Identifying genomic architecture features that contribute to critical phenotypes in shellfish

PIs: Matthew George (University of Washington), Mackenzie Gavery (NOAA and University of Washington), Steven Roberts (University of Washington)

Shellfish are a key component of domestic seafood production. Shellfish aquaculture is one of the most economically important sectors of the US industry, with major species including oysters and clams. As is the case with all farmed species, there are a suite of desirable phenotypes that directly correspond to increased environmental and economic sustainability. The ability to identify genomic predictors of phenotype offer a framework to increase aquaculture production. In shellfish aquaculture key phenotypes continue to be resilience and stress tolerance. Understanding the physiological underpinnings of these phenotypes in oysters and clams has been a focus in our group. To this end we have archived hundreds of samples from families with diverse phenotypic responses to stress. For example, as part of one effort to examine the influence of ploidy on oyster stress tolerance we have Standard Metabolic Rate (SMR) and enzyme activity data on oysters that reveal diverse physiological profiles.

In response to the NRSP-8 Small Funding Possibilities for US Aquaculture Groups, we are proposing to 1) identify genomic architecture variation contributing to desired phenotypes in shellfish and 2) develop a community platform to share data and analytical approaches. These objectives are in direct response to Program Objective 2: *Advance genome-to-phenome prediction by implementing strategies and tools to identify and validate genes and allelic variants predictive of biologically and economically important phenotypes and traits.* Additionally the proposed work will address Program Objective 1, by ... *providing a deep functional annotation of assemblies, and comparison across species to understand structure and function of animal genomes.*

To carry out these objectives we will leverage our library of Pacific oyster tissue samples that include individuals with a range of phenotypes (e.g., SMR, survival, growth). Fifteen individuals representative of the best and worst performing cohorts will be selected for whole genome sequencing (WGS). We will address genomic architecture variation by evaluating ribosomal DNA (rDNA) copy number variation. This genomic feature has received limited attention, however rDNA encodes for ribosome biogenesis, one of the most central processes in cellular biology from a functional perspective because of its close connections to growth, development, and metabolism. rDNA is an emerging genomic determinant of phenotype, with respect to both sequence and copy number variation. Using WGS will characterize rDNA copy number variation while also assessing variability across other features including transposable elements, another feature with characteristics that have correlations with phenotype in marine invertebrates. We will also be able to assess genomic sequence variation. $10,000 is requested to develop and sequence thirty WGS libraries. To complement this effort on our archived samples, we will also evaluate WGS data submitted to NCBI from oysters and clams, prioritizing data where phenotype information is available. Computational approaches, data, and summaries of how genomic architecture predicts phenotype will be made available online in a manner similar to that found at https://robertslab.github.io/resources/Genomic-Resources. This project will primarily benefit the shellfish aquaculture community, though the informatic procedures will be applicable to the broader research community.