Organism-environment interactions shape responses to stress in a changing world

As high resolution, genomic data is becoming straightforward to generate, biologists are faced with the challenge of causally linking molecular-level changes to phenotypes. Determining these connections is complicated by additional factors that can influence phenotype besides the genome – the environment, the epigenome, and the microbiome. My lab studies how organisms interact with their environment and how the environment shapes organismal traits, specifically in the context of rapidly changing environments and stress. I will present new data from two major themes in the lab. First, we are examining the interactive role of temperature and microbes on development and fitness. Using the purple sea urchin, *Strongylocentrotus purpuratus*, as a model, we have found that the microbial community experienced during early development impacts host growth, chromatin accessibility, and ultimately gene regulation. This novel finding challenges what we know about how host phenotypes and gene expression can be altered by the environment. Second, we investigate the role of phenotypic plasticity and adaptation in organismal responses to stress. Tropical species' range shifts can rapidly alter the community composition, productivity, and species diversity in temperate ecosystems. My lab has is using community science data, whole genome re-sequencing, and establishing population specific polyp lines to enable us to test mechanisms underlying the range expansion of the upside-down jellyfish, *Cassiopea,* in Florida, which has economic and ecological consequences. With these studies, my lab addresses mechanistic questions on the molecular level that relate to key evolutionary and ecological processes.