# Symbiodinium community composition for individual A. cervicornis from Elliot Key, Florida during 2014 and 2015 (EMUCoReS project)

Website: https://www.bco-dmo.org/dataset/709909

Data Type: Other Field Results

Version: 1

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### **Project**

» RAPID: A hyper-thermal anomaly in the Florida Reef Tract: An opportunity to explore the mechanisms underpinning patterns of coral bleaching and disease (EMUCoReS)

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### Abstract

Symbiodinium community composition for individual A. cervicornis from Elliot Key, Florida during 2014 and 2015 (EMUCoReS project)

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# Coverage

**Spatial Extent**: Lat:25.488 Lon:-90.109 **Temporal Extent**: 2014-09-05 - 2015-10-13

# **Dataset Description**

Symbiodinium community composition for individual A. cervicornis. Sampled from Biscayne Bay Coral Nursery near Elliot Key, Florida.

### **Associated Publications:**

Seibeck et al., 2006: Monitoring coral bleaching using a colour reference card

### Methods & Sampling

At indicated dates, individual corals were visually assessed for bleaching. Bleaching was noted for those corals paling or entirely lacking in pigmentation. A reference color card (Seibeck et al., 2006) was used as a pigmentation reference. The normal level of pigmentation was C3 or darker (not bleached). Colors lighter than C3 were considered bleached. Using bone cutters, a small sub-apical piece was broken off of each coral. On the boat, samples were transferred to CHAOS buffer (listed below) and extracted for DNA:

### **Chaos Buffer:**

4.5M Guanidinium thiocyanate 2% N-lauroylsarcosine (sarcosyl) 50mM EDTA 25mM Tris-HCl, pH 7.5 0.2% antifoam A (Sigma) 0.1M b-mercaptoethanol (BME)

# **Binding buffer (BB):**

6 M GuSCN 1 , (Guanidine Thiocyanate) 20 mM EDTA pH 8.0 10 mM Tris-HCl pH 7.5 4% Triton X-100

### Protein wash buffer (PWB):

70 mL of ethanol (96%) was thoroughly mixed with 26 mL of BB (stable at 20 deg C for1 week).

## Wash buffer (WB):

ethanol (60%), 50 mM NaCl 10 mM Tris-HCl pH 7.4 0.5 mM EDTA pH 8.0 (stored at -20 deg C)

- -Allow coral fragments to sit covered in CHAOS buffer in 1.5 2.0 mL tube for days- weeks.
- -Pipet the Supernatant mixture into a silica spin column placed in a 2 ml collection tube. Centrifuge at  $6000 \times g$  (8000 rpm) for 1 min. Discard flow-through. Repeat as needed to load entire sample.
- -Add 700 ul PWB to column, and centrifuge for 1 min at 6000 x g (8000 rpm). Discard flow-through.
- -Repeat 2x (3 washes total).
- -Add 700 ul WB to column and centrifuge for 1 min at 20,000 x g (14,000 rpm). Discard flow-through.
- -Repeat wash and centrifuge for 3 min at 20,000 x g (14,000 rpm) to dry the DNeasy membrane.
- -Discard flow-through and collection tube.
- -Place the spin column in a clean 1.5 ml or 2 ml microcentrifuge tube, and pipet 100 ul 0.1x TE directly onto the spin column.
- -Incubate at room temperature for 1 min, and then centrifuge for 1 min at  $6000 \times g$  (8000 rpm) to elute. (May repeat with another  $100 \text{ ul of } 0.1 \times \text{TE}$ ).

Purified DNA was sent to MR DNA in stillwater Texas for Illumina sequencing of the cp-23S gene for Symbiodinium typing.

# **Data Processing Description**

Data was processed with MR DNA's proprietary pipeline.

# **BCO-DMO Processing Notes:**

- modified parameter names to conform with BCO-DMO naming conventions
- filled all blank cells with nd

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# **Data Files**

# File

**symbiodinium.csv**(Comma Separated Values (.csv), 46.06 KB)

MD5:bd876c275a50e065b7d4d2a13726b170

Primary data file for dataset ID 709909

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# **Related Publications**

Siebeck, U. E., Marshall, N. J., Klüter, A., & Hoegh-Guldberg, O. (2006). Monitoring coral bleaching using a colour reference card. Coral Reefs, 25(3), 453–460. doi: <a href="https://doi.org/10.1007/s00338-006-0123-8">10.1007/s00338-006-0123-8</a> Methods

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# **Parameters**

Parameter	Description	Units
genet_clonalPopulation_ID	Azexual clone identifier; A through X	unitless
ramet_individualColony_ID	Individual coral ID within each genet; 1 through 10	unitless
visit	Month sampled: September 14; March 15; October 15	unitless
bleaching	Presence or absence of bleaching categorically binned as bleaching, or healthy	unitless
disease	Presence or absence of disease categorically binned as: no disease; white band disease; or rapid tissue loss	unitless
mortality	Relative partial mortality categorically binned as; no mortality; partial mortality; mostly dead; or dead	unitless

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# **Deployments**

Coral\_Bleaching\_FRRP

Website	https://www.bco-dmo.org/deployment/640250
Platform	shoreside Florida_Coral_Reefs
Start Date	2014-01-01
End Date	2015-08-20
Description	Coral reef surveys as part of the project "RAPID: A hyper-thermal anomaly in the Florida Reef Tract: An opportunity to explore the mechanisms underpinning patterns of coral bleaching and disease". Single location entered: Florida Reef Tract, 24.8684, -80.6435 in order to 'ground' the datasets.

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# **Project Information**

RAPID: A hyper-thermal anomaly in the Florida Reef Tract: An opportunity to explore the mechanisms underpinning patterns of coral bleaching and disease (EMUCoReS)

**Coverage**: Florida Reef Tract (24.868358, -80.643495)

### Description from NSF award abstract:

Coral reefs are among the most biologically diverse and economically important ecosystems on the planet. However, coral reefs are in a state of global decline due to effects of climate change, disease outbreaks, and other stressors. Mass coral bleaching events, a breakdown of the association between corals and their symbiotic algae, are predicted to become more frequent and severe in response to climate change, and it is expected that subsequent disease outbreaks will become more common. Beginning in August 2014, nearly all coral species in the Florida Reef Tract have undergone severe bleaching, in some cases followed by coral mortality and/or disease outbreaks. This widespread, thermal-induced event presents a unique time-sensitive opportunity to explore the mechanisms underpinning the patterns of coral bleaching, disease, and recovery. The mechanisms linking patterns of bleaching, disease, mortality, and recovery remain relatively unexplored. This research will explore the influences that genotype combinations of host polyps, their algal symbionts, and associated bacterial have on bleaching/disease likelihood and recovery/mortality predisposition of coral specimens. By providing a mechanistic understanding of the processes that underlie coral bleaching and subsequent recovery this research will contribute to measures in support of preserving this invaluable natural resource. The study will further involve students from diverse backgrounds as well as provide project internship opportunities for high school students. A web based radio blog will disseminate project results and other relevant developments to the broad audiences

Mass coral bleaching events are predicted to become more frequent and severe in response to climate change, and it is expected that subsequent disease outbreaks will become more common. The lack of a baseline genetic datasets for coral holobionts prior to previous natural bleaching events has hindered our understanding of recovery patterns and physiological tolerance to thermal stress, also known as coral bleaching. An extensive pre-thermal stress baseline of genotypic identity of coral hosts, Symbiodinium, and associated bacterial community offers a unique opportunity to analyze changes associated with current bleaching event along the Florida coastline and to document holobiont compositions most and least resistant/resilient to bleaching and disease. Repeated sampling of the same coral colonies will allow the investigators to compare holobiont composition before, during and after bleaching of both healthy and diseased individuals. This bleaching event is a time-sensitive natural experiment to examine the dynamics of microbes (Symbiodinium and bacteria) associated with affected colonies, including their potential influence on disease susceptibility and resistance of reef corals. This effort would constitute the first time that high throughput sequencing of coral, Symbiodinium endosymbiont, and the coral-associated bacterial community genotypes are together used to explain patterns of disease, recovery, and mortality following natural bleaching. This study will likely change the way investigators study emerging wasting diseases of keystone species that define marine benthic communities.

# Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1503483
NSF Division of Ocean Sciences (NSF OCE)	OCE-1503430

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