

Acropora cervicornis fragment growth during bleaching events in the Florida Reef Tract from 2014-2015 (EMUCoReS project)

Website: <https://www.bco-dmo.org/dataset/640108>

Data Type: Other Field Results

Version: 1

Version Date: 2016-03-10

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)

| Contributors | Affiliation | Role |
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Abstract

Growth of *Acropora cervicornis* fragments were measured before and after three months during the summer bleaching events of 2014 and 2015.

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Coverage

Spatial Extent: Lat:25.488 Lon:-80.109

Temporal Extent: 2014 - 2015

Methods & Sampling

Bleached and unbleached *Acropora cervicornis* fragments were measured for total linear extension immediately after being collected from nursery block platforms and after three months. The number of branches formed on each fragment was also recorded.

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Data Files

| File |
|---|
| frag_growth.csv (Comma Separated Values (.csv), 1.50 KB) MD5:b93ab0321517bb2b6117d603f76ae94a |
| Primary data file for dataset ID 640108 |

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Supplemental Files

| File |
|--|
| Florida Reef Tract Coral Bleaching Response Plan filename: Coral-Bleaching-Response-Plan-6.pdf(Portable Document Format (.pdf), 4.77 MB) MD5:778dec6b2e19ea77546308c185116a71 |

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Parameters

| Parameter | Description | Units |
|------------------------------|--|-----------------|
| Coral_number | coral sample number | number |
| lat | latitude of measurement; in this case the Nursery Bowl | decimal degrees |
| lon | longitude of measurement; negative is West; in this case the Nursery Bowl | decimal degrees |
| enviro_condition | the environmental conditions under which the coral existed in the nursery; two choices: bleached or unbleached. Original name: "Treatment" | text |
| total_linear_extension_start | measurement of total length of branch at the beginning of the study | centimeters |
| numb_branches_start | number of branches at the start of the study | number |
| total_linear_extension_end | measurement of total length of branch at the conclusion of the study | centimeters |
| numb_branches_end | number of branches at the conclusion of the study | number |

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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 | <p>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.</p> <p>Methods & Sampling These locations were from a single site, actually. 24.868, -80.643</p> |

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 |