Accession numbers of symbiotic algae in coral collected from the Florida Keys, Bahamas, Panama, and Mexico during 2010 (SymBioSys project)

Website: https://www.bco-dmo.org/dataset/546040
Version: 2015-01-15

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

Contributors	Affiliation	Role
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Dataset Description

Links to GenBank accession numbers of symbiotic algae in *Eunicea flexuosa* coral.

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

Samples from host, *Eunicea flexuosa*,were amplified and sequenced following (Prada & Hellberg 2013). We amplified and sequenced Symbiodinium samples from *Eunicea flexuosa*, following earlier protocols [(LaJeunesse 2002) for ITS2; [(Moore et al. 2003) for psbA; (Santos et al. 2002) for cp23s-rDNA]. We also sequenced a subset of samples (42) from all populations (three locations and two depths) using the flanking region of the microsatellite B7SYM15, following previous procedures (Pettay & La- Jeunesse 2007). Amplicons were directly sequenced in both directions (except B7SYM15, forward only) in an ABI 3100 using BigDye chemistry v 3.1 and both amplification primers. The COI region from *Symbiodinium* from a western Pacific *Cassiopea* (obtained from Shedd Aquarium, Chicago, IL) was amplified and sequenced following Holland et al (2004).

References:

Drummond AJ, Ashton B, Cheung M et al. (2009) GENEIOUS v4.5.4. Available from http://www.geneious.com.

Holland, B.S., Dawson, M.N., Crow, G.L., Hofmann, D.K., 2004. Global phylogeography of *Cassiopea* (Scyphozoa: Rhizostomeae): molecular evidence for cryptic species and multiple invasions of the Hawaiian Islands. Mar. Biol. 145 (6), 1119–1128.

LaJeunesse TC (2002) Diversity and community structure of symbiotic dinoflagellates from Caribbean coral

reefs. Marine Biology, 141, 387–400.

Moore RB, Ferguson KM, Loh WKW, Hoegh-Guldberg O, Carter DA (2003) Highly organized structure in the non-coding region of the psbA minicircle from clade C *Symbiodinium*. International Journal of Systematic and Evolutionary Microbiology, 53, 1725–1734.

Pettay DT, LaJeunesse TC (2007) Microsatellites from clade B *Symbiodinium* spp. specialized for Caribbean corals in the genus *Madracis.* Molecular Ecology Notes, 7, 1271–1274.

Prada C, Hellberg ME (2013) Long pre-reproductive selection and divergence by depth in a Caribbean candelabrum coral. Proceedings of the National Academy of Sciences of the USA, 119, 53–60.

Santos SR, Taylor DJ, Kinzie RA, Hidaka M, Sakai K, Coffroth MA (2002) Molecular phylogeny of symbiotic dinoflagellates inferred from partial chloroplast large subunit 23sr DNA sequences. Molecular Phylogeetics and Evolution, 23, 97–111.

Data Processing Description

All sequences were edited and assembled using GENEIOUS v4.5.5 (Drummond et al. 2009).

BCO-DMO Processing:

- original file: Coffroth_Links to GenBank submissions.xlsx
- added conventional header with dataset name, PI name, version date, reference information
- changed parameter names to be BCO-DMO compatible
- replaced spaces with underscores

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Data Files

File
accession_nums.csv (Comma Separated Values (.csv), 1.44 KB) MD5:89270aa6b6910ff6037bcdf885140a43 Primary data file for dataset ID 546040

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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
description	sequenced organism and gene	unitless
reference_paper	citation of published sequence reference	unitless
Genbank_accession_num	GenBank accession number	unitless
accession_link	GenBank accession number url link	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

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