Oyster morphometric, condition, and parasite infection data from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2018-2020

Website: https://www.bco-dmo.org/dataset/1004478
Data Type: Other Field Results
Version: 1
Version Date: 2026-08-11

Project
» CAREER: Linking genetic diversity, population density, and disease prevalence in seagrass and oyster ecosystems (Seagrass and Oyster Ecosystems)

Contributors	Affiliation	Role
Hughes, A. Randall	Northeastern University	Principal Investigator
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Abstract
This dataset contains individual-level morphometric, condition, and parasite infection measurements for eastern oysters (Crassostrea virginica, urn:lsid:marinespecies.org:taxname:140657) sampled from 12 experimental restored reefs in Ninigret Pond, Rhode Island, USA, as part of a multi-year oyster reef restoration experiment using oysters sourced from four commercial hatcheries along the U.S. Atlantic coast. Morphometric and condition measurements, including shell height (mm), shell length (mm), dry tissue mass (g), dry shell mass (g), and condition index (dry tissue mass multiplied by 100 divided by dry shell mass), are provided for 515 individuals sampled in fall 2018 and fall 2020. Parasite infection data are provided for fall 2018 individuals only, and include presence/absence of infection by four oyster parasites: the macroparasites mud blister worm (Polydora sp.) and boring sponge (Cliona spp.), and the microparasites Haplosporidium costale and Perkinsus marinus. Infection intensity measurements are provided for the two most prevalent parasites, P. marinus and mud blister worm. The primary genetic cluster assignment for each individual is also provided; these assignments correspond to one of four genetic clusters identified with SNP genotype data, which broadly correspond to the four commercial hatchery sources (Maine, Massachusetts, New York, and Virginia) as described in the related genetic assignments dataset. This dataset also contains supplemental data on reef-level prevalence of infection by the four oyster parasites summarized by oyster genetic cluster for the 12 experimental restored reefs. For each parasite, the reef-level dataset includes the total number of individuals sampled, the number infected, and the proportion infected, reported separately for oysters assigned to each genetic cluster on the 12 focal restored reefs.

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Coverage

Location: Ninigret Pond, Charlestown, Rhode Island
Spatial Extent: **Lat**:41.3549 **Lon**:-71.6929
Temporal Extent: 2018-11 - 2020-10

Methods & Sampling

These data were published in Truskey et al. 2025 (Evolutionary Applications).

In fall 2018, we haphazardly collected live oysters from each reef by scuba or snorkel. We repeated sampling in fall 2020, when lower live oyster densities resulted in variable sample sizes among reefs. Following collection, oysters were placed on ice, transported to the Northeastern University Marine Science Center, and stored at −80°C until subsequent processing and analysis.

Measuring oyster traits

To assess variation in oyster traits associated with genetic cluster identity, we recorded the following size-related measurements for all oysters sampled in fall 2018 and 2020: shell height (mm) from the hinge to the outer shell edge; shell length (mm) from one lateral shell edge to the other at the widest point perpendicular to height; total mass (g); dry tissue and shell mass (g; tissue and shells dehydrated in drying oven for ≥ 48 h). We calculated oyster condition index as dry tissue mass × 100 divided by dry shell mass (i.e., dry tissue weight: dry shell weight ratio; Lucas and Beninger 1985; Mann 1978).

Additionally, for oysters sampled in fall 2018, we assessed infection by four common oyster parasites: the microparasites *Perkinsus marinus* (urn:lsid:marinespecies.org:taxname:562957) and *Haplosporidium costale* (urn:lsid:marinespecies.org:taxname:394948), the causative pathogens of Dermo disease and SSO disease, respectively, and the macroparasites, *Cliona* spp. boring sponges and *Polydora* sp. mud blister worms. To assess infection by the microparasites, we used DNA extracted from the 32 oysters sampled per reef in 2018 and performed a polymerase chain reaction (PCR) assay protocol developed for SSO (Stokes and Burreson 2001) and a quantitative polymerase chain reaction (qPCR) assay for Dermo (De Faveri et al. 2009). For macroparasite presence, we surveyed the shells of individual oysters for physical signatures of macroparasites (i.e., holes characteristic of boring sponge; interior blisters indicating burrowing by mud blister worms). In addition to infection presence, we also report infection intensities (parasite load or concentration, per infected host) for the two most prevalent oyster parasites (*P. marinus* and mud blister worm) as an additional axis of potential variation in the response (tolerance) of oysters to parasites. Standardized intensity values for *P. marinus* were generated through the above cited qPCR protocol. For mud blister worm intensity, we quantified the overall proportion of parasite-affected shell area using ImageJ (Abràmoff et al. 2004) following protocols from Hanley et al. (2023).

Data Processing Description

Individual-level trait data

Outlier flags are provided for individuals identified as statistical outliers for condition index and shell height in collections from 2018 and from 2020 based on the Rosner Test.

Dermo intensity values represent the *log10-transformed* copy number of *Perkinsus marinus* generated from the standardized qPCR protocol.

Reef-level parasite prevalence by genetic cluster

To evaluate patterns of parasite infection by genetic cluster, we calculated the prevalence of each parasite as the proportion of individuals infected (the number infected/the total number of individuals sampled for an observed parasite) for each genetic cluster on each reef.

BCO-DMO Processing Description

- Loaded file Truskey_EVA2025_ind_traits_parasites_combined_bcodmo.csv
- Stripped trailing unit suffixes (_g, _mm) from column names total_tissue_dryweight_g, total_shell_dryweight_g, shell_height_mm, shell_length_mm, renaming them to total_tissue_dryweight, total_shell_dryweight, shell_height, shell_length in compliance with BCO-DMO parameter guidelines
- Replaced value "x" with "1" in columns taggedoutlier_ci and taggedoutlier_height
- Set remaining null/missing values in taggedoutlier_ci to 0, keeping already-converted 1 values, cast to integer

- Set remaining null/missing values in taggedoutlier_height to 0, keeping already-converted 1 values, cast to integer
- Output file as 1004478_v1_ind_traits_parasites.csv

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Related Publications

Abràmoff, M.D, Magalhães, P.J., Ram, S.J. 2004. Image processing with ImageJ. Biophotonics International 11(7): 36−42
Software

De Faveri, J., Smolowitz, R. M., & Roberts, S. B. (2009). Development and Validation of a Real-Time Quantitative PCR Assay for the Detection and Quantification of Perkinsus marinus in the Eastern Oyster, Crassostrea virginica. Journal of Shellfish Research, 28(3), 459–464. https://doi.org/10.2983/035.028.0306
Methods

Hanley, T. C., Grabowski, J. H., Schneider, E. G., Barrett, P. D., Puishys, L. M., Spadafore, R., McManus, G., Helt, W. S. K., Kinney, H., Conor McManus, M., & Randall Hughes, A. (2023). Host genetic identity determines parasite community structure across time and space in oyster restoration. Proceedings of the Royal Society B: Biological Sciences, 290(1995). https://doi.org/10.1098/rspb.2022.2560
Results

Lucas, A., & Beninger, P. G. (1985). The use of physiological condition indices in marine bivalve aquaculture. Aquaculture, 44(3), 187–200. https://doi.org/10.1016/0044-8486(85)90243-1
Methods

Mann, R. 1978. " A Comparison of Morphometric, Biochemical, and Physiological Indexes of Condition in Marine Bivalve Molluscs." In Energy and Environmental Stress in Aquatic Systems, edited by J. H. Thorp and J. W. Gibbons, vol. 48, 484–497. US Department of Energy Symposium Series. https://seagrant.whoi.edu/wp-content/uploads/2015/01/WHOI-R-77-016-Mann-Roger-A-Comparison.pdf
Methods

Stokes, N.A. & Burreson, E.M. (2001). Differential Diagnosis Of Mixed *Haplosporidium Costale* And *Haplosporidium Nelsoni* Infections In The Eastern Oyster, *Crassostrea Virginica*, Using DNA Probes. Journal Of Shellfish Research, 20(1), 207-213. https://scholarworks.wm.edu/vimsarticles/475
Methods

Truskey, S., Sotka, E., Grabowski, J., Kollars-Kjersten, N. M., Lotterhos, K. E., Schneider, E., & Hughes, A. R. (2025). Non-Random Mortality in an Experimental Oyster Restoration. Evolutionary Applications, 18(7). Portico. https://doi.org/10.1111/eva.70128
Results

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Related Datasets

IsRelatedTo

Hughes, A. R., Truskey, S. (2026) **Genetic diversity metrics for oyster genetic clusters from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2018-2020.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-12 http://lod.bco-dmo.org/id/dataset/1004745 [view at BCO-DMO]
Relationship Description: Related dataset with genetic diversity estimates at the oyster genetic cluster-level from restored reefs

Hughes, A. R., Truskey, S. (2026) **Genetic relatedness estimates calculated from SNP genotype data of oysters from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2018-2020.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-05 http://lod.bco-dmo.org/id/dataset/1003777 [view at BCO-DMO]
Relationship Description: Related dataset with pairwise individual genetic relatedness estimates from restored reefs

Hughes, A. R., Truskey, S. (2026) **Oyster genetic assignment data from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2017-2020.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-07 http://lod.bco-dmo.org/id/dataset/1004242 [view at BCO-DMO]
Relationship Description: Companion dataset with individual genetic cluster assignments for oysters

Hughes, A. R., Truskey, S. (2026) **Sequence metadata for all sampled oysters from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2017-2020.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-07 http://lod.bco-dmo.org/id/dataset/1003894 [view at BCO-DMO]
Relationship Description: Sequence metadata for larger sample set

References

Northeastern University. Non-random mortality in an experimental oyster restoration. 2025/06. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA1280068. NCBI:BioProject: PRJNA1280068.

Truskey, S. B., & Hughes, A. R. (2025). Non-random mortality in an experimental oyster restoration [Data set]. Northeastern University. https://hdl.handle.net/2047/D20775066

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Parameters

Parameter	Description	Units
yearcoll	Year and season of sample collection (e.g., F2018 = Fall 2018, F2020 = Fall 2020)	unitless
ind_id	Unique identifier for each individual oyster. This identifier corresponds to the associated FASTQ sequence file name	unitless
reef	Restored reef from which an individual was collected. Letter refers to experimental block and number refers to the reef number within a block (e.g., D3)	unitless
block	Experimental block in which a restored reef was situated (A - D)	unitless
primary_genetic_assignment	Assigned genetic cluster for an individual using the primary genetic assignment set applied to all main text analyses (DAPC approach, SNP set filtered for MAF > 0.01, LD pruning, and Fall 2020 missing data). Label names correspond to the state of origin of the hatchery source associated with a given genetic cluster (gME, gMA, gNY, gVA)	unitless
library	RADseq library batch in which an individual was processed and sequenced	unitless
total_tissue_dryweight	Total dry weight of soft tissue from an individual oyster	grams (g)
total_shell_dryweight	Total dry weight of shell from an individual oyster	grams (g)

condition_index_eq	Condition index, calculated as (dry tissue weight / dry shell weight) * 100	unitless (ratio)
shell_height	Maximum shell height measured in mm from the hinge to the outer shell edge	millimeter (mm)
shell_length	Maximum shell length measured in mm from one lateral edge of shell to the other at the widest point perpendicular to height	millimeter (mm)
taggedoutlier_ci	Flag indicating whether the individual was identified as an outlier for condition index (1) or not tagged (0)	unitless
taggedoutlier_height	Flag indicating whether the individual was identified as an outlier for shell height (1) or not tagged (0)	unitless
mb_present	Presence (1) or absence (0) of blisters on shell associated with mud blister worm *Polydora sp.* infection	unitless
bs_present	Presence (1) or absence (0) of holes in shell associated with boring sponge *Cliona spp.* infection	unitless
sso_present	Presence (1) or absence (0) of *Haplosporidium costale* infection based on PCR assay	unitless
dermo_present	Presence (1) or absence (0) of *Perkinsus marinus* infection based on qPCR assay	unitless
dermo_intensity	Intensity of *Perkinsus marinus* infection reflected as the mean concentration (copy number based on gBlocks standard) per wet weight oyster tissue (in mg); calculated for infected oysters only	log10-transformed copy number Perkinsus marinus per mg of oyster tissue
mb_intensity	Mean percent of oyster shell (top and bottom valves) with blisters characteristic of mud blister worm *Polydora sp*. infection ((total infected area/total shell area)*100), calculated for infected oysters only	percent

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Manual Biota Sampler
Dataset-specific Description	In fall 2018, we haphazardly sampled live oysters from each reef on scuba or snorkel (N = 512 individuals total, 32 per reef). Oysters were put on ice and transported to the Northeastern University Marine Science Center where they were held at −80°C until DNA extraction.
Generic Instrument Description	"Manual Biota Sampler" indicates that a sample was collected in situ by a person, possibly using a hand-held collection device such as a jar, a net, or their hands. This term could also refer to a simple tool like a hammer, saw, or other hand-held tool.

Dataset-specific Instrument Name	
Generic Instrument Name	qPCR Thermal Cycler
Dataset-specific Description	Standardized intensity values for P. marinus were generated through the above cited qPCR protocol.
Generic Instrument Description	An instrument for quantitative polymerase chain reaction (qPCR), also known as real-time polymerase chain reaction (Real-Time PCR).

Dataset-specific Instrument Name	
Generic Instrument Name	scale or balance
Dataset-specific Description	We calculated oyster condition index as dry tissue mass × 100 divided by dry shell mass (i.e., dry tissue weight: dry shell weight ratio; Lucas and Beninger 1985; Mann 1978).
Generic Instrument Description	Devices that determine the mass or weight of a sample.

Dataset-specific Instrument Name	scuba
Generic Instrument Name	Self-Contained Underwater Breathing Apparatus
Dataset-specific Description	In fall 2018, we haphazardly sampled live oysters from each reef on scuba or snorkel (N = 512 individuals total, 32 per reef). Oysters were put on ice and transported to the Northeastern University Marine Science Center where they were held at −80°C until DNA extraction.
Generic Instrument Description	The self-contained underwater breathing apparatus or scuba diving system is the result of technological developments and innovations that began almost 300 years ago. Scuba diving is the most extensively used system for breathing underwater by recreational divers throughout the world and in various forms is also widely used to perform underwater work for military, scientific, and commercial purposes. Reference: https://oceanexplorer.noaa.gov/technology/technical/technical.html

Dataset-specific Instrument Name	
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	To assess infection by the microparasites, we used DNA extracted from the 32 oysters sampled per reef in 2018 and performed a polymerase chain reaction (PCR) assay protocol developed for SSO (Stokes and Burreson 2001) and a quantitative polymerase chain reaction (qPCR) assay for Dermo (De Faveri et al. 2009).
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Project Information

CAREER: Linking genetic diversity, population density, and disease prevalence in seagrass and oyster ecosystems (Seagrass and Oyster Ecosystems)

Coverage: Coastal New England

NSF Award Abstract:
Disease outbreaks in the ocean are increasing, causing losses of ecologically important marine species, but the factors contributing to these outbreaks are not well understood. This 5-year CAREER project will study disease prevalence and intensity in two marine foundation species - the seagrass Zostera marina and the Eastern oyster Crassostrea virginica. More specifically, host-disease relationships will be explored to understand how genetic diversity and population density of the host species impacts disease transmission and risk. This work will pair large-scale experimental restorations and smaller-scale field experiments to examine disease-host relationships across multiple spatial scales. Comparisons of patterns and mechanisms across the two coastal systems will provide an important first step towards identifying generalities in the diversity-density-disease relationship. To enhance the broader impacts and utility of this work, the experiments will be conducted in collaboration with restoration practitioners and guided by knowledge ascertained from key stakeholder groups. The project will support the development of an early career female researcher and multiple graduate and undergraduate students. Students will be trained in state-of-the-art molecular techniques to quantify oyster and seagrass parasites. Key findings from the surveys and experimental work will be incorporated into undergraduate courses focused on Conservation Biology, Marine Biology, and Disease Ecology. Finally, students in these courses will help develop social-ecological surveys and mutual learning games to stimulate knowledge transfer with stakeholders through a series of workshops.

The relationship between host genetic diversity and disease dynamics is complex. In some cases, known as a dilution effect, diversity reduces disease transmission and risk. However, the opposite relationship, known as the amplification effect, can also occur when diversity increases the risk of infection. Even if diversity directly reduces disease risk, simultaneous positive effects of diversity on host density could lead to amplification by increasing disease transmission between infected and uninfected individuals. Large-scale field restorations of seagrasses (Zostera marina) and oysters (Crassostrea virginica) will be utilized to test the effects of host genetic diversity on host population density and disease prevalence/intensity. Additional field experiments independently manipulating host genetic diversity and density will examine the mechanisms leading to dilution or amplification. Conducting similar manipulations in two marine foundation species - one a clonal plant and the other a non-clonal animal - will help identify commonalities in the diversity-density-disease relationship. Further,

collaborations among project scientists, students, and stakeholders will enhance interdisciplinary training and help facilitate the exchange of information to improve management and restoration efforts. As part of these efforts, targeted surveys will be used to document the perceptions and attitudes of managers and restoration practitioners regarding genetic diversity and its role in ecological resilience and restoration.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1652320

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