NCBI accession numbers and related metadata for an SRA archive of the seagrass, Zostera marina

Website: https://www.bco-dmo.org/dataset/958698
Data Type: Other Field Results
Version: 1
Version Date: 2025-04-10

Project
» RUI: Collaborative Research: Trait differentiation and local adaptation to depth within meadows of the foundation seagrass Zostera marina (ZosMarLA)

Contributors	Affiliation	Role
Hanley, Torrance C.	Northeastern University	Co-Principal Investigator
Hays, Cynthia	Keene State College (Keene)	Co-Principal Investigator
Hughes, A. Randall	Northeastern University	Co-Principal Investigator
Sotka, Erik	Grice Marine Laboratory - College of Charleston (GML-CoC)	Co-Principal Investigator
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Using recent advances in indirect genetic methods applied to both adult plants and dispersed seeds, we find that the mean seed dispersal in a threatened marine foundation plant (the seagrass Zostera marina) is approximately 100-200 meters. We documented strong phenotypic variation and genome-wide differentiation among plants separated by less than the spatial scale of mean realized dispersal, which suggests genetic isolation by environment in response to depth-related environmental gradients. Within all meadows, the ratio of effective to census size (or Ne/Nc) approximated 0.1%, indicating that a fraction of existing plants provides the genetic variation to allow adaptation to environmental change. The SRA dataset at NCBI contains the raw sequencing reads that were used to create genotypes and genotype likelihoods.

Table of Contents

Coverage

Location: Massachusetts, USA
Spatial Extent: **N**:42.596758 **E**:-70.65518121 **S**:42.419022 **W**:-70.91758865
Temporal Extent: 2019-06 - 2019-10

Methods & Sampling

During the June peak of seasonal flowering in 2019, divers on SCUBA collected a single vegetative shoot at each node within each sampling grid for genetic analysis (n=15 ramets per grid, 45 per depth, 90 per site). At approximately alternating nodes (i.e., 5-7 of the 15 nodes in each grid, depending on the location of bare

patches), divers also harvested all shoots from within a 25 × 25 centimeter (cm) quadrat (n = 15-21 per depth) to estimate shoot density and canopy characteristics. Samples were returned to the lab on ice for processing. The second and third leaves of each genetic sample were preserved in silica.

After the flowering season and once seeds had dropped (September 2019; von Staats et al. 2021), we returned to each sampling grid to collect dispersed seeds. Sediment cores (10 cm in diameter and 10 cm in depth) were taken at three locations within each grid at Curlew Beach and at four locations within each grid at the other three field sites (n=9 or 12 cores per depth). Sediment cores were bagged and kept cold (4 degrees Celsius (°C)) until they could be processed; each core was hand-sieved for intact seeds within 3 days of collection. We counted all intact seeds encountered and assessed viability by firmness (the squeeze test; Marion and Orth 2010). Seeds deemed viable were individually weighed and stored in microfuge tubes and frozen at -80°C until DNA extraction.

Leaf samples (2 to 4 milligrams (mg) of dried tissue from the middle third of the leaf) were ground with a Retsch mixer mill MM400; seeds were ground by hand with a micropestle after removing the seed coat. DNA extraction was done with the Omega Bio-Tek E-Z 96 Tissue DNA kit, and samples were stored at -20°C. We prepared one genomic library of 464 individuals (359 adults, 105 seeds) by following the ddRADseq protocol of Parchman et al. (2012) and sequenced the library using two lanes of Illumina Novaseq. We digested gDNA with two restriction enzymes, EcoRI and MseI, and ligated adaptors containing unique 8-10bp barcodes to the digested DNA of each individual. The products were then PCR-amplified in two independent reactions with standard Illumina primers. All amplicons were pooled and shipped to the University of Texas Genomic Sequencing and Analysis Facility, which used Blue Pippen Prep to isolate the 300-450bp fraction. This fraction was then single-read-sequenced (approximately 100bp) with both lanes of an Illumina Novaseq machine. We used custom scripts to demultiplex into sample-specific FASTQ- formatted files.

Data Processing Description

These are the raw sequences from the Illumina sequencer after the demultiplex step (see methods above).

BCO-DMO Processing Description

- Imported original file "BioSampleObjects_wLatLon_final.csv" into the BCO-DMO system.
- Renamed fields to comply with BCO-DMO naming conventions.
- Saved final file as "958698_v1_z_marina_genbank_accessions.csv".

[table of contents | back to top]

Data Files

File	
958698_v1_z_marina_genbank_accessions.csv	(Comma Separated Values (.csv), 28.74 KB) MD5:24d4dbf425fca51a6786182bdc991c67
Primary data file for dataset ID 958698, version 1	

[table of contents | back to top]

Related Publications

Marion, S. R., & Orth, R. J. (2010). Innovative Techniques for Large-scale Seagrass Restoration Using Zostera marina (eelgrass) Seeds. Restoration Ecology, 18(4), 514–526. https://doi.org/10.1111/j.1526-100x.2010.00692.x https://doi.org/10.1111/j.1526-100X.2010.00692.x
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

Sotka, E. E., Hughes, A. R., Hanley, T. C., & Hays, C. G. (2024). Restricted Dispersal and Phenotypic Response to Water Depth in a Foundation Seagrass. Molecular Ecology, 33(23). Portico. https://doi.org/10.1111/mec.17565
Results

Von Staats, D. A., Hanley, T. C., Hays, C. G., Madden, S. R., Sotka, E. E., & Hughes, A. R. (2020). Intra-Meadow Variation in Seagrass Flowering Phenology Across Depths. Estuaries and Coasts, 44(2), 325–338. doi:10.1007/s12237-020-00814-0
Methods

[table of contents | back to top]

Related Datasets

IsRelatedTo

College of Charleston. Restricted dispersal and phenotypic response to water depth in a foundation seagrass. 2024/02. 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/PRJNA1073956. NCBI:BioProject: PRJNA1073956. https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1073956

Erik Sotka. (2024). esotka/ZosteraSNPs: 1.0 (ZosteraSNPs) [Computer software]. Zenodo. https://doi.org/10.5281/ZENODO.13798979 https://doi.org/10.5281/zenodo.13798979

[table of contents | back to top]

Parameters

Parameter	Description	Units
Accession	GenBank BioSample number	unitless
Sample_Name	Sample Name (note: the S and A at the end of the names are seed vs adults; the S vs D at the 2nd character are deep vs shallow depths)	unitless
adult_seed	A = Adult or S = seed	unitless
site	One letter population code (D = Curlew, N = Niles, W = West, L = Lynn)	unitless
SvD	Depth of site. s = shallow or d = deep	unitless
quad_name	Within-site position in a transect (1st six places); 2 digit individual ID	unitless
lon	Longitude of opulation collection site	decimal degrees
lat	Latitude of population collection site	decimal degrees
YearCollected	Year of collection	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina Novaseq machine
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Retsch mixer mill MM400
Generic Instrument Name	Homogenizer
Generic Instrument Description	A homogenizer is a piece of laboratory equipment used for the homogenization of various types of material, such as tissue, plant, food, soil, and many others.

Dataset-specific Instrument Name	sediment cores
Generic Instrument Name	Sediment Corer
Generic Instrument Description	A generic term for a coring device that allows for relatively undisturbed penetration of the sediment. Generally, core samplers consist of a core barrel (a hollow pipe or box) and a core cutter (or cutting head), located at the advancing end of the core barrel to facilitate the sampler's advancement into the sediment. Core catchers are commonly inserted into the cutting head to prevent sample loss during retrieval.

Dataset-specific Instrument Name	SCUBA
Generic Instrument Name	Self-Contained Underwater Breathing Apparatus
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

[table of contents | back to top]

Project Information

RUI: Collaborative Research: Trait differentiation and local adaptation to depth within meadows of the foundation seagrass Zostera marina (ZosMarLA)

Coverage: Massachusetts, USA

NSF Award Abstract:
Understanding how species cope with spatial variation in their environment (e.g. gradients in light and temperature) is necessary for informed management as well as for predicting how they may respond to change. This project will examine how key traits vary with depth in common eelgrass (Zostera marina), one of the most important foundation species in temperate nearshore ecosystems worldwide. The investigators will use a combination of experiments in the field and lab, paired with fine-scale molecular analyses, to determine the genetic and environmental components of seagrass trait variation. This work will provide important information on the microevolutionary mechanisms that allow a foundation species to persist in a variable environment, and thus to drive the ecological function of whole nearshore communities. The Northeastern University graduate and Keene State College (KSC) undergraduate students supported by this project will receive training in state-of-the-art molecular techniques, as well as mentorship and experience in scientific communication and outreach. A significant portion of KSC students are from groups under-represented in science. Key findings of the research will be incorporated into undergraduate courses and outreach programs for high school students from under-represented groups, and presented at local and national meetings of scientists and stakeholders.

Local adaptation, the superior performance of "home" versus "foreign" genotypes in a local environment, is a powerful demonstration of how natural selection can overcome gene flow and drift to shape phenotypes to match their environment. The classic test for local adaptation is a reciprocal transplant. However, such experiments often fail to capture critical aspects of the immigration process that may mediate realized gene flow in natural systems. For example, reciprocal transplant experiments typically test local and non-local phenotypes at the same (often adult) life history stage, and at the same abundance or density, which does not mirror how dispersal actually occurs for most species. In real populations, migrants (non-local) often arrive at low numbers compared to residents (local), and relative frequency itself can impact fitness. In particular, rare phenotypes may experience reduced competition for resources, or relative release from specialized pathogens. Such negative frequency dependent selection can reduce fitness differences between migrants and residents due to local adaptation, and magnify effective gene flow, thus maintaining greater within-population genetic diversity. The investigators will combine spatially paired sampling and fine-scale molecular analyses to link seed/seedling trait variation across the depth gradient at six meadows to key factors that may drive these patterns: local environmental conditions, population demography, and gene flow across depths. The team will then experimentally test the outcome of cross-gradient dispersal in an ecologically relevant context, by reciprocally out-planting seeds from different depths and manipulating relative frequency in relation to both adults and other seedling lineages. The possible interaction between local adaptation and frequency-dependence is particularly relevant for Zostera marina, which represents one of the best documented examples of the ecological effects of genetic diversity and identity. Further, a better understanding of seagrass trait differentiation is not simply a matter of academic interest, but critical to successful seagrass restoration and conservation.

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.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1851262

[table of contents | back to top]