

may be limiting diversification of pharyngeal skeletal elements. A similar pattern was observed in a hybrid mapping population, allowing us to determine the extent to which phenotypic integration is reflected by the genotype-phenotype map. Using QTL mapping and qPCR, we identify *smad7* as a robust candidate gene driving integration between bones, providing important insights into the mechanisms of diversification and constraint acting on the pharyngeal skeleton.

Staghorn or stingray? High-resolution network analysis of cartilaginous trabeculae

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Sharks and rays possess cartilaginous skeletons supported by a cortex of mineralized tiles (tesserae) encasing the unmineralized core, imparting dynamic compressive stiffness to skeletal elements. In certain hard prey-feeding stingrays, an additional reinforcement exists, hollow mineralized trabeculae coursing throughout the unmineralized cartilage like support beams in a building. We combined high-resolution micro-CT imaging and custom quantitative network analyses in a multi-scale characterization of this trabecular network in a series of cownose rays (*Rhinoptera*). We demonstrate that trabeculae are highly aligned toward the occlusion surface, thickest near their origins, on the non-occlusal side of the jaw, before branching into smaller struts under the teeth. In the labiolingual direction, the trabeculae are considerably more mineralized under the functional teeth, with those under the forming dentition appearing distinctly wispy in microCT. The upright branching morphology of trabeculae gives the network the appearance of colonies of staghorn coral, with the finer branching near the teeth suggesting trabeculae may compartmentalize the unmineralized cartilage in addition to providing compressive reinforcement. Notably, the interaction between trabeculae and the jaw cortex is complex: trabeculae are also formed by individual tesserae but exposed to the external environment via pores in the cortex. The pores suggest a potential growth mechanism for trabeculae through cortical invaginations into unmineralized cartilage, indicating that trabeculae could provide novel models for understanding factors driving cartilage mineralization, growth and mechanics.

Shifts in salamander body sizes in response to 60 years of climate change

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Climate change impacts species distributions and abundances and can also affect body size, a fundamental trait that influences energetics, competition, and reproductive success. Many endotherms have exhibited body size declines in response to warming, but research on ectotherms, especially amphibians, remains limited. We examined body size shifts in seven species of Plethodontid salamanders in the Balsam Mountains, Southwest Virginia, USA. These species span a range of habitat preferences, from aquatic to terrestrial environments. We used historical data from 1957-1959 as a baseline and resurveyed salamanders in 2021 and 2023. We then examined the role of temperature and precipitation changes in driving body size shifts over time. We hypothesized that warmer and wetter conditions would lead to body size declines in the salamander species. Over the 60-year period, we found a general increase in temperature and precipitation across the resurvey sites. Contrary to our hypothesis, not all species showed body size declines: some species showed significant reductions in body size, others showed significant increases, and some showed no change over time. These differences may be due to variation in the natural history of the salamanders; body sizes of more terrestrial species declined while more aquatic species increased. These varying responses suggest that the influence of climate change on body size is species-specific and may be driven by a combination of factors, including different habitat preferences.

Do distributions of host susceptibility reflect the evolution of pathogen specialism or generalism?

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Pathogen life history strategies vary from specialists infecting a single host species to extreme generalists that successfully exploit multiple taxonomically distant host species. Further specialization occurs as pathogens evolve higher infection of a particular host type or population within a species. We propose that the degree of pathogen specialization or local adaptation can be detected by quantifying the continuous distribution of host susceptibilities to that pathogen, a well-described method in disease ecology. We develop a framework that uses these methods to detect specialist vs generalist life history strategies and local adaptation. First, we assume a Gamma distribution of host susceptibilities to pathogen infection and consider this model for three cases: 1) pathogen specialism and local adaptation, 2) non-specialism and local maladaptation, and 3) a pseudo-generalist pathogen. We then present examples from two empirical systems of animal viruses: an NPV infecting the butterfly species *Dione vanillae*, and