

Sample key for *Symbiodinium* species and abundance in *Dendrogyra cylindrus* from 3 regions of the Florida Reef Tract April - Dec. 2014 (EMUCoReS project)

Website: <https://www.bco-dmo.org/dataset/700077>

Data Type: Other Field Results, experimental

Version:

Version Date: 2017-05-17

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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Coverage

Spatial Extent: N:25 E:-80.4 S:24.47 W:-81.75

Temporal Extent: 2014-04-01 - 2014-12-01

Dataset Description

This dataset includes a key to samples of *Dendrogyra cylindrus* which were analyzed for 23S on an Illumina platform from three sites in the Florida Reef Tract, one each in the upper, middle and lower Keys in 2014. Tube numbers are matched to sample name, status (pre-bleach, pale, bleached, recovery), region, locations, sampling time point, total number of colonies and number of colonies sampled.

Data Processing Description

BCO-DMO Processing Notes:

- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions

Data Files

File
sample_key_Dcyl_2014.csv (Comma Separated Values (.csv), 9.60 KB) MD5:b1b185dfd26c560003c12c9619b1608f
Primary data file for dataset ID 700077

Parameters

Parameter	Description	Units
sample	sample tube	unitless
sample_ID	sample identifier ((yyyymmdd.site.colony-num)	unitless
region	region of Florida Reef Tract: upper/middle/lower	unitless
status	bleaching status: prebleach - April 2014; bleached - Sept 2014; Recovery - Oct 2014 and Dec 2014	unitless
date_sampled	date sampled	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is postivie	decimal degrees
depth	sampling depth	meters
total_num_colonies	total number of Dendrogyra cylindrus colonies	colonies
num_colonies_sampled	number of Dendrogyra cylindrus colonies sampled	colonies

Instruments

Dataset-specific Instrument Name	Illumina platform
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	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.

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.

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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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