# Viral consortia in Stony Coral Tissue Loss Disease- affected, disease-exposed, and disease-unexposed coral colonies from a transmission experiment conducted on samples collected from Rupert's Rock in St. Thomas, U.S. Virgin Islands in 2019

**Website**: https://www.bco-dmo.org/dataset/875283
**Data Type**: experimental
**Version**: 1
**Version Date**: 2022-06-29

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

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## Abstract

To understand the extent to which (if any) viruses are associated with stony coral tissue loss disease (SCTLD) in stony corals of the U.S. Virgin Islands, we leveraged viral metatranscriptomes generated from SCTLD-affected, SCTLD-exposed, and control (unexposed) coral holobionts sampled during a SCTLD transmission experiment. Sequence data is available in NCBI Genbank under BioProject accession PRJNA788911.

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# Coverage

**Spatial Extent**: **Lat**:18.3276666667 **Lon**:-64.9259722222
**Temporal Extent**: 2019-04-11 - 2019-04-12

## Methods & Sampling

This dataset represents collections of *Montastraea cavernosa*, *Porites astreoides*, and *Pseudodiploria strigosa*

colonies, no larger than 25 centimeters (cm) × 25 centimeters (cm), from Rupert's Rock (18°19′39.6″N 64°55′33.5″W) in St. Thomas, U.S. Virgin Islands. The corals were collected by divers on SCUBA with hammers and chisels (March 2019) and preserved for analysis in April 2019.

**Methodology:**
Samples were preprocessed by Novogene Co., Ltd. (Davis, CA, USA) 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.

**Sampling and analytical procedures:**
Samples were flash frozen in liquid nitrogen and stored at -80 degrees C until further processing. Total RNA was extracted using the RNAqueous-4PCR total RNA isolation kit (Invitrogen, Life Technologies AM1914). Tissues were lysed using a refrigerated Qiagen TissueLyser II microcentrifuge at 30 oscillations per second for 30 seconds. The elution stage consisted of two consecutive 30-milliliter (mL) elutions. Contaminating DNA and chromatin were removed from the total RNA using the Ambion DNase I (RNase-free) kit (Invitrogen, Life Technologies AM2222).

A combination of reads from stony coral tissue loss disease affected, stony coral tissue loss disease exposed and control (unexposed) holobiont metatranscriptomes (*Montastraea cavernosa*, *Porites astreoides* and *Pseudodiploria strigosa*) were generated from the following samples: Mcav_c3, Mcav_c6, Mcav_c7, Mcav_d2, Mcav_d3, Mcav_d4, Mcav_d6, Mcav_d8, Past_c6, Past_d4, Past_d6 and Pstrig_d5 and given the NCBI accession number: OM030231.

A combination of reads from stony coral tissue loss disease affected, stony coral tissue loss disease exposed and control (unexposed) holobiont metatranscriptomes (*Montastraea cavernos*a, *Porites astreoides* and *Pseudodiploria strigosa*) were generated from the following samples: Mcav_c3, Mcav_c6, Mcav_c7, Mcav_d2, Mcav_d3, Mcav_d4, Mcav_d6, Mcav_d8, Past_c6, Past_d4 and Pstrig_d5 and given the NCBI accession number: OM030232.

Sequence data is available in NCBI Genbank under BioProject accession PRJNA788911 and including NCBI SRA run SRR17230316 - SRR17230326.

**Data Processing Description**

**Data Processing:**
All bioinformatic tools were run using default parameters unless otherwise specified. BBSplit (BBMap v38.90) was used to map quality-filtered (fastp v0.20.1) reads to coral or Symbiodiniaceae transcriptomes and generate three read files: (i) coral, (ii) Symbiodiniaceae, and (iii) noncoral/non-Symbiodiniaceae. Noncoral/non-Symbiodiniaceae reads were combined and normalized using BBnorm.sh within BBMap. Normalized reads were assembled using the program TransPi. Multiple assemblies were generated using rnaSPADES v3.14.0 (kmer: 75,85,91,107 nucleotides), Trans-ABySS v2.0.1 (kmer: 25,35,55,75,85 nucleotides), SOAPdenovo-Trans v1.03 (kmer: 25,35,55,75,85 nucleotides), Trinity v2.9.1 (kmer: 35 nucleotides), and Velvet v1.2.12/Oases v0.2.09 (kmer: 65,71,81,87,91,97,101 nucleotides). The multiple assemblies were concatenated into a single file, and the EvidentialGene tr2aacds pipeline v2019.05.14 was used to collapse duplicates and remove misassembled contigs from the assembly file. VirSorter2 was used to detect RNA viruses from the nonredundant metatranscriptome-assembly file (minimum length, 300 nucleotides). Viral genomes similar to known members of the Alphaflexiviridae were identified by aligning translated open reading frames (ORFs) to the proteic version of the Reference Virus Database with DIAMOND BLASTx v2.0.11.149 in "ultra-sensitive" mode. Cenote-Taker 2 was used to annotate identified viral genomes with similarity to the Alphaflexiviridae and calculate the genome coverage using the normalized reads. The alphaflexivirus read count per sample library was estimated by mapping nonnormalized reads to the nonredundant assembly using bowtie2 with the align_and_estimate_abundance.pl script.

**BCO-DMO Processing:**
- Converted dates to format (YYYY-MM-DD)
- Adjusted field/parameter names to comply with BCO-DMO naming conventions
- Missing data identifier 'NA' replaced with 'nd' (BCO-DMO's default missing data identifier)
- Added a conventional header with dataset name, PI names, version date
- Latitude and longitude columns were split from the location columns

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## Data Files

| File |
|------|
| **viral_consortia.csv** (Comma Separated Values (.csv), 1.72 KB)<br>MD5:c4a4a41056eac03c8234c325518ea518<br><br>Primary data file for dataset ID 875283 |

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## Related Publications

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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## Related Datasets

### IsRelatedTo

University of Texas at Arlington. Novel Alphaflexiviridae Genomes Associated with Stony Coral Tissue Loss Disease (SCTLD)-Infected, Disease-Exposed and Unexposed Coral Colonies in the U.S. Virgin Islands. 2021/12. 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/PRJNA788911. NCBI:BioProject: PRJNA788911.

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## Parameters

| Parameter | Description | Units |
|-----------|-------------|-------|
| Sample_Name | name of sample | unitless |
| Preservation_Date | date of preservation of sample in format YYYY-MM-DD | unitless |
| Depth | depth of sample | meters (m) |
| Location | location of sample site | unitless |
| Latitude | latitude of sample site | decimal degrees |
| Longitude | longitude of sample site | decimal degrees |
| Coral_Species | species of coral | unitless |
| Colony_health_status | status of coral colony health | unitless |
| Experimental_bin_ID | experimental bin ID | unitless |
| SRA_Run | SRA Run ID | unitless |
| Bio_Project | Bio Project ID | unitless |

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | Hammer and Chisel |
| **Generic Instrument Name** | Manual Biota Sampler |
| **Generic Instrument Description** | "Manual Biota Sampler" indicates that a sample was collected in situ by a person, possibly using a hand-held collection device such as a jar, a net, or their hands. This term could also refer to a simple tool like a hammer, saw, or other hand-held tool. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **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. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | Self-Contained Underwater Breathing Apparatus |
| **Generic Instrument Description** | The self-contained underwater breathing apparatus or scuba diving system is the result of technological developments and innovations that began almost 300 years ago. Scuba diving is the most extensively used system for breathing underwater by recreational divers throughout the world and in various forms is also widely used to perform underwater work for military, scientific, and commercial purposes.<br>Reference: http://oceanexplorer.noaa.gov/technology/diving/diving.html |

## 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:*

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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.

## Funding

| Funding Source | Award |
|---|---|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1928609 |