Coral 16s rRNA sequence accession, sample, and experimental treatment information from white plague disease exposed corals at Brewer's Bay, St. Thomas, The U.S. Virgin Islands in June of 2017

Website: https://www.bco-dmo.org/dataset/841008
Data Type: Other Field Results
Version: 1
Version Date: 2021-02-17

Project
» Immunity to Community: Can Quantifying Immune Traits Inform Reef Community Structure? (Coral Immune Traits)

Contributors	Affiliation	Role
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Abstract
Coral 16s rRNA sequence accession, sample, and experimental treatment information from white plague disease exposed corals. Seven Caribbean coral species were exposed to white plague at Brewer's Bay, St. Thomas, The U.S. Virgin Islands in June of 2017. Sequence data can be found in the NCBI SRA database under the National Center for Biotechnology Information BioProject PRJNA667272.

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Coverage

Spatial Extent: **Lat**:18.34403 **Lon**:-64.98435
Temporal Extent: 2017-06

Dataset Description

Sequence data referenced in this dataset can be found in the NCBI SRA database under the National Center for Biotechnology Information BioProject PRJNA667272.

Methods & Sampling

Location: Brewer’s Bay (18.34403, -64.98435), St. Thomas, The U.S. Virgin Islands

Processing of fragments included freezing the coral tissue in liquid nitrogen and storing at -80˚C for 16S rRNA analysis. DNA from the coral samples were extracted at the University of Texas at Arlington (UTA) using DNeasy Powersoil Isolation kits (MO BIO Laboratories, Carlsbad, CA). Roughly 0.25g of tissue was removed from each of the coral fragments. Tissue from healthy-state fragments (“control”) was extracted from the center of the fragment. Tissue was extracted in a similar manner from fragments exposed to WPD that did not display lesions by the end of the experiment (“disease-exposed”). For fragments that developed a lesion(s) (“disease-infected”), tissue was extracted approximately 2 to 3mm horizontally from the lesion margin.

Tissue samples were sent to MR DNA Molecular Research LP (Shallowater, TX) for 16S rRNA gene amplification using 515F and 806R primers for the V4 region and sequenced on an Illumina MiSeq 2x250bp PE reads. Before sequencing, coral DNA was amplified using 515F and 806R primers through 30 PCR cycles using HotStarTaq Plus Master Mix Kit (Qiagen, USA) under the following conditions: 94°C for 3 minutes, followed by 30-35 cycles of 94°C for 30 seconds, 53°C for 40 seconds and 72°C for 1 minute, after which a final elongation step at 72°C for 5 minutes was performed. PCR products were checked for amplification intensity and integrity on a 2% agarose gel and then bands of similar weight were pooled, purified using Ampure XP beads and used for illumina DNA library prep. Libraries were sequenced at MR DNA on an illumina MiSeq and then bioinformatically processed to combine homologous sequences, depleted barcodes, sequences <150bp removed, and sequences with ambiguous base calls removed using the MR DNA analysis pipeline (MR DNA, Shallowater, TX, USA).

Libraries were sequenced at MR DNA on an illumina MiSeq and then bioinformatically processed to combine homologous sequences, depleted barcodes, sequences <150bp removed, and sequences with ambiguous base calls removed using the MR DNA analysis pipeline (MR DNA, Shallowater, TX, USA). Sequences were grouped into operational taxonomic units (OTU’s) with a 3% tolerated divergence (97% similarity) and taxonomically annotated using BLASTn against the NCBI database.

Instruments:
DNeasy Powersoil Isolation kits (MO BIO Laboratories, Carlsbad, CA)
Illumina MiSeq 2x250bp PE reads
HotStarTaq Plus Master Mix Kit (Qiagen, USA)
MR DNA analysis pipeline (MR DNA, Shallowater, TX, USA)
Taxonomically annotated using BLASTn against the NCBI database

Coral species list in this dataset:

ScientificName,AphiaID
Colpophyllia natans,289697
Montastraea cavernosa,287962
Orbicella annularis,758260
Orbicella faveolata,758261
Porites astreoides,288889
Porites porites,207238
Siderastrea siderea,207516

Data Processing Description

BCO-DMO data manager processing notes:
* Data submitted in file BCO DMO EAGER Microbiome metadata.xlsx sheet 1 extracted to csv
* Modified parameter names to conform with BCO-DMO naming conventions: only A-Za-z0-9 and underscore allowed. Can not start with a number. (spaces, +, and - changed to underscores).
* Unique species list of species names in this dataset checked using the World Register of Marine Species (WoRMS) taxa match tool. All names were exact matches to accepted names as of 2021-02-17. Species list and AphiaIDs added to the metadata.
* "sample_title" column had no values so it was removed from the dataset.
* The combined lat_lon e.g. values "18.34 N 64.98 W" were removed and separate columns for latitude and longitude were added in decimal degrees using the value provided in the metadata.
* commas in geolocation replaced with semicolons. "USA: St thomas, Brewer's Bay" changed to "USA: St thomas; Brewer's Bay"

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Related Datasets

IsReferencedBy

Mydlarz, L., Brandt, M., MacKnight, N. (2020) **Phenotypic information collected from white plague disease exposure in a controlled environment at The University of the Virgin Islands Center for Marine and Environmental Studies in June of 2017.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2020-11-17 doi:10.26008/1912/bco-dmo.829113.1 [view at BCO-DMO]
Relationship Description: The same coral samples used.

References

The University of Texas at Arlington. Species-specific microbial dysbiosis reflect disease resistance in Caribbean corals. 2020/10. In: NCBI:BioProject: PRJNA667272. [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA667272.

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Parameters

Parameters for this dataset have not yet been identified

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq 2x250bp PE reads
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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Project Information

Immunity to Community: Can Quantifying Immune Traits Inform Reef Community Structure? (Coral Immune Traits)

Coverage: US Virgin Islands

NSF abstract:

Coral diseases have increased significantly throughout the past 30 years. Climate change and other detrimental environment factors are likely to blame. Unhealthy coral reefs cannot support the fish and other life that make the reef a vibrant and diverse ecosystem. Corals reefs in the Caribbean Sea are disease hotspots and many reefs have experienced population collapses due to outbreaks of disease. Importantly, coral species vary in their susceptible to disease, but the reasons behind this variation are unknown. This project will quantify coral susceptibility to disease by examining coral immunity using several novel approaches and experiments. Seven species of coral that differ in disease susceptibility, growth rates, growth form and reproductive strategies will be used. Immune responses of each species of coral will be measured by exposing the corals to bacterial immune stimulators. Susceptibility to white plague disease, a prevalent disease affecting many species of corals, will also be measured by exposing the corals to active white plague disease and calculating disease transmission rates. The immune response and disease transmission data for each coral species will be used to develop a predictive model to determine how different coral communities will respond to disease threats under climate change scenarios. This project will support graduate students at University of Texas, Arlington (Hispanic-serving Institution) and University of Virgin Islands (Historically Black University) and many undergraduate students at all three institutions (Mote Marine Laboratory). This research will be highlighted at outreach events at all three institutions which take place regularly and include Earth Day Texas in Dallas, TX, Mote's Living Reef Exhibit and Aquarium in Sarasota, FL and "Reef Fest" and Agricultural fairs in the U.S. Virgin Islands.

Environmental changes, such as ocean warming, have led to an increase in the prevalence of coral diseases, causing region-wide population collapses in some locations. However, not all coral species, or even populations within species, are affected by disease equally. Some species are host to many different types of diseases, but have limited mortality. Other species suffer significant disease-related mortality. How and why disease susceptibility differs among species and the effects of this differential susceptibility on reef community structure and composition are currently unknown. This project will use immune-challenge experiments that will quantify novel components of the innate immune system of corals, coupled with the application of a trait-based model, to fulfill three goals: 1) Determine variability of coral immune traits in seven common coral species found on Caribbean reefs, 2) Determine the variability in resistance to white plague disease transmission in the same coral species 3) Develop a predictive model of coral community assemblage that incorporates immune traits. Quantification of coral immunity will also incorporate unique approaches, such as combining full transcriptome sequencing with protein activity assays for a gene-to-phenotype analysis. Data will be mapped onto immune pathways for comprehensive pathway evaluation between coral species and these will serve as trait inputs into a "traitspace" model. These traits will provide continuous data within the model, which will create a probability density function (PDF) for the trait distributions of each species. These PDFs will then be used to determine the probability of species under different disease exposure scenarios. Model analyses will determine which traits influence community structure and characterize how disease exposure and the immune response will predict community assemblages through space and time. The completion and application of a trait-base model that incorporates extensive immunity parameters (none of which have been applied to trait models within coral ecosystems) is a distinct product from this project.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1712134
NSF Division of Ocean Sciences (NSF OCE)	OCE-1712240
NSF Division of Ocean Sciences (NSF OCE)	OCE-1712540

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