Shoot measurements (sheath length and width) for the eelgrass (Zostera marina) shoots sampled for whole genome sequencing collected from Bodega and Tomales Bay, CA, USA from July to September 2019

Website: https://www.bco-dmo.org/dataset/924808
Data Type: Other Field Results
Version: 1
Version Date: 2024-04-10

Project
» Using genomics to link traits to ecosystem function in the eelgrass Zostera marina (ZosteraEcoGenomics)

Contributors	Affiliation	Role
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Abstract

This dataset provides shoot measurements for the shoots sampled for whole genome sequencing for Tomales Bay and Bodega Harbor (see related datasets for access to sequence data). Sheath width is measured on the terminal shoot using calipers at the abscission point (point where leaves emerge from the sheath). Sheath length is measured using a ruler to the nearest mm from the base to the abscission point. These data were used to record any differences in plant phenotype among the populations sampled. Shoot Length was not measured since it is susceptible to breakage and density was not measured as we could not ascribe density to a genetic individual.

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Coverage

Location: Tomales Bay and Bodega Harbor in California
Spatial Extent: **N**:38.3334 **E**:-122.846 **S**:38.105 **W**:-123.06
Temporal Extent: 2019-07-16 - 2019-09-30

Methods & Sampling

We collected 2 to 3 shoots attached by a rhizome from fifteen putative genets (separated by approximately 5 to 10 meters) at 14 sites across Tomales Bay and Bodega Harbor from a height below 0.0 mean lower low water (MLLW) (i.e., not sampling the uppermost or lowermost vertical distribution of *Zostera marina*). For two of the sites sampled in Bodega Harbor (Mason's Marina and Westside Park), we also collected a deeper set of specimens (at least -0.6 meters below MLLW) to test for differences between shallower versus deeper plants. We transported plants back to the University of California, Davis in a cooler with ice packs, and stored them for no more than 1 day in a recirculating seawater table before measuring the terminal shoot sheath width using calipers and sheath length using a ruler. The sheath width was measured at the abscission point and the length from the abscission point to the base of the shoot. Once measurements were made, we dissected out the tissue from within the leaf sheath and flash-froze them in liquid nitrogen and stored at -80 degrees Celsius (°C).

BCO-DMO Processing Description

- Imported original file "Zm_TomBod_morpohmetrics.xlsx" into the BCO-DMO system.
- Imported original file "WGS_LS_TomalesBodega.xlsx" into the BCO-DMO system.
- Added the "collection_date" column from "WGS_LS_TomalesBodega.xlsx" to the shoot morphometrics file, matching on individual sample ID number
- Converted date field to YYYY-MM-DD format.
- Saved final file as "924808_v1_shoots_sampled_for_sequencing.csv".

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Data Files

File
924808_v1_shoots_sampled_for_sequencing.csv(Comma Separated Values (.csv), 11.83 KB) MD5:cc2f379b9ab6d53d9c4995fcd245756a Primary data file for dataset ID 924808, version 1

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Related Datasets

IsRelatedTo

Stachowicz, J. J. (2024) **Sample collection information and sequence accessions at the National Center for Biotechnology Information (NCBI) for whole genome sequencing of eelgrass (Zostera marina) collected at Bodega and Tomales Bay, CA, USA from July to September 2019.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2024-04-10 doi:10.26008/1912/bco-dmo.924786.1 [view at BCO-DMO]
Relationship Description: These datasets were collected concurrently as part of a study of parallel genomic adaptation of Zostera marina in northern California estuaries published in Scheibelhut, et al. (2023).

Stachowicz, J. J. (2024) **Temperature data recorded using HOBO Pendant MX2201 loggers deployed at 14 sites in Tomales Bay and Bodega Harbor during August 2019.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2024-04-09 doi:10.26008/1912/bco-dmo.924671.1 [view at BCO-DMO]
Relationship Description: These datasets were collected concurrently as part of a study of parallel genomic adaptation of Zostera marina in northern California estuaries published in Scheibelhut, et al. (2023).

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Parameters

Parameter	Description	Units
INDV	sample name	unitless
SITE	B=Bodega Bay; T= Tomales Bay; two letter code indicates site within each Bay from Schiebelhut et al 2023.	unitless
collection_date	Date of sample collection	unitless
Latitude	Latitude	decimal degrees
Longitude	Longitude	decimal degrees
sheath_length	length of the seagrass sheath from the base to the abscission point	millimeters (mm)
sheath_width	width of the sheath at the abcission point	millimeters (mm)
depth	intertidal (0 to - 0.5m below mllw) or subtidal (deeper than 0.5 m below MLLW)	unitless
mean_temp_C	mean temperature at the site during the day of sampling	degrees Celsius

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Instruments

Dataset-specific Instrument Name	calipers
Generic Instrument Name	calipers
Generic Instrument Description	A caliper (or "pair of calipers") is a device used to measure the distance between two opposite sides of an object. Many types of calipers permit reading out a measurement on a ruled scale, a dial, or a digital display.

Dataset-specific Instrument Name	ruler
Generic Instrument Name	ruler
Generic Instrument Description	A device used for measuring or for drawing straight lines, consisting of an elongated piece of rigid or semi-rigid material marked with units for measurement. Device that allows one or more physical dimensions of a sample or specimen to be determined by visible comparison against marked graduations in units of measurement of dimension length.

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Project Information

Using genomics to link traits to ecosystem function in the eelgrass Zostera marina (ZosteraEcoGenomics)

Coverage: In Zostera marina beds worldwide, including western and eastern margins of both the Atlantic and Pacific Oceans. Project centered in Bodega Bay, CA 38.31 N; 123.059 W

NSF Award Abstract:
Seagrass ecosystems provide important services to coastal regions, including primary production, carbon storage, nutrient cycling, habitat for fisheries species, and erosion control. At the same time, eelgrass is threatened by direct destruction, pollution, and other human impacts on the environment. We know that genetic diversity in eelgrass enhances seagrass bed growth and persistence, but application of this knowledge to restoration and conservation is limited. This work will guide restoration programs by considering what specific aspects of diversity are important to conservation and restoration of seagrass ecosystems, helping to guide the selection of source material to improve restoration success (which is often low). The project integrates the effects of multiple components of diversity and clarifies the extent to which genetic and ecological uniqueness can predict ecosystem functions.

Intellectual Merit: Genetic diversity as measured by the number of genetically distinct individuals (genets) in an assemblage influences critical ecosystem functions in a wide range of ecosystems. Functional diversity, the presence of key traits, or population flexibility to respond to environmental change are all potential mechanisms underlying these patterns, but distinguishing among them requires a clear link between genetic diversity and the phenotypes present in an assemblage. The investigators, and others, have previously demonstrated that genet diversity in eelgrass (Zostera marina) increases stand productivity, animal community diversity, and resilience to environmental change. These genet diversity effects are associated with increases in genetically determined trait diversity. Predicting trait diversity without having to measure traits of every genet remains a major barrier to wider application of functional diversity approaches in restoration and management. In this project, the investigators assess the association between Single Nucleotide Polymorphisms (SNPs) across the genome and performance-related traits that we will measure at the individual, population, and seascape-scale. They also assess environmental correlates of trait differentiation from field sampling. Finally, the research team will compare the predictive power of genomic SNP diversity versus other metrics of intraspecific diversity for the functioning (productivity, invertebrate abundance) of field planted eelgrass assemblages. If genomic variation can reliably be used to predict functional traits, then the value of genomic sequencing efforts for informing management will be greatly enhanced. Broader Impacts: Seagrass restoration and mitigation is currently of major interest in California and elsewhere and the project results will inform current initiatives regarding eelgrass management in California through the state's Ocean Protection Council. In addition to recruiting individual students from diverse backgrounds to work on the project, the project broadens participation of students in STEM fields through its partnership with three existing outreach/training programs at UC Davis.

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.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1829976

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