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**Damage or defenses: An examination of how the sea urchin proteome changes in response to ultraviolet radiation**

Anthropogenically induced ozone depletion and climate change have increased the importance in understanding how marine organisms, especially planktonic embryos and larvae that float in surface waters, respond to and protect themselves from abiotic stress. Marine organisms living in shallow waters are most vulnerable to damaging levels of ultraviolet radiation (UVR), which may act synergistically with other stressors including temperature, lower pH and changes in salinity. Over a century of research has demonstrated that echinoids, especially sea urchins, embryos and larvae are a powerful model organisms for studying effects of UVR on development, cellular targets, protein regulation, effects on whole organisms, and protection against damage. In addition to providing a large number of synchronously developing embryos amenable to cellular, biochemical, molecular, and single cell analyses, the purple sea urchin, *Strongylocentrotus purpuratus*, also offers an annotated genome, making it an excellent model for studying proteome dynamics and identifying protein biomarkers of stress. Our studies have highlighted some ways the proteome of *S. purpuratus* changes during development and in response to UV-induced stress. These changes include variation in protein levels as well as many post-translational modifications, such as phosphorylation, glycosylation, ubiquitination, and acetylation. Post-translational modifications may provide embryos with a fine-tuned, rapid-response to stress during early stages, especially during pre-blastula stages that rely on maternally derived defenses rather than responses through gene transcription.

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**Variation in immune responsiveness and tolerance of Mycoplasma infection between house finch populations**

Revealing how population differences in immune defenses impact pathogen load and shedding will greatly improve predictive models of disease spread. However, such links remain poorly understood in natural systems. Here, we present population differences in host immune responses, disease pathology, and pathogen load in a naturally occurring host-pathogen system, house finches (*Carpodacus mexicanus*) infected with *Mycoplasma gallisepticum* (MG). This bacterial pathogen causes severe conjunctivitis and, since emerging in 1993, has spread rapidly across North America. In this study, wild-caught birds from two populations with different histories of pathogen co-evolution were experimentally infected in the same captive environment. MG arrived in the exposed population (Alabama) in the mid-1990s, but, as of capture, had not been detected in the naive population (Arizona). While the Red Queen Hypothesis predicts that an exposed population should evolve increased resistance (the ability to reduce pathogen load more rapidly/completely), the populations displayed similar pathogen loads. However, early disease pathology (mass loss and conjunctival lesions) was less pronounced in the exposed population. This result suggests that tolerance of infection (reduced pathology per unit parasite), rather than resistance, may have evolved in the exposed population. Immunologically, the initial, inflammatory response (fever) began later in the exposed population, while subsequent, MG-specific antibody levels tended to be higher in that population. These data suggest that prioritization of different types of immune defense may help drive population differences in tolerance. We will discuss potential consequences of such differences in tolerance, rather than resistance, for disease spread and the evolution of virulence.

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**The insulin-like growth factor axis as a mediator of life history trade-offs**

Classic life-history theory predicts trade-offs between the lifetime fecundity and lifespan of an individual. However, little is known about the mechanisms that control these trade-offs. Two genetically divergent ecotypes of *Thamnophis elegans*, the Western garter snake, provide a natural experiment to explore genetic and hormonal mechanisms that are involved in these trade-offs. Populations of the fast-living ecotype live along rocky outcrops of Eagle Lake, in the Sierra Nevada Mountains. This ecotype has on average eight young each year, and has an average life span of four years. In contrast, the slow-living ecotype lives in the mountain meadows above Eagle Lake, has an average lifespan of eight years and average litter sizes of four, but reproduction is dependent upon food availability. One proposed mechanism involved in these trade-offs is the regulation of the insulin-like-growth-factor (IGF) axis. The IGF axis is involved in a broad spectrum of cellular functions, particularly those of cell proliferation, cell differentiation, and the inhibition of programmed cell death. At the organismal level, these genes affect an organism's physiological processes, including those of aging and reproduction. In this study, we explored sequence and expression variation in the genes IGF-1, IGF-2, IGF-1R, and IGF-2R. We found little variation in gene sequences between ecotypes. However, expression of IGF-2, IGF-1R, and IGF-2R mRNA was several fold higher in the fast-living ecotype than the slow-living. No difference was observed in expression of IGF-1 mRNA between ecotypes. We discuss the significance of these results in the context of variation in both life-history strategies between the two ecotypes and in environmental conditions between the two habitats.

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**Evolutionary morphology of the caudal musculoskeletal system in syngnathid fish: from swimming to prehension ... in different ways**

Seahorses and pipehorses possess the unique characteristic of extensive tail bending, allowing them to grasp onto the substrate. Current phylogenetic hypotheses suggest that grasping performance evolved more than once, as it seems to have arisen independently in pipehorses and seahorses. Pipehorse species with prehensile tail are nested within pipefish species (that lack this prehensile tail), hence are not sister group to the seahorses. Considering the different evolutionary strategies giving rise to a prehensile tail (starting from a rigid one), it is hypothesised that some crucial (and hence shared) structural modifications occurred at the level of (1) body armour organisation, (2) vertebra organisation, (3) interaction between plates on vertebra and (4) muscle organisation. To test these hypotheses, the caudal system in pipefish (ancestral condition), pipehorse and seahorse are compared, using histological and micro-CT data. The results confirm some hypotheses, but not all. As such, body armour organisation in pipehorse proved to be different from that of seahorses, providing both an increased capacity for flexibility between consecutive segmented plates (overall to partial plate reduction). Modifications in the musculature are also extensive, where seahorses represent a unique organisation of the muscle-tendon complexes for syngnathids (plate-like versus ancestral conical myoseptal organisation, and muscle fiber extension). This study thus confirms that within a single clade (syngnathids), at least two different evolutionary strategies have independently yielded an adaptive solution for a novel function, i.e. tail prehension.