Oyster genetic assignment data from an experimental oyster reef restoration in Ninigret Pond, Rhode Island (USA) in 2017-2020

Website: https://www.bco-dmo.org/dataset/1004242
Data Type: Other Field Results
Version: 1
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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 genetic cluster assignments for 619 eastern oysters (Crassostrea virginica, urn:lsid:marinespecies.org:taxname:140657) sampled as part of an experimental oyster reef restoration in Ninigret Pond, Rhode Island, USA. Oysters include 104 juvenile individuals from source hatchery-labeled samples collected prior to reef construction and 515 individuals sampled from 12 experimental restored reefs in fall 2018 and again in fall 2020. Juvenile oysters were sourced from four commercial hatcheries spanning a broad geographic range along the U.S. Atlantic coast (Maine, Massachusetts, New York, and Virginia). Each individual oyster was assigned to one of four genetic clusters identified using discriminant analysis of principal components (DAPC) and sparse non-negative matrix factorization (sNMF) applied to SNP genotype data. The dataset includes a primary genetic cluster assignment used in downstream analyses, as well as assignments generated from all combinations of the two analytical genetic assignment approaches and 12 SNP sets varying in filtering parameters (24 'assignment sets' in total). These additional assignments sets were included to assess both the consistency of genetic assignments as a whole and the robustness of downstream ecological inferences to certain upstream bioinformatic decisions (i.e., how we filtered the SNP data and generated individual genetic assignments).

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Coverage

Location: Ninigret Pond, Charlestown, Rhode Island
Spatial Extent: **Lat**:41.3549 **Lon**:-71.6929
Temporal Extent: 2017-11 - 2020-10

Methods & Sampling

These data were published in Truskey et al. 2025 (Evolutionary Applications). All figure numbers and supplementary materials mentioned refer to Truskey et al. 2025 (Evolutionary Applications).

Restoration experiment and sample collection

In April 2017, we collaborated with local oyster farmers to source oyster eyed-larvae from four commercial hatcheries for the construction of new experimental oyster reefs in Ninigret Pond (Charlestown, Rhode Island, USA). Hatchery sources were selected across a broad geographic sampling range to maximize diversity (Figure 1a of Truskey et al. 2025). They included two regional hatcheries, one from Massachusetts (MA) and one from New York (NY), and two more distant hatcheries, one from Maine (ME) and one from Virginia (VA). A local Rhode Island hatchery facility received oyster eyed-larvae from each source hatchery, set the eyed-larvae on dead oyster and/or clam shell (hereafter referred to as spat-on-shell oysters), and distributed the spat-on-shell oysters to three local oyster growers (Grower 1: MA; Grower 2: ME, NY, VA; Grower 3: NY, VA) who maintained these juvenile oysters on separate leased oyster farm plots prior to reef construction. Immediately prior to reef construction, we collected 20 juvenile spat-on-shell oysters from each grower-hatchery source combination for genetic analysis ($n = 6$ combinations; Grower 1-MA; Grower 2-ME; Grower 2-NY; Grower 2-VA; Grower 3-NY; Grower 3-VA).

In October and November 2017, we constructed 16 subtidal reefs within a no-harvest Shellfish Management Area in Ninigret Pond. Reefs were created across four 0.025-acre experimental blocks, with four reefs per block (Figure 2 of Truskey et al. 2025). Each reef consisted of a base layer of 0.25 cubic yards of dead oyster or clam shell deployed in October and topped with 1.25 cubic yards of spat-on-shell oysters in early November from the stock grown out by the local oyster growers. Our experiment was originally designed to seed three reefs per block with a different single hatchery source from the four available hatchery sources and to seed the fourth reef per block with a mixed combination of the three sources (e.g., Reef 1: ME, Reef 2: MA, Reef 3: NY, Reef 4: ME+MA+NY). However, analysis of the hatchery samples from oyster growers collected prior to reef construction revealed an early, unintended mixing of some of the sources (Appendix S1 of Truskey et al. 2025; Figure S1 of Truskey et al. 2025), resulting in mixtures of multiple sources on 12 out of the 16 constructed reefs. Thus, we focused our analyses on the actual genetic composition of each reef as determined by genetic sampling at two time points (fall 2018, fall 2020).

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. By the fall of 2020, live oyster densities on all experimental reefs had declined, reflecting mortality of the original planted oysters and a lack of recruitment, consistent with other data from this system (Barrett et al. 2024). To assess whether this mortality was associated with a consistent change in the genetic composition of surviving oysters on reefs, we repeated our sampling in fall 2020 and compared the resulting reef genetic profiles to those from fall 2018. Reef sample sizes varied at this time point due to low live abundances ($N = 249$ individuals total, ranging from 8 to 32 per reef).

DNA extraction, RADseq library preparation, and bioinformatics

Genomic DNA was extracted using the E-Z 96 Tissue DNA Kit (Omega-Biotek, Norcross, GA) following the animal tissue protocol with tissue centrifugation. Double-digest restriction-site-associated DNA (ddRAD) libraries with individually barcoded samples were prepared in three batches following Parchman et al. (2012): (1) initial hatchery samples (n = 120), (2) fall 2018 reef samples (n = 480; 30 oysters per reef across 16 reefs), and (3) fall 2020 reef samples (n = 248). For additional details on ddRAD library preparation, see Appendix S2 of Truskey et al. 2025. All libraries were sequenced with 100-bp single-end reads on an Illumina platform. The initial and fall 2020 batches were sequenced on a single lane of the Illumina HiSeq 2500 at Tufts University Core Facility Genomics; the fall 2018 batch was sequenced on two lanes of the Illumina NovaSeq 6000 at the University of Texas at Austin Genomic Sequencing and Analysis Facility.

Data Processing Description

SNP calling, filtering, and defining datasets

Raw sequence quality was assessed with FastQC v0.11.9 (Andrews 2010), and files were demultiplexed using the process_radtags function in STACKS v2.41 (Catchen et al. 2013). Read trimming, mapping, SNP calling, and genotyping were performed with the dDocent pipeline v2.9.4 (Puritz et al. 2014), with reads mapped to the *C. virginica* genome pruned for haplotigs (Puritz et al. 2024). Variant calling was performed using Freebayes v1.3.6 (Garrison and Marth 2012). SNP loci were then filtered using vcftools v0.1.16 (Danecek et al. 2011)

following standard iterative quality filtering procedures for RADseq-generated SNP data (O'Leary et al. 2018), including filters for minor allele count, base quality, genotype call rate, and read depth, followed by individual-level filtering for missing data. Because genetic assignment approaches can be sensitive to the SNP dataset used, we generated 12 SNP sets varying in minor allele frequency (MAF) threshold, locus-level filtering for missingness specific to the fall 2020 library, and pruning for high linkage disequilibrium (LD), to evaluate the robustness of downstream genetic cluster assignments to these bioinformatic decisions. Filtering outcomes for each SNP set are detailed in Table S1 of Truskey et al. 2025.

Individual genetic assignments

Individual genetic assignments to one of four genetic clusters (K = 4) were generated using discriminant analysis of principal components (DAPC; adegenet v2.1.10, Jombart 2008) and sparse non-negative matrix factorization (sNMF; LEA v3.10.0, Frichot and Francois 2015), applied independently to each of the 12 SNP sets, yielding 24 genetic assignment sets in total. Both approaches supported an optimal K = 4 (Figures S3-S4 of Truskey et al. 2025). For sNMF, individual assignments reflect the single cluster assignment with the highest admixture coefficient under K = 4. The primary genetic assignment referred to in the dataset and used in downstream analyses reflects DAPC assignments from the LD-pruned SNP set filtered for MAF > 0.01 and fall 2020 library-specific missingness. Additional details on DAPC and sNMF runs and outcomes are provided in Appendix S3 of Truskey et al. 2025.

The individuals presented in this dataset are those retained after SNP filtering steps and not sampled from single-source reefs at the start of the experiment in fall 2018 as reflected by the individual genetic assignments. Genetic assignments for all individuals retained after SNP filtering (n=803), including those from single-source fall 2018 reefs, are provided in the related Sequence Metadata dataset.

BCO-DMO Processing Description

- Loaded table Truskey_EVA2025_ind_genetic_assignments_combined_bcodmo.csv, using filename as table name, with header row on row 1; set missing value sentinels to "", "nd", and "NA"
- Exported file as 1004242_v1_ind_genetic_assignments.csv

Problem Description

Genetic analysis of the pre-construction hatchery source samples revealed unintended mixing of oyster sources associated with samples provided by Grower 2, prior to reef construction. Samples labeled by Grower 2 as ME (Grower 2-ME) appear to have been mislabeled and likely represent a mixture of sources, primarily clustering with the NY-labeled group from Grower 3. The sample labeled by Grower 2 as VA (Grower 2-VA) also did not cluster with the VA-labeled sample from Grower 3, and instead likely represents the ME hatchery source. These inconsistencies were detected consistently across independent analyses using different SNP datasets and genotyping approaches, supporting the interpretation that they reflect true mislabeling or source mixing prior to reef construction rather than technical artifacts. In the dataset, hatchery source labels for Grower 2 samples are flagged with an asterisk.

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Related Publications

Andrews S. (2010). FastQC: a quality control tool for high throughput sequence data. Available online at: http://www.bioinformatics.babraham.ac.uk/projects/fastqc
Software

Barrett, P. D., Schneider, E. G., Grabowski, J. H., Hanley, T. C., McManus, M. C., Helt, W., Kinney, H., & Hughes, A. R. (2024). Evaluating Multiple Oyster Reef Restoration Practices Across Space and Time in Coastal Rhode Island. Ecological Restoration, 42(3), 193–204. https://doi.org/10.3368/er.42.3.193
Methods

Catchen, J., Hohenlohe, P. A., Bassham, S., Amores, A., & Cresko, W. A. (2013). Stacks: an analysis tool set for population genomics. Molecular Ecology, 22(11), 3124–3140. Portico. https://doi.org/10.1111/mec.12354
Software

Danecek, P., Auton, A., Abecasis, G., Albers, C. A., Banks, E., DePristo, M. A., Handsaker, R. E., Lunter, G., Marth, G. T., Sherry, S. T., McVean, G., & Durbin, R. (2011). The variant call format and VCFtools. Bioinformatics, 27(15), 2156–2158. https://doi.org/10.1093/bioinformatics/btr330
Software

Frichot, E., & François, O. (2015). LEA: An R package for landscape and ecological association studies. Methods in Ecology and Evolution, 6(8), 925–929. Portico. https://doi.org/10.1111/2041-210x.12382 https://doi.org/10.1111/2041-210X.12382
Methods

Garrison, E., & Marth, G. (2012). *Haplotype-based variant detection from short-read sequencing* (Version 2). arXiv. https://doi.org/10.48550/ARXIV.1207.3907 https://doi.org/10.48550/arXiv.1207.3907
Software

Jombart, T. (2008). *adegenet*: a R package for the multivariate analysis of genetic markers. Bioinformatics, 24(11), 1403–1405. https://doi.org/10.1093/bioinformatics/btn129
Software

O'Leary, S. J., Puritz, J. B., Willis, S. C., Hollenbeck, C. M., & Portnoy, D. S. (2018). These aren't the loci you're looking for: Principles of effective SNP filtering for molecular ecologists. Molecular Ecology, 27(16), 3193–3206. Portico. https://doi.org/10.1111/mec.14792
Methods

Parchman, T. L., Gompert, Z., Mudge, J., Schilkey, F. D., Benkman, C. W., & Buerkle, C. A. (2012). Genome-wide association genetics of an adaptive trait in lodgepole pine. Molecular Ecology, 21(12), 2991–3005. Portico. https://doi.org/10.1111/j.1365-294x.2012.05513.x https://doi.org/10.1111/j.1365-294X.2012.05513.x
Methods

Puritz, J. B., Guo, X., Hare, M., He, Y., Hillier, L. W., Jin, S., Liu, M., Lotterhos, K. E., Minx, P., Modak, T., Proestou, D., Rice, E. S., Tomlinson, C., Warren, W. C., Witkop, E., Zhao, H., & Gomez-Chiarri, M. (2024). A second unveiling: Haplotig masking of the eastern oyster genome improves population-level inference. Molecular Ecology Resources, 24(1). Portico. https://doi.org/10.1111/1755-0998.13801
Methods

Puritz, J. B., Hollenbeck, C. M., & Gold, J. R. (2014). *dDocent*: a RADseq, variant-calling pipeline designed for population genomics of non-model organisms. PeerJ, 2, e431. https://doi.org/10.7717/peerj.431
Software

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 morphometric, condition, and parasite infection data 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-

08-11 http://lod.bco-dmo.org/id/dataset/1004478 [view at BCO-DMO]
Relationship Description: Related dataset with trait measurements for oysters from restored reefs

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 all archived genetic samples associated with this project

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
ind_id	Unique identifier for each individual oyster. This identifier corresponds to the associated FASTQ sequence file name	unitless
sampling_group	Indicator for whether an individual was sampled from either an experimental reef or pre-reef construction from an initial hatchery group	unitless
yearcoll	Year and season of sample collection (e.g., F2018 = Fall 2018, F2020 = Fall 2020, Init = hatchery-sourced samples taken before reef deployment)	unitless
reef	For reef samples only. 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

grower	For initial hatchery samples only. Oyster grower that provided the grown-out hatchery-source sample (e.g., Grower1, Grower3)	unitless
hatcherysource_label	For initial hatchery samples only. Original source hatchery ID as provided by oyster grower labels, corresponding to the state of origin of the respective hatcheries (e.g., NY, MA, VA, ME). *asterisk denotes a source that is likely mislabelled; see Problems/Issues section for details on the unintended mixing of hatchery-sourced samples prior to reef construction	unitless
grower_by_hatcherysource_label	For initial hatchery samples only. Combined identifier for oyster grower and original source hatchery label (e.g., Grower1_MA). *asterisk denotes a source that is likely mislabelled; see Problems/Issues section for details on the unintended mixing of hatchery-sourced samples prior to reef construction.	unitless
library	RADseq library batch in which an individual was processed and sequenced	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

dapc_assigned_genetic_cluster_g90maf01_ldprunedrsq05	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.01 and pruned for LD	unitless
dapc_assigned_genetic_cluster_g90maf01_g20f2020	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.01 and pruned for Fall 2020 missing data	unitless
dapc_assigned_genetic_cluster_g90maf01	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.01	unitless
dapc_assigned_genetic_cluster_g90maf025_g20f2020_ldprunedrsq05	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.025, pruned for LD and Fall 2020 missing data	unitless
dapc_assigned_genetic_cluster_g90maf025_ldprunedrsq05	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.025 and pruned for LD	unitless
dapc_assigned_genetic_cluster_g90maf025_g20f2020	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.025 and pruned for Fall 2020 missing data	unitless
dapc_assigned_genetic_cluster_g90maf025	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.025	unitless
dapc_assigned_genetic_cluster_g90maf05_g20f2020_ldprunedrsq05	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.05, pruned for LD and Fall 2020 missing data	unitless

dapc_assigned_genetic_cluster_g90maf05_ldprunedrsq05	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.05 and pruned for LD	unitless
dapc_assigned_genetic_cluster_g90maf05_g20f2020	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.05 and pruned for Fall 2020 missing data	unitless
dapc_assigned_genetic_cluster_g90maf05	Individual genetic cluster assignments using DAPC approach with SNP set filtered for MAF > 0.05	unitless
snmf_primary_ancestry_cluster_g90maf01_g20f2020_ldprunedrsq05	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.01, pruned for LD and Fall 2020 missing data	unitless
snmf_primary_ancestry_cluster_g90maf01_ldprunedrsq05	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.01 and pruned for LD	unitless
snmf_primary_ancestry_cluster_g90maf01_g20f2020	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.01 and pruned for Fall 2020 missing data	unitless
snmf_primary_ancestry_cluster_g90maf01	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.01	unitless
snmf_primary_ancestry_cluster_g90maf025_g20f2020_ldprunedrsq05	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.025, pruned for LD and Fall 2020 missing data	unitless

snmf_primary_ancestry_cluster_g90maf025_ldprunedrsq05	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.025 and pruned for LD	unitless
snmf_primary_ancestry_cluster_g90maf025_g20f2020	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.025 and pruned for Fall 2020 missing data	unitless
snmf_primary_ancestry_cluster_g90maf025	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.025	unitless
snmf_primary_ancestry_cluster_g90maf05_g20f2020_ldprunedrsq05	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.05, pruned for LD and Fall 2020 missing data	unitless
snmf_primary_ancestry_cluster_g90maf05_ldprunedrsq05	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.05 and pruned for LD	unitless
snmf_primary_ancestry_cluster_g90maf05_g20f2020	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.05 and pruned for Fall 2020 missing data	unitless
snmf_primary_ancestry_cluster_g90maf05	Individual genetic cluster assignments using sNMF approach with SNP set filtered for MAF > 0.05	unitless

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq 2500
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	The initial and fall 2020 batches were sequenced on a single lane of the Illumina HiSeq 2500 at Tufts University Core Facility Genomics; the fall 2018 batch was sequenced on two lanes of the Illumina NovaSeq 6000 at the University of Texas at Austin Genomic Sequencing and Analysis Facility.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Illumina NovaSeq 6000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	The initial and fall 2020 batches were sequenced on a single lane of the Illumina HiSeq 2500 at Tufts University Core Facility Genomics; the fall 2018 batch was sequenced on two lanes of the Illumina NovaSeq 6000 at the University of Texas at Austin Genomic Sequencing and Analysis Facility.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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	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

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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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