Results from experiment examining Zostera marina genotype response to warming from the Bodega Marine Laboratory

Website: https://www.bco-dmo.org/dataset/645524
Data Type: experimental
Version: 17 May 2016
Version Date: 2016-05-17

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

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Dataset Description

Zostera marina genotype-specific traits after transplantation, a 5-week warming event, and a 5-week recovery.

The experiment is described in:
Reynolds LK, DuBois K, Abbott JM, Williams SL, Stachowicz JJ (2016) Response of a Habitat-Forming Marine Plant to a Simulated Warming Event Is Delayed, Genotype Specific, and Varies with Phenology. PLoS ONE 11(6): e0154532. doi:10.1371/journal.pone.0154532

Methods & Sampling

The experiment is described in:
Reynolds LK, DuBois K, Abbott JM, Williams SL, Stachowicz JJ (2016) Response of a Habitat-Forming Marine Plant to a Simulated Warming Event Is Delayed, Genotype Specific, and Varies with Phenology. PLoS ONE 11(6): e0154532. doi:10.1371/journal.pone.0154532

Data Processing Description

BCO-DMO processing:
- modified parameter names to conform with BCO-DMO naming conventions;
- replaced "." with "nd" (missing data/no data);
- rounded columns to 2 decimal places: leafpro_grams, leafpro, above_below, alpha, ETR_max, NO3.

Data Files

File
warming_experiment.csv(Comma Separated Values (.csv), 23.40 KB) MD5:450f9fbcafcc55708f0dfa0ea272b08b Primary data file for dataset ID 645524

Parameters

Parameter	Description	Units
time_point	Time point of sampling: after acclimation (1), a 5 week warming event (2), and after a 5 week recovery (3).	dimensionless
treatment	Treatment type: Warm vs Control.	dimensionless
genotype	Individual clone.	dimensionless
bin	Replicate mesocosm.	dimensionless
shootpro_grams	Biomass of new shoots produced (cumulative over time).	grams (g)
leafpro_grams	Leaf biomass productivity measured with the marking technique.	grams per day (g day-1)
shootpro	Number of new shoots produced (cumulative over time).	counts
leafpro	Leaf area productivity measured with the marking technique.	square centimeters per day (cm2 day-1)
rhizome_len	Cumulative rhizome length.	centimeters (cm)
above_below	Above to below ground biomass ratio.	dimensionless
max_leaf_len	Maximum leaf length of terminal shoot.	centimeters (cm)
sheath_width	Maximum leaf width of terminal shoot at the top of the sheath.	centimeters (cm)
leaves	Number of leaves on the terminal shoot.	count

DA_yield	Terminal shoot Dark adapted yield (FV/Fm measured by Pulse Amplitude Modulation).	dimensionless
alpha	Terminal shoot alpha (the initial slope of the curve—a measure of light harvesting efficiency by Pulse Amplitude Modulation).	dimensionless
ETR_max	Terminal shoot ETRMAX (the asymptote of the curve—a measure of photosystem capacity to use absorbed light by Pulse Amplitude Modulation).	dimensionless
NO3	Terminal shoot nitrate uptake rate normalized to plant biomass.	micromoles per gram per minute (micromol g-1 min-1)

Deployments

BML_Stachowicz

Website	https://www.bco-dmo.org/deployment/645707
Platform	lab Bodega Marine Laboratory

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.

Funding

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