Sample and treatment information for the environmental metagenome of paired bleaching and nonbleaching Pocillopora cf. meandrina corals in Mo'orea, French Polynesia in March of 2016

Website: https://www.bco-dmo.org/dataset/844868
Data Type: experimental, Other Field Results
Version: 1
Version Date: 2021-03-12

Project
» Collaborative Research: Viral Reefscapes: The Role of Viruses in Coral Reef Health, Disease, and Biogeochemical Cycling (Moorea Virus Project)

Contributors	Affiliation	Role
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Abstract
Sample and treatment information for the environmental metagenome of paired bleaching and nonbleaching Pocillopora cf. meandrina corals in Mo'orea, French Polynesia in March of 2016. All sequences are available in the Short Read Archive (SRA) at The National Center for Biotechnology Information (NCBI)under BioProject PRJNA647466 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA647466).

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Coverage

Spatial Extent: **Lat**:-17.28 **Lon**:-149.49
Temporal Extent: 2016-03

Dataset Description

A processed version of these data were published in Messyasz et al. (2020) (all tables and figures).

All sequences are available in the Short Read Archive (SRA) at The National Center for Biotechnology Information (NCBI). BioSample and SRA accessions can be accessed from the BioProject PRJNA647466 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA647466).

Methods & Sampling

Location: Mo’orea, French Polynesia, Pacific Ocean.

Sampling and analytical procedures:

Pocillopora spp. coral fragments were collected in situ on SCUBA using bone-cutters. For each coral sample, fragments were airbrushed with 1.5 mL of Qiagen Dneasy Kit lysis buffer and the resulting coral tissue slurry was used for whole community DNA extraction with a Dneasy Kit. For metagenome generation, the extracted DNA from the coral fragments were cleaned with Zymo DNA Clean and Concentrator- 5 Kits and eluted into Ultra-pure H2O for sequencing. DNA from each coral sample was prepared for sequencing with the PrepX DNA Library Kit, then sequenced on the Illumina HiSeq 3000 platform (2 × 150 paired-end).

Data Processing Description

The only data processing was done by the sequencing facility which included stripping of sequencing primers and bar codes. No other data manipulation was done.

BCO-DMO Data Manager Notes:
* Data in file "biosample_result.txt" imported into the BCO-DMO data system.
* Sample latitude, longitude, year and month added to the data table from information under the BioSamples at NCBI.
* Modified parameter (column) 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).
* Converted Date format to ISO 8601 format yyyy-mm-dd

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Data Files

File
sra_bleach_nonbleach.csv (Comma Separated Values (.csv), 694 bytes) MD5:343cd85f84a8d111bc7ddcd185a1a259 Primary data file for dataset ID 844868

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Related Publications

Messyasz, A., Rosales, S. M., Mueller, R. S., Sawyer, T., Correa, A. M. S., Thurber, A. R., & Vega Thurber, R. (2020). Coral Bleaching Phenotypes Associated With Differential Abundances of Nucleocytoplasmic Large DNA Viruses. Frontiers in Marine Science, 7. doi:10.3389/fmars.2020.555474
Results

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Related Datasets

IsRelatedTo

Oregon State University. Comparison of Viral Metagenomes from Bleached and Non-Bleached Pocillopora spp. Corals. 2020/07. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA647466.
NCBI:BioProject: PRJNA647466.

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Parameters

Parameter	Description	Units
Sample_ID	Unique sample identifier consistent within the study.	unitless
BioSample	BioSample accession identifier at NCBI. The associated Sequence Read Archive (SRA) sequences can be found by searching by BioSample.	unitless
Description	Type of data (all are environmental metagenomes)	unitless
Species	Species identified. Pocillopora in Moâ€™orea form a species complex that is morphologically indistinguishable, while these were most similar to Pocillopora meandrina, they are indicated as Pocillopora sp.	unitless
Treatment	Corals were either bleached (having lost their photosynthetic symbionts) or non-bleached.	unitless
Replicate	Paired corals were collected adjacent to each other with one being bleached and the other not. Corals with the same replicate ID were adjacent to each other on the reef at the time of collection.	unitless
Year	Sample year in format yyyy.	unitless
Month	Sample month (numeric month)	unitless
Lat	Sample latitude (South is negative).	decimal degrees
Lon	Sample longitude (West is negative)	decimal degrees

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq 3000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Sequencing was performed on the Illumina HiSeq 3000 sequencing platform at the Center for Genome Research and Biocomputing at Oregon State University.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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Project Information

Collaborative Research: Viral Reefscapes: The Role of Viruses in Coral Reef Health, Disease, and Biogeochemical Cycling (Moorea Virus Project)

Coverage: Moorea, French Polynesia, Pacific 17 S 150 W

Ecologically and economically, coral reefs are among the most valuable ecosystems on Earth. These habitats are estimated to harbor up to nine million species, contribute ~30 billion US dollars annually to the global economy, and are tropical epicenters of biogeochemical cycling. Global (climate change) and local (nutrient pollution and overfishing) stressors are drivers of coral reef decline that can disrupt the symbiotic associations among corals and resident microbial communities, including dinoflagellate algae, bacteria, and viruses. Viruses interact with all living cellular organisms, are abundant in oceans, and integral to marine ecosystem functioning. This project will be the first to quantify the variability of viral infection in corals across different reef habitats and across time. This will increase our understanding of the total diversity of coral viruses and illuminate the full suite of factors that trigger viral outbreaks on reefs. At the same time the project will evaluate how carbon and nitrogen cycling are altered on coral reefs as a result of global and local stressors that trigger viral infection. This project will ultimately broaden our understanding of the impacts of viruses on reefs beyond their role as putative disease agents. Results of the project will be communicated broadly in scientific arenas, in K-12, undergraduate, and graduate education and training programs, and to the general public through video and multimedia productions, as well as outreach events. 2-D Reef Replicas from our field sites across Moorea will be constructed, allowing children and adults in the US and French Polynesia to 'become' marine scientists and use quadrats, transect tapes, and identification guides to quantify metrics of reef change. Three graduate students will be involved in all aspects of the research and an effort will be made to recruit and support minority students. All datasets will be made freely available to the public and newly developed methods from this project will serve as an important set of springboard tools and baselines for future lines of inquiry into the processes that influence reef health.

Coral reefs, found in nutrient-poor shallow waters, are biodiversity and productivity hotspots that provide substantial ecological and societal benefits. Corals energetically subsidize these oligotrophic ecosystems by releasing significant amounts of mucus (an organic carbon and nitrogen-rich matrix) into the surrounding seawater. Viral production in reef waters can be a significant portion of total reef carbon cycling, accounting for ~10% of gross benthic carbon fixation in reef ecosystems. Viruses are also ~10 times more abundant on coral surfaces than in the water column meaning that viral infection experienced by corals during stress likely results is an increase in carbon and perhaps nitrogen flux to the water column. Thus phages and eukaryotic viruses may be responsible for shifting reef health and function directly via coral and symbiont infection and by altering biogeochemical cycling in host colonies and the adjacent reef system. The main goal of this project is to experimentally interrogate and then model the links among viral infections, declines in coral and reef health, and associated shifts in biogeochemical cycling in reef ecosystems. Lab and field experiments will be conducted at the Moorea Coral Reef LTER to characterize the spatiotemporal dynamics of viruses within two dominant reef-building coral species that differ in their susceptibility to abiotic stress. A novel viral infection and induction approach will be coupled with stable isotopic pulse-chase experiments to quantify and track carbon and nitrogen flux out of coral holobionts (host and microbial symbionts) and into dissolved and particulate pools. In these experiments, virus, bacteria, and symbiont abundance, diversity, and function will be measured simultaneously with the health and activity of the host. Pulse-chase techniques, as well as flux- and niche-based modeling, will result in a holistic understanding of how corals and associated viruses impact reef energy budgets and the ramifications of carbon and nitrogen flux for reef communities. Ultimately, this project will quantify and describe an integrated mechanism by which environmental stressors alter viral, microbial, and coral diversity and, consequently, ecosystem function.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1635798
NSF Division of Ocean Sciences (NSF OCE)	OCE-1635913

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