Hatchery-reared spat data from laboratory experiments performed to investigate the effect of salinity on juvenile oyster growth in 2019 and 2020

Website: https://www.bco-dmo.org/dataset/895791
Data Type: experimental
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 (see "Related Datasets" section for methods and results of wild spat experiments). A second experiment used hatchery reared oyster larvae set in one of four different salinity conditions (results reported in this dataset). Those spat were maintained in settlement salinities 22, 16, 10 and 6 for two to three weeks post-settlement, then measured before fully factorial transfer into new salinity conditions with measurement three weeks later. 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

This methodology describes this hatchery spat dataset as well as the related wild spat dataset:

This study examined how salinity and salinity history influence oyster spat growth . This was tested using two experiments, one using wild spat placed into different salinity treatments in the laboratory (referred to as Wild Spat Experiment, see Related Datasets section for methods) and another using hatchery raised spat which grew from larvae set in different salinities then transferred into new salinities after three weeks postset (referred to as Hatchery Spat Experiment, results reported in this dataset). Wild spat provided observations linked to pre-experiment conditions in the wild (larval dispersal, settlement, and early postset growth) to provide results of greater potential relevance to understanding effects of the natural estuarine gradient. The datasets provide the size of the oyster spat at the time they were placed into the final salinity treatments and at the end of the experiment.

See methodology in methods and results published in Manuel et al., 2023

Though laboratory-based, the geospatial range for Delaware Bay is used for this dataset due to use of some Delaware Bay oysters used to produce the animals, and filtered sea water from Delaware Bay was used.

Instruments

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

Data Processing Description

Data processing

Data provided are average size for a given experimental unit.

BCO-DMO Data Manager Processing Notes:
* Sheet 1 of file "HatcherySpatSizes.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]
* 7th data column with name column name "Final Salinity (average um)" renamed to "Final_Size_average" as it was described in provided metadata. This was reviewed by the data submitter.

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Data Files

File
salin_hatchery_spat.csv(Comma Separated Values (.csv), 3.42 KB) MD5:c30ef4b087fa68370b30fdff114d1a5c Primary data table for dataset 895791.

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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

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

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Parameters

Parameter	Description	Units
Initial_Salinity	The salinity that the post-set spat were exposed to before the start of the experiment. For the Selected spat, this exposure was 2 weeks in duration; for the Hybrid spat this exposure was 3 weeks in duration.	Practical Salinity Units (PSU)
Final_Salinity	The spat were moved to a new salinity regime for the experiment. These salinities were replicated. Both spat types were in this final salinity for a duration of 3 weeks.	Practical Salinity Units (PSU)
Replicate	Each combination of initial and final salinity was replicated four times (named A, B, C, D). Where a replicate is missing for a given combination of treatments in this dataset, the given replicate tank was lost or there were insufficient spat surviving to the end of the experiment.	unitless
Spat_Type	Spat type (Hybrid or Selected, see methodology)	unitless
Initial_Size_average	Spat length was measured for ten randomly selected spat in each experimental unit (treatment combination and replicate). The reported size is the spat length (hinge to growing edge) in micrometers (um) for the average across the ten measured spat.	micrometers (um)
Coefficient_of_Variation_Initial_Size	The standard deviation across all individual spat measured in each experimental unit (treatment combination and replicate) was calculated. Coefficient of variation is the ratio of the standard deviation to the average initial size.	micrometers (um)
Final_Size_average	Spat length was measured for ten randomly selected spat in each experimental unit (treatment combination and replicate). The reported size is the spat length (hinge to growing edge) in micrometers (um) for the average across the ten measured spat. The duration of time for the experiment was 3 weeks (21 days), meaning the difference in growth from initial to final size is the average growth over 21 days.	micrometers (um)
Coefficient_of_Variation_Final_Size	The standard deviation across all individual spat measured in each experimental unit (treatment combination and replicate) was calculated. Coefficient of variation is the ratio of the standard deviation to the average final size.	micrometers (um)

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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.

Funding