Symbiodinium species and relative abundance in Dendrogyra cylindrus from 3 regions of the Florida Reef Tract, 2015-2016 (EMUCoReS project)

Website: https://www.bco-dmo.org/dataset/700149
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)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: **N**:25 **E**:-80.4 **S**:24.47 **W**:-81.75
Temporal Extent: 2015-04-01 - 2016-04-30

Dataset Description

This dataset includes the relative abundance 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 2015-2016.

Methods & Sampling

Dendrogyra cylindrus tissue sampling: syringe micro-sampling method (described in Kemp et al. 2008); samples filtered with Swinnex filter holder (13mm) with 3.0µm glass fiber filter; filter preserved in 95% ETOH.

DNA extraction: DNeasy Plant Mini kit (Qiagen) with modifications:

5 min bead beating – acid-washed glass beads
20µl Proteinase K - incubate 1 hr at 56°C

amplicon sequencing: partial chloroplast large subunit 23S rDNA Domain V gene hyper-variable region (Santos et al 2003)

Data Processing Description

MR DNA analysis pipeline: MR DNA, Shallowater, TX, USA
Mothur software v1.37.2 (Schloss e t al. 2009) Operational taxonomic units (OTUs) generated, 0.03 similarity cutoff

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

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Data Files

File
abund_Dcyl_Symb_2015_16.csv (Comma Separated Values (.csv), 118.69 KB) MD5:7a647ff60145773589e635eb25e9728e Primary data file for dataset ID 700149

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Related Publications

Kemp, D. W., Fitt, W. K., & Schmidt, G. W. (2007). A microsampling method for genotyping coral symbionts. Coral Reefs, 27(2), 289–293. doi:10.1007/s00338-007-0333-8
Methods

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
Methods

Schloss, P. D., Westcott, S. L., Ryabin, T., Hall, J. R., Hartmann, M., Hollister, E. B., … Weber, C. F. (2009). Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. Applied and Environmental Microbiology, 75(23), 7537–7541. doi:10.1128/aem.01541-09 https://doi.org/10.1128/AEM.01541-09
Software

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Parameters

Parameter	Description	Units
OTU_id	operational taxonomic unit identity	unitless
species	Symbiodinium species identification	unitless
sample_785_thru_1292	relative abundance of OTU	percent

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Instruments

Dataset-specific Instrument Name	Illumina Mi-Seq - MR.DNA Next Generation Sequencing, Shallowater, Texas (www.mrdnalab.com)
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.

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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.

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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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