# Laboratory results on symbiont type in recovering Porites divaricata corals collected from the Florida Keys, Bahamas, Panama, and Mexico during 2010 (SymBioSys project)

**Website**: https://www.bco-dmo.org/dataset/546152
**Version**: 2015-01-29

**Project**
» Ontogenic change in Cnidarian-algal symbioses: A genomic and ecologic perspective (SymBioSys)

| Contributors | Affiliation | Role |
|---|---|---|
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## Dataset Description

Data on symbiont type in recovering corals (*Porites divaracata*) by treatment following inoculation with a specific symbiont type following heat-induced bleaching.

**Related Reference:**

Coffroth MA, Poland DM, Petrou EL, Brazeau DA, Holmberg JC (2010) Environmental Symbiont Acquisition May Not Be the Solution to Warming Seas for Reef-Building Corals. PLoS ONE 5(10): e13258. doi:10.1371/journal.pone.0013258. http://journals.plos.org/plosone/article?id=10.1371/journal.pone.0013258

### Methods & Sampling

All cultures were obtained from the BURR Culture Collection and used to inoculate bleached colonies of *Porites divaricata*. Collections were made in the vicinity of Long Key, FL, oceanside (N24$^{o}$ 49.791' W80$^{o}$ 45.743') and experimentation was performed at the Keys Marine Laboratory, Long Key, FL

Coral colonies were sampled a total of 4 times throughout the experiment. Symbionts present in the tissue samples were characterized based on sequence variation in the symbiont chloroplast 23S rDNA following the protocols of Santos et al. 2003, Mar.Biotech. 5:130-140

**Reference:**
- Santos SR, Gutiérrez-Rodríguez C, Coffroth MA (2003) Phylogenetic identification of symbiotic dinoflagellates via length heteroplasmy in domain V of chloroplast large subunit (cp23S)-rDNA sequences. Mar Biotech 5: 130-140 for technique to characterize symbionts based on of chloroplast large subunit (cp23S)-rDNA

### Data Processing Description

**BCO-DMO Processing:**

- original file: Coffroth et al 2010_ Data Summary_cp-type.xlsx
- added conventional header with dataset name, PI name, version date, reference information
- changed parameter names to be BCO-DMO compatible
- combined 7 tables and reformated data to flat file
- removed or replaced spaces with underscores
- replaced > with gt_ and < with lt_
- changed 'no amp' to 'no_amplification'

**Revisions:**
2015-01-29: small formatting changes to strong and weak bp columns
2015-01-15: originally submitted data

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## Data Files

| File |
|---|
| **symb_type.csv** (Comma Separated Values (.csv), 57.30 KB) MD5:8f061fb69199b3fac69ca7a2e373a0f2 Primary data file for dataset ID 546152 |

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| lab | laboratory identification; for mapping puposes | unitless |
| lat | latitude of lab; north is positive | decimal degrees |
| lon | londitude of lab; east is positive | decimal degrees |
| genotype | 23S chloroplast genotype | unitless |
| treatment_inoculant | infection treatment of Porites: Symbiodinium types A188; B211; B224 and D206 (letter=clade code; number=base pair size of the particular cp23S-rDNA domain V allele) | unitless |
| sample_id | specimen identification: Pd=Porites divaricata | unitless |
| date | sampling date | yyyy-mm-dd |
| description | whether sampling was pre- or post-bleaching | unitless |
| strong_base_pairs | sequence variation of strong base pairs of symbiont chloroplast 23S rDNA | unitless |
| weak_base_pairs | sequence variation of weak base pairs of symbiont chloroplast 23S rDNA | unitless |
| comments | comments | unitless |

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | Automated Sequencer |
| **Generic Instrument Name** | Automated DNA Sequencer |
| **Dataset-specific Description** | LI-COR 4200 NENH Global IR2 DNA sequencing system (LI-COR Biosciences, Lincoln, NE,USA) |
| **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. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | Spectrophotometer |
| **Generic Instrument Name** | Spectrophotometer |
| **Dataset-specific Description** | Nano-Drop ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE) |
| **Generic Instrument Description** | An instrument used to measure the relative absorption of electromagnetic radiation of different wavelengths in the near infra-red, visible and ultraviolet wavebands by samples. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | Thermal Cycler |
| **Generic Instrument Name** | Thermal Cycler |
| **Dataset-specific Description** | Stratagene Mx3005P QPCR System (Stratagene, La Jolla, CA.) |
| **Generic Instrument Description** | A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html) |

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## Deployments

### Coffroth_2010

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/546058 |
| **Platform** | SUNY-Buffalo |
| **Start Date** | 2010-01-01 |
| **End Date** | 2015-12-31 |
| **Description** | laboratory-based research on coral symbionts |

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## Project Information

**Ontogenic change in Cnidarian-algal symbioses: A genomic and ecologic perspective (SymBioSys)**

**Coverage**: Florida Keys, Bahamas, Panama, Mexico

PROJECT SUMMARY:
The symbiosis between corals (Cnidaria:Hexacorallia:Scleractinia) and photosynthetic dinoflagellate symbionts (Alveolata: Dinophycea: Symbiodinium) provides the foundation and structure of the coral reef ecosystem, as well as significant contributions to global carbon and biogeochemical cycles. Given the importance of this symbiosis to the coral-algal holobiont and the reef ecosystem, understanding the mechanisms governing the establishment and long term maintenance of this symbiosis is essential. The overall aim of this project is to identify the mechanisms and selective processes that lead to the final assemblage of symbionts harbored by adult hosts. This question will be approached from two perspectives, ecologic and genomic, with the specific aims of determining (1) if different Symbiodinium strains differentially affect fitness of corals as the adult settles into a mature symbiosis (2) if competition among symbionts or environmental conditions contribute to the final host-symbiont pairing and (3) how host/symbiont transcriptomes varying as the symbiont community within a host is winnowed to the final assemblage found in the adult host. Traits that directly affect coral fitness (i.e. growth, survivorship, energy production) will be measured under different environmental conditions over the ontogeny of coral recruits that are experimentally infected with different types of Symbiodinium. Concurrently, high throughput gene expression profiling will be used to follow changes in gene expression between host and symbiont. Together, these data will be used to validate or falsify the hypotheses that the final symbiont assemblage found in the adult host is determined by (a) host selection (b) competition among symbionts and/or (c) environmental condition.

This study pools the expertise of two labs that have focused on these aspects of the symbiosis. The Coffroth lab pioneered the studies on early ontogeny of the symbiosis and symbiont diversity and will continue to take the lead in the ecological studies. The Medina lab is at the forefront in the development and utilization of genomic technology to study transcriptomic changes during the establishment and breakdown of the symbiosis. Furthermore, the Medina lab has the coral microarrays to be used in this study and in 2009 will also have oligo arrays for two Symbiodinium species based on 454 EST data. Although several groups have initial studies of the host transcriptome, none have combined an approach that examines the host and the symbiont in a single experiment. This will be a powerful approach as it will allow the investigators to track complementary changes in gene expression between host and symbiont and relate those to turnover in the symbiont community as the final symbiont complement is established.

The data resulting form the study will bridge an important gap in our understanding of the establishment and maintenance of coral-Symbiodinium symbiosis. Understanding the mechanism(s) regulating the establishment of the symbiosis will broaden our knowledge and help to predict the response of this symbiosis to future climate conditions. As in the past, the genomic tools (arrays, ESTs) will be made readily available to researchers via array distribution at cost, microarray analysis training, or sequence data, providing valuable resources to continue exploring these systems.

In conjunction the Aquarium of Niagara, Coffroth will develop educational and outreach programs to train and disseminate information on coral reefs to local area teachers and the general public. The Medina lab will continue to produce science and environment podcasts in multiple languages (English, Spanish and Hmong) with undergraduate students at UC Merced and will continue to collaborate with the California Academy of Sciences (CAS) in their coral reef outreach efforts. Additionally, this work will result in the training and

mentoring of a postdoctoral fellow, at least one graduate student and at least 2 undergraduates. Through this project these students will have the opportunity to participate in research in both a lab and field setting, learning a range of ecological, molecular and algal culturing techniques. The extensive culture collection housed at the University at Buffalo is an important resource that is available to researchers worldwide which the proposed funding will help to maintain. Our EST annotations are publicly available through our EST database (http://montastraea.psu.edu/SymBioSys/).

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## Funding


| Funding Source | Award |
|---|---|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-0926822 |
| NSF Division of Ocean Sciences (NSF OCE) | OCE-0424996 |


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