Accession numbers and characteristics of 33 microsatellite loci developed for Gracilaria vermiculophylla

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 is a supplemental file (PeerJ_TableS1.docx) 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 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, N_A, $\pm$ standard error (SE); mean allelic richness, A_E, based on the smallest global sample size of 46 alleles (23 diploid individuals) $\pm$ SE; mean observed heterozygosity, H_O, $\pm$ SE; mean expected heterozygosity, H_E, $\pm$ SE.

Red Invasive Seaweed - Raw Genotypes (PeerJ_genotype_data.xlsx)

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Data Files

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accession_numbers.csv(Comma Separated Values (.csv), 9.72 KB)
MD5:995b5ce1d4c8338b015df30b79c717fc
Primary data file for dataset ID 630041

Parameters

Parameter	Description	Units
locus	Locus identifier.	dimensionless
accession_num	Genbank accession number.	dimensionless
motif	Sequence motif.	dimensionless
primer_sequence	Primer sequences.	dimensionless
profile	One- or multi- locus genetic determinism. "no amp." indicates non-amplification.	dimensionless
accession_URL	Hyperlink to Genbank for the accession number.	dimensionless

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.

Funding

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