

Eelgrass (*Zostera marina*) diversity metrics from 15-month field experiment in Bodega Bay, CA starting in the summer of 2013

Website: <https://www.bco-dmo.org/dataset/725627>

Data Type: Other Field Results

Version: 1

Version Date: 2018-01-31

Project

» [Connecting genetic diversity to ecosystem functioning: links between genetic diversity, relatedness and trait variation in a seagrass community](#) (Genetic Div to Ecosys Functioning)

Contributors	Affiliation	Role
Stachowicz, John J.	University of California-Davis (UC Davis)	Principal Investigator, Contact
York, Amber D.	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

Field experiment assessing the relative importance of genotype richness, genetic relatedness, and trait diversity on eelgrass performance. The 15-month experiment was started in July of 2013 and ended in October 2015.

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Coverage

Spatial Extent: Lat:38.32353 Lon:-123.04778

Temporal Extent: 2013-07 - 2015-11

Methods & Sampling

Field experiment assessing the relative importance of genotype richness, genetic relatedness, and trait diversity on eelgrass performance. 41 genotypes across three tidal heights at five sites were collected in Bodega Harbor, California, USA in May 2012 and propagated in outdoor tanks at the UC Davis Bodega Marine Laboratory to produce enough shoots for deployment in a 15-month field experiment starting in the summer of 2013. More details can be found in Abbott et al., 2017 and Abbott et al., in press.

Location: Bodega Harbor, CA. Latitude: 38.32353 N Longitude: -123.04778 W.

Eelgrass collection locations can be found in the dataset: "Eelgrass transect information" <https://www.bco-dmo.org/dataset/725435>.

Physical and morphological traits of the eelgrass used in this experiment can be found in the dataset "Eelgrass traits" <https://www.bco-dmo.org/dataset/725483> measured between March of 2013 and August of 2014.

Data Processing Description

BCO-DMO Data Manager Processing Notes:

- * added a conventional header with dataset name, PI name, version date
- * modified parameter names to conform with BCO-DMO naming conventions
- * rounded all numeric values with more than three decimal places to three decimal places
- * changed values "ND" to "nd" indicating no data for BCO-DMO system compatibility

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Data Files

File
RichnessRelatedness.csv (Comma Separated Values (.csv), 9.73 KB) MD5:fcc77c4bfb563ef3d84f11ecb86f22bc Primary data file for dataset ID 725627

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Related Publications

Abbott, J. M., DuBois, K., Grosberg, R. K., Williams, S. L., & Stachowicz, J. J. (2018). Genetic distance predicts trait differentiation at the subpopulation but not the individual level in eelgrass, *Zostera marina*. *Ecology and Evolution*, 8(15), 7476–7489. Portico. <https://doi.org/10.1002/ece3.4260>
Results

,
Methods

Abbott, J. M., Grosberg, R. K., Williams, S. L., & Stachowicz, J. J. (2017). Multiple dimensions of intraspecific diversity affect biomass of eelgrass and its associated community. *Ecology*, 98(12), 3152–3164.
doi:[10.1002/ecy.2037](https://doi.org/10.1002/ecy.2037)

Results

,
Methods

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Parameters

Parameter	Description	Units
Block	block refers to spatial location of the plots in the blocked design of the experiment	unitless
Treatment	treatment in the form of number-word; number refers to initial number of genotypes and words refers to relatedness (high-med-low)	unitless
Richness_initial	initial number of genotypes planted in the plot	unitless
Ave_Relatedness_Intitial	average pairwise relatedness of the genotypes initially planted. Relatedness ranges from -1 (as unrelated as possible) to +1 (genetically identical)	unitless

Ave_Relatedness_findI	average pairwise relatedness of the genotypes left at the end of the experiment	unitless
Relatedness_weighted_findI	measure of the relatedness of genotypes present at the end of the experiment weighted by their relative abundance (analogous to Rao's Q)	unitless
Rao_intial	Rao's Q (trait diversity) of the genotypes initially planted	unitless
Rao_findI	Rao's Q (trait diversity) of the genotypes left at end of experiment - unweighted	unitless
Rao_findI_weigthed	Rao's Q (trait diversity) of the genotypes left at end of experiment - weighted by relative abundance of genotypes	unitless
Rao_FindI_propogation_traits	Rao's Q (trait diversity) of the genotypes left at end of experiment - unweighted only for traits related to propogation	unitless
Rao_FindI_Nutrient_uptake_traits	Rao's Q (trait diversity) of the genotypes left at end of experiment - unweighted only for nitrate and ammonium uptake rate	unitless
genotypic_richness_findI	final genotypic richness	unitless
genotypic_diversity	final genotypic shannon diversity	unitless
genotypic_evenness	final genotypic evenness	unitless
Aboveground_biomass	total aboveground biomass	grams (g)
rhizome_biomass	total rhizome biomass	grams (g)
Root_biomass	total root biomass	grams (g)
Belowground_biomass	total belowground biomass	grams (g)
total_biomass	total biomass (above + below)	grams (g)

Leaf_Growth	leaf growth rate	centimeters squared per day (cm ² /day)
Ratio_above_to_below_ground_biomass	ratio of above to belowground biomass	dimensionless
Invert_richness_per_g_eelgrass	invertebrate richness per gram of eelgrass sampled	unitless
Invert_abundance_per_g_eelgrass	invertebrate abundance per gram of eelgrass sampled	unitless
Invert_Abund_per_plot	invertebrate abundance per plot (abundance/g X total aboveground biomass)	unitless
Invert_raw_richness	raw richness per plot (total richness per sampled of 3 shoots)	unitless

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Deployments

Stachowicz_Eelgrass_Transects_2012

Website	https://www.bco-dmo.org/deployment/725439
Platform	Bodega Harbor

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Project Information

Connecting genetic diversity to ecosystem functioning: links between genetic diversity, relatedness and trait variation in a seagrass community (Genetic Div to Ecosys Functioning)

There is growing evidence that genetic variation within and among populations of key species plays an important role in marine ecosystem processes. Several experiments provide compelling evidence that the number of genotypes in an assemblage (genotypic richness) can influence critical ecosystem functions including productivity, resistance to disturbance and invasion or colonization success. However, these studies use only the number of genotypes as a measure of genetic diversity. Recent analyses of species diversity experiments show that phylogenetic diversity may be a more reliable predictor of ecosystem functioning than simply the number of species. However, such approaches have not yet been applied to understanding the effects of genetics on ecosystem functioning. While genetic relatedness within a species holds the potential to predict the outcome of intraspecific interactions, and the functioning of ecosystems that depend on those species, we currently have few data to assess the shape or strength of this relationship. The investigators will build on their own previous work, and that of others, in eelgrass (*Zostera marina*) ecosystems showing strong effects of genotypic richness on a spectrum of critical ecosystem processes. The investigators will ask whether genotypic richness, or - as in studies at the level of species diversity - genetic relatedness/distance better predicts ecosystem functioning? If genetic relatedness measures are better predictors, then what mechanisms underlie this relationship? Can genetic relatedness predict ecological relatedness?

Although the current focus is on eelgrass, the research should be applicable to many systems. The project will

assess the relationship between genetic relatedness and phenotypic distinctiveness of a key marine foundation species and use manipulative experiments to test the relative importance of the number of genotypes in an assemblage vs. their genetic relatedness and trait diversity for ecosystem functioning. Specifically, experiments will:

- (1) characterize the relationship between genetic relatedness and trait similarity among individual genotypes of eelgrass, including responses to experimental warming;
- (2) compare the effects of genetic relatedness and trait similarity among genotypes on the outcome of intraspecific competitive interactions; and
- (3) test the relative effect of genetic relatedness vs. number of genotypes of eelgrass on the growth of eelgrass, its associated ecosystem functions it (e.g., primary production, nutrient dynamics, trophic transfer, habitat provision, and detrital production and decomposition).

Seagrass ecosystems provide important services to coastal regions including primary production, nutrient cycling, habitat for fisheries species, and erosion control. Previous studies have shown these services can be compromised by reduction in the numbers of species of grazers or genotypes, but this study will allow a more predictive approach to diversity loss by integrating the effects of multiple components of diversity and clarifying the extent to which diversity effects can be predicted by the genetic or ecological uniqueness of component genotypes.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1234345

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