Pyrosequencing reads (454) of marine RNA virus metagenomes collected Kaneohe Bay, HI during 2009 (Diversity and ecology of marine RNA viruses project)

Website: https://www.bco-dmo.org/dataset/636479
Data Type: Other Field Results
Version: 2016-01-26

Project
» Diversity and ecology of marine RNA viruses (Diversity and ecology of marine RNA viruses)

Contributors	Affiliation	Role
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Dataset Description

This datasest links to accessions at the iMicrobe data repository containing fasta formatted nucleic acid sequences. Samples are from Surface waters of Kaneohe Bay, a tropical embayment on eastern shore of Oahu, HI, 21° 25’ 46.80” N, 157° 47’ 31.51” W.

Sample Name: CAM_SMPL_000815 (collected Aug 1, 2009)
Link: http://data.imicrobe.us/sample/view/333

Sample Name: CAM_SMPL_000824 (collected Jun 3, 2010)
Link: http://data.imicrobe.us/sample/view/324

Related References:

Culley AI, JA Mueller, M Belcaid, EM Wood-Charlson, G Poisson, GF Steward (2104). The characterization of RNA viruses in tropical seawater using targeted PCR and metagenomics. *mBio* 5(3):e01210-14. doi:10.1128/mBio.01210-14.

Steward GF, AI Culley, JA Mueller, EM Wood-Charlson, M Belcaid, G Poisson (2013). Are we missing half the viruses in the sea? *ISME Journal* 7(3) 627-679.

Methods & Sampling

454 Pyrosequencing on the GS FLX Titanium platform (Roche Diagnostics Corporation) was used to generate the sequence data.

Data Processing Description

Sequences were processed though the quality control pipeline of the RAST metagenomics server (http://metagenomics.anl.gov/?page=Home) to remove short and low-quality reads as well as artificial replicates.

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Data Files

File
virus_metagenome.csv (Comma Separated Values (.csv), 384 bytes) MD5:a6b7378f5e435b3b3b87252b1e046354 Primary data file for dataset ID 636479

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Parameters

Parameter	Description	Units
sample	sample description	unitless
sample_type	analysis type	unitless
date	collection date; local time	yyyy-mm-dd
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
temp	surface temperature	degrees Celsius
iMicrobe_accession	iMicrobe accession number with link	unitless

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	GS FLX Titanium platform (Roche Diagnostics Corporation)
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.

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Deployments

KaneoheBay_Steward

Website	https://www.bco-dmo.org/deployment/636485
Platform	lab UHawaii_SOEST
Start Date	2009-08-01
End Date	2010-06-03
Description	surface water samples for genomics studies

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Project Information

Diversity and ecology of marine RNA viruses (Diversity and ecology of marine RNA viruses)

Viruses are an integral component of the marine food web contributing to the disease and mortality of essentially every type of marine life, yet the diversity of marine viral assemblages remains very poorly characterized. This is especially true of the RNA-containing viruses. There are several reports of isolations of RNA-containing viruses that infect marine protists, but the number of isolates and the number of cultivation-independent surveys of RNA viral diversity are still very limited. Previous studies in coastal British Columbia and in coastal Oahu have shown RNA viruses are diverse and persistent in both temperate and tropical waters. Many of these novel gene sequences appear to derive from viruses of marine protists and their high diversity suggests that viral infections are a persistent force shaping protistan community composition in the sea. It is now clear that the few available isolates of marine RNA viruses are just the tip of the iceberg; novel RNA viruses are still being discovered with each new sample analyzed and the cultivated representatives are not adequately representative. Quantifying the abundance, diversity, and dynamics of these viruses, and obtaining additional representative isolates are some of the important first steps we need to take to incorporate the RNA viruses into the ecology of the sea. Our tasks in this project were to 1) determine the diversity of RNA viruses in coastal and offshore seawater 2) determine whether the RNA viruses make a significant numerical contribution to the total virus pool and 3) isolate and characterize new RNA viruses that infect phytoplankton.

We estimated the relative abundance of RNA viruses using RNA and DNA assays of purified and fractionated viral assemblages harvested from seawater and we characterized the genomic diversity of RNA viruses in a subtropical environment using a metagenomics approach. We found that RNA viruses are probably much more abundant than had been assumed. New bioinformatic tools and approaches specifically designed to handle metagenomic data were tested and implemented and should prove useful for characterizing short reads from viral metagenomic studies. We also initiated a cultivation effort and identified a large number of putative phytoplankton viruses. A number of these have now been confirmed to be viral. One of these has been confirmed to be an RNA-containing virus in the Order *Picornavirales* and its genome has been fully sequenced. This appears to be the first isolation of a virus infecting a pennate diatom. It is expected that the final output from this project will be of interest and value to researchers in a range of disciplines including microbial oceanographers, evolutionary biologists, virologists, and protistan ecologists.

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Funding

Funding Source	Award
NSF Division of Biological Infrastructure (NSF DBI)	DBI-0424599
NSF Division of Ocean Sciences (NSF OCE)	OCE-0826650
Gordon and Betty Moore Foundation (GBMF)	GBMF1799
National Institutes of Health (NIH)	NIH-P20GM103516
National Institutes of Health (NIH)	NIH-P20GM103466

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