

Alana Luzzio

Advisor: Dr. Sarah Kingston

Edward E. Langbein Sr. Summer Fellowship

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

Bivalves are integral members of the benthic community in both estuarine and oceanic environments. They 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-growing. This allows the clam to sequester significant environmental data in its shell as it calcifies and *A. islandica* is often used in paleotemperature model reconstructions.

In order to assess how the bivalves are reacting to the changing water quality parameters there needs to be genetic, phenotypic, and environmental analysis to achieve a full picture. To do this, my project has multiple dimensions. The first part is the genetic component. I had previously sent *N. proxima* for Next Generation Sequencing at the University of Texas at Austin. This assay investigates correlations between highly

multilocus genotype and environmental parameters and will help assess the impact the variation in water quality has on population composition of these bivalves. I received the sequences and assessed them using bioinformatics pipelines in Spring 2017.

This summer with funding from the Edward E. Langbein Sr. Summer Fellowship as well as guidance from my advisor Dr. Sarah Kingston, I was able to delve deeper into this project. This summer, I applied the Next Generation Sequencing assay to *A. islandica* populations. To detail this process out further, I performed a library prep on 171 samples of *A. islandica*. I performed a size purification on the pippin prep to ensure the size was between 300 and 500bp and then sent off for a run on an Illumina HiSeq 4000 at the University of Texas at Austin for single end reads of 150bp in size. I recently received the sequences this summer and have started to analyze the results using a bioinformatic pipeline. This genetic component allows me to assess the genetic variation in these species.

These clam's physical phenotype of shell shape and structure reflects both genetic variation in their abilities to calcify their hard parts as well as the impact local water quality has on this ability. To assess this, I started to delve into their shell chemistry composition. This summer, I utilized a protocol to cleaned the shells of organic matter and then using the Scanning Electron Microscope (SEM) in the Earth and Oceanographic Sciences department assessed the calcium / magnesium and strontium / magnesium ratios in the shell. These measured ratios tell us how bioavailable these compounds were during calcification.

In conclusion, this summer I was able to prepare all 171 samples of *A. islandica* for sequencing using library prep techniques to purify and concentrate the samples before sending them off for sequencing. I recently received the sequences and have started to analyze them. For the shell chemistry, I have cleaned the organic matter from each shell in preparation for SEM analysis. To date, I have started to analyze the shell chemistry composition on the SEM. I am continuing to analyze the shell chemistry and run data through the bioinformatic pipeline for both species to attempt to hypothesize how the environmental variables and genetics are interacting and how this relationship is manifested as a phenotype. This study will add to the body of literature and clarify how benthic dwelling Gulf of Maine bivalves are faring in the face of changing water quality variables.