

# Site information for eelgrass (*Zostera marina*) transects in Bodega Bay, CA in May of 2012

**Website:** <https://www.bco-dmo.org/dataset/725435>

**Data Type:** Other Field Results

**Version:** 2

**Version Date:** 2018-06-12

## 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
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## Abstract

Site information for *Zostera marina* physiological and morphological traits sample transects in Bodega Bay, CA in May of 2012.

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## Coverage

**Spatial Extent:** N:38.33352 E:-123.04258 S:38.30498 W:-123.05932

**Temporal Extent:** 2012-05

## Methods & Sampling

In May 2012 we collected 20 ramets harvested at 2 m intervals along a 40 m transect at each of three tidal heights (high intertidal, low intertidal, and subtidal) at five sites within Bodega Harbor, CA. The five eelgrass collection sites are distributed throughout the harbor, between 0.45 and 3.2 km apart.

The dataset "Eelgrass diversity" <https://www.bco-dmo.org/dataset/725627> references the Site\_Code and Tidal\_Height data parameters in this "Eelgrass Transect Information" dataset.

Related dataset:

\* Eelgrass traits: <https://www.bco-dmo.org/dataset/725483>

## Data Processing Description

BCO-DMO Data Manager Processing Notes (Data version 2 - 2018-06-12):

\* data version 2 replaces (2018-06-12) data version 1 (2018-01-30). Data updated to correct transect latitude and longitudes.

- \* made longitude in decimal degrees negative
- \* added site codes provided in last data version

BCO-DMO Data Manager Processing Notes (Data version 1 - 2018-01-30):

- \* added a conventional header with dataset name, PI name, version date
- \* added column for site code and concatenated all site information vertically
- \* added columns for lat/lon degrees, minutes, and direction from provided lat/lon in degrees decimal minutes format which had formatting inconsistencies (spaces, minute symbols)
- \* added lat/lon in decimal degree format
- \* added column for full location name
- \* original file had start and stop lat/lons in the same columns with another column with values (start|end). Separated start and end lat/lons so there are now four columns (lat\_start,lon\_start,lat\_end,lon\_end).

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## Data Files

File
<b>site_list.csv</b> (Comma Separated Values (.csv), 1.02 KB) MD5:76991e8a71e9162f55218c0bc0a379db
Primary data file for dataset ID 725435

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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
Site_Name	Site name	unitless
Site_Code	Site code (MM=mason's marina; WP = westside park; CC = Campbell Cove; DP = Doran Park; J = jetty)	unitless
Tidal_Elevation	Description of tidal height (high intertidal; low intertidal; subtidal)	unitless
Tidal_Code	Code for tidal height (HI=high intertidal; LI=low intertidal; S=subtidal)	unitless
Start_Transect_Lat	Transect start latitude	decimal degrees
Start_Transect_Lon	Transect start longitude	decimal degrees
End_Transect_Lat	Transect end latitude	decimal degrees
End_Transect_Lon	Transect end longitude	decimal degrees

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## Deployments

### Stachowicz Eelgrass Transects 2012

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/725439">https://www.bco-dmo.org/deployment/725439</a>
<b>Platform</b>	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
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1234345</a>

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