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Edward E. Langbein Sr. Summer Fellowship

Assessing Genomic Variation in a Population of Bivalves from the Gulf of Maine

Bivalves are integral member0.2 (nt)m ben5T 50.2 ric communi5T 50.2 y in bo5T 50.2 r es5T 50. oceanic environmen5T The 2 are essential parts of the ecosystem as they create complex structural substrate for other organisms, nurseries for juveniles, and filter particles out of the water. Changes in water quality and chemistry can impact population health, in particular, because since bivalves are marine calcifiers they rely on the quality of the water to create their shells and survive. It has been shown, in the laboratory, that when water quality variables like pH are decreased, the ability of bivalves to calcify their hard parts decreases (Talmage & Gobler 2010).

In the Gulf of Maine, bivalves represent important fisheries (both wild and aquacultured) and assessing the impacts of the effect water quality has on bivalve populations is imperative. As part of my internship during the summer of 2015, bivalves were sampled from the coastal benthic zone Boothbay Harbor to the Kennebec River region using a grab sampler. A water quality sonde was also sent down with each grab sample to assess spatial variation in water quality. The sonde measured variables such as pH, salinity, dissolved oxygen. When the grabs were collected, a portion of the sediment was separated and sent off for analysis at the University of Maine at Orono. The sediment was analyzed according to grain size and broadly classified as mud, sand and gravel.

Some of the most abundant bivalve species were the clams *Nucula proxima* and *Arctica islandica*. This was particularly intriguing because *Arctica islandica* is recognized in the literature as a "climate change clam" since it is so long-lived and slow-

multilocus genotype and environmental parameters and will help assess the impact the