, in a single outcrop, located at the Viviparus Bed Member of the Vega de Pas Formation (Hauterivian-Barremian). In the Cameros Basin, remains have been collected from fifteen different sites found within the Oncala Group (Tithonian-Berriasian), Urbión Group (uppermost Berriasian-lower Aptian) and Enciso Group (Aptian). These fish assemblages show general similarities with the ichthyofaunas from the Purbeck and Weald of Europe. The Cameros Basin faunas are the most similar to those previously known from the Early Cretaceous of Spain: Galve (Teruel, Maestrazgo Basin), Las Hoyas (Cuenca, Iberian Basin), and Montsec (Lérida, South Pyrenean Zone), although all these localities present a high percentage of endemic taxa, at least at specific level. In addition to the overall faunistic similarities, the new ichthyofaunas from both basins show evidence of endemisms as well, involving several new taxa currently under study.

Romer Prize Session, Thursday 10:30

#### VARIATION, VARIABILITY, AND PROBABILITY IN ASSESSING THE EVOLUTIONARY HISTORY OF VERTEBRATE FOSSILS BASED ON DISCRETE SKELETAL CHARACTERS

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Although the geological record provides us the only direct window into the evolutionary history of Life, it often does not supply us with the specimens necessary to recognize the full complexity of the morphological transformations that it preserves. Developmental biology combined with phylogenetic systematics is broadening our perspectives on the role of intraspecific variation in the evolution of morphology and its applications to the fossil record. These perspectives include conceptualizing variability as a reflection of the evolutionary history of underlying developmental pathways rather than solely the result of population-level phenomena working largely independent of phylogenetic history. This view provides a theoretical context for studying variability as synapomorphy, which in turn provides not only the means to objectively estimate variability in extinct lineages but also the emphasis to do so. Unfortunately, our current understanding of variation in the skeleton of extant vertebrates and its distribution through space and time is largely inadequate to support meaningful conclusions with regards to what degree the evolution of variability affects our perception of evolutionary history based on the fossil record. I undertook a series of studies, using cryptodire turtles as a model, which examined variation in discrete skeletal characters to determine how that variation is distributed across a range of hierarchical levels. Results indicate that variation data are not randomly distributed through space and time and therefore informative patterns do exist. These patterns, not surprisingly, are often complex and closely related to postnatal trajectories of growth and skeletal remodeling. The presence of phylogenetic information in variation data supports the notion that meaningful phylogenetic brackets can be used to infer variability in extinct lineages and to assess confidence in the phylogenetic position of a fossil specimen. Such confidence also is applicable to the inference of all secondary biological properties dependent on tree topology and therefore can be used to strengthen the contribution of paleontological data to broader biological questions.

Technical Session V, Wednesday 3:15

#### THE ENIGMATIC FOSSILS *EXOSTINUS* AND *RESTES*: RESOLVING THE STEM AND THE CROWN OF *XENOSAURUS*, THE KNOB-SCALED LIZARDS

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Two lizard clades, Xenosauridae (Pan-*Xenosaurus*) and Shinisauridae, both with extensive fossil records and relict extant distributions, are important in reconstructing relationships within Anguimorpha, an ancient clade whose composition and internal relationships remain controversial. Xenosauridae and Shinisauridae preserve plesiomorphic characters within Anguimorpha that are lost in the highly derived Anguinae and Varanoidea. In the course of my work on Anguioidea (Xenosauridae + Anguinae), and with the aid of CT scans, I examined the anatomy of all extinct and most extant Xenosauridae in an attempt to produce the first phylogeny of the clade. These taxa included the extinct *Exostinus lancensis* (Cretaceous), *Exostinus serratus* (Oligocene), and *Restes rugosus* (Paleocene), the latter two known from substantial but inadequately described cranial material, and eight species within the crown clade *Xenosaurus*. Phylogenetic resolution of the clade is complicated by the derived nature of putative outgroups. Nevertheless, my results suggest that *R. rugosus* is sister to the others, resolv-

ing a polytomy with other Anguimorpha recovered by previous work. Its anterior skull roof osteoderms are primitively platey, but its posterior osteoderms filled apomorphic "knob-scales," demonstrating the early appearance of this characteristic feature. *E. lancensis* is problematic in that referred specimens may represent several distinct taxa. One of these appears to be sister to *E. serratus* + *Xenosaurus*, making *Exostinus* paraphyletic. *Exostinus serratus* emerges as sister to *Xenosaurus*; however, it is autapomorphic in its shortened rostrum and narial elongation. Finally, *Xenosaurus* comprises flattened, crevice-dwelling lizards whose distribution follows the great mountain ranges of southern North America. For parts of a group until recently thought to include but three species, the eight examined species are remarkably distinct. A northern clade comprises *X. newmanorum* and *X. platyceps*; the remaining taxa are united as a southern clade. North-south splits within Xenosauridae mirror those of several other lizard clades and may be the legacy of the equatorial contraction of early Tertiary tropical forests

Technical Session XII, Friday 1:45

#### RECONSTRUCTION OF PALEOECOLOGIES AND PALEOCLIMATES OF CENOZOIC MAMMALS FROM NORTHWEST CHINA BASED ON STABLE ISOTOPES

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The Linxia Basin is located in Gansu Province, China, on the NE margin of the Tibetan Plateau and the present-day climate is strongly influenced by the East Asian monsoon system. The uplift of the Tibetan Plateau during the Cenozoic is considered to be the driving force in the development of the Asian monsoons, and the timing of this development is important to the understanding of mammalian evolution in China. The sedimentary sequences in the Linxia Basin span almost continuously from the L. Oligocene to the Holocene and contain abundant and well-preserved mammalian fossils. Bulk carbon and oxygen isotope analyses of teeth from 160 mammalian individuals, including bovinds, horses, rhinos, cervids, giraffes, pigs, and elephants, and serial analyses of tooth enamel from 38 of those individuals ranging in age from 25 Ma to the present, have allowed reconstruction of the paleoecologies of those taxa and seasonality in the region throughout the late Cenozoic. Bulk and serial  $\delta^{13}\text{C}$  values for samples older than 2.5 Ma indicate a pure C3 diet for all individuals. A positive shift in bulk  $\delta^{13}\text{C}$  values after 2.5 Ma, indicating a change to a mixed C3/C4 diet, suggests that C4 grasses may have not spread into the basin until after 2.5 Ma, which is much later than the proposed global C4 expansion during the Late Miocene. It was hypothesized that the late C4 expansion into the Linxia Basin was driven by the strengthening of the East Asian Summer Monsoon after ~2-3 Ma, as C4 plants require summer precipitation. The serial  $\delta^{13}\text{C}$  values show greater ranges after 2.5 Ma, indicating a seasonal shift in diet from a C4-based or mixed C3/C4 diet during summer months to a C3-based diet in winter months. The seasonal patterns from individuals younger than 2.5 Ma are consistent with the seasonal isotopic patterns in modern precipitation in the summer monsoon region of East Asia, whereas the seasonal patterns from individuals older than 2.5 Ma correspond to modern precipitation records outside the summer monsoon region. This change in seasonal isotopic patterns recorded in individual teeth provides strong evidence indicating a strengthening of the East Asian summer monsoon after ~2-3 Ma.

Technical Session XII, Friday 1:30

#### DIETARY NICHE PARTITIONING AMONG FOSSIL BOVIDS IN LATE MIOCENE C<sub>3</sub> HABITATS: CONSILIENCE OF FUNCTIONAL MORPHOLOGY AND STABLE ISOTOPE ANALYSIS

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Teeth of late Miocene Bovini (bovid clade including living oxen, buffaloes, and bison) possess morphology-larger size, higher crowns, increased enamel surface area-that is reflective of feeding on a rougher diet, probably graze. In contrast, teeth of fossil "Boselaphini" bear simpler, more plesiomorphic dental morphology indicative of a diet with a greater reliance on softer food items such as browse. A paleoecological implication of the comparative dental morphology is that late Miocene bovines inhabited drier, more open habitats than did boselaphines. In order to test this hypothesis, I analyzed the stable carbon isotopes from fossil teeth from well-dated localities between 7.9 and 8.3 Ma in age from the Siwalik deposits, Pakistan. All  $\delta^{13}\text{C}$  values (PDB) lie between -9.5‰ and -12.5‰, indicating that both bovines and boselaphines at this time had pure C<sub>3</sub> diets. The mean  $\delta^{13}\text{C}$  for bovine teeth (-10.4‰) is more positive than that for boselaphines (-10.9‰), and the differences between these two series is statistically significant. Fossil bovine and boselaphine  $\delta^{13}\text{C}$  values for the most part do not overlap, separating at -10.7‰. Stable isotope analysis results support the hypothesis developed on the basis of dental functional morphology that early bovines evolved inhabiting more open habitats than did contemporaneous boselaphines. The scenario whereby the bovine clade owes its origins to a boselaphine lineage that adapted to drier, more open habitats is supported by the general context of climatic and faunal change