

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

Website: <https://www.bco-dmo.org/dataset/895783>

Data Type: Other Field Results

Version: 1

Version Date: 2023-05-09

Project

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

Contributors	Affiliation	Role
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Abstract

Higher salinity habitats tend to support faster oyster growth, while lower salinity habitats act as a refuge from predation and disease but tend to slow growth. Two experiments were performed to investigate the effect of salinity juvenile oyster (also known as spat) growth. One experiment used wild oyster spat collected from three distinct Delaware Bay salinity zones that were then transplanted into various salinity conditions in the laboratory where growth was monitored (results reported in this dataset). Transplanting into low salinity led to decreased growth compared to transplanting to higher salinity, and growth of oyster spat was overall highest for spat from the lowest salinity source. A second experiment used hatchery reared oyster larvae set in one of four different salinity conditions (see "Related Datasets" section for methods and results of hatchery spat experiments). Lower final salinity treatments were associated with lower growth, lower initial salinity treatments were associated with faster final treatment growth, and final growth depended on the interaction between initial and final salinity. As increased freshwater events due to climate change are expected in the Delaware Bay and regionally in the Northeast, these results indicate that nonlinear early life stress responses are important to quantify to better understand oyster stock resilience and plan management.

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Coverage

Spatial Extent: N:39.43333 E:-74.83333 S:38.75 W:-75.6666

Temporal Extent: 2019-10 - 2020-12

Methods & Sampling

Instruments

Equipment for these experiments included tanks, algal paste, microscopes, micrometers and calipers.

Data Processing Description

Data provided are raw individual oyster sizes.

BCO-DMO Data Manager Processing Notes:

* Sheet 1 of file "WildSpatSizes.xlsx " was imported into the BCO-DMO data system

* Column names adjusted to conform to BCO-DMO naming conventions designed to support broad re-use by a variety of research tools and scripting languages. [Only numbers, letters, and underscores. Can not start with a number]

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Data Files

File
salin_wild_spat.csv (Comma Separated Values (.csv), 12.21 KB) MD5:da6773e426533d69308b7bf12f7944f7 Primary data table for dataset 895783.

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Related Publications

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>

Results

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Related Datasets

IsRelatedTo

Hare, M., Munroe, D., North, E. (2024) **Archived Oyster Samples Collected from the Delaware Bay from 2018 to 2021 (SEGO project)**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-03-23 doi:10.26008/1912/bco-dmo.872323.1 [[view at BCO-DMO](#)]

Munroe, D., Hare, M. (2023) **Hatchery-reared spat data from laboratory experiments performed to investigate the effect of salinity on juvenile oyster growth 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.895791.1 [[view at BCO-DMO](#)]

Relationship Description: Related experiment performed to investigate the effect of salinity on juvenile oyster spat growth.

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Parameters

Parameter	Description	Units
Year	This is the year of spat collection, making it the year of spat settlement (cohort year), and year of the experiment. Years include 2019 and 2020 only.	unitless
Spat_ID	Provides an unique spat identification code. Each spat was measured repeatedly so the growth associated with that ID is from size over time for that individual.	unitless
Salinity_Source_Zone	This is the salinity region of the Delaware Bay from which the individual spat was collected. High salinity beds are located further downbay than moderate and low. In 2019, spat likely experienced average daily salinities of 16-20 ppt in the high salinity zone and 13-18 ppt in the moderate salinity zone. Spat likely experienced average salinities of 18-19 ppt in the high salinity zone, 14-17 ppt in the moderate salinity zone, and 8.5-12.5 ppt in the low salinity zone.	unitless
Final_Salinity_Treatment	This is the salinity treatment that the spat was placed into for the experiment. In 2019, these final salinities were replicated in triplicate. In 2020, these final salinity treatments were replicated quadruplicate. Final salinities differ between experimental years.	Practical Salinity Units (PSU)
Replicate	Indicates the replication of the final salinity treatments. In 2019, these include A, B, C. In 2020, these are indicated by A, X, Y, Z.	units
Initial_Length	Spat length was measured individually for each spat. The reported size is the spat length (hinge to growing edge) in millimeters (mm) at the beginning of the experiment.	millimeters (mm)
Final_Length	Spat length was measured individually for each spat. The reported size is the spat length (hinge to growing edge) in millimeters (mm) at the end of the experiment which ran for 6 weeks duration, thus the change in size from initial to final represents growth over 6 weeks.	millimeters (mm)

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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
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756698
NSF Division of Ocean Sciences (NSF OCE)	OCE-1756592

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