NCBI Sequence Read Archive (SRA) accession numbers for fastq sequence files of 16S amplicons from a longitudinal study of SCTLD at St. John, U.S. Virgin Islands from 2020 to 2024

Website: https://www.bco-dmo.org/dataset/986592
Data Type: Other Field Results
Version: 1
Version Date: 2025-11-18

Project
» A multi-scale approach to predicting infectious multi-host disease spread in marine benthic communities (Multi-scale multi-host disease spread)

Contributors	Affiliation	Role
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Abstract
In St. John, U.S. Virgin Islands, a longitudinal study of Colpophyllia natans was conducted. Six corals per site (two sites) were tagged and repeatedly sampled from July 2020 through March 2024, during which time, stony coral tissue loss disease (SCTLD) arrived on the reefs. As the tagged corals contracted SCTLD, coral tissue and near-coral seawater (2-5 centimeters from colony surface) were collected. Coral tissue was separated from the coral skeleton, and the seawater was filtered through 0.2-micrometer (µm) filters. DNA was extracted from the tissue and filters, and 16S ribosomal RNA gene sequencing was done to determine the bacteria and archaea communities that live within and near the corals. The goal of the study was to determine how coral-associated microbiomes are affected by the arrival of SCTLD through time. This data set contains the fastq files of the 16S amplicon sequencing of the coral tissue and near-coral seawater communities. National Center for Biotechnology Information (NCBI) SRA: SRP550314; BioProject: PRJNA1194595

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Coverage

Location: St. John, U.S. Virgin Islands

Spatial Extent: **N**:18.337967 **E**:-64.704017 **S**:18.31462 **W**:-64.7642
Temporal Extent: 2020-07-16 - 2024-03-07

Methods & Sampling

Samples were collected on day-trips aboard a University of the Virgin Islands powerboat in the U.S. Virgin Islands from July 2020 through March 2024. On SCUBA, 60 milliliters (mL) of seawater was collected 2-5 centimeters (cm) above the colony surface, then the coral fragment was collected; upon surfacing, samples were put on ice. Seawater was passed through 0.2-micrometer (µm) filters, and the tissue was removed from the skeleton using PBS solution and an airbrush. DNA was extracted from the coral tissue, seawater filters, and processing controls using the Qiagen DNeasy PowerBiofilm Kit. PCR was used to amplify the V4 region of the small subunit rRNA gene of bacteria and archaea using primers 515FY and 806RB with standard barcodes. To purify the PCR product from seawater, the Qiagen PCR Purification Kit was used. Purification of PCR products from coral tissue proceeded by running products in a 1.5% agarose gel and excising bands of 450 bp. Gel excisions were purified using the Qiagen Gel Extraction Kit. PCR products were diluted to 1 nanogram per microliter (ng/µL) and sequenced on an Illumina MiSeq (paired reads, 2x250 nt) at the University of Georgia's Georgia Genomics and Bioinformatics Core and University of Illinois Urbana-Champaign's Roy J. Carver Biotechnology Center.

BCO-DMO Processing Description

- Imported original file "sra_result.csv" into the BCO-DMO system.
- Renamed fields to comply with BCO-DMO naming conventions.
- Saved the final file as "986592_v1_ncbi_sra.csv".

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Data Files

File	
986592_v1_ncbi_sra.csv	(Comma Separated Values (.csv), 36.40 KB) MD5:01b778f9b8d15875af642be2015d8644
Primary data file for dataset ID 986592, version 1	

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Related Datasets

IsRelatedTo

Woods Hole Oceanographic Institution. Longitudinal microbiomes of coral and near-coral seawater influenced by disease phase. 2024/12. 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/PRJNA1194595. NCBI:BioProject: PRJNA1194595.

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Parameters

Parameter	Description	Units
Experiment_Accession	NCBI experiment accession number	unitless
Instrument	Sequencing instrument used	unitless
Study_Accession	NCBI study accession number	unitless
Study_Title	Title of study on NCBI	unitless
Sample_Accession	NCBI sample accession number	unitless
Library_Name	Sample name used during the experiment	unitless
Collection_date	Date that the sample was collected from reef site	unitless
Latitude	Latitude of reef site	decimal degrees
Longitude	Latitude of reef site	decimal degrees

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Instruments

Dataset-specific Instrument Name	agarose gel
Generic Instrument Name	Agarose Gel Electrophoresis System
Dataset-specific Description	Purification of PCR products from coral tissue proceeded by running products in a 1.5% agarose gel and excising bands of 450 bp.
Generic Instrument Description	A gel electrophoresis system that is used to separate DNA or RNA molecules by size, achieved by moving negatively charged nucleic acid molecules through an agarose matrix with an electric field.

Dataset-specific Instrument Name	Illumina MiSeq V2
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Samples were sequenced on an Illumina MiSeq V2.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	SCUBA
Generic Instrument Name	Self-Contained Underwater Breathing Apparatus
Dataset-specific Description	Samples were collected by SCUBA divers.
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. Reference: https://oceanexplorer.noaa.gov/technology/technical/technical.html

Dataset-specific Instrument Name	PCR
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	PCR was used to amplify the V4 region of the small subunit rRNA gene of bacteria and archaea using primers 515FY and 806RB with standard barcodes.
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)

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Project Information

A multi-scale approach to predicting infectious multi-host disease spread in marine benthic communities (Multi-scale multi-host disease spread)

Coverage: United States Virgin Islands

NSF Award Abstract:
Marine diseases have devastating impacts on ocean ecosystems and this work will directly examine the framework for understanding disease transmission in the ocean. A team of ecologists, ocean connectivity and disease modelers, microbiologists, and coral immunologists (from the University of Virgin Islands (UVI), Louisiana State University (LSU), Rice University, University of Texas-Arlington and the Woods Hole Oceanographic Institution) will develop a model that predicts transmission of a devastating Caribbean coral disease that has the potential to impact the economic value of coral reefs, including those located in the U.S. This project will support multidisciplinary field and laboratory research experiences of graduate students at multiple minority-serving institutions, and will provide undergraduate students with hands-on training in modeling, ecological and molecular analysis techniques. UVI and LSU are in EPSCoR jurisdictions and have

diverse student bodies, including numerous under-represented minority (URM) students. The research team will collaboratively provide URM students with research experiences in STEM fields. Project findings will be broadly communicated through virtual public programming, and through the Virgin Islands Coral Disease Advisory Committee with updates on the vicoraldisease.org website. A coral disease response workshop for the U.S. Virgin Islands will also be held, in which project results will be presented and used to support disease response planning.

Over the last four decades, marine diseases have decimated ecosystem engineers in marine coastal ecosystems, including the rocky intertidal, seagrasses and coral reefs. The pathogens driving these diseases have frequently been challenging to isolate, characterize and confirm, in part because they affect multiple host species and can spread by ocean currents, as well as through individual contact. Here, we propose a multi-scale epidemic model for studying marine disease that addresses both within-host and within-patch disease dynamics, and explicitly acknowledges the dispersal of pathogens between populations. Our interdisciplinary research team of ecologists, connectivity and disease modelers, microbiologists, and coral immunologists will integrate the largest set of predictors of marine disease spread to date: individual host species traits that allow for disease resistance or susceptibility, local transmission within communities that may have unique community structure, and hydrodynamic connectivity among susceptible communities. Modeling will be supported with rich data sets of within- and among-patch population characteristics and disease dynamics as well as molecular data on species-level disease responses. This project will advance knowledge of infectious diseases by integrating multidimensional scales and differential host susceptibilities into existing epidemiological models. This model will particularly advance the framework for studying marine diseases and has the potential to elucidate the transmission properties of a devastating Caribbean coral disease (stony coral tissue loss disease) that fits the most confounding and notorious hallmarks of marine diseases: infection of multiple hosts by an elusive pathogen.

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-2109622

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