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### The evolutionary response of populations of the blue mussel (*Mytilus edulis*) populations to climate change

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Jenna Watling

Since early July, I've been working on three projects. I've been studying parrotfish speciation, dissecting green crabs, and collecting samples of muscle tissue from blue mussels. My primary occupation is the study of parrotfish speciation with Dr. Carlon. He has found evidence of speciation through hybridization, which is has not been commonly observed. During the 2013-2014 academic year, he and I extracted DNA from fin or scale samples from Pacific parrotfish. Throughout the year and during this summer, we have been amplifying specific genes—nuclear and mitochondrial—using a polymerase chain reaction, confirming the amplification via gel electrophoresis, and preparing the samples for Sanger sequencing, which is done by the Nevada Genomics Center. Once we receive the sequencing results electronically, I use the program Geneious to check the quality of the individual sequences and resolve ambiguous calls (e.g., whether a specific base pair is an arginine or a cytosine) and align the sequences so we can compare them base pair by base pair. By examining both nuclear and mitochondrial genes, which evolve at different rates, we can hypothesize about the way in which different species arise.

Green crab (*Carcinus maenas*) dissection is an early step in Aidan Short's analysis of their diet. I assist in collecting tissue samples. We collect muscle tissue from the crabs' claws. These samples will allow Aidan to differentiate between the crabs' food and the crabs themselves. Then their carapaces are cut open and their entire stomachs are collected. In the near future, Aidan will use next-generation sequencing to identify any species present in the crab stomachs and quantify the abundance of these species' DNA. Sequencing the crabs' stomach contents is more precise and more complete than the older method of hard part analysis. The green crabs' diet is of interest because green crabs are an invasive species and have been implicated in loss of sea grass beds and decreasing soft shell clam populations.

Collection of tissue from blue mussels (*Mytilus edulis*) and bay mussels (*M. trossulus*) is a preliminary step for Dr. Sarah Kingston's investigation of the genetic basis of variation in shell calcification rate under environmental conditions possible due to ocean acidification. She collects mussels from various sites along the Maine coast, marks each with a color and number, and records their buoyant weight. The buoyant weight allows Dr. Kingston to determine the mass of the shells without having to kill the mussels. In the first round of experiments, Dr. Kingston determined which of three experimental schemes (involving the manipulation of food levels, temperature, and pH) resulted in the greatest variation of shell calcification after two weeks. The harshest scheme—no food, high temperature, and low pH—resulted in the greatest variation, and this scheme will be used in the experiment going forward. After the experimental period, the mussels are re-weighed and tissue samples are collected. I assist in tissue sample collection; we cut open the mussels and remove the foot and the adductor muscle. In the next round of experiments, I will further assist by participating in mussel collection, monitoring tank conditions during the experimental period, and labeling and weighing the specimens. The DNA libraries obtained from the tissue samples will be sent away for next generation sequencing, and Dr. Kingston will begin looking for genetic variation associated with calcification rates.