Local or long-distance recruitment of the Atlantic Sea Scallop (Placopeceten magellanicus) in Coastal Maine

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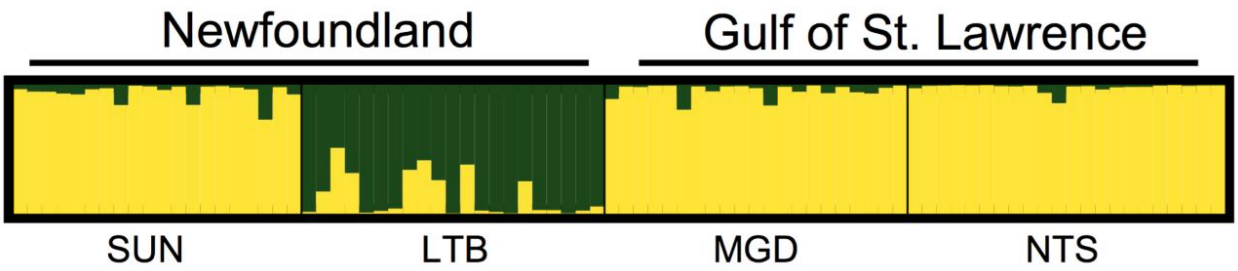
This summer I spent 9 weeks working in the Kingston lab continuing a long-term study conducted in conjunction with the Hurricane Island Foundation regarding the source populations of inshore Atlantic sea scallops in coastal Maine. The Atlantic sea scallop is a member of the mollusk phylum and is most closely related to other bivalves such as clams, oysters and mussels. Atlantic sea scallops are found solely in the northwest Atlantic Ocean, primarily between Cape Hatteras of North Carolina and the northern tip of Newfoundland, Canada. The coastal sea scallop industry is of economic interest in Maine, especially as local fishermen are looking to diversify their fisheries. Identifying source populations and further understanding the relationship between inshore and offshore populations is not only of interest for local fishermen and scientists but also for informing management efforts.

Rolling closures are the primary fisheries management tool used along the coast of Maine and are implemented when it is believed that a temporary relief of harvesting efforts would benefit a particular environment or population. Closures can be very effective in maintaining stable populations however only if there is a significant understanding of the target population. This, unfortunately, is not currently the case for Atlantic sea scallops.

The research that I have been performing on behalf of the Kinston lab will contribute to a more in-depth understanding of Maine's scallop populations and how to sustain them. In order to do this, I extracted the DNA from the adductor muscle tissue samples of local scallop populations of interest near Penobscot Bay as well farther-flung populations along the coast and offshore (George's Bank). After this, I assessed the quality of the extracted DNA to ensure that it was intact and had not been sheared (broken up) in the process. To do this, I used a NanoDrop spectrophotometer to assess DNA concentration and a Lonza gel to assess molecular weight. I also transferred all the project samples, in addition to all other samples collected, to long-term preservation grade ethanol to another in hopes of better preserving them. It is important that samples are preserved appropriately so as to prevent degredation.

The main objective of this project is to eventually perform a next generation sequencing-based genome reduction technique -- double digest RADsequencing -- on the samples in order to identify any single nucleotide polymorphisms (often called SNPs - a change in one of the base pairs A, T, C or G at a particular location – found at 10s of 1000s of loci) that a scallop may possess and to use this knowledge to infer ancestry. If two organisms share multiple SNPs, it is reasonable to suggest that they share a more common ancestor than two organisms that do not. During my time at Bowdoin this summer, I was able to complete all of the RADseq library preparation necessary to sequence 40 of the 100 target samples. Future work would involve finishing the remaining 60 samples and then using the sequencing results to identify SNPs and infer which scallops are more closely related. This information could then be used to inform stakeholders where certain populations are thought to come from and how best to protect them. This research was truly fascinating and I was so lucky to have had this opportunity.

Faculty Mentor: Sarah Kingston



Source: VanWyngaarden_et_al-2017 figure.png

This is an example of the type of image that can be generated once the genetic material has been sequenced and once the number of common SNPs have been identified. Each column represents an individual scallop while each color represents a different population.