

A re-sampling of historical population genetic surveys of *Zostera marina* from Bodega, Tomales, and San Francisco Bays USA; study performed at Bodega Marine Laboratory in 2014-15

Website: <https://www.bco-dmo.org/dataset/661446>

Data Type: experimental

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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

A re-sampling of historical population genetic surveys of *Zostera marina* from Bodega (BB), Tomales (TB), and San Francisco Bays (SFB) USA. Plant (*Zostera marina*) samples were collected from Bodega Bay, Tomales Bay, and San Francisco Bay in 2013. DNA was extracted and amplified in the Stachowicz and Grosberg labs at UCDavis, and fragments were analyzed at the UCDavis core facility during 2014-2015. Data are presented as number of base pairs.

Methods & Sampling

Both sampling and analyses are described in the manuscript in press in the journal *Heredity*, titled "Temporal stability in patterns of genetic diversity and structure of a marine foundation species (*Zostera marina*)".

Briefly, we re-sampled *Z. marina* populations previously described genetically in the literature. Because the goal of sampling these populations was to compare changes over time within each region, we designed the re-sampling to match the previously published studies as closely as possible. Consequently, sampling schemes (haphazard collection (SFB) vs. quadrat sampling (TB and BB)) differed between regions. DNA from all samples was analyzed at 12 microsatellite loci.

Data Processing Description

We amplified 12 previously characterized microsatellite loci (CT12, CT19 (Reusch 2000), CT3, GA2, GA3 (Reusch et al. 1999), CL32 Contig 2, ZMC 12075, ZMC 13053, ZMC 19017, (Oetjen & Reusch 2007), CL 559 Contig 1, CL172 Contig 1, ZMC 19062 (Oetjen et al. 2010)). We analyzed fragments on an ABI 3010XL at the UC Davis DNA sequencing facility, and visualized the fragments using STRand software (Toonen & Hughes 2001).

BCO-DMO Processing:

- modified parameter names to conform with BCO-DMO naming conventions; appended "a1" (allele 1) or "a2" (allele 2).
- added columns containing the full name/meaning for region, meadow, and tidal height codes.

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Data Files

File
heredity.csv (Comma Separated Values (.csv), 45.69 KB) MD5:3a3ea8a4838bad910f017d03aadf71c0
Primary data file for dataset ID 661446

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Parameters

Parameter	Description	Units
region_code	Code assigned to region where samples were collected	unitless
region	Region where samples were collected	unitless
meadow_code	Code assigned to meadow within the region where samples were collected	unitless
meadow	Meadow within the region where samples were collected	unitless
tidal_height_code	Code assigned to tidal height. NA = Not applicable because samples were collected over a gradient	unitless
tidal_height	Description of tidal height of area sampled	unitless
CL32_Con2_a1	Locus CL32 Contig 2 (Oetjen & Reusch 2007 Molecular Ecology); allele 1; reported in number of base pairs.	unitless
CL32_Con2_a2	Locus CL32 Contig 2 (Oetjen & Reusch 2007 Molecular Ecology); allele 2; reported in number of base pairs.	unitless

CL559_Con1_a1	Locus CL 559 Contig 1 (Oetjen et al. 2010 Marine Biology); allele 1; reported in number of base pairs.	unitless
CL559_Con1_a2	Locus CL 559 Contig 1 (Oetjen et al. 2010 Marine Biology); allele 2; reported in number of base pairs.	unitless
ZMC12075_a1	Locus ZMC 12075 (Oetjen & Reusch 2007 Molecular Ecology); allele 1; reported in number of base pairs.	unitless
ZMC12075_a2	Locus ZMC 12075 (Oetjen & Reusch 2007 Molecular Ecology); allele 2; reported in number of base pairs.	unitless
ZMC13053_a1	Locus ZMC 13053 (Oetjen & Reusch 2007 Molecular Ecology); allele 1; reported in number of base pairs.	unitless
ZMC13053_a2	Locus ZMC 13053 (Oetjen & Reusch 2007 Molecular Ecology); allele 2; reported in number of base pairs.	unitless
CL172_Con1_a1	Locus CL172 Contig 1 (Oetjen et al. 2010 Marine Biology); allele 1; reported in number of base pairs.	unitless
CL172_Con1_a2	Locus CL172 Contig 1 (Oetjen et al. 2010 Marine Biology); allele 2; reported in number of base pairs.	unitless
ZMC19017_a1	Locus ZMC 19017 (Oetjen & Reusch 2007 Molecular Ecology); allele 1; reported in number of base pairs.	unitless
ZMC19017_a2	Locus ZMC 19017 (Oetjen & Reusch 2007 Molecular Ecology); allele 2; reported in number of base pairs.	unitless
ZMC19062_a1	Locus ZMC 19062 (Oetjen et al. 2010 Marine Biology); allele 1; reported in number of base pairs.	unitless
ZMC19062_a2	Locus ZMC 19062 (Oetjen et al. 2010 Marine Biology); allele 2; reported in number of base pairs.	unitless
CT12_a1	Locus CT12 (Reusch 2000 Molecular Ecology); allele 1; reported in number of base pairs.	unitless
CT12_a2	Locus CT12 (Reusch 2000 Molecular Ecology); allele 2; reported in number of base pairs.	unitless
CT19_a1	Locus CT19 (Reusch 2000 Molecular Ecology); allele 1; reported in number of base pairs.	unitless

CT19_a2	Locus CT19 (Reusch 2000 Molecular Ecology); allele 2; reported in number of base pairs.	unitless
CT3_a1	Locus CT3 (Reusch et al. 1999 Marine Biology); allele 1; reported in number of base pairs.	unitless
CT3_a2	Locus CT3 (Reusch et al. 1999 Marine Biology); allele 2; reported in number of base pairs.	unitless
GA2_a1	Locus GA2 (Reusch et al. 1999 Marine Biology); allele 1; reported in number of base pairs.	unitless
GA2_a2	Locus GA2 (Reusch et al. 1999 Marine Biology); allele 2; reported in number of base pairs.	unitless
GA3_a1	Locus GA3 (Reusch et al. 1999 Marine Biology); allele 1; reported in number of base pairs.	unitless
GA3_a2	Locus GA3 (Reusch et al. 1999 Marine Biology); allele 2; reported in number of base pairs.	unitless

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Instruments

Dataset-specific Instrument Name	ABI 3010XL
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	We analyzed fragments on an ABI 3010XL at the UC Davis DNA sequencing facility, and visualized the fragments using STRand software (Toonen & Hughes 2001).
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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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.

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