Symbiodiniaceae communities (via ITS-2 rDNA amplicon sequencing) in reef-associated fish feces, corals, water and sediments

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Version: 1
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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
SRA accessions and collection information for ITS-2 rDNA amplicon data from fish feces, corals, water and sediments sampled from Mo'orea, French Polynesia in August 2019. Sequences will be made available at the National Center for Biotechnology Information (NCBI).

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Coverage

Temporal Extent: 2019-01-01

Methods & Sampling

Methodology summary:

ITS-2 rDNA Symbiodiniaceae community libraries were prepared and PE 300bp reads were generated using Illumina MiSeq platform.

Sampling and analytical procedures:

Samples were preserved in DNA/RNA shield (Zymo Research, CA) and stored at -20°C until further processing. DNA was extracted using the ZymoBIOMICs DNA/RNA Miniprep kit (Zymo Research, CA) from 20-200 mg of feces, small coral tissue sections (~5 mm2), 250 ml sediments and ~1890 ml water using a ZymoBIOMICs DNA/RNA Miniprep kit (Zymo Research, CA).

Sample subject list with aphiaIDs for taxonomic names:

Acropora, 205469
Amanses scopas, 212242

Chaetodon citrinellus, 218744
Chaetodon lunulatus, 398549
Chaetodon ornatissimus, 273352
Chaetodon pelewensis, 273353
Chaetodon reticulatus, 273359
Chlorurus spilurus, 712772
Ctenochaetus flavicauda, 277560
Ctenochaetus striatus, 219659
Pocillopora, 206938
Porites, 206485
Sediment
Water

Data Processing Description

The sequencing data were processed using Symportal (Hume et al., 2019). Samples with <1,000 reads were discarded and sequencing depth was assessed using rarefaction curves. ITS2-profiles were reduced to number of reads per Symbiodiniaceae genus and expressed as percentages. All data were analysed using R version 3.6.1 (R Core Team, 2019).

BCO-DMO data manager processing notes:
* Data submitted in Excel file "Correa Grupstra 121620 metadata.xlsx" extracted to csv.
* Taxonomic names verified using the World Register or Marine Species taxa match tool. All names matched exactly to accepted taxonomic names (as of 2021-03-09).

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Related Publications

Grupstra, C. G. B., Rabbitt, K. M., Howe-Kerr, L. I., & Correa, A. M. S. (2020). Fish predation on corals promotes the dispersal of coral symbionts. doi:10.1101/2020.08.10.243857
Results

R Core Team (2019). R: A language and environment for statistical computing. R v3.6.1. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/
Software

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Parameters

Parameters for this dataset have not yet been identified

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq platform
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.

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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
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