Viral metagenomes derived from an apparently healthy M. cavernosa coral and a heat-stressed M. cavernosa coral analyzed in the Vega Thurber lab at Florida International University, North Miami, FL (Coral Virus project)

Website: https://www.bco-dmo.org/dataset/558294
Version: 12 May 2015
Version Date: 2015-05-12

Project
» Effects of Viruses on Coral Fitness (Coral Virus)

Contributors	Affiliation	Role
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Dataset Description

These two viral metagenomes were derived from 1) an apparently healthy *Montastrea cavernosa* coral maintained in 28.0 degrees C, and 2) a heat stressed *M. cavernosa* coral which was exposed to 31.5 degrees C for 12 hours.

The experiment was conducted in North Miami, Florida, USA, at Florida International University. Specimens were collected at Key West, FL, USA.

Status Note [12 May 2015]: These data are stored at the MG-RAST Server http://metagenomics.anl.gov/metagenomics.cgi?page=MetagenomeSearch under ID numbers: 44551158.3 and 44551159.3. However, at this time, these data are not publicly available. Links will be provided here once the data are available online through MG-RAST.

Methods & Sampling

For complete details see Correa et al. (2012).

Following treatment, the tissue layer from each fragment was removed using an airbrush and 0.02 mm filtered viral-free 1_ PBS (pH 7.8). Coral and coral symbiont homogenates were collected in sterile tri-pour containers and pre-filtered with an 1-mm nucleopore filter (Whatman, Piscataway, NJ,USA). VLPs were concentrated from 27 ml of homogenate using ultracentrifugation of four-layer (1.2, 1.35, 1.5 and 1.7 g ml-1) cesium chloride density gradients (Vega Thurber et al., 2009). A gray band formed in the 1.2 g ml-1 density layer (Supplementary Figure 1a) and was harvested using an 18-gage needle and sterile syringe. Before and following a 0.22-mm Sterivex (Millipore, Billerica,MA, USA) filtration step (for details, see Vega Thurber et al. (2009)), this fraction was visualized using epifluorescence microscopy and SYBR Gold (Invitrogen, Carlsbad, CA, USA) staining (Noble and Fuhrman, 1998; Vega Thurber et al., 2009).

Related publications:
Correa, A.M., Welsh, R.M., and Vega Thurber, R.L. 2012. Unique nucleocytoplasmic dsDNA and +ssRNA

viruses are associated with the dinoflagellate endosymbionts of corals. ISME J., 7(1): 13-27. doi:10.1038/ismej.2012.75

Data Processing Description

Approximately 2 ug of cDNA of each sample was pyrosequenced on a Roche Titanium 454 platform at the Broad Institute (Massachusetts Institute of Technology, Cambridge, MA, USA). SFF files were converted to FASTA and FASTAQ files, and each read was parsed and assigned an alphanumeric name. Reads were archived at the National Center for Biotechnology Information (NCBI) Sequence Read Archive (SRA) (ID SRA052068), as well as at CAMERA (IDs CAM_SMPL_000711 and CAM_SMPL_000712) (Sun et al., 2011) and MG-RAST (IDs 4455158.3 and 4455159.3).

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Parameters

Parameters for this dataset have not yet been identified

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Deployments

Vega_Thurber_Coral_Virus

Website	https://www.bco-dmo.org/deployment/558381
Platform	lab_FIU

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Project Information

Effects of Viruses on Coral Fitness (Coral Virus)

Coverage: St. Thomas, US Virgin Islands, USA; Heron Island, QLD, Australia; Orpheus Island, QLD, Australia; Kona ,Hawaii, USA; Moorea, French Polynesia.

Description from NSF Award Abstract:
Corals are important ecosystem engineers, providing habitat and nutrient recycling to tropical reefs. However, coral species richness and abundance are in decline world-wide, due in large part to anthropogenic impacts stemming from global industrialization and human population growth. Over the past several decades, global coral cover is estimated to have declined between ~20 to 60%, and approximately one-third of all known reef-building corals currently face an elevated risk of extinction. Coral disease is a major contributor to this decline of tropical reefs, and therefore, investigations into the causes of and remedies to these diseases are of critical importance. Currently little is known about viruses that infect corals. This project will address this issue.

Herpes-like viruses have been shown to be produced in coral tissues after acute episodes of stress.Viral diversity characterization, however, does not inform scientists about the effects of viral infection on coral hosts. This project will investigate whether viral infection in corals leads to disease and/or reductions in coral reproductive fitness. Specifically, this project aims to compare and contrast the relative abundance and diversity of viruses present in coral tissues during episodes of diseases, particularly, growth anomalies in Porites species and white plague disease in Montastraea species. Pyrosequencing of viral DNA will be conducted on healthy and diseased corals to: i) characterize new viral types, ii) determine whether viral types are associated with particular diseases, and iii) address the central hypothesis that viruses contribute to reduced coral fitness. Sequence analysis and functional annotation of coral viromes will determine the phylogenetic and evolutionary relationships of these viruses and identify viral mechanisms of host infection and

disease. The role of viruses in host fitness will be further explored using coral fecundity and larval survivorship and settlement experiments on the model coral, Acropora millepora. Viruses will be isolated from adults, egg bundles, and larvae, in order to determine the transmission mode and ontogenic fitness effects of viral infection.

This proposal will expand the coral taxa, diseases, developmental stages, and geographic regions from which viruses have been characterized, broadening our general knowledge about the diversity of these coral parasites. The examination of viral consortia in healthy and diseased corals combined with viral inoculation experiments will then take the next step and provide scientists clues about the ecological roles that viruses play in coral reef ecosystems. This combination of high-throughput sequencing and microscopy-based methods will lead to a more comprehensive picture of the diversity and role(s) of coral viruses in holobiont fitness and disease. Lastly, insight into how viruses are transmitted will give policymakers better information about how to control viral outbreaks, including limiting the spread of infection and disease.

Recent metagenomics work has begun to uncover unique viral assemblages associated with a variety of ecosystems. To a large extent, this work has focused on phages from the open ocean and temperate coasts. This project will use similar methods to investigate viruses in tropical stony corals, a group of highly threatened organisms which provide a multitude of ecosystem services to marine organisms and local communities. The characterization of viral consortia in healthy, diseased, and different life stages of corals will provide scientists clues about the roles that viruses play in the establishment, health, and resilience of these critical ecosystem engineers.

Note: Funding for this project has transferred from award OCE-0960937 to OCE-1242064, coincident with Principal Investigator's affiliation change.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1242064
NSF Division of Ocean Sciences (NSF OCE)	OCE-0960937

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