

## **Project Report**

PSMFC Subaward 23-084G for the period **Feb 1<sup>st</sup> through April 30<sup>th</sup> 2024**

Project Title: Gene activity and genetic selection in Pacific cod reared under thermal stress

Objective: Predict organismal and population outcomes of Pacific cod exposed to elevated temperature

Summary: Recent heat wave stress in the Gulf of Alaska has resulted in significant declines of Pacific cod, *Gadus macrocephalus*, in that region. The physiological and transcriptional responses of Pacific cod and whether selective mortality is present under thermal stress are unknown. The proposed project will address these questions critical to their survival under climate change by identifying regions of the genome and epigenome that respond to thermal stress. Juvenile Pacific cod will be reared in several temperatures then an integrated genomic approach will identify genes, gene variants, and epigenetic markers that respond to thermal stress and confer resilience. To complement the genomic approaches and further investigate temperature influences on energy resources, we will perform lipid analyses. This work will inform predictions of genetic selection and molecular response of Pacific cod in the Gulf of Alaska under climate change.

## **Progress and results**

For this reporting period effort included analyses of lipid samples at Oregon State University. In addition, RNA-seq data analysis efforts have progressed to evaluate the Gene Ontology terms associated with genes differentially expressed based on temperature. In warmer conditions, decreased activity is observed in genes related to mitosis and cell adhesion, suggesting impacts on liver health and overall resilience. Inflammation-related genes were less active, which was unexpected and warrants further investigation. DNA extracted for bisulfite sequencing was sent off for library preparation and sequencing. It was determined by the sequencing facility that the DNA integrity was not optimum to proceed therefore it was determined that we would revisit sample selection for epigenetic analysis.

## **Challenges**

None to report.