Wasting disease prevalence and severity and seagrass length and density based on subpopulations of Zostera marina on the North Shore of Massachusetts surveyed in July and September 2016

Website: https://www.bco-dmo.org/dataset/851122
Data Type: Other Field Results
Version: 1
Version Date: 2021-05-04

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, Contact
Schenck, Forest	Northeastern University	Co-Principal Investigator
Heyl, Taylor	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

This dataset includes wasting disease infection prevalence and severity in four Zostera marina subpopulations located along a 30 kilometer stretch of coastline on the North shore of Massachusetts. Surveys of subpopulations were conducted in July and September 2016.

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Coverage

Spatial Extent: **N**:42.5971 **E**:-70.6559 **S**:42.4206 **W**:-70.9158
Temporal Extent: 2016-07 - 2016-09

Methods & Sampling

Wasting disease and Zostera morphology: We assessed wasting disease infection prevalence and severity in four *Zostera* subpopulations located at least 4 kilometers (km) apart along a 30 kilometer (km) stretch of coastline on the north shore of Massachusetts: Niles Beach, Gloucester (NB, 42° 35.8268’ N, 70° 39.3553’ W); West Beach, Beverly (WB, 42° 33.9155’ N, 70° 47.1102’ W); Lynch Park, Beverly (LP, 42° 32.6925’ N, 70° 51.5057’ W); and Curlew Beach, Nahant (CB, 42° 25.2378’ N, 70° 54.9474’ W). These subpopulations share similar depth profiles (ranging from 1-2 meter MLLW) and occur seaward of sandy beaches. We surveyed the CB subpopulation in July 2016 and the NB, WB, and LP subpopulations in September 2016. These dates fall within the time of year of peak disease prevalence reported for temperate *Zostera* meadows (Burdick et al., 1993; Bockelmann et al., 2013). Within 12 quadrats (0.0625 m2) at each subpopulation, we counted *Zostera* shoot density and haphazardly collected ten *Zostera* shoots. Quadrats were spaced 2 meters apart along a 25 meter transect running parallel to shore.

We stored shoots in coolers of seawater and scored the third youngest leaf of each shoot for the presence and percent cover of lesions characteristic of wasting disease within 6 hours of collection. We focused on this leaf because it has been shown to harbor the highest intensity of wasting disease (Bockelmann et al., 2013). We used published descriptions and photographs of lesions associated with wasting disease to guide our scoring (Burdick et al., 1993; Groner et al., 2014; Groner, Burge, et al., 2016). In addition, we measured the length of each shoot from the base of the stem (1st node) to the tip of the longest leaf.

Data Processing Description

Statistical Analyses: To examine differences in wasting disease prevalence among subpopulations, we summed the number of *Zostera* shoots collected per quadrat with and without wasting disease present on the third youngest leaf and used a binomial generalized linear model (GLM) with a logit link followed by Tukey HSD post hoc tests. We calculated quadrat-level wasting disease lesion severity as the mean lesion percent cover on the third leaf. We excluded leaves without lesions from the lesion severity calculation to avoid confounding these results with lesion prevalence. We used non-parametric Kruskal-Wallace tests to examine the effect of subpopulation on lesion severity and shoot density due to non-normality and Wilcoxon rank sum tests to differentiate among subpopulations. We calculated quadrat-level canopy height as the mean length of the ten shoots collected from each quadrat. We used one-way ANOVAs to examine differences in canopy height among subpopulations, followed by Tukey HSD post hoc tests to differentiate among subpopulations when relevant.

BCO-DMO processing description:
- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Missing data identifier ‘NA’ replaced with 'nd' (BCO-DMO's default missing data identifier)
- Added a conventional header with dataset name, PI names, version date

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Data Files

File
wasting_disease_exp.csv (Comma Separated Values (.csv), 20.08 KB) MD5:24cde9972b2dd318e69f5f50edd830bd Primary data file for dataset ID 851122

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Related Publications

Bockelmann, A.-C., Tams, V., Ploog, J., Schubert, P. R., Reusch, T. B. H. (2013). Quantitative PCR reveals strong spatial and temporal variation of the wasting disease pathogen, Labyrinthula zosterae in northern European eelgrass (Zostera marina) beds. PLoS ONE, 8(5), e62169.
Results

Burdick, D. M., Short, F. T., & Wolf, J. (1993). An index to assess and monitor the progression of wasting disease in eelgrass Zostera marina. Marine Ecology-Progress Series, 94, 83-83.
Methods

Burge, C. A., Friedman, C. S., Getchell, R., House, M., Lafferty, K. D., Mydlarz, L. D., Prager, K. C., Sutherland, K. P., Renault, T., Kiryu, I., Vega-Thurber, R. (2016). Complementary approaches to diagnosing marine diseases: a union of the modern and the classic. Philosophical Transactions of the Royal Society B: Biological Sciences, 371, 20150207.
Methods

Groner, M. L. Maynard, J.,Breyta, R., Carnegie, R. B., Dobson, A., Friedman, C. S., Froelich, B., Garren, M., Gulland, F. M. D., Heron, S. F., Noble, R. T., Revie, C. W., Shields, J. D., Vanderstichel, R., Weil, E., Wyllie-

Echeverria, S., Harvell, C. D. (2016). Managing marine disease emergencies in an era of rapid change. Philosophical transaction of the Royal Society B: Biological Sciences, 371, 1689.
Methods

Groner, M. L., Burge, C. A., Couch, C. S., Kim, C. J. S., Siegmund, G.-F., Singhal, S., Smoot, S. C., Jarrell, A., Gaydos, J. K., Harvell, C. D., Wyllie-Echeverria, S. (2014). Host demography influences the prevalence and severity of eelgrass wasting disease. Disease of Aquatic Organisms, 108, 165-175.
Methods

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Related Datasets

IsRelatedTo

Hughes, A. R., Schenck, F. (2022) **Seagrass responses to Labyrinthula zosterae inoculation base on a subpopulation from mesocosm experiments conducted in Nahant, Massachusetts.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-05-04 doi:10.26008/1912/bco-dmo.851047.1 [view at BCO-DMO]

Hughes, A. R., Schenck, F. (2022) **Seawater temperature and salinity of mesocosms and a field location collected while conducting experiments on seagrass in Nahant, Massachusetts.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-05-04 doi:10.26008/1912/bco-dmo.851059.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
subpopulation	Descriptor of the subpopulation of Zostera marina plants	Unitless
latitude	Latitude of Zostera subpopulation	Decimal degrees
longitude	Longitude of Zostera subpopulation	Decimal degrees
quad	Unique numeric identifier assigned sampling locations within each Zostera marina subpopulation	Unitless
shoot_id	Unique alphabetic identifier assigned to shoots sampled within each sampling location	Unitless
length	Length of Zostera marina shoot: measured from the first node to the tip of the longest leaf	Centimeters
no_leaves	The number of leaves of Zostera marina shoot	Unitless
lesion_cover	Estimated percent of Zostera marina leaf area covered by lesions characteristic of wasting disease on each Zostera marina focal leaf from sheath top to leaf tip	Unitless
focal_leaf_no	Descriptor of the relative age of the focal Zostera marina leaf: 1 (the youngest leaf); relative leaf age increases as the value of the integer increases	Unitless
leaf_broken	Descriptor of the wholeness of the focal leaf: N (focal leaf completely intact); Y (section of focal leaf broken off)	Unitless
density	The number of Zostera marina shoots per meters squared	Shoot per meter squared

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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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