

# Data describing bleaching in algae collected from Antarctica, Fiji, and California when stressed by heat, cold, or low salinity.

**Website:** <https://www.bco-dmo.org/dataset/743763>

**Data Type:** Other Field Results

**Version:** 1

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

## Project

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

Contributors	Affiliation	Role
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## Abstract

Data describing bleaching in algae collected from Antarctica, Fiji, and California when stressed by heat, cold, or low salinity.

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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

Bleaching scores of introduced seaweed when stressed by heat, cold, or low salinity.

## Methods & Sampling

These data are described in detail in Sotka et al., 2018. From May until October 2015, we collected live thalli at each of 40 populations: 15 Japanese (six source and nine nonsource), five western North American, 10 eastern North American, and 10 European populations. We exposed a haphazardly chosen set of approximately 20 thalli per population to extreme heat (1, 2, and 4 hr in 40°C), extreme cold (45, 75, and 105 min at -20°C), and low salinities (8 days at 0, 5, and 10 ppt). For the heat tolerance assay, four apices per thallus were individually placed into unsealed 2- ml microcentrifuge tubes containing 175 µl of seawater. A control apex was kept in a 15°C growth chamber, while three apices were placed in a 40°C water bath for 1, 2, and 4 hr. For the cold tolerance assay, four apices were independently placed into sealed 250 µl PCR tubes containing 200 µl seawater. A control apex was kept in a 15°C incubator, while three apices were placed in a -20° C freezer for 45, 75, and 105 min. Apices were then placed into randomly assigned wells of 12- well

tissue culture plates (2.21- cm- diameter wells) filled with 4 ml of seawater and incubated at 15°C for 8 days with a 12- hr light/dark cycle. For the salinity tolerance assay, four apices were independently placed directly into the 12- well tissue culture plates filled with 4 ml of seawater at a titration of salinities diluted to 0, 5, and 10 ppt, with 30 ppt serving as a control. Every 2 days for 8 days, we changed water and assessed thallus bleaching (i.e., loss of photosynthetic pigments; Figure S2) as a proxy of mortality, itself an important component of fitness. We generated a Bleaching Score (BS), where “1” indicated no bleaching, “2” indicated partial bleaching or color change to pink or white, and “3” indicated full bleaching.

## Data Processing Description

### BCO-DMO Data Processing Notes:

-Reformatted column names to comply with BCO-DMO standards

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## Data Files

File
<b>bleaching_scores.csv</b> (Comma Separated Values (.csv), 1.91 MB) MD5:9481c843e38a97e88a6a6267737b9e14
Primary data file for dataset ID 743763

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## Related Publications

Sotka, E. (2018). Bleaching scores - laboratory experiments [Data set]. Figshare.  
<https://doi.org/10.6084/m9.figshare.6441818.v1>  
*Results*

Sotka, E. E., Baumgardner, A. W., Bippus, P. M., Destombe, C., Duermit, E. A., Endo, H., ... Krueger-Hadfield, S. A. (2018). Combining niche shift and population genetic analyses predicts rapid phenotypic evolution during invasion. *Evolutionary Applications*, 11(5), 781–793. doi:[10.1111/eva.12592](https://doi.org/10.1111/eva.12592)  
*Results*  
,  
*Methods*

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## Parameters

Parameter	Description	Units
assay	Type of assay; heat, cold, or salinity assay.	unitless
ind_type	Common garden vs field collected samples	unitless
pop	Three letter abbreviation; see Sotka et al. 2018 Evolutionary Applications	unitless
ind	Individual ID	unitless
trt	Levels of treatment	unitless
day	Day 0, 2, 4, 6, 8 after treatment started	days
bleach_score	1=healthy; 2=partially healthy; 3=bleached	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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