

# Symbiodinium cultures isolated from the octocoral *Antilloporia bipinnata* in the Florida Keys and processed at Coffroth lab at the University at Buffalo in 2008, 2013 and 2016 (Host Symbiont Temp Response project)

Website: <https://www.bco-dmo.org/dataset/728215>

Data Type: experimental

Version: 1

Version Date: 2018-02-16

## Project

» [RUI: Collaborative Research: Genetic variation as a driver of host and symbiont response to increased temperature on coral reefs](#) (Host Symbiont Temp Response)

Contributors	Affiliation	Role
<a href="#">Coffroth, Mary Alice</a>	State University of New York at Buffalo (SUNY Buffalo)	Principal Investigator
<a href="#">terHorst, Casey</a>	California State University Northridge (CSU-Northridge)	Co-Principal Investigator
<a href="#">Biddle, Mathew</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Abstract

Symbiodinium cultures isolated from the octocoral *Antilloporia bipinnata* in the Florida Keys and processed at Coffroth lab at the University at Buffalo in 2008, 2013 and 2016.

---

## Table of Contents

- [Coverage](#)
- [Dataset Description](#)
  - [Acquisition Description](#)
  - [Processing Description](#)
- [Related Publications](#)
- [Parameters](#)
- [Instruments](#)
- [Deployments](#)
- [Project Information](#)

- [Funding](#)
- 

## Coverage

**Spatial Extent:** N:25.1326 E:-80.26195 S:24.54955 W:-81.75458

**Temporal Extent:** 2008 - 2016

---

## Dataset Description

*Symbiodinium* cultures isolated from adult colonies of the octocoral *Antilloporia bipinnata* in 2008, 2013 and 2016, grown at either 26 or 30 degrees C.

Cultures initially isolated from *Antilloporia bipinnata* colonies collected in the lower keys in the vicinity of Looe Key (24 32.973'N 81 22.849'W) in 2008, the middle keys near Tennessee Reef (24 45.150'N 81 45.275'W) in 2013 and the upper keys at Pickles Reef (24 59.016'N 80 24.832'W) and Elbow Reef (25 07.956'N 80 15.810'W and 25 07.925'N 80 15.717'W). Culture have been maintained in the Coffroth lab, University at Buffalo.

## Acquisition Description

Symbionts were isolated from adult colonies of *Antilloporia bipinnata* following the protocol outline in Santos et al 2001. Briefly, a small piece (1-2 cm) of the branch was ground in a glass tissue homogenizer with 2 ml of filtered seawater (FSW) and poured through a series of meshes (250  $\mu$ m on top, then 120  $\mu$ m, then 70  $\mu$ m mesh) into a 15 ml tube. The mesh was washed with 1 ml FSW several times for a final volume between 3 and 10 ml. This slurry was spun for 5 min at 500-800 rpm on a Beckman J6-HC centrifuge to pellet symbiont cells, the supernatant removed and resuspended in 10 ml of FSW. This step was repeated again and then the pellet was resuspended in 1.0 ml of F/2 (Gulliard and Ryther 1962). Cultures were started by using 20-50  $\mu$ l of the resuspended pellets to inoculate 30ml of F/2 and incubated at the appropriate temperature.

Clade identity and Cp-type were determined following the protocols outline in Santos et al (2003). Briefly, DNA was amplified using the primers HYPERUP and HYPERDN on and MJ96 or BioRad thermocyclers. PCR products were visualized and scored using size standards on a LI-COR 4200 NEN® Global IR2 DNA sequencing system as specified in Santos et al (2003). Putative species identity was based on sequence analysis of B7SYM15 flanking region (LaJeunesse et al. 2012, Parkinson et al. 2015). Briefly, the B7SYM15 flanking region was amplified and directly sequenced in 5' and 3' directions on a 3730XL DNA Analyzer (High Throughput Genomics Center, University of Washington). Sequences were compared to

known species within the GenBank database using BLAST- Basic Local Alignment Search Tool (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>).

## Processing Description

### BCO-DMO processing:

- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- converted latitude and longitude format from degrees, decimal minutes, hemisphere (DD MM.MMH) to decimal degrees (DD.DDDD).
- Adjusted the Incubation\_Temperature values to remove the additional units from the values. (eg. 16\_C converted to 16).

[ [table of contents](#) | [back to top](#) ]

---

## Related Publications

Guillard, R. R. L., & Ryther, J. H. (1962). STUDIES OF MARINE PLANKTONIC DIATOMS: I. CYCLOTELLA NANA HUSTEDT, AND DETONULA CONFERVACEA (CLEVE) GRAN. *Canadian Journal of Microbiology*, 8(2), 229–239. doi:[10.1139/m62-029](https://doi.org/10.1139/m62-029)

Lajeunesse, T. C., Parkinson, J. E., & Reimer, J. D. (2012). A genetics-based description of *Symbiodinium minutum* sp. nov. and *S. psymgophilum* sp. nov. (Dinophyceae), two dinoflagellates symbiotic with cnidaria. *Journal of Phycology*, 48(6), 1380–1391. doi:[10.1111/j.1529-8817.2012.01217.x](https://doi.org/10.1111/j.1529-8817.2012.01217.x)

Parkinson, J. E., Coffroth, M. A., & LaJeunesse, T. C. (2015). New species of Clade B *Symbiodinium* (Dinophyceae) from the greater Caribbean belong to different functional guilds: *S. aenigmaticum* sp. nov., *S. antillogorgium* sp. nov., *S. endomadraxis* sp. nov., and *S. pseudominutum* sp. nov. *Journal of Phycology*, 51(5), 850–858. doi:[10.1111/jpy.12340](https://doi.org/10.1111/jpy.12340)

Santos, S. R., Gutierrez-Rodriguez, C., & Coffroth, M. A. (2003). Phylogenetic identification of symbiotic dinoflagellates via length heteroplasmy in Domain V of chloroplast Large Subunit (cp23S)-Ribosomal DNA Sequences. *Marine Biotechnology*, 5(2), 130–140. doi:[10.1007/s10126-002-0076-z](https://doi.org/10.1007/s10126-002-0076-z)

Santos, S. R., Taylor, D. J., & Coffroth, M. A. (2001). GENETIC COMPARISONS OF FRESHLY ISOLATED VERSUS CULTURED SYMBIOTIC DINOFLAGELLATES: IMPLICATIONS FOR EXTRAPOLATING TO THE INTACT SYMBIOSIS. *Journal of Phycology*, 37(5), 900–912. doi:[10.1046/j.1529-8817.2001.00194.x](https://doi.org/10.1046/j.1529-8817.2001.00194.x)

## Parameters

Parameter	Description	Units
Culture_ID	Identification of sample; culture name (08-0689.4; 08-0689.6; 08-0690.1; 13-117; 13-143; etc.)	unitless
Incubation_Temperature	Temperature at which the culture is maintained	degree Celsius (C)
Host	Octocoral from which the symbiont was isolated. Note - In the vast majority of cases; the culture is NOT representative of the host symbiont population (Santos et al 2001)	unitless
Putative_Species	Putative species based on sequence analysis of B7 SYM15 flanking region (LaJeunesse et al 2012; Parkinson et al 2015)	unitless
Location	Location where adult colony was collected	unitless
Latitude	Latitude of sample location; positive north.	decimal degrees
longitude	Longitude of sample location; positive east	decimal degrees
State_Country	State/Country where adult colony was collected	unitless
Ocean	Ocean where adult colony was collected	unitless
Host_stage	Developmental stage of host	unitless
Axenic	Whether or not the culture is axenic	unitless
Isolated_by	Researcher who isolated the culture	unitless
Year_isolated	The year in which the culture was isolated in four digit year format	years
Clade	Clade designation	unitless
cp_type	Fragment length of the hypervariable region of Domain V of symbiont 23S rDNA (Santos et al 2003) as base pairs	unitless

## Instruments

<b>Dataset-specific Instrument Name</b>	LI-COR 4200 NEN® Global IR2 DNA
<b>Generic Instrument Name</b>	Automated DNA Sequencer
<b>Dataset-specific Description</b>	DNA was amplified using the primers HYPERUP and HYPERDN on and MJ96 thermocycler and PCR products were visualized and scored using size standards on the LI-COR 4200 NEN® Global IR2 DNA sequencing system as specified in Santos et al (2003).
<b>Generic Instrument Description</b>	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.

<b>Dataset-specific Instrument Name</b>	3730XL DNA Analyzer
<b>Generic Instrument Name</b>	Automated DNA Sequencer
<b>Dataset-specific Description</b>	The B7SYM15 flanking region was amplified and directly sequenced in 5' and 3' directions on a 3730XL DNA Analyzer (High Throughput Genomics Center, University of Washington).
<b>Generic Instrument Description</b>	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.

<b>Dataset-specific Instrument Name</b>	Beckman J6-HC centrifuge
<b>Generic Instrument Name</b>	Centrifuge
<b>Dataset-specific Description</b>	This slurry was spun for 5 min at 500-800 rpm on a Beckman J6-HC centrifuge to pellet symbiont cells, the supernatant removed and responded in 10 ml of FSW.
<b>Generic Instrument Description</b>	A machine with a rapidly rotating container that applies centrifugal force to its contents, typically to separate fluids of different densities (e.g., cream from milk) or liquids from solids.

[ [table of contents](#) | [back to top](#) ]

---

## Deployments

## Coffroth\_2008-16

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/728864">https://www.bco-dmo.org/deployment/728864</a>
<b>Platform</b>	SUNY-Buffalo
<b>Start Date</b>	2008-01-01
<b>End Date</b>	2016-12-31

[ [table of contents](#) | [back to top](#) ]

---

## Project Information

**RUI: Collaborative Research: Genetic variation as a driver of host and symbiont response to increased temperature on coral reefs (Host Symbiont Temp Response)**

**Coverage:** Florida Keys, Caribbean

Description from NSF award abstract: On coral reefs, mutualisms with single celled algae (Symbiodinium) and reef species literally and figuratively form the foundation of reef ecosystems. Coral reefs are among the most threatened ecosystems under a changing climate and are rapidly declining due to increasing levels of environmental stress, namely increased temperatures. Climate change is resulting in even warmer ocean temperatures that threaten associations between Symbiodinium and their hosts. In this project the investigators examine the genetic diversity of Symbiodinium and the potential for this important species to evolve in response to temperature. The project will also address whether the ecological and evolutionary dynamics of the Symbiodinium population affect the performance of their host. If so, this suggests that the evolution of microscopic organisms with short generation times could confer adaptation to longer-lived host species on ecologically and economically vital coral reefs. Given that diversity is already being lost on many reefs, considering how evolutionary changes in Symbiodinium will affect reef species is crucial for predicting the responses of reefs to future climate change. This project provides training for two graduate students and several undergraduates at a Hispanic-serving institution. This work includes outreach to the students and the general public through the Aquarium of Niagara, local K-12 schools, and web-based education modules. The effects of evolution on contemporary ecological processes are at the forefront of research in evolutionary ecology. This project will answer the call for experiments elucidating the effects of genetic variation in Symbiodinium performance and the effect on the response of the holobiont (host and symbiont) to increased temperature. These experiments examine the effects of temperature through both ecological and evolutionary mechanisms and

will determine the relative importance of adaptation and acclimatization in replicated experimental populations. The investigators will examine how genetic variation within a species (*Symbiodinium antillogorgium*) affects symbiont performance in culture and in the host and how this affects the response of the holobiont to increased temperature. Further, the project examines whether holobiont response to increased temperature associated with climate change depends on particular GxG host-symbiont combinations. Moreover, the investigators will examine the effects of symbiont history on mutualist hosts, which have been largely ignored in eco-evolutionary studies. These experiments provide a first step in predicting whether invertebrate hosts on coral reefs will respond to global change via adaptation of their symbionts.

[ [table of contents](#) | [back to top](#) ]

---

## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1559286</a>

[ [table of contents](#) | [back to top](#) ]