The genotypes from 9 microsatellites generated on individuals of the red invasive seaweed Gracilaria vermiculophylla

Website: https://www.bco-dmo.org/dataset/629302
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Project
» Cascading effects of an invasive seaweed on estuarine food webs of the southeastern US (Gracilaria effects)

Contributors	Affiliation	Role
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Dataset Description

This dataset contains the genotypes from 9 microsatellites generated on individuals of the red invasive seaweed *Gracilaria vermiculophylla*.

This is a supplemental file (PeerJ_genotype_data.xlsx) of the manuscript:
Kollars, N. M., S. a. Krueger-Hadfield, J. E. Byers, T. W. Greig, A. E. Strand, F. Weinberger, and E. E. Sotka. 2015. Development and characterization of microsatellite loci for the haploid–diploid red seaweed *Gracilaria vermiculophylla*. PeerJ 3:e1159. doi: 10.7717/peerj.1159

Related supplemental files:
Table S1: Characteristics of 33 microsatellite loci developed for *Gracilaria vermiculophylla* that showed monomorphism, non-amplification, or multi-locus genetic determinism.

Table S2: Null allele frequencies for the microsatellite loci developed for *Gracilaria vermiculophylla*. Frequencies were directly estimated in the haploid subpopulations, whereas frequencies in each of the diploid subpopulations at Akkeshi, Elkhorn Slough, Fort Johnson and Nordstrand were calculated using maximum likelihood and the software MLNullFreq.

Table S3: Short allele dominance analysis for microsatellite loci developed for *Gracilaria vermiculophylla* including number of pooled size classes used in regression analysis (following Wattier *et al.* 1998), *No. of classes*, and linear regression statistics. Loci Gverm_10367 and Gverm_2790 only exhibited two alleles in our sampled populations and consequently, short allele dominance analysis was not applicable (NA).

Table S4: Linkage disequilibrium analysis for microsatellite loci developed for *Gracilaria vermiculophylla*. Darkened cells indicate pairs of loci that show significant linkage disequilibrium after Bonferroni correction (*p*-value threshold < 0.006 at $\alpha = 0.05$).

Table S5: Genetic features per locus of four populations of *Gracilaria vermiculophylla*, including: number of alleles at each locus, *NA*, + standard error (SE); mean allelic richness, *AE*, based on the smallest global sample size of 46 alleles (23 diploid individuals) + SE; mean observed heterozygosity, *HO*, + SE; mean expected heterozygosity, *HE*, + SE.

Methods & Sampling

Data were generated on an ABI genotyper.

Briefly, from Kollars et al. (2015):
A library of contigs for *G. vermiculophylla* was generated using the 454 next-generation sequencing platform (Cornell University Life Sciences Core Laboratory Center) from a single individual collected fromCharleston, South Carolina, USA. Total genomic DNA was isolated and loci were amplified on a thermocycler (BioRad). Samples were electrophoresed on an ABI 3130xL genetic analyzer equipped with 36 cm capillaries (Applied Biosystems). Alleles were scored manually using GENEMAPPER ver. 4 (Applied Biosystems) and allele sizes were binned with TANDEM ver. 1.08 software.

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Data Files

File
raw_genotypes.csv (Comma Separated Values (.csv), 15.00 KB) MD5:6a5a80c7aa8f72a8802e7f3bf2e55db8 Primary data file for dataset ID 629302

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Parameters

Parameter	Description	Units
individual	Individual identifier.	dimensionless
population	Population.	dimensionless
range	Range (native or non-native).	dimensionless
Gverm_1203	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_1203b	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_6311	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_6311b	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_8036	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_8036b	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_804	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_804b	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_10367	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_10367b	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_5276	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_5276b	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_2790	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_2790b	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_3003	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_3003b	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_1803	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless
Gverm_1803b	Name of loci (with two columns per locus to capture the diploid genotypes).	dimensionless

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Instruments

Dataset-specific Instrument Name	ABI 3130xL genetic analyzer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Samples were electrophoresed on an ABI 3130xL genetic analyzer equipped with 36 cm capillaries (Applied Biosystems).
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	Thermocycler
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	Loci were amplified on a thermocycler (BioRad). The PCR program included 2 min at 95 degrees C, 30 cycles of 30 s at 95 degrees C, 30 s at 55 degrees C and 30 s at 72 degrees C, and a final 5 min at 72 degrees C.
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Project Information

Cascading effects of an invasive seaweed on estuarine food webs of the southeastern US (Gracilaria effects)

Coverage: Georgia and South Carolina coasts

Description from NSF award abstract:
During the last decade, the Asian seaweed, *Gracilaria vermiculophylla*, has proliferated along high-salinity mudflats in several Georgia and South Carolina estuaries. The invasion is noteworthy because the mudflats in these estuaries were historically devoid of macrophyte-based primary production and structure. *Gracilaria* has few native analogues in these mudflat environments, and thus represents an opportunity to examine the ecosystem consequences of an invasion within an historically-unexploited niche. In theory, *Gracilaria* affects populations of species that are directly dependent on the invader for structure and food, as well as altering community- and ecosystem-level processes such as detrital production and food web structure. Through a combination of manipulative field experiments, laboratory assays and stable isotope analysis, the investigators will test three mechanisms by which *Gracilaria* influences native community structure. The novel structure and primary production generated by *Gracilaria vermiculophylla* may be 1) increasing rates of secondary production, 2) increasing levels of mudflat microbial production through leeching of dissolved nutrients, and 3) increasing detrital input to microbial and macrobial food webs.

This project will provide a mechanistic understanding of the multiple cascading impacts of an invasive species within the estuarine community. Species invasions that alter ecosystem functions are usually the most profound. These alterations are often generated by a small number of invaders that create physical structure, including important biogenic habitat, de novo. By altering physical structure, these non-native ecosystem engineers alter local abiotic conditions, interactions between species, and species composition. Highly influential invaders may also change food web structure and trophic flow of energy and materials. Such substantive food web changes can occur when an influential invader provides nutrients or resources that are different in quality, quantity or both. An invasive species that both provisions new physical structure and fundamentally alters food web structure could exert an overwhelming influence on native communities when these mechanisms act in synergy.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1057707
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