

Towards a Classificatory Scheme and Nomenclature of Bone Histology

Armand J. de Riquelès; Collège de France, UPMC, MNHN, CNRS, UMR 7179. Equipe "Squelette des Vertébrés", UPMC 2-4 place Jussieu, 75221 Paris, France (ricqles@ccr.jussieu.fr)

Current research in bone tissue biology still demonstrates a great diversity in the terminology used by various authors. This creates misunderstandings because a given word may carry different meanings (homonymy) and, conversely, a given structure (or concept) may be known under various terms (synonymy). A common language is a desirable goal. However, while classifications of bone as a tissue and related nomenclatorial systems have been in use for almost two centuries, it appears that incomplete progress has been made towards standardization. This suggests that bone tissue classification and nomenclature is a complex subject, replete with contradictory or even conflicting demands. Accordingly, before any new system of bone tissue classification and nomenclature can be proposed, it seems necessary to critically analyze the various aims and purposes it should fulfill, as well as the factors which necessarily will act as its major constructional constraints. We review these herewith: 1) history and stability. Names (and concepts) have been coined for bone tissue structures for centuries. Nomenclature implies stability over time. 2) Bone and bones. Tissue classification/terminology should address their proper hierarchic level of integration. 3) Why classify? Structural variability at the tissue level (histodiversity) should be recognized because it has biological significance. 4) Significance. Objective classification (tissue typology) as a basis for comparative descriptions should be able to express simultaneously several signals: structural, phylogenetic and functional. 5) Aim. A proper tissue classification/terminology should integrate all of the above points of view. 6) How to classify? Additive (open) versus subtractive (closed) schemes.

Ontogeny, Morphology and Mechanics of the Tessellated Skeleton of Cartilaginous Fishes

Mason Dean; Ecology and Evolutionary Biology, 321 Steinhaus Hall, University of California, Irvine, CA 92697 USA (mdean@uci.edu)

The cyclic loading of the feeding and swimming modes of elasmobranch fishes (sharks, rays and relatives) is not compatible with the fact that cartilage cannot repair. Materials counteract the gradual build-up of fatigue damage through either being overbuilt (with an excessive safety factor) or resistant to fatigue. As the former is unlikely in active animals, I posit that elasmobranch skeletons are inherently fatigue-resistant and that this is a function of the calcification of the tissue. The uncalcified hyaline-like cartilage core of each element is overlain by a tessellated bark of abutting mineralized tiles (tesserae), adjoined by a fibrous phase. I employ a diversity of imaging techniques and ontogenetic tissue series to investigate the development, ultra-scale morphology and mechanics of the tessellated skeleton in a species of stingray. Tesserae form in histotroph embryos and gradually widen and thicken with ontogeny. Chondrocytes flatten and are engulfed by tesserae to form cell-rich laminae with communicating passageways between entombed lacunae. Elasmobranch chondrocytes decrease in size and density with age as in endochondral ossification, yet do not hypertrophy and die as in tetrapods. Nanoindentation tests show that the mineralized tissue behaves as a nearly elastic tissue and is an order of magnitude stiffer than the uncalcified layer, which is highly viscoelastic. Mathematical models suggest that, during skeletal bending, this layered biological composite acts to distribute damaging tensile stresses to the compressive portion of the mineralized phase where the elastic modulus is more than three times higher and therefore better able to resist applied forces.

Axial Muscle Function During Locomotion in the Salamander *Ambystoma maculatum*

Stephen M. Deban,¹ and Nadja Schilling²; ¹Department of Biology, University of South Florida, Tampa, USA (sdeban@cas.usf.edu), ²Institute of Systematic Zoology and Evolutionary Biology, Friedrich-Schiller-University Jena, Germany

Trunk muscles were examined in the spotted salamander, *Ambystoma maculatum*, to determine the relationships between anatomical position, fiber type composition, and muscle activation pattern during swimming. All epaxial and hypaxial muscles examined are activated out of phase (180–270 degrees) with maximum bending, the exact phase relationship varying with undulation rate and segment number. Most muscles at a

given body segment show simultaneous activity in a large burst associated with segment lengthening (i.e., bending to the contralateral side), and are electrically silent when bending to the ipsilateral side is greatest. Some muscles show a smaller secondary burst of activation when the segment is shortening. In the epaxial muscles, no effect of the fiber type composition or distance from the vertebral column is apparent in the activation patterns during swimming. Similar patterns of activation are seen in fast twitch muscles (m. dorsalis trunci profundus, m. rectus lateralis, and m. subvertebralis pars ventralis), slow twitch muscles (m. interspinalis, m. dorsalis trunci superficialis), and even regionalized muscles (m. subvertebralis pars transversalis). Differences in activation between fast and slow twitch muscles and among those with different mechanical advantages may become evident in slower and/or terrestrial locomotion.

Feeding Functional Morphology of Extant Amphibians

Stephen M. Deban; Department of Biology, University of South Florida, Tampa, USA (sdeban@cas.usf.edu)

Understanding the relationship between form and function is critical for correctly interpreting the fossilized remains of organisms and for assigning plausible evolutionary relationships and character transformations. The relationship between feeding function and cranial morphology in extant amphibians is useful in this regard because it is well studied and the anatomical correlates of feeding functions are relatively clear and generalizable. Living amphibians use their skull, jaws, and hyobranchial apparatus to feed using four modes: jaw prehension, tongue prehension, suction feeding, and suspension feeding. Jaw prehension can be used in combination with the others; however, suction/suspension feeding versus tongue prehension appear to be conflicting functions that require compromises in structure, most evident in extreme forms. Suction feeding taxa possess a robust, often mineralized or ossified hyobranchial apparatus whereas tongue prehension is associated with slender, cartilaginous hyobranchial elements. Jaw prehension taken to the extreme requires robust jaws and skull, and is observed in both suction feeding and tongue protracting species. The interplay of form and function in the feeding systems of living amphibians may provide insights that allow more confident assessments of lissamphibian ancestry among the tetrapod taxa of the late Paleozoic.

Advances in Molecular and Phylogenetic Studies of Xenarthra

Frédéric Delsuc,¹ Mariella Superina,² Marie-Ka Tilak,¹ Emmanuel J.P. Douzery,¹ and Alexandre Hassanin³; ¹Laboratoire de Paléontologie, Phylogénie et Paléobiologie, Institut des Sciences de l'Evolution, UMR 5554-CNRS, Université Montpellier II, Montpellier, France (delsuc@isem.univ-montp2.fr), ²Department of Biological Sciences, University of New Orleans, New Orleans, USA, ³Origine, Structure et Evolution de la Biodiversité UMR 5202-CNRS, Département Systématique et Evolution, Service de Systématique Moléculaire, Muséum National d'Histoire Naturelle, Paris, France

The introduction of molecular data has had profound effects on mammalian systematics and evolution. Living xenarthrans, that represent one of the four main placental lineages, have been no exception to this trend. Indeed, to early attempts based on morphological, cytological, immunological, and protein characters, have followed up more recent phylogenetic studies based on mitochondrial and nuclear genes. Reviewing the recent advances made in xenarthran molecular systematics, we show how molecular data allowed reconstructing the phylogeny of living xenarthrans at the genus level, but left uncertain the position of Xenarthra within placental mammals. Moreover, we present new results on the phylogenetic position of the enigmatic pink-fairy armadillos (genus *Chlamyphorus*) based on sequences of mitochondrial and nuclear genes obtained from museum specimens. The resulting phylogenetic framework is subsequently used to define a molecular timescale for the evolutionary history of extant xenarthrans. These molecular dating analyses reveal a striking synchronicity between some diversification events in xenarthran phylogeny and the major environmental changes that occurred in South America during the Tertiary.

Dental Microwear Methodology of Dietary Assessment for the Paleoeological Reconstruction of *Procervulus* (Artiodactyla, Cervidae)

Daniel DeMiguel,^{1,2} Beatriz Azanza,² Jorge Morales,¹ and Mikael Fortelius³; ¹Museo Nacional de Ciencias Naturales, Madrid, Spain, ²Universidad de