

# GenBank accession numbers for algae species sequenced in Antarctica, California, and Fiji.

**Website:** <https://www.bco-dmo.org/dataset/743771>

**Data Type:** Other Field Results

**Version:** 1

**Version Date:** 2018-08-20

## Project

» [Detecting genetic adaptation during marine invasions](#) (Genetic Adaptation Marine Inv)

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## Coverage

**Spatial Extent:** N:38.32 E:-64.05 S:-64.77 W:-123.04

**Temporal Extent:** 1996 - 2014

## Dataset Description

GenBank accession numbers for the algae species sequenced.

## Methods & Sampling

These data are described in detail in Demko, A. M., C. D. Amsler, M. E. Hay, J. D. Long, J. B. McClintock, V. J. Paul, and E. E. Sotka. 2017. Declines in plant palatability from polar to tropical latitudes depend on herbivore and plant identity. *Ecology* 98:2312–2321. We quantified the relative palatability of 50 seaweeds by offering each generalist herbivore a pairwise choice between each test seaweed and a control in artificial feeding assays with finely ground lyophilized tissue. For each assay, 8 g of freeze-dried and ground powder (ground via Wiley Mill) of one experimental seaweed and the *Ulva* control were rehydrated with 28 mL distilled water and mixed with 72 mL molten agar (2% by mass). Seaweed mixes were then poured into side-by-side lanes in a mold on window screen (192 mm squares) in a thickness of approximately 2 mm. After cooling, the screen was then cut into strips with approximately 80 squares of each food type separated by 2 cm. Individual strips were then isolated with approximately 30 separate crabs and 50 separate urchins, and removed before the entirety of either food was consumed or until 24–30 h had elapsed. Replicates in which <10% or >95% of all food offered was consumed were removed before statistical analysis because of their low power to infer feeding choice. Our sample size for each seaweed–herbivore combination ranged from  $n = 10$  to 46. Palatability of each seaweed to each herbivore was quantified as the proportion of the experimental seaweed consumed divided

by the total consumption of experimental and control seaweed within a replicate (%T).

## Data Processing Description

### BCO-DMO Data Processing Notes:

- Added links to NCBI accession numbers
- Reformatted column names to comply with BCO-DMO standards

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## Data Files

File
<b>accession_numbers.csv</b> (Comma Separated Values (.csv), 13.88 KB) MD5:38ebfb090e9f20ea261d8810738e2203
Primary data file for dataset ID 743771

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## Related Publications

Demko, A. M., Amsler, C. D., Hay, M. E., Long, J. D., McClintock, J. B., Paul, V. J., & Sotka, E. E. (2017). Declines in plant palatability from polar to tropical latitudes depend on herbivore and plant identity. *Ecology*, 98(9), 2312-2321. doi:[10.1002/ecy.1918](https://doi.org/10.1002/ecy.1918)

*Methods*

,  
*Results*

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## Parameters

Parameter	Description	Units
species	Genus and species of alga	unitless
sequence_types	Gene name	unitless
location	Antarctica (64.77 deg S 64.05 deg W); California (32.72 deg N 117.16 deg W and 38.32 deg N 123.04 deg W); Fiji (18.00 deg S 179.00 deg E)	unitless
accession_number	Accession number and link to information at NCBI	unitless

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## Project Information

### Detecting genetic adaptation during marine invasions (Genetic Adaptation Marine Inv)

**Coverage:** Estuaries of NW and NE Pacific; estuaries of NW and NE Atlantic

*Description from NSF award abstract:*

Biological introductions, defined as the establishment of species in geographic regions outside the reach of

their natural dispersal mechanisms, have dramatically increased in frequency during the 20th century and are now altering community structure and ecosystem function of virtually all marine habitats. To date, studies on marine invasions focus principally on demographic and ecological processes, and the importance of evolutionary processes has been rarely tested. This knowledge gap has implications for management policies, which attempt to prevent biological introductions and mitigate their impacts. The Asian seaweed *Gracilaria vermiculophylla* has been introduced to every continental margin in the Northern Hemisphere, and preliminary data indicate that non-native populations are both more resistant to heat stress and resistant to snail herbivory. The project will integrate population genetics, field survey and common-garden laboratory experiments to comprehensively address the role of rapid evolutionary adaptation in the invasion success of this seaweed. Specifically, the PIs will answer the following. What is the consequence of introductions on seaweed demography and mating systems? How many successful introductions have occurred in North America and Europe? Where did introduced propagules originate? Do native, native-source and non-native locations differ in environmental conditions? Do native, native-source and non-native populations differ in phenotype?

The intellectual merit of this project is based on three gaps in the literature. First, while biological invasions are widely recognized as a major component of global change, there are surprisingly few studies that compare native and non-native populations in their biology or ecology. Native and non-native populations will be surveyed in a similar manner, allowing assessment of differences in population dynamics, mating system, epifaunal and epiphytic communities, and the surrounding abiotic and biotic environment. Second, *G. vermiculophylla* exhibits a life cycle typical of other invasive species (including some benthic invertebrates), yet we still lack data on the effects of decoupling the haploid and diploid stages on genetic structure, and in turn, on the evolvability of their populations. Finally, this project will provide unequivocal evidence of an adaptive shift in a marine invasive. To our knowledge, such evolutionary change has been described previously for only a complex of marine copepod species. *G. vermiculophylla* will serve as a model for understanding evolution in other nuisance invasions, and perhaps lead to novel methods to counter future invasions or their spread.

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1357386</a>

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