Information about sequences of coral, Acropora cervicornis, collected from host colonies at the Mote Marine Laboratory in situ coral nursery in Looe Key, Lower Florida Keys in November and December 2019

Website: https://www.bco-dmo.org/dataset/924394
Data Type: experimental, Other Field Results
Version: 1
Version Date: 2024-04-04

Project
» CAREER: Applying phenotypic variability to identify resilient Acropora cervicornis genotypes in the Florida Keys (Resilient Acerv)
» Collaborative Research: Tracking the interacting roles of the environment, host genotype, and a novel Rickettsiales in coral disease susceptibility (Coral Rickettsiales)

Contributors	Affiliation	Role
Muller, Erinn M.	Mote Marine Laboratory (Mote)	Principal Investigator
Klinges, Grace J.	Oregon State University (OSU)	Scientist
Williams, Sara D.	Mote Marine Laboratory (Mote)	Scientist
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This dataset contains information about sequences of coral, Acropora cervicornis, collected from host colonies (genets) at the Mote Marine Laboratory in situ coral nursery in Looe Key, Lower Florida Keys in November and December 2019. The sequence data can be found in the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) database under accession number PRJNA769275. The objective of the study was to characterize and compare the microbiomes of apparently healthy Acropora cervicornis genotypes that were originally collected from different regions of Florida's Coral Reef and sampled after residing within Mote Marine Laboratory's in situ nursery near Looe Key, FL for multiple years. By using 16S rRNA high-throughput sequencing, we described the microbial communities of 74 A. cervicornis genotypes originating in the Lower Florida Keys(n=40 genotypes), the Middle Florida Keys (n=15 genotypes), and the Upper Florida Keys (n=19 genotypes). Data were collected and curated by Drs. Sara Williams and Grace Klinges. Results of the data analysis are published in Williams, et al. (2022) (DOI: 10.7717/peerj.13574).

Table of Contents

Coverage

Location: Mote Marine Laboratory’s in-situ nursery near Looe Key, FL (USA) in the Lower Keys
Spatial Extent: **Lat**:24.5627 **Lon**:-81.4005
Temporal Extent: 2019-11-01 - 2019-12-31

Methods & Sampling

Complete methods are published in Williams, et al. (2022) and summarized here. 74 genotypes of *Acropora cervicornis* in Mote Marine Laboratory's in situ nursery in the Lower Florida Keys were fragmented and collected between November and December 2018. The fragments were flash-frozen using liquid nitrogen and were then immediately stored at -80 degrees Celsius (°C) until further processing. DNA was isolated from the frozen coral fragments (sub-sampled for 4-5 polyps first) using DNeasy PowerSoil Kits (QIAGEN, Germantown, MD, USA) with modifications to the manufacturer's protocol. Sample bacterial communities were determined using 16S rRNA Illumina sequencing on the MiSeq platform. DNA was sent to MR DNA (http://www.mrdnalab.com, Shallowater, TX, USA) for barcoding, amplification, and sequencing. Amplification of the 16S rRNA gene variable region (V4) was conducted using primers 515F and 806R. A polymerase chain reaction was performed using the HotStarTaq Plus Master Mix Kit (QIAGEN, Germantown, MD, USA) and products were checked on a 2% agarose gel to determine the success of amplification and the relative intensity of bands. Samples were pooled and then purified using calibrated Agencourt Ampure XP beads (Beckman Coulter, CA, USA). The pooled DNA library was made using the Illumina TruSeq DNA library preparation protocol. Paired-end sequencing (sequencing read length of 300 base pairs) was performed at MR DNA using a single flow cell on a MiSeq following the manufacturer's guidelines.

BCO-DMO Processing Description

- Imported original file "BCODMO_Sample_MetaData_ACER16S_Williams_etal.csv" into the BCO-DMO system.
- Converted "Collection_Date" from Excel format to YYYY-MM-DD.
- Reordered columns.
- Removed "N" and "W" from "Latitude" and "Longitude" columns.
- Made longitude values negative to indicate West direction.
- Saved the final file as "924394_v1_a_cerv_sequence_metadata_williams_et_al_2022.csv"

[table of contents | back to top]

Related Publications

Williams, S. D., Klinges, J. G., Zinman, S., Clark, A. S., Bartels, E., Villoch Diaz Maurino, M., & Muller, E. M. (2022). Geographically driven differences in microbiomes of Acropora cervicornis originating from different regions of Florida's Coral Reef. PeerJ, 10, e13574. Portico. https://doi.org/10.7717/peerj.13574
Results

[table of contents | back to top]

Related Datasets

IsRelatedTo

Mote Marine Laboratory. Geographically driven differences in microbiomes of Acropora cervicornis originating from different regions of Florida's Coral Reef. 2021/10. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA769275. NCBI:BioProject: PRJNA769275.

[table of contents | back to top]

Parameters

Parameter	Description	Units
BioProject	NCBI BioProject identifier	unitless
SRA_Study	SRA study identifier	unitless
BioSample	SRA BioSample identifier	unitless
Sample_Name	Sample Name	unitless
SRA_Run	SRA run identifier	unitless
SRA_Sample	SRA sample identifier	unitless
SRA_Experiment	SRA experiment identifier	unitless
Experiment_Title	SRA experiment title	unitless
SRA_title	Descriptive title of SRA study	unitless
Library_Strategy	Type of library prep ("AMPLICON")	unitless
Library_Source	Source of genetic material ("METAGENOMIC")	unitless
Library_Selection	Library selection method ("PCR")	unitless
Library_Layout	Library layout ("PAIRED")	unitless
Platform	Sequencing platform ("ILLUMINA")	unitless
Instrument_Model	Sequencing instrument model ("Illumina MiSeq")	unitless
Design	Sequencing design description	unitless
DataStore_FileType	File type of data stored on SRA ("fastq")	unitless
Site	Sampling site	unitless
Collection_Date	Date of sampling as year-month-day (YYYY-MM-DD)	unitless
Latitude	Sampling latitude; positive values = North	decimal degrees
Longitude	Sampling longitude; negative values = West	decimal degrees
Host_Organism	Host from which microbiome samples were collected	unitless
Genotype_MoteID	Microsatellite genotype identifier used by Mote Marine Laboratory	unitless
Origin	Original collection location of host organism prior to moving to Mote's in situ coral nursery. Locations are within the Florida Keys, USA.	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina MiSeq platform
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	PCR
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)

[table of contents | back to top]

Project Information

CAREER: Applying phenotypic variability to identify resilient Acropora cervicornis genotypes in the Florida Keys (Resilient Acerv)

Coverage: Florida Keys, Summerland Key, FL 24.563595°, -81.278572°

NSF Award Abstract:
Caribbean staghorn coral was one of the most common corals within reefs of the Florida Keys several decades ago. Over the last 40 years disease, bleaching, overfishing and habitat degradation caused a 95% reduction of the population. Staghorn coral is now listed as threatened under the U.S. Endangered Species Act of 1973. Within the past few years, millions of dollars have been invested for the purpose of restoring the population of staghorn coral within Florida and the U.S. Virgin Islands. Significant effort has been placed on maintaining and propagating corals of known genotypes within coral nurseries for the purpose of outplanting. However, little is known about the individual genotypes that are currently being outplanted from nurseries onto coral reefs. Are the genotypes being used for outplanting resilient enough to survive the three major stressors affecting the population in the Florida Keys: disease, high water temperatures, and ocean acidification? The research within the present study will be the first step in answering this critically important question. The funded project will additionally develop a research-based afterschool program with K-12 students in the Florida Keys and U.S. Virgin Islands that emphasizes an inquiry-based curriculum, STEM research activities, and peer-to-peer mentoring. The information from the present study will help scientists predict the likelihood of species persistence within the lower Florida Keys under future climate-change and ocean-acidification scenarios. Results of this research will also help guide restoration efforts throughout Florida and the Caribbean, and lead to more informative, science-based restoration activities.

Acropora cervicornis dominated shallow-water reefs within the Florida Keys for at least the last half a million years, but the population has recently declined due to multiple stressors. Understanding the current population level of resilience to three major threats - disease outbreaks, high water temperatures, and ocean acidification conditions - is critical for the preservation of this threatened species. Results from the present study will answer the primary research question: will representative genotypes from the lower Florida Keys provide enough phenotypic variation for this threatened species to survive in the future? The present proposal will

couple controlled laboratory challenge experiments with field data and modeling applications, and collaborate with local educators to fulfill five objectives: 1) identify *A. cervicornis* genotypes resistant to disease, 2) identify *A. cervicornis* genotypes resilient to high water temperature and ocean acidification conditions, 3) quantify how high water temperature and ocean acidification conditions impact disease dynamics on *A. cervicornis*; 4) determine tradeoffs in life-history traits because of resilience factors; and 5) apply a trait-based model, which will predict genotypic structure of a population under different environmental scenarios.

Collaborative Research: Tracking the interacting roles of the environment, host genotype, and a novel Rickettsiales in coral disease susceptibility (Coral Rickettsiales)

Coverage: at Oregon State University and in the Florida Keys at Mote Marine Laboratory

NSF Award Abstract:
Historically one of the most abundant reef-building corals in Florida and the wider Caribbean, the staghorn coral, *Acropora cervicornis*, is now listed as critically endangered primarily because of previous and reoccurring disease events. Understanding the holistic mechanisms of disease susceptibility in this coral is a top concern of practitioners engaged in conservation and restoration. The investigators recently discovered a group of parasitic bacteria common within the microbial community of *A. cervicornis* that can reduce the growth and health of corals when reefs are exposed to nutrient polluted waters. Determining how interactions among the coral host, this parasitic microbe, and the environment are linked to disease susceptibility provides critical insight and greater success of future restoration efforts. Yet the complexity of animal microbiomes and the contextual nature of disease make it difficult to identify the specific cause of many disease outbreaks. In this project, the investigators conduct experiments to explore the interactions among different genetic strains of coral and these bacteria in various nutrient scenarios to better understand how this bacterium affects the susceptibility of staghorn coral to diseases. This project also characterizes the genomics, host range, and local and global distribution of this bacterial coral parasite to determine how its evolutionary history and physiology drive disease susceptibility in this important coral species. The project trains two postdocs, one technician, and seven students (one graduate, six undergraduates) in integrative sciences that span marine science, physiology, genetics, microbiology, omics, and statistical modeling. A research-based after school program in Florida is expanded to include microbiology and create a new program module called Microbial warriors, with a focus on women in science. The investigators produce documentary style films and outreach materials to broadly communicate the project science and conservation efforts to local and national communities via presentations at Mote Marine Lab and the Oregon Museum of Science and Industry. This project is co-funded by the Biological Oceanography Program in the Division of Ocean Sciences and the Symbiosis, Defense, and Self-recognition Program in the Division of Integrative Organismal Systems.

The investigators recently identified a marine *Rickettsiales* bacterium that, in corals, can be stimulated to grow in the presence of elevated nitrogen and phosphorous species. Based on genomic reconstruction and phylogeography, this bacteria is classified as a novel bacterial genus, *Candidatus Aquarickettsia*, and showed that it is broadly associated with scleractinian corals worldwide. Importantly, using a model system, the endangered *Acropora cervicornis* coral, the team has also shown that the growth of this bacterium in vivo is associated with reduced host growth and increased disease susceptibility. This project aims to more completely evaluate the mechanisms behind and impacts of these inducible infections on coral physiology and host-bacterial symbiosis. The investigators conduct nutrient dosing experiments on different coral genotypes with various *Rickettsiales* abundances. Using a range of omics and microscopy techniques, the team quantifies the resulting effects on holobiont phenotypes. The investigators are also comparing the genomes of these bacteria in the different Acroporid hosts and other coral genera to evaluate facets of the bacterium's evolutionary history, as well as to identify possible mechanisms of its proliferation, virulence, and host specificity. This interdisciplinary project mechanistically links nutrients to temporal changes in host, algal symbiont, and bacterial parasite physiology and also explain why there is natural variation in these responses by exploring how host and parasite genotypes and growth dynamics combined with environmental contextuality alter holobiont phenotypes.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1452538
NSF Division of Ocean Sciences (NSF OCE)	OCE-1923836
National Fish and Wildlife Foundation (NFWF)	62145

[table of contents | back to top]