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**The genetic basis of digit identity and evolution of the avian wing**  
Digits are an excellent model for studying the evolution and development of individuality in serial homologs. How digit identity is regulated or, indeed, whether digits have stable transcriptomic profiles that indicate discrete regulatory states, is unclear. While a number of genes have been identified as markers of digit identities, for example low expression of *Hoxd11* seems to mark digit I of amniotes, comprehensive and comparative analyses of gene expression in digits are lacking. To discover the genetic basis of digit identity, we analyzed transcriptomes of developing limbs of American alligator (*Alligator mississippiensis*), green anole (*Anolis carolinensis*), and mouse (*Mus musculus*), chicken (*Gallus gallus*), and human (*Homo sapiens*). Limbs were sampled at comparable developmental stages, after digital condensation and once inter-digital webbing has begun reducing. RNA-Seq was performed on dissected digits and their associated, posterior inter-digital webbing, a known source of signals for digital identity. In situ hybridization was used to validate patterns of expression of identified candidate digit-identity genes. These analyses inform the variational independence and modularity of amniote digits, mechanistic hypotheses of limb morphogenesis, and human developmental malformations. Further, we identify stable transcriptomic profiles in chicken between the fore- and hindlimb. These analyses suggest a scenario for the evolution of the avian wing wherein the digits of chicken forelimb correspond to digits I, III, IV of other species.

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**Functional trade-offs in salamander feeding performance due to morphological divergence**

Salamanders use the hyobranchial apparatus to depress the floor of the mouth during aquatic suction feeding and to project the tongue from the mouth during terrestrial feeding. We hypothesized that morphological and functional compromises in the hyobranchial apparatus will yield decreased prey capture performance for semi-aquatic species that feed in both air and water when compared to fully aquatic species. We found the fully aquatic newt, *Paramesotriton labiatus*, has increased mineralization of the hyobranchial apparatus, as well as relatively more robust ceratobranchial I + II complexes and epibranchials, compared to semi-aquatic newts, and that this increased robustness is correlated with increased aquatic feeding performance. Maximum hyobranchial depression acceleration was found to be approximately three times greater than in semi-aquatic species, at 50 m/s/s. Particle image velocimetry revealed peak and average fluid velocities generated during suction feeding events (0.6 m/s and 0.2 m/s, respectively) were more than double those produced by all semi-aquatic species. These findings reveal that a more robust hyobranchial apparatus increases aquatic feeding performance in a fully aquatic newt and accompanies specialization for suction feeding.

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**The Covert Dragon: Phylogeography of the Seadragons (Syngnathidae) along the Temperate Australian coast**

The southern coastline of Australia is home to a unique biota that has been exposed to complex changes throughout the glacial cycles. Glacial impacts on marine organisms of the region are less understood than in the northern hemisphere and detailed reconstructions of population histories were often hampered by the limited availability of genetic markers. Here, we investigate patterns of genetic structuring of two species of syngnathid fishes that are sympatric in parts of Australia's temperate coast. Both leafy seadragons (*Phycodurus eques*) and common seadragons (*Phyllopteryx taeniolatus*) are known for their remarkable camouflage mimicking seagrass and kelp. We used range-wide sampling of both species and sequenced ~1000 Ultraconserved Elements (UCEs) for >250 individuals. The genetic data is integrated with information on life history and geology to elucidate the phylogeographic structure and demographic history of each species and compare patterns between them. Both seadragons showed strong geographic structuring, consistent with their low dispersal potential. Considerable differences in genetic diversity existed regionally, some of which bearing signatures of recent changes in population size. A genetic break between populations of common seadragons in the southeastern part of the range coincides with the historical location of a land bridge connecting Tasmania to mainland Australia. Reopening of the seaway ~14,000 years ago resulted in opportunities for secondary contact and we found low levels of gene flow across the phylogeographic barrier. Overall, the high-throughput data provide a detailed picture of histories of both species and point towards complex factors influencing marine organisms in southern Australia.

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**A Short-snouted, Middle Triassic Phytosaur May Indicate Salt-Water Tolerance is Ancestral for Archosauria**

Following the end-Permian extinction, terrestrial vertebrate diversity recovered by the Middle Triassic and was dominated by reptiles. However, these reptilian clades, including archosaurs and their closest relatives, are not commonly found until ~30 million years later in Late Triassic deposits despite time-calibrated phylogenetic analyses predicting an early Middle or even Early Triassic divergence for those clades. One of these groups from the Late Triassic, Phytosauria, is well known from a near-Pangean distribution, and this easily recognized clade bears an elongated rostrum with posteriorly retracted nares and numerous postcranial synapomorphies, particularly of the pectoral girdle, that are unique compared with all other contemporary reptiles. Here, we recognize the exquisitely preserved, nearly complete skeleton of *Diandongosuchus fuyuanensis* as the oldest and basalmost phytosaur. The Middle Triassic age and lack of the characteristically-elongated rostrum fill a critical morphological and temporal gap in phytosaur evolution, indicating that the postcranial modifications of phytosaurs occurred prior to rostral elongation. The cranial modifications that are present in *Diandongosuchus* suggest early modifications for prey acquisition, paralleling the trend that is later observed in crocodylomorph evolution. Based on the paleogeographic location and possible marine paleoenvironment of *Diandongosuchus*, we hypothesize salt-water tolerance as the mechanism for Phytosauria's pan-Tethyan distribution, adding to the growing body of evidence that the saltwater tolerance of birds and crocodylians was present in their most recent common ancestor and closest relatives.