RNAseq data from apparently healthy and Stony Coral Tissue Loss Disease-affected Montastraea cavernosa coral collected from St. Thomas, US Virgin Islands in 2020

Website: https://www.bco-dmo.org/dataset/935630
Data Type: Other Field Results, experimental
Version: 1
Version Date: 2024-12-10

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

Contributors	Affiliation	Role
Mydlarz, Laura	University of Texas at Arlington (UT Arlington)	Principal Investigator
Beavers, Kelsey	University of Texas at Arlington (UT Arlington)	Scientist
Merchant, Lynne M.	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
These data include raw RNAseq reads from Montastraea cavernosa collected from two reefs in St. Thomas, United States Virgin Islands. Samples were collected from two reefs showing signs of active stony coral tissue loss disease (SCTLD) in February of 2020: Buck Island and Black Point. Black Point, a nearshore reef, first exhibited cases of SCTLD between December 2018 and January 2019, whereas Buck Island, situated near an offshore undeveloped island, recorded its first cases of SCTLD in October 2019. At both sites, one coral fragment was collected from each apparently health colony (Buck Island, n = 3; Black Point, n = 3), termed apparently healthy tissue on an apparently healthy colony (HH). Two fragments were collected from each diseased colony: one immediately adjacent to the SCTLD lesion line (Buck Island, n = 3: Black Point, n = 5), termed lesion tissue on a diseased colony (LD), and one as far away from the lesion line as possible (approximately 10 cm from the lesion line) (Buck Island, n = 3; Black Point, n = 5), termed apparently healthy tissue on a diseased colony (HD). Sample and data analysis was performed in January 2024. Sequences were used in a feature selection algorithm to identify the genes in M. cavernosa and its dominant algal endosymbiont, Cladocopium goreaui, that best discriminate between the three SCTLD health states. By characterizing the gene expression profiles associated with various tissue health states in M. cavernosa and C. goreaui, this data supports evidence that SCTLD causes dysbiosis between the coral host and its Symbiodiniaceae and describes the metabolic and immune shifts that occur as the holobiont transitions from an apparently healthy state to a diseased state.

Table of Contents

Coverage

Location: St. Thomas, United States Virgin Islands
Spatial Extent: **N**:18.3445 **E**:-64.89833 **S**:18.27883 **W**:-64.98595
Temporal Extent: 2020-02

Methods & Sampling

Golf ball-sized coral fragments were collected by divers on SCUBA with hammers and chisels from two reefs in St. Thomas, United States Virgin Islands (USVI) showing signs of active SCTLD in February of 2020: Buck Island (18.27883˚, –64.89833˚) and Black Point (18.3445˚, –64.98595˚). Black Point, a nearshore reef, first exhibited SCTLD cases between December 2018 and January 2019, as documented in Brandt et al. (2021). Buck Island, situated near an offshore undeveloped island, recorded its first cases of SCTLD in October 2019, also documented in Brandt et al. (2021). Current

environments at both sites are similar. SCTLD-affected corals were identified based on displaying acute multifocal lesions consistent with the SCTLD case definition at the time (*SCTLD Case Definition,* 2018). Lesions were bright white where the skeleton had recently been denuded of tissue, with no visible algal colonization at the skeletal/tissue boundary, indicating actively expanding lesions.

At both sites, one coral fragment was collected from each apparently healthy colony (Buck Island, n=3; Black Point, n=3), termed apparently healthy tissue on an apparently healthy colony (HH). Two fragments were collected from each diseased colony: one immediately adjacent to the SCTLD lesion line (Buck Island, n=3; Black Point, n=5), termed lesion tissue on a diseased colony (LD), and one as far away from the lesion line as possible (approximately 10 cm from the lesion line) (Buck Island, n=3; Black Point, n=5), termed apparently healthy tissue on a diseased colony (HD). The sampling scheme aimed to capture the variability in gene expression across different tissue health states while ensuring consistency in sampling methodology. Coral fragments were placed in individual bags that were sealed and transported to land on ice before being flash-frozen at -80˚C.

Total RNA was extracted from all 22 coral fragments following the protocol outlined in Beavers et al. (2023) using the RNAqueous-4PCR Total RNA Isolation Kit from Invitrogen (Life Technologies AM1914). About one gram of frozen coral tissue was scraped off each fragment into a 2 mL microcentrifuge tube using a sterilized bone cutter. Lysis buffer was added to each microcentrifuge tube followed by mechanical disruption using a refrigerated Qiagen Tissuelyser II at 30 oscillations/s for 60 s. Elution was performed in two 30 µL steps at a time. After combining elutions, contaminating DNA and chromatin were removed using the Ambion DNase I kit from Invitrogen (Life Technologies AM 2222). Resulting total RNA samples were sent to Novogene Co., LTD (Beijing, China) for quality assessment using an Agilent Bioanalyzer 2100. All 22 samples passed quality assessment with RNA integrity (RIN) values ≥ 7 and were preprocessed for mRNA enrichment using polyA tail capture. cDNA libraries were prepared using the NEBNext Ultra II RNA Library Prep Kit from Illumina and sequenced on the Illumina NovaSeq 6000 for 150 bp, paired-end sequencing. Sample and data analysis was performed in January 2024.

The data have been deposited with links to BioProject accession number PRJNA1062758 in the NCBI BioProject database (https://www.ncbi.nlm.nih.gov/bioproject/).

Data Processing Description

The data presented are raw RNAseq reads and have not undergone any processing besides that done at the sequencing facility.

BCO-DMO Processing Description

Processed submitted file named BCO-DMO.xlsx with frictionless BCO-DMO Laminar tool.

Removed the duplicate column named Collection_month/year containing the collection month and year because another column named Collection_month_year contains the same information.

Renamed the columns according to BCO-DMO naming conventions where no units are included in the column names. Removed the units from the columns named Reef_depth_m, Disease_Colony_Sample_Distance_cm, Temperature_C, and Salinity_psu.

Converted the date format in the column Collection_month_year from Month name and two digit year to the ISO8601 format of YYYY-MM.

Renamed the column Collection_month_year to Collection_Date.

Checked the Coral Species name "Montastraea cavernosa" with the World Register of Marine Species (WoRMS) website to verify this is the accepted species name.

Saved the dataset to the primary data file named 935630_v1_rna_seq_montastraea_cavernosa.

[table of contents | back to top]

Data Files

File
935630_v1_rna_seq_montastraea_cavernosa.csv (Comma Separated Values (.csv), 15.94 KB) MD5:44e11ec63cae80c32749fd12e36dcb95 Primary data file for dataset ID 935630, version 1

[table of contents | back to top]

Related Publications

Beavers, K. M., Gutierrez-Andrade, D., Van Buren, E. W., Emery, M. A., Brandt, M. E., Apprill, A., & Mydlarz, L. D. (2024). Characterizing gene expression profiles of various tissue states in stony coral tissue loss disease using a feature selection algorithm. https://doi.org/10.1101/2024.11.05.622084
Results

Beavers, K. M., Van Buren, E. W., Rossin, A. M., Emery, M. A., Veglia, A. J., Karrick, C. E., MacKnight, N. J., Dimos, B. A., Meiling, S. S., Smith, T. B., Apprill, A., Muller, E. M., Holstein, D. M., Correa, A. M. S., Brandt, M. E., & Mydlarz, L. D. (2023). Stony coral tissue loss disease induces transcriptional signatures of in situ degradation of dysfunctional Symbiodiniaceae. Nature Communications, 14(1). https://doi.org/10.1038/s41467-023-38612-4
Methods

Brandt, M. E., Ennis, R. S., Meiling, S. S., Townsend, J., Cobleigh, K., Glahn, A., Quetel, J., Brandtneris, V., Henderson, L. M., & Smith, T. B. (2021). The Emergence and Initial Impact of Stony Coral Tissue Loss Disease (SCTLD) in the United States Virgin Islands. Frontiers in Marine Science, 8. https://doi.org/10.3389/fmars.2021.715329
Methods

SCTLD Case Definition. (2018). Florida Coral Disease Response Research & Epidemiology Team. https://floridadep.gov/sites/default/files/Copy%20of%20StonyCoralTissueLossDisease_CaseDefinition%20final%2010022018.pdf
Methods

[table of contents | back to top]

Related Datasets

IsRelatedTo

Apprill, A., Brandt, M. (2021) **Application of a rapid microbiome characterization pipeline to corals afflicted with Stony Coral Tissue Loss Disease in St. Thomas, US Virgin Islands.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2020-12-07 doi:10.26008/1912/bco-dmo.833133.1 [view at BCO-DMO]

University of Texas at Arlington (2025). RNASeq data from multiple SCTLD health states of Montastraea cavernosa from a natural reef environment in the US Virgin Islands. 2025/01. NCBI:BioProject: PRJNA1062758 [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1062758.

[table of contents | back to top]

Parameters

Parameter	Description	Units
Sample_ID	Sample identifier	unitless
NCBI_BioProject_accession	NCBI BioProject accession number	unitless
NCBI_BioSample_accession	NCBI BioSample accession number	unitless
NCBI_SRA_accession	NCBI SRA accession number	unitless

Sample_type	Type of sample collected. Tissue fragment = a golf ball-sized fragment of coral tissue + skeleton that we later extracted RNA from	unitless
Coral_species	Species of Coral collected: All samples were collected from Montastraea cavernosa colonies	unitless
Reef_Name	The name of the reef that samples were collected from	unitless
Reef_type	Indicates the reef type that samples were collected from	unitless
Collection_Date	Indicates the month and year of sample collection	unitless
Latitude	Sampling location latitude, south is negative	decimal degrees
Longitude	Sampling location longitude, west is negative	decimal degrees
SCTLD_duration_months	Indicates in months how long SCTLD had been present at that location prior to sampling	unitless
Reef_depth	The depth of the sample collected	meters (m)
Temperature	The temperature of sample environment	Celcius (degC)
Salinity	The salinity of the sample environment	psu
pH	The pH of the sample environment	unitless
Colony_status	The health status of the colony sampled. (Diseased = SCTLD; Healthy = Apparently healthy)	unitless
Frag_condition	The tissue status of the sample (Apparently healthy = apparently healthy (visibly); Lesion = immediately adjacent to the SCTLD lesion)	unitless
Tissue_Health_State	The health state identifier of the sample (HH = apparently healthy tissue from an apparently healthy colony; HD = apparently healthy tissue from a SCTLD-affected colony; LD = lesion tissue from a SCTLD-affected colony)	unitless
Disease_Colony_Sample_Distance	Indicates how far away the apparently healthy tissue was sampled from the SCTLD lesion (only applies to HD tissue). nd = not collected (HH or LD)	centimeters (cm)
Library_strategy	RNA-Seq = samples were prepared for RNA sequencing	unitless
Sequencing_Strategy	all RNA samples were prepared for 150 base-pair, paired-end sequencing	unitless
Sequencing_Instrument_model	All RNA samples were sequenced on the Illumina NovaSeq 6000	unitless

Sequencing_strategy_details	All RNA samples were processed for polyA-tail enrichment to remove non-eukaryotic reads	unitless
RNA_extraction_method	Indicates how the RNA was extracted from each sample.	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina NovaSeq 6000
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Agilent Bioanalyzer 2100
Generic Instrument Name	Bioanalyzer
Generic Instrument Description	A Bioanalyzer is a laboratory instrument that provides the sizing and quantification of DNA, RNA, and proteins. One example is the Agilent Bioanalyzer 2100.

Dataset-specific Instrument Name	Qiagen TissueLyser II
Generic Instrument Name	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.

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

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

[table of contents | back to top]