Feeding trials: Effects of diversity in feeding trials, conducted at Bodgea Marine Laboratory, using detritus from eelgrass (Zostera marina) genotypes (clones) as a food source and either one or a combination of invertebrate grazers

Website: https://www.bco-dmo.org/dataset/714942
Data Type: experimental
Version: 1
Version Date: 2017-09-15

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

Seagrass meadows are among the world's most productive ecosystems, and as in many other systems, genetic diversity is correlated with increased production. However, only a small fraction of seagrass production is directly consumed, and instead much of the secondary production is fueled by the detrital food web. Here, we study how plant genotype influences detrital consumption. We used three common mesograzers—an amphipod, Ampithoe lacertosa, an isopod, Idotea resecata, and a polychaete, Platynereis bicanaliculata. Each grazer consumed eelgrass detritus at rates greater than live eelgrass or macroalgae. This detrital consumption, however, was not spread evenly over leaves shed from different eelgrass

clones. Palatability and consumption varied because of genotype specific differences in leaf texture, secondary metabolites (phenolics), and nutritional quality (nitrogen). Further, detritus derived from some eelgrass genotypes was palatable to all grazers, while detritus from other genotypes was preferentially consumed by only one grazer species. These data are illustrated in figures 2 and 3 of Reynolds et al., 2017 (DOI:10.1111/oik.04471).

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Dataset Description

In this project, we examined the effect of eelgrass genetic and invertebrate species diversity on detrital consumption and animal survival rates in a series of laboratory experiments. This dataset contains chemical traits for individual eelgrass clones and feeding rates for each grazer type (isopods, amphipods, polychaetes).

Abstract:
Seagrass meadows are among the world's most productive ecosystems, and as in many other systems, genetic diversity is correlated with increased production. However, only a small fraction of seagrass production is directly consumed, and instead much of the secondary production is fueled by the detrital food web. Here, we study how plant genotype influences detrital consumption. We used three common mesograzers—an amphipod, *Ampithoe lacertosa*, an isopod, *Idotea resecata*, and a polychaete, *Platynereis bicanaliculata*. Each grazer consumed eelgrass detritus at rates greater than live eelgrass or macroalgae. This detrital consumption, however, was not spread evenly over leaves shed from different eelgrass clones. Palatability and consumption varied because of genotype specific differences in leaf texture, secondary metabolites (phenolics), and nutritional quality (nitrogen). Further, detritus derived from some eelgrass genotypes was palatable to all grazers, while detritus from other genotypes was preferentially consumed by only one grazer species.

These data are illustrated in figures 2 and 3 of the manuscript:
Reynolds LK, KM Chan, E Huynh, SL Williams, and JJ Stachowicz (in press) Plant genotype

indentity and diversity interact with mesograzer species diversity to influence detrital consumption in eelgrass meadows. DOI:10.1111/oik.04471

Acquisition Description

We conducted a series of food choice experiments using detritus from cultured eelgrass (Zostera marina) genotypes (clones) as a food source and either one or a combination of the following invertebrate grazers: the tube dwelling amphipod *Ampithoe lacertosa*, the free swimming isopod *Idotea resecata*, and/or the tube building polychaete *Platynereis bicanaliculata*.

All feeding trials were conducted by placing pre-weighed fragments of each choice (approximately 4 cm in length) in 140 mL cups (7 cm tall, 6 cm diameter) covered with a 250 um mesh cloth and submerged in a flowing seawater bath in an indoor tank. Food choices were marked using colored zip ties, and trials were terminated before any food item was reduced in size by one half. Consumption was calculated as ([Hi X Cf/Ci] - Hf), where Hi and Hf were initial and final wet masses of tissue exposed to consumers, and Ci and Cf were initial and final masses in controls.

In addition to feeding trials, we grew invertebrates for one month (in similar containers and feeding trial conditions) with food sources that varied in number of seagrass clones present. Animal survival was assessed weekly, and food was replaced.

The chemical traits for individual eelgrass clones were also assessed. We measured the pressure required to penetrate and tear each genotype. We clamped in place below a needle (17G / 19mm length), which was held in place with a metal sleeve and which supported a cup to which dry sand was added a few milligrams at a time until the pin pierced completely through the plant tissue. The mass of the dry sand and the apparatus were then weighed to determine the mass needed to pierce the leaf (Duffy & Hay 1991). Tensile strength was measured using a tensiometer. Leaf segments were clamped to a hanging balance equipped with a maximum mass indicator and pulled by hand until the leaf failed. Phenolic content was determined on an approximately 4 mg subsample using a modified Folin-Ciocalteu method (see Bolser et al. 1998). An approximately 3 mg subsample was analyzed for carbon and nitrogen concentration on a Thermo Flash EA 1112 Soil elemental analyzer.

Processing Description

BCO-DMO Processing:
- separated original Excel file into 3 datasets: feeding trials, biodiversity experiments,

invertebrate survival;
- modified parameter names to conform with BCO-DMO naming conventions: replaced % with pcnt, replaced spaces with underscores.

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Related Publications

Reynolds, L. K., Chan, K. M., Huynh, E., Williams, S. L., & Stachowicz, J. J. (2017). Plant genotype identity and diversity interact with mesograzer species diversity to influence detrital consumption in eelgrass meadows. Oikos, 127(2), 327–336. doi:10.1111/oik.04471

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Parameters

Parameter	Description	Units
Genotype	Individual clone	unitless
Nitrogen_pcnt	Detrital leaf nitrogen content	percent (%)
Carbon_pcnt	Detrital leaf carbon content	percent (%)
Tear_g	The mass recordered by a tensiometer reqired to break a detrial leaf	grams (g)
Penetrate_g	The mass needed to push a needle through a detrial leaf	grams (g)
Phenolic_pcnt	Phenolic concentration measured by the Folin Ciocalteu method	percent (%)
Isopod_feeding_rate_mg_day	Isopod (Idotea rescata) feeding rate	milligrams per day (mg/day)
Amphipod_feeding_rate_mg_day	Amphipod (Amphithoe lacertosa) feeding rate	milligrams per day (mg/day)
Polychaete_feeding_rate_mg_day	Polychaete (Platynereis bicanicalulata) feeding rate	milligrams per day (mg/day)

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Instruments

Dataset-specific Instrument Name	indoor tank
Generic Instrument Name	Aquarium
Dataset-specific Description	Pre-weighed fragments of eelgrass were covered with a 250 um mesh cloth and submerged in a flowing seawater bath in an indoor tank.
Generic Instrument Description	Aquarium - a vivarium consisting of at least one transparent side in which water-dwelling plants or animals are kept

Dataset-specific Instrument Name	Thermo Flash EA 1112 Soil elemental analyzer
Generic Instrument Name	Elemental Analyzer
Dataset-specific Description	Carbon and nitrogen concentrations were measured on a Thermo Flash EA 1112 Soil elemental analyzer.
Generic Instrument Description	Instruments that quantify carbon, nitrogen and sometimes other elements by combusting the sample at very high temperature and assaying the resulting gaseous oxides. Usually used for samples including organic material.

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Deployments

BML_Stachowicz

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

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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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