

Using genomics to understand differences in sea scallop *Placopecten magellanicus* populations

Samuel J. Gurr, NRC Research Associates Program at NEFSC Milford, currently: Coastal Oregon Marine Experiment Station, Oregon State University
Jonathan B. Puritz Department of Biological and Environmental Sciences, University of Rhode Island; **Dvora Hart** Woods Hole, NEFSC, NOAA;

Lisa Milke and **Shannon Meseck** Milford Laboratory, NEFSC, NOAA;

Katherine McFarland NEFSC Milford Laboratory, Currently: National Ocean Service Office for Coastal Management, NOAA; **Mackenzie Gavery** Seattle, NWFSC, NOAA

Introduction

The Atlantic sea scallop, *Placopecten magellanicus*, is the largest wild caught scallop fishery in the world (~\$450 million United States dollars). Scallop habitat range has been shifting northward as water temperatures increase, and recent research suggests that growth slows as ocean acidification (OA) intensifies. Population genetics are important to understand the capacity of an organism to evolve to long-term ecosystem-scale changes. Preliminary studies suggest that there might be genetic differentiation between southern and northern populations of sea scallops. We propose to **build and annotate the chromosome-scale genome** for *P. magellanicus* to serve as an open-source reference for fisheries management. Wild sea scallops were harvested across a latitudinal gradient from the Northeast US Atlantic to investigate genetic variation between populations. Sea scallops from 2 different populations were exposed for 2 weeks to two different temperatures (9°C and 15°C) and two different OA conditions (ambient and ~150 μatm $p\text{CO}_2$). Hemolymph and gill samples were taken to understand how each populations respond to changing ocean conditions. Through a combination of manipulative experiments and -omics, we can start to understand the capacity for the sea scallop to evolve and adapt to long-term ecosystem changes.

Methods

PROBLEM: Population genetics are essential to improve the predictive accuracy of risk assessments, identifying selective genetic regions that may permit sensitive species to adapt under long-term ecosystem-scale change

SOLUTION: We funded assembly and annotation of the *P. magellanicus* genome and employed multi-omics resequencing of different populations and under an **experimental challenge**

APPROACH: Wild juvenile sea scallops spanning the Northeast US were collected (Fig. 1) for population genetics and a subset were exposed to a 14-day challenge. Chosen conditions represented the current summer and projected **warming** and **acidification** in the GoM (Table 1).

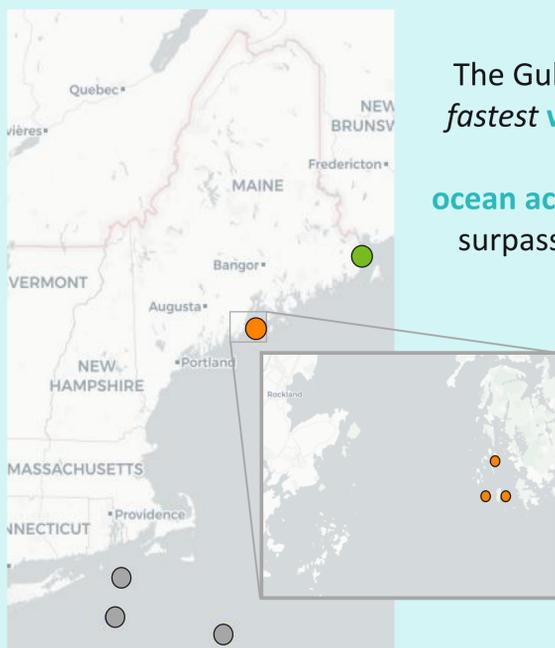
- genome assembly and annotation
- multi-omics suite (IcWGS, ATACseq, and RNAseq)
- hemocyte viability



Photos: (left) The ocean acidification laboratory at the Downeast Institute, (top right) sea scallops in experimental units, and (bottom right) Tessa Houston extracting hemolymph from a scallop. *photo credit: S. Gurr and B. Beal*



Photos: (right) Madison Meier (Hurricane Island Center for Science and Leadership) scuba diving for wild scallops in May 2025. (left) Wild collections targeted juveniles 1-2 years in age. *photo credit: Hurricane Island Staff*



The Gulf of Maine (GoM) is the **fastest warming** system globally

ocean acidification is projected to surpass physiological limits for marine calcifiers

Figure 1. Wild scallops were collected (north to south) from **Cobscook Bay, Hurricane Island, and the Mid-Atlantic Bight**

Results

PROBLEM: An open-source reference genome is a fundamental and invaluable product for end-users as we collectively experience the prolific research initiatives proceeding the publicized reference genomes; there is currently no genome for *P. magellanicus*

SOLUTION: Using multi-omics approaches and the new reference genome, understand mechanisms behind the interactions of adaptation and acclimation to **warming × OA**

- completed genome assembly and annotation, 19 chromosomes
- hemocyte viability was unaffected by treatment, fewer live hemocytes at low temperature
- pending -omics data to determine the contribution of genomic (adaptation) and non-genetic (rapid acclimation) regulation of gene expression under **warming × OA**

Table 1. Seawater chemistry from experiment challenge

Treatment	Temperature	$p\text{CO}_2$	Temperature (°C)	pH (total scale)	$p\text{CO}_2$ (μatm)
High	High		13.3 ± 0.3	7.70 ± 0.01	856 ± 27
High	Low		13.6 ± 0.3	7.77 ± 0.03	746 ± 55
Low	High		9.3 ± 0.3	7.84 ± 0.07	687 ± 43
Low	Low		9.4 ± 0.2	7.83 ± 0.09	612 ± 33

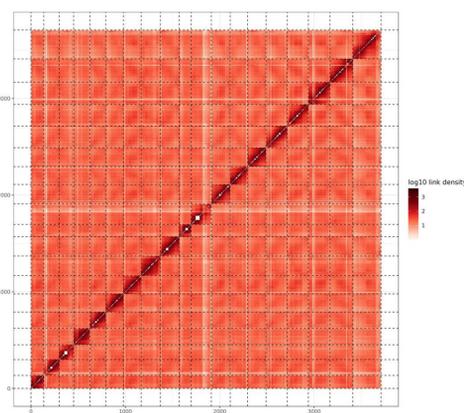


Figure 2. Scaffolding heatmap of the *P. magellanicus* genome, containing 19 chromosomes

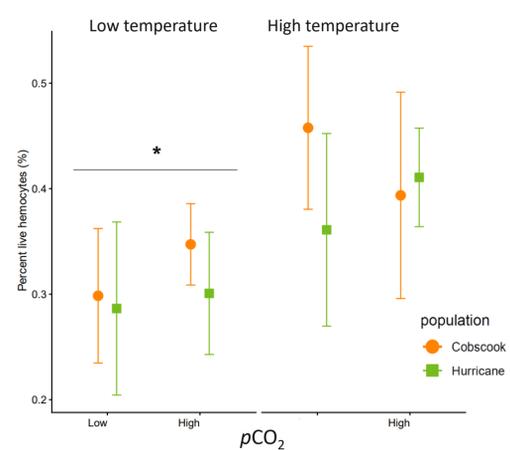


Figure 3. *In-vivo* cytology found low temperature reduced hemocyte viability, and GoM populations did not differ.

In the pipeline..

Synthesize the full-omics suite

- adaptive loci
- open chromatin
- gene expression



..to determine the contribution of genomic (adaptation) and non-genetic (rapid acclimation) regulation of gene expression under **warming** and **ocean acidification**.

Funding Source



NOAA Ocean Acidification Program, Project number 25199
 "Disentangling adaptation from acclimation: Identification of genetic and non-genetic traits that enable environmental tolerance among populations of Atlantic sea scallop *Placopecten magellanicus*"

Contributors



Co-PIs

THE UNIVERSITY OF RHODE ISLAND

Conclusions

1) We completed assembly and annotation of the chromosome-level reference genome for the Atlantic sea scallop *P. magellanicus*

2) Sea scallops from southern and northern Gulf of Maine showed no difference in hemocyte viability under **warming × acidification**