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

Website: https://www.bco-dmo.org/dataset/924786
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
Stachowicz, John J.	University of California-Davis (UC Davis)	Principal Investigator
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Abstract
This dataset includes 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, California, USA from July and September of 2019. Sequence Read Archive (SRA) Experiments and BioSamples can be accessed from the NCBI BioProject PRJNA887384 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA887384/). Results summary as described in Scheibelhut, et al. (2023): We examine genomic signals of selection in the eelgrass Zostera marina across temperature gradients in adjacent embayments. Although we find many genomic regions with signals of selection within each bay there is very little overlap in signals of selection at the SNP level, despite most polymorphisms being shared across bays. We do find overlap at the gene level, potentially suggesting multiple mutational pathways to the same phenotype. Using polygenic models we find that some sets of candidate SNPs are able to predict temperature across both bays, suggesting that small but parallel shifts in allele frequencies may be missed by independent genome scans. Together, these results highlight the continuous rather than binary nature of parallel evolution in polygenic traits and the complexity of evolutionary predictability.

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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 in California 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 genetic 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 dissecting out the tissue from within the leaf sheath of all shoots within a genet and they were then flash-frozen in liquid nitrogen and stored at -80 degrees Celsius (°C). Using the inner leaf sheath tissue allowed us to minimize the amount of noneelgrass DNA by selecting tissue that was free of epibionts and had lower chloroplast concentrations. We extracted DNA from up to 200 milligrams (mg) of frozen tissue by grinding with a plastic pestle and liquid nitrogen in a 1.5 milliliter (mL) tube until powdered and then by using a modified CTAB chloroform extraction (see details and references in Schiebelhut et al., 2023).

Briefly, tissue was resuspended in 800-microliter (µL) CTAB (0.1 M Tris-HCl [pH 8.0], 0.02 M EDTA [pH 8.0], 3% CTAB, 1.4 M NaCl, 0.2% β-mercaptoethanol), after the first chloroform isoamyl alcohol step, the upper aqueous phase was transferred to a new tube and treated with 2 µL of RNAse A at 37°C for 1 hour, followed by an additional chloroform-isoamyl alcohol step before completing the remaining steps. We quantified DNA on a Qubit fluorometer and adjusted the concentration to ~13 nanograms per microliter (ng/µL); in cases where the concentration was lower than 17 ng/µL the concentration was not adjusted. DNA quality was visually assessed on a 2% agarose gel. We submitted genomic DNA for 240 individuals to the Genomics and Bioinformatics Services Texas A&M Agrilife Research Centre (College Station, Texas, USA) for library preparation using the high-throughput PerkinElmer NEXTFLEX Rapid XP DNA-Seq Kit and paired-end 150 base pair (bp) sequencing (targeting 10× coverage with ~5.8 Gb/sample) on two lanes of a NovaSeq 6000 S4 X.

BCO-DMO Processing Description

- Imported original file "WGS_LS_TomalesBodega.xlsx" into the BCO-DMO system.
- Converted date field to YYYY-MM-DD format.
- Saved the final file as "924786_v1_whole_genome_sequencing_eelgrass.csv".

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Data Files

File
924786_v1_whole_genome_sequencing_eelgrass.csv (Comma Separated Values (.csv), 25.73 KB) MD5:a76e9bc7e49dcd3c4208f11121ccd512 Primary data file for dataset ID 924786, version 1

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Related Publications

Schiebelhut, L. M., Grosberg, R. K., Stachowicz, J. J., & Bay, R. A. (2023). Genomic responses to parallel temperature gradients in the eelgrass Zostera marina in adjacent bays. Molecular Ecology, 32(11), 2835–2849. Portico. https://doi.org/10.1111/mec.16899
Results

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Related Datasets

IsRelatedTo

Schiebelhut, L., Grosberg, R., Stachowicz, J. J., & Bay, R. (2023). *Data and code associated with: Genomic responses to parallel selection in the eelgrass Zostera marina in adjacent bays* (Version 7) [Data set]. Dryad.

https://doi.org/10.6071/M3DD4F

Stachowicz, J. J. (2024) **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.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2024-04-10 doi:10.26008/1912/bco-dmo.924808.1 [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).

University of California, Merced. Genomic responses to parallel selection in the eelgrass Zostera marina in adjacent bays. 2022/10. 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/PRJNA887384. NCBI:BioProject: PRJNA887384.

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Parameters

Parameter	Description	Units
accession	NCBI accession number	unitless
sample_name	sample name	unitless
bioproject_accession	NCBI BioProject number	unitless
Site	Geographic Site Name	unitless
organism	Organism name	unitless
collection_date	Date of sample collection	unitless
isolation_source	Upper (0 m mllw) vs Lower (-0.5 to -1.0 m mllw) intertidal zone	unitless
latitude	latitude	decimal degrees
longitude	longitude	decimal degrees

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Instruments

Dataset-specific Instrument Name	2% agarose gel
Generic Instrument Name	Agarose Gel Electrophoresis System
Generic Instrument Description	A gel electrophoresis system that is used to separate DNA or RNA molecules by size, achieved by moving negatively charged nucleic acid molecules through an agarose matrix with an electric field.

Dataset-specific Instrument Name	NovaSeq 6000 S4 X
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	Qubit fluorometer
Generic Instrument Name	Fluorometer
Generic Instrument Description	A fluorometer or fluorimeter is a device used to measure parameters of fluorescence: its intensity and wavelength distribution of emission spectrum after excitation by a certain spectrum of light. The instrument is designed to measure the amount of stimulated electromagnetic radiation produced by pulses of electromagnetic radiation emitted into a water sample or in situ.

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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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