NCBI accession numbers for RNAseq data from five coral species experimentally exposed to Stony Coral Tissue Loss Disease (SCTLD) at the University of the Virgin Islands in 2019

Website: https://www.bco-dmo.org/dataset/881776
Data Type: experimental
Version: 1
Version Date: 2022-09-30

Project
» RAPID: Collaborative Research: Predicting the Spread of Multi-Species Coral Disease Using Species Immune Traits (Multi-Species Coral Disease)

Contributors	Affiliation	Role
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Abstract
Raw RNA sequence data were obtained from a disease transmission experiment carried out at the University of the Virgin Islands in which five reef-building coral species, Colpophyllia natans, Orbicella annularis, Pseudodiploria strigosa, Porites astreoides, and Montastraea cavernosa, were exposed to Stony Coral Tissue Loss Disease (SCTLD) in mesocosms. Sequences were used to compare the differential expression of host and endosymbiont genes between disease states (control, disease-exposed, and disease-infected) and to elucidate a transcriptomic model of the holobiont response to SCTLD. This dataset includes National Center for Biotechnology Information (NCBI) accession numbers and related data for those five coral species examined in the experiment.

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Coverage

Spatial Extent: **Lat**:18.3277 **Lon**:-64.926
Temporal Extent: 2019-03-17 - 2019-04-12

Methods & Sampling

A Stony Coral Tissue Loss Disease (SCTLD) transmission experiment was carried out at the University of the Virgin Islands (UVI) in April of 2019 and is described in Meiling et al. (2021).

Coral colonies were collected from Rupert's Rock Reef (18.3277 N, -64.926 E) from March 17 to April 02 of 2019. One fragment from five species of stony coral was placed into a control mesocosm equidistant from a central healthy coral colony. Corresponding genet fragments were placed into an experimental mesocosm equidistant from a SCTLD-infected coral colony. This paired design was replicated for a total of 8 genets per species. Experimental coral fragments that developed lesions were removed and stored at -80ºC for RNA

sequencing when 30% tissue loss was achieved. Corresponding control coral fragments were removed and stored at the same time. Tissue samples were harvested from the fragments and total RNA was extracted using the RNAqeous-4PCR total RNA isolation kit (Invitrogen, Life Technologies AM1914) as explained in Veglia et al. (2022). Tissues were lysed using a refrigerated Qiagen TissueLyser II microcentrifuge at 30 oscillations per second for 30 seconds. Contaminating DNA and chromatin were removed from the total RNA using the Ambion DNase I (RNase-free) kit (Invitrogen, Life Technologies AM2222). Samples were preprocessed by Novogene Co., Ltd. for mRNA enrichment using polyA tail capture; the mRNA libraries underwent 150-bp, paired-end sequencing on an Illumina NovaSeq 6000 instrument using the NEBNext Ultra II RNA library prep kit.

Data Processing Description

BCO-DMO Processing:
- converted date columns to YYYY-MM-DD format.

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Data Files

File	
accessions_five_coral_species.csv	(Comma Separated Values (.csv), 7.09 KB) MD5:ee26dbba27afcfe6a9bf034fbf1f8df0
Primary data file for dataset ID 881776	

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Related Publications

Meiling, S. S., Muller, E. M., Lasseigne, D., Rossin, A., Veglia, A. J., MacKnight, N., Dimos, B., Huntley, N., Correa, A. M. S., Smith, T. B., Holstein, D. M., Mydlarz, L. D., Apprill, A., & Brandt, M. E. (2021). Variable Species Responses to Experimental Stony Coral Tissue Loss Disease (SCTLD) Exposure. Frontiers in Marine Science, 8. https://doi.org/10.3389/fmars.2021.670829
Results

Veglia, A. J., Beavers, K., Van Buren, E. W., Meiling, S. S., Muller, E. M., Smith, T. B., Holstein, D. M., Apprill, A., Brandt, M. E., Mydlarz, L. D., & Correa, A. M. S. (2022). Alphaflexivirus Genomes in Stony Coral Tissue Loss Disease-Affected, Disease-Exposed, and Disease-Unexposed Coral Colonies in the U.S. Virgin Islands. Microbiology Resource Announcements, 11(2). https://doi.org/10.1128/mra.01199-21
Results

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Parameters

Parameter	Description	Units
Sample_Name	Sample ID number	unitless
Organism	Coral species	unitless
Dive_Site	Dive site where the colony was taken	unitless
Lat	Latitude where the colony was taken	degrees North
Lon	Longitude where the colony was taken	degrees East
Collection_Date	Date of colony collection in format YYYY-MM-DD; time zone: Atlantic Standard Time (AST)	unitless
Experiment_Mesocosm	Mesocosm (Control or Diseased; #1-8) where the fragment was placed	unitless
Freeze_Date	Date of fragment removal from experiment and freezing in format YYYY-MM-DD; time zone: Atlantic Standard Time (AST)	unitless
BioProject	NCBI BioProject number	unitless
Biosample_Accession	NCBI BioSample accession number	unitless
SRA_accession	NCBI SRA accession number	unitless

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Instruments

Dataset-specific Instrument Name	Illumina NovaSeq 6000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	mRNA libraries underwent 150-bp, paired-end sequencing on an Illumina NovaSeq 6000 instrument.
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	Qiagen TissueLyser II
Generic Instrument Name	Qiagen TissueLyser II
Dataset-specific Description	Tissues were lysed using a refrigerated Qiagen TissueLyser II.
Generic Instrument Description	The Qiagen TissueLyser II is a tissue processor designed to disrupt biological samples through high-speed shaking in plastic tubes with stainless steel, tungsten carbide, or glass beads. It is used for high-throughput disruption of human, animal, and plant tissues, bacteria, and yeast to access biological information for genomics, transcriptomics, and proteomics applications. It automates the purification of DNA, RNA, and protein from 1 to 96 samples. Disruption and homogenization are achieved through the beating and grinding effect of beads on the sample material as they are shaken together in the grinding vessels. Using the appropriate adapter set, up to 48 or 192 samples can be processed at the same time. Alternatively, a grinding jar set can be used to process large samples. A range of beads, bead dispensers, and collection microtubes and caps are also available. It can be programmed to provide variable speeds from 3 to 30 Hz (180-1800 oscillations per minute) and run times from 10 seconds to 99 minutes.

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Project Information

RAPID: Collaborative Research: Predicting the Spread of Multi-Species Coral Disease Using Species Immune Traits (Multi-Species Coral Disease)

Coverage: St. Thomas, U.S. Virgin Islands

NSF Award Abstract:
Coral reef ecosystems provide substantial economic resources to the societies of the United States Virgin Islands (USVI) and other US locations in the forms of tourism, fishing and coastal protection. However, reefs are among the most threatened marine environments, and coral disease is having a devastating impact on these valued systems. In early 2019, a multi-species rapid tissue loss disease matching the description of stony coral tissue loss disease (SCTLD) was found severely affecting a reef off the southwest coast of St. Thomas in the US Virgin Islands (USVI). SCTLD has been devastating coral reef communities in southeast

Florida for the last four years, and was very recently reported from disparate areas around the Caribbean, including Mexico, Jamaica, and St. Martin. Rapid surveys by the investigators at the University of the Virgin Islands believe that a 50 km2 area southwest of St. Thomas is the initial incidence area of the disease, but will likely spread across the USVI, British Virgin Islands, and Puerto Rico. This study performs experiments to understand how this disease affects coral species immune traits and compares the microbiology and physiology of disease samples in the USVI to samples from Florida. It also examines how changing the species composition of a coral community affects the spread and impact of the disease. The overall aim is to produce a model to predict the impact of multi-species disease spread on reefs based on coral species assemblages. The project contributes to the research training of at least 2 undergraduates, 2 M.S. students, and 3 Ph.D. students, who benefit from cross-investigator mentoring. The research team includes representatives to the Coral Disease Advisory Committees for the USVI and Florida, which ensures rapid communication of findings to management bodies in both regions.

Coral disease is a significant and increasing threat to Caribbean coral reef systems. Recent results demonstrate that coral species immune traits can predict disease resistance, and thus, forecast impacts to coral community structure, under multi-species coral disease. The onset of this epizootic in the USVI offers an unprecedented opportunity to test hypotheses about the impact of coral resistance, tolerance and immune traits on disease spread during the early stages of an outbreak that could profoundly change the diversity of Caribbean reefs. It is hypothesized that the abundance of highly susceptible species dictates 1) the onset of disease at reef sites downstream of the initial incidence area, and 2) the spread of disease within reef sites. Furthermore, 3) downstream reef sites where highly susceptible species are removed or treated show lower immune responses in all susceptible corals, later onset of disease, and slower within-site disease spread. To test these hypotheses, two experiments directly compare species responses to disease exposure and test the effect of species assemblage on coral immune function and disease spread. Results from these experiments aim to inform a generalizable model to predict the impact of multi-species disease spread on reefs based on coral species assemblages. Results of this project include direct comparison of the USVI disease to Florida SCTLD and a better understanding of how the abundance of highly susceptible host species impacts the spread of disease during the early onset of a multi-species panzootic.

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.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1928771

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