Archived Oyster Samples Collected from the Delaware Bay from 2018 to 2021 (SEGO project)

Website: https://www.bco-dmo.org/dataset/872323
Data Type: Other Field Results
Version: 1
Version Date: 2022-03-23

Project
» Collaborative Research: Spatial analysis of genetic differences in salinity tolerance resulting from rapid natural selection in estuarine oysters (SEGO)

Contributors	Affiliation	Role
Hare, Matthew	Cornell University (Cornell)	Principal Investigator
Munroe, Daphne	Rutgers University	Co-Principal Investigator
North, Elizabeth	University of Maryland Center for Environmental Science (UMCES/HPL)	Co-Principal Investigator
Newman, Sawyer	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
The Selection along Estuarine Gradients in Oysters (SEGO) project is a collaborative NSF-funded effort to measure and understand the dynamics of short term adaptive change at small spatial scales. We focused on eastern oysters as an example of a common marine life history – high fecundity, complex life cycle with early larval dispersal, and sedentary (sessile for oysters) life after larval settlement. The data assembled in this data table are collections made over three years for two types of genomic analysis: (1) annual adult samples collected along the axis of the Delaware Bay estuary to capture a gradient in potentially stressful low salinities, (2) adult samples collected from mid-bay for experimental low-salinity challenge experiments, and (3) spat and broodstock collected for low salinity challenge experiments directly on wild spat or on larval progeny of broodstock collected from low vs. moderate salinity, respectively. Transect adults were collected by dredge in 2018, 2019 and 2021 from the same 5 subset of sites, each year, that the Rutgers Haskin lab consistently monitors every year to manage the oyster fishery. By piggy backing on the Haskin monitoring effort, the SEGO project has benefited from the long term data and deep understanding that Rutgers scientists have built about the Delaware Bay oyster population. 2021 was an exception because adults from an additional three sites were collected and analyzed. Two replicate challenge experiments on adults were accomplished in 2019 and 2020 using similar-size oysters collected from the highest oyster density part of the Delaware Bay population where environmental variation seems to generate the least mortality. Full details on the wild transect samples (genotype-environment association tests) and from the challenge experiment results comparing survivors vs. nonsurvivors are being prepared for publication. Spat collected in 2020 from across the salinity gradient were used for low salinity challenge experiments – results are published in Manuel et al. 2023. Broodstock collected in low vs. moderate salinity regions of the estuary in April 2021 were spawned to conduct a low salinity challenge experiment on their larvae, but larval performance and survival was too low for meaningful results.

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Coverage

Spatial Extent: **N**:39.442 **E**:-75.248 **S**:39.2358 **W**:-75.518
Temporal Extent: 2018-10-19 - 2021-06-28

Methods & Sampling

Sampling and analytical procedures:

Spat and adult samples dredge-collected from the James Joseph research vessel were based on standard operating procedures for the Haskin Shellfish Research Laboratory annual dredge survey to monitor the natural oyster (seed) beds on the New Jersey side of Delaware Bay. Annual stock assessment workshop reports related to these samples (Rutgers oyster SAW reports) are available at https://hsrl.rutgers.edu/documents/delaware-bay-oyster-stock-assessment-reports/ and should be consulted for dredge method details and definitions for spat versus adult life stages. Additional published reports describing aspects of the oyster population are given below.

In general for transect analysis samples, sample collections for the SEGO project piggy-backed on Haskin monthly monitoring program collections. The Haskin program consistently samples oysters from the same grids every month (see SAW reports for a definition of grid). Dredge contents were hand sorted to find spat if present. All spat were collected. A sample of 50 adult oysters from each site was haphazardly (without size selection) culled, cleaned of fouling organisms, measured for shell height (hinge to longest dimension), and shucked for tissue dissection and preservation in ethanol. For challenge experiments, many more dredge hauls were required from the same area to find sufficient numbers of similar-sized adults. They were processed by cleaning them of fouling organisms and arranging them in four ambient-salinity and room temperature raceways and fed frozen shellfish diet according to manufacturers protocols: 0.18 mL per animal based on 10g meat weight. Feces and pseudo-fences were siphoned out every day and water was changed approximately every 4th day throughout the challenge experiment. Challenge experimental protocols will be reported in conjunction with genomic analyses.

BCO-DMO Processing Description

- Dates converted from mm/dd/yyyy format to yyyy-mm-dd format
- Latitude and longitude fields rounded consistently to 5 decimal places
- Temperature and salinity fields rounded consistently to 1 decimal place
- Dissolved oxygen field rounded to 2 decimal places

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Data Files

File
nsf_oyster_tissues_bco-dmo-1.csv — (Comma Separated Values (.csv), 8.00 KB) MD5:c67797051528fd198c00d61f39cde3df
File processed with laminar pipeline "872323_v1_delaware_bay_oyster_samples" at path 872323/1/data/nsf_oyster_tissues_bco-dmo-1.csv

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Related Publications

Howlander, A., E. North, D. Munroe, M.P. Hare. Predicting the salinity history of oysters in Delaware Bay using observing systems data and nonlinear regression. Estuaries and Coasts, in revision.
Results

Manuel, E. C., Hare, M. P., & Munroe, D. (2023). Consequences of Salinity Change, Salinity History, and Shell

Morphology on Early Growth of Juvenile Oysters. Journal of Shellfish Research, 42(1). https://doi.org/[10.2983/035.042.0103](https://doi.org/10.2983/035.042.0103)
Results

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Results

Munroe, D., Tabatabai, A., Burt, I., Bushek, D., Powell, E. N., & Wilkin, J. (2013). Oyster mortality in Delaware Bay: Impacts and recovery from Hurricane Irene and Tropical Storm Lee. Estuarine, Coastal and Shelf Science, 135, 209–219. https://doi.org/[10.1016/j.ecss.2013.10.011](https://doi.org/10.1016/j.ecss.2013.10.011)
Related Research

Powell, E. N., Ashton-Alcox, K. A., Kraeuter, J. N., Ford, S. E., & Bushek, D. (2008). Long-term Trends in Oyster Population Dynamics in Delaware Bay: Regime Shifts and Response to Disease. Journal of Shellfish Research, 27(4), 729–755. https://doi.org/10.2983/0730-8000(2008)27[729:ltiopd]2.0.co;2 [https://doi.org/10.2983/0730-8000(2008)27[729:LTIOPD]2.0.CO;2](https://doi.org/10.2983/0730-8000(2008)27[729:LTIOPD]2.0.CO;2)
Related Research

Simon, A., E.C. Manuel, D. Monroe, H. Borchardt-Wier and M.P. Hare. In prep. Microgeographic variation in gene expression plasticity: Transcriptomic responses to osmotic stress in Crassostrea virginica juveniles.
Results

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Related Datasets

IsRelatedTo

Munroe, D., Hare, M. (2023) **Wild spat data from experiments performed to investigate the effect of salinity juvenile oyster growth using spat collected from three salinity zones in Delaware Bay in 2019 and 2020.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2023-05-09 doi:10.26008/1912/bco-dmo.895783.1 [[view at BCO-DMO](#)]
Relationship Description: These datasets were collected and analyzed as part of the same collaborative NSF SEGO project.

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Parameters

Parameter	Description	Units
Date	Date of sample collection	unitless
Species	Latin name (Crassostrea genus abbreviated "C")	unitless
location_1	Name of estuary	unitless
location_2	Name of oyster bed	unitless
lat	Latitude in decimal degrees; positive values represent Northern coordinates	decimal degrees
lon	Longitude in decimal degrees; negative values represent Western coordinates	decimal degrees
No_individ	Number of individuals in a sample	unitless
life_stage	Adults/spat/larvae	unitless
tissue_type	Type of tissue dissected and preserved	unitless
Experiment	Specific experiment the sample was used for	unitless
preservative	Name of chemical preservative	unitless
collector	List of collectors, primary listed first	unitless
vessel	Name of research vessel	unitless
method	Method of oyster collection	unitless
Temp	Temperature	degrees Celsius
Salinity	Salinity	practical salinity units
DO	Dissolved oxygen	mg/L
Notes	Sample notes	unitless

Instruments

Dataset-specific Instrument Name	YSI handheld Pro2030
Generic Instrument Name	Conductivity Meter
Dataset-specific Description	YSI handheld Pro2030 calibrated for conductivity at the start of the season and again mid-season.
Generic Instrument Description	Conductivity Meter - An electrical conductivity meter (EC meter) measures the electrical conductivity in a solution. Commonly used in hydroponics, aquaculture and freshwater systems to monitor the amount of nutrients, salts or impurities in the water.

Project Information

Collaborative Research: Spatial analysis of genetic differences in salinity tolerance resulting from rapid natural selection in estuarine oysters (SEGO)

Coverage: Delaware Bay, NJ side of channel: 39.43 N, -75.50 W to 39.14 N, -75.14 W

NSF abstract:

Many marine animals have a bipartite life cycle consisting of a stationary bottom-dwelling adult stage and a mobile larval stage. The flow of water transports these larval offspring, and their genes, to different habitat patches. It is thought that animals from nearby patches will be more genetically similar than animals in patches that are further in proximity, but these patterns of genetic similarity may not be maintained if the nearby patches have different habitat characteristics. This idea is fundamental to our understanding of adaptation and evolution, but it has not been adequately tested with respect to the effects of rapid selection. This study applies new technologies to test if the genetic signatures of marine animals change even when patches with different environmental characteristics are closer together than the dispersal distance of larvae. This research focuses on eastern oysters (Crassostrea virginica) in Delaware Bay, and their ability to withstand variability in the amount of salt in the water. This study will provide new insights on factors that control oyster survival and growth in estuaries with different salinity profiles. The three investigators are sharing study results with resource managers and stakeholders to improve shellfish restoration and oyster stock management in Delaware Bay, Chesapeake Bay, and New York. A postdoctoral scholar at Cornell and graduate student at the University of Maryland are being trained and mentored during the project. The investigators are also working with teacher training programs in New York and New Jersey to develop and disseminate new curriculum materials on oyster ecology for middle-school students.

The project will investigate whether hyposalinity tolerance of oysters is a function of viability selection during larval dispersal and after settlement. Gene flow across salinity zones within an estuary is expected to be high enough that adaptive differentiation will not result from Darwinian multigenerational processes. Instead, recurrent viability selection in each generation is expected to generate spatial variation in this trait at small spatial scales. This type of recurrent within-generation adaptation has been referred to as phenotype-environment mismatches and has been hypothesized to generate balanced polymorphisms, but it has never been studied beyond single gene cases. The project team is testing for spatially discrete patterns of selection by first collecting oysters from different salinity zones, measuring variation in their tolerance to low salinity and then testing for associations between this trait and genomic variation using whole genome sequencing. Experimental hyposalinity challenges enable within-generation, before/after genomic comparisons to identify

DNA variants that change as a result of strong viability selection. Candidate genes and selectively neutral control loci will be assayed in larval, juvenile, and adult samples from the same salinity zones to test for an association between variation at candidate loci and lifetime hyposalinity exposure. Two years of environmental data will be collected and added to an existing long-term data set to map salinity variation. The observed spatial distribution of hyposalinity tolerance and genomic variation associated with it provide a test that could definitively reject the prevalent assumption that all larvae have similar capabilities. If larvae differ by parental source for traits that differentially affect their viability in the plankton, then phenotype-environment mismatches can have profound consequences for population connectivity. This project improves understanding about mechanisms that shape realized larval dispersal and recruitment variation in oyster populations.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756712

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