Coral associated microbes on coral, sediment and water sampled from coral reefs in Mo'orea, French Polynesia in 2017 and 2018

Website: https://www.bco-dmo.org/dataset/845039
Data Type: Other Field Results
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Project
» Collaborative Research: Viral Reefscapes: The Role of Viruses in Coral Reef Health, Disease, and Biogeochemical Cycling (Moorea Virus Project)

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Abstract
Three species of coral, plus water and sediment, were sampled at 21 sites around the island of Mo'orea, French Polynesia during the dry and rainy seasons in 2017 and 2018. Coral associated microbes (bacteria and archaea) were investigated and their community composition characterized through sequencing of the 16S rRNA gene.

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Coverage

Spatial Extent: **N**:-17.4721 **E**:-149.762 **S**:-17.58 **W**:-149.921
Temporal Extent: 2017-09 - 2018-03

Acquisition Description

Coral, water and sediment were sampled at 21 sites around the island of Mo'orea, French Polynesia in September 2017 and March 2018. Locations included Forereef on the oceanic side of the reef crest, Backreef on the lagoonal side of the reef crest, and Fringing Reef adjacent to the shoreline.

Coral: Individual corals from three species (*Acropora hyacinthus*, *Porites lobata*, and *Pocillopora sp.*) were tagged and repeatedly sampled twice a year in the rainy and dry seasons at depths between 1 and 10 meter water depth. Note that *Pocillopora* are a species complex on the Island of Mo'orea and while all individuals appeared to be *Pocillopora meandrina*, different species of this genus are morphologically indistinguishable at the size of these corals. Sampling was done free-diving or on SCUBA, with individual corals sampled using bone cutters (or chisels for *P. lobata*) that had been flame sterilized prior to each day's collection and were used only for that species to eliminate cross-species contamination. Corals with the same ID are the same individual sampled over time. All collections were done while wearing nitrile gloves. Upon return to the boat, coral fragments were placed in Zymo DNA/RNA shield and kept cold on Techni ice (frozen to -80 degrees C) until processing.

Sediment: 2 milliliters of sediment were collected by gloved hands in sterile 'snap-cap' vials. Upon return to the boat samples were added to Zymo DNA/RNA shield and kept cold on Techni ice (frozen to –80 degrees C) until processing.

Water: 500 milliliters of seawater was collected and kept chilled until it was filtered onto a 0.1 micron filter, then put into Zymo DNA/RNA shield and kept cold on Techni ice (frozen to –80 degrees C) until processing.

Sample processing:
Initial processing included bead beating of all samples prior to them being frozen at -80 degrees C and shipped back to either Rice University or Oregon State University. Coral and sediment were extracted using the ZYMO quick-DNA extraction kit and water samples with Qiagen Powerwater DNA extraction kit. DNA was amplified (at OSU) following the Earth Microbiome Project protocols, using the updated primers of 515f (Parada et al. 2016) and 806r (Apprill et al. 2015). Due to co-amplification of eukaryotic 12S rRNA genes, DNA was size selected using Blue Pippin (Sage Scientific) prior to sequencing to minimize 12S sequence generation. Sequencing was performed on the Illumina MiSeq platform using the V.2 chemistry at the Center for Genome Research and Biocomputing at Oregon State University. While we used forward and reverse barcoding for sequencing, reverse read quality scores were not acceptable and only forward reads were used and uploaded to the SRA. In certain cases, there were repeated sequencing runs for individual samples. That is indicated with different numbers.

Accession numbers of DNA sequences generated as part of this project are archived and available in the National Center for Biotechnology Information (NCBI) Short Read Archive under BioProject Identifier PRJNA684406 (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA684406).

Processing Description

Data processing:
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 processing description:
The original data submitted in CSV file "AroundIsland_Metadata_final.csv" was modified during processing:
- Adjusted field/parameter names to comply with database requirements
- Added a conventional header with dataset name, PI names, version date, and BioProject
- Added separate columns for Latitude and Longitude and converted to decimal degrees
- Split column "collection_date" to show separate "Month" and Year" columns

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Related Publications

Apprill, A., McNally, S., Parsons, R., & Weber, L. (2015). Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. Aquatic Microbial Ecology, 75(2), 129–137. doi:10.3354/ame01753 https://doi.org/http://doi.org/10.3354/ame01753
Methods

Parada, A. E., Needham, D. M., & Fuhrman, J. A. (2015). Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. Environmental Microbiology, 18(5), 1403–1414. doi:10.1111/1462-2920.13023 https://doi.org/http://doi.org/10.1111/1462-2920.13023
Methods

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Related Datasets

IsRelatedTo

Oregon State University. Moorea Virus Project - Longitudinal Coral Microbiome Study at the Mo'orea LTER. 2020/12. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA684406. NCBI: BioProject PRJNA684406.

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Parameters

Parameter	Description	Units
BioSample_accession	NCBI Short Read Archive BioSample accession identifier	unitless
Sample_name	Unique Sample ID	unitless
Organism	Host organism from which environmental metagenome was made	unitless
Year	Year of sample collection from environment	dimensionless
Month	Month of sample collection from environment	dimensionless
Depth	Seawater depth from which the sample was collected	meters
Env_Local_Scale	Reef type (forereef= oceanic side of the reef crest, backreef= lagoonal side of the reef crest, fringing reef= adjacent to the shoreline)	unitless
Geo_Loc_Name	Geographic location	unitless
Latitude	Latitude of sample collection	decimal degrees
Longitude	Longitude of sample collection	decimal degrees
Host	Sediment, Water, or Coral species	unitless
Host_Subject_ID	Identification of individual tagged corals that were repeatedly sampled. (Water and sediment have only one sample at each site)	unitless
Sequencing_Replicate	Repeated sequencing runs for individual samples	unitless

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq platform
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina MiSeq platform using the V.2 chemistry at the Center for Genome Research and Biocomputing at Oregon State University.
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	
Generic Instrument Name	Diving Mask and Snorkel
Dataset-specific Description	Samples were collected by free diving
Generic Instrument Description	A diving mask (also half mask, dive mask or scuba mask) is an item of diving equipment that allows underwater divers, including, scuba divers, free-divers, and snorkelers to see clearly underwater. Snorkel: A breathing apparatus for swimmers and surface divers that allows swimming or continuous use of a face mask without lifting the head to breathe, consisting of a tube that curves out of the mouth and extends above the surface of the water.

Dataset-specific Instrument Name	SCUBA
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. Reference: http://oceanexplorer.noaa.gov/technology/diving/diving.html

Dataset-specific Instrument Name	BluePippin
Generic Instrument Name	Agarose Gel Electrophoresis System
Dataset-specific Description	BluePippin is a an automated DNA Size Selection System, a preparative electrophoresis platform that uses agarose gel plates. For this dataset, DNA was size selected using Blue Pippin (Sage Scientific) prior to sequencing to minimize 12S sequence generation
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.

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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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