and life-history plasticity (development and growth rates) were measured. Morphological changes were analyzed by both multivariate and geometric morphometric methods. Results obtained by the two methods were in concordance. Shape analysis allows us to discriminate predator-induced, competitor-induced and drying-induced morphotypes. Life-history traits under isolated environmental factors were also consistent with precedent studies. In complex environments we observed that life-history plasticity was governed by abiotic factors, whereas a mixture of morphological traits was observed in response to exposure to complex environments.

Developmental Basis of Morphological Integration of Brain and Skull in Craniosynostosis

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Skull and brain are commonly studied separately, building upon a perception of these tissues as developmentally and genetically distinct. The evolutionary history of Mammalia provides strong evidence that the morphology of skull and brain change jointly in evolution. In a recent study we used 3D computed tomography and magnetic resonance images of human children diagnosed with two types of premature closure of cranial sutures (craniosynostosis) and found evidence of strong phenotypic integration of brain and skull. We have expanded this study to examine patterns of association between neural and skull tissues in other forms of isolated craniosynostosis and some forms of syndromic craniosynostosis. Though patterns of association between skull and brain differ between diagnostic categories, the basis for these relationships is unknown. To initiate analyses of the genes and their regulatory programs responsible for the phenotypic associations that we have discovered, we introduce our work with a knock-in mouse model for Apert syndrome that has a S252W mutation in fibroblast growth factor receptor 2. The $Fgfr2^{+/S252W}$ mouse model provides the opportunity to closely investigate proliferation, differentiation, and altered cell fate determination of progenitor cells in cranial phenotypes while monitoring the various signaling networks that are responsible for development of the head.

Gross Anatomical Brain Region Approximation (Gabra): A New Technique for Assessing Brain Structure in Dinosaurs and Other Fossil Archosaurs

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Tracking brain evolution through the fossil record is difficult, because the bony endocranial cavity is the only proxy available for study. Although for some groups (mammals, birds) a cranial endocast is a fair representation of brain size and morphology, for many reptile groups the brain does not fill the cavity and an endocast is a poor proxy. Thus, quantitative studies of relative brain size or qualitative studies of brain region evolution often require untested assumptions and speculation. We present a new technique called Gross Anatomical Brain Region Approximation (GABRA) which addresses these problems using 3D digital analysis to estimate brain morphology in fossils based on a variety of comparative anatomical criteria. 3D digital endocasts are extracted from CT scan datasets of fossil archosaurs and then imported into modeling software (Maya). Virtual models of the underlying brain regions are produced using 3D ellipsoids based on the osteological correlates of various soft-tissue structures within the cerebral cavity, as identified by comparison with extant taxa. These discernable structures (neurovascular canals, dural sinuses, fossae produced by the brain itself, etc.) provide limits on the location and size of major brain regions (e.g., cerebral hemispheres, cerebellum, optic lobes, olfactory bulbs). GABRA allows moving beyond studying the cranial endocast as a singular entity to studying the evolution of the brain and its different parts, allowing hypotheses of neurological mosaic evolution to be better tested. Moreover, revised estimates of brain (and brain region) size will put quantitative analyses of relative brain size on a better footing.

Comparative Ontogeny and Phylogeny in Reptiles

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Statements of homology are low-level theories of character evolution that are based on a variety of empirical criteria such as those obtained by comparative ontogenetic investigations. Reptiles provide a number of classic examples that illustrate the importance of comparative ontogeny for the inference of homology. One famous example is the ontogeny and evolution of the manus in the transition from theropod dinosaurs to birds. Another example concerns the evolution of the astragalus, which involves two consecutive events of ontogenetic repatterning, one in lepidosaurs and turtles, the other in chameleons. Controversy also surrounds re-development of limbs, or parts thereof, in squamate taxa nested deeply inside limb-reduced lineages. The recent push towards broad-scale phylogenetic analyses as are required for the assembly of the tree of life highlights further difficulties of homology assessment. The AToL "Deep Scaly" Project aims at the reconstruction of squamate (lizards, amphisbaenians and snakes) interrelationships using genomic and morphological data. This approach reveals morphological homology statements to be restricted in scope. A striking example is provided by the developmentally and functionally tightly integrated palatobasal articulation between the dermal palate and the base of the braincase. I will argue on both developmental and functional grounds that the basipterygoid process in snakes, where present, is not homologous to that of other gnathostomes. The consequence of such argument is the creation of an "incomplete" character for phylogenetic analysis.

Forelimb Muscle Activity in Swimming Sliders and Sea Turtles: Are Neuromotor Patterns Conserved?

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Tetrapod limbs have been modified numerous times through evolution to yield a diverse array of forms. New locomotor behaviors might arise through evolutionary changes in anatomy, changes in activation of muscles producing limb motion, or a combination of both. Turtles provide an excellent model to test for such changes because they display diverse locomotor styles and morphologies. Most freshwater turtles swim via asynchronous anteroposterior forelimb rowing, but sea turtles swim via synchronous dorsoventral flapping of forelimbs modified as flippers. Muscular arrangements differ between these groups, but comparisons of their forelimb motor patterns have not been performed. We collected high-speed video and electromyographic (EMG) data from forelimbs of swimming red-eared sliders (*Trachemys scripta*) to provide a baseline for comparison to previous motor pattern data from the derived, flipper-shaped forelimbs of loggerhead sea turtles (*Caretta caretta*). Limb cycles were defined as a recovery phase (sea turtles: abduction, sliders: protraction) followed by a thrust phase (sea turtles: adduction, sliders: retraction). Although relative durations of these phases differ between the species (recovery phase = 30% cycle duration in sliders, 50% in sea turtles), aspects of their motor patterns are similar relative to landmark kinematic events. For example, latissimus dorsi (humeral abductor and protractor) becomes active about 10% before the start of protraction and remains active until 10% before maximal humerus protraction and abduction in both species. These data indicate the potential for conservation of motor patterns in the evolution of turtle limb function despite dramatic evolutionary changes in anatomical structure. Supported by NIH (R01-DC005063-06A1).

Schmelzmuster of *Alticola strelzovi* and *Lasiopodomys brandtii* (Arvicolinae, Rodentia) and Its Evolutionary Polarization

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Enamel Schmelzmuster offers plenty of information for phylogenetic and mechanical interpretations. Although the arvicoline Schmelzmuster is taxonomically well known, it remains undetected in some species. In this study, we analyzed the Schmelzmuster of the first lower molars of two Asiatic arvicolines, *Alticola strelzovi* and *Lasiopodomys brandtii*, using SEM. In *A. strelzovi*, the leading edges are built of a very thin layer of inner radial enamel, middle layer of a thick lamellar enamel and an outer layer of relatively thin radial enamel. The trailing edges