# cDNA expressed sequence tags for the corals Acropora palmate and Orbicella faveola in Mexico, Panama, and the Florida Keys in 2003 (SymBioSys project)

**Website**: https://www.bco-dmo.org/dataset/627996
**Data Type**: experimental
**Version**: 2016-02-01

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

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

This dataset includes links to NCBI accession pages for cDNA EST's for the corals *Acropora palmate* and *Orbicella faveola* (*Montastraea faveolata*).

**Related References:**


Desalvo, MK., CR. Voolstra, S. Sunagawa, JA. Schwarz, JH. Stillman, MA. Coffroth, AM. Szmant and M. Medina (2008) Differential gene expression during thermal stress and bleaching in the Caribbean coral *Montastraea faveolata.* Molecular Ecology, doi: 10.1111/j.1365-294X.2008.03879.x

Desalvo, MK., S. Sunagawa, PL. Fisher, CR. Voolstra, R. Iglesias-Prieto and M. Medina (2010) Coral host transcriptomic states are correlated with Symbiodinium genotypes. Molecular Ecology, 19, 1174–1186 doi: 10.1111/j.1365-294X.2010.04534.x

DeSalvo MK., S Sunagawa, CR. Voolstra, M. Medina (2010) Transcriptomic responses to heat stress and bleaching in the elkhorn coral *Acropora palmate.* Mar Ecol Prog Ser, 402: 97–113, doi: 10.3354/meps08372

DeSalvo MK., A. Estrada, S. Sunagawa, M. Medina (2011) Transcriptomic responses to darkness stress point to common coral bleaching mechanisms. Coral Reefs, doi 10.1007/s00338-011-0833-4.

Schwarz JA, PB Brokstein, C Voolstra, AY Terry, DJ Miller, AM Szmant, MA Coffroth and M Medina (2008) Coral life history and symbiosis: Functional genomic resources for two reef building Caribbean corals, *Acropora palmata* and *Montastraea faveolata*. BMC Genomics, 9:97, doi:10.1186/1471-2164-9-97.

Voolstra CR., JA. Schwarz, J Schnetzer,S Sunagawa,MK. Desalvo, AM. Szmant, MA Coffroth and M Medina (2009) The host transcriptome remains unaltered during the establishment of coral–algal symbioses. Molecular Ecology, 18, 1823–1833, doi: 10.1111/j.1365-294X.2009.04167.x


### Methods & Sampling

Coral spawn and adult fragments were collected in the Florida Keys in a shallow reef environment at 30 ft. by scuba. RNA was extracted following standard protocols from Ambion kits. Samples were QCed with Nanodrop and Bionalyzer instruments and cDNA libraries were built for EST sequencing.

**Protocols:**
Coral RNA isolation protocol (for small prep's in 1.5mL or 2mL tubes)
Coral RNA isolation (for large prep's in 15mL Falcon tubes)

**Data Processing Description**

Raw sequence data have been submitted to NCBI.

**BCO-DMO Processing:**
- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard
- added species column and links to NCBI accessions were added to the EST accession numbers.
- split lats and lon into separate columns
- replaced spaces with underscores

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## Data Files

| File |
|---|
| **EST_accnums.csv** (Comma Separated Values (.csv), 19.48 MB)<br>MD5:e737ba82a53edcf8fb4e6545ec12e807<br>Primary data file for dataset ID 627996 |

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| species | coral species | unitless |
| experiment | description of experiment | unitless |
| molecule_type | type of molecule that was sequenced: mRNA | unitless |
| lat_PMor_Mex | Puerto Morelos, Mexico latitude; north is postive | unitless |
| lon_PMor_Mex | Puerto Morelos, Mexico longitude; east is postive | unitless |
| lat_KLar_FL | Key Largo, Florida latitude; north is postive | unitless |
| lon_KLar_FL | Key Largo, Florida longitude; east is postive | unitless |
| lat_CZap_Pan | Cayos Zapatillas, Panama latitude; north is postive | unitless |
| lon_CZap_Pan | Cayos Zapatillas, Panama longitude; east is postive | unitless |
| lat_ISol_Pan | Isla Solarte, Panama latitude; north is postive | unitless |
| lon_ISol_Pan | Isla Solarte, Panama longitude; east is postive | unitless |
| lat_CraK_Pan | Cayos Zapatillas, Panama latitude; north is postive | unitless |
| lon_CraK_Pan | Cayos Zapatillas, Panama longitude; east is postive | unitless |
| comment | comments | unitless |
| GenBank_GI | linked accession number of the EST runs deposited at NCBI; a gi number (genInfo identifier) is a unique integer which identifies a particular sequence; the gi number will change every time the sequence changes. | unitless |
| GenBank_ACC | GenBank accession number | unitless |
| EST_Name | identifier of the Expressed Sequence Tags | unitless |
| direction_seq | sequencing direction: 5 is 5' and 3 is 3' | unitless |

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **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. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | Thermal Cycler |
| **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

**Medina_genomics**

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/637648 |
| **Platform** | U_Cal-Merced |
| **Start Date** | 2003-01-01 |
| **End Date** | 2007-12-31 |
| **Description** | coral genomics studies |

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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-0926906 |


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