Genbank accession numbers for genome sequences of cyanomyoviruses collected from the coastal waters of North America

Website: https://www.bco-dmo.org/dataset/658729
Data Type: Other Field Results
Version: 2
Version Date: 2021-06-10

Project
» Evolutionary ecology of marine cyanophages (Cyanophage Evolutionary Ecology)
» Cyanophage-Synechococcus interactions in complex communities (Cyanophage-Synechococcus interactions)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: **N**:48.5005 **E**:-70.4469 **S**:32.5593 **W**:-122.692
Temporal Extent: 2007-08-01 - 2010-09-30

Dataset Description

Cyanomyovirus auxiliary metabolic genome accessions at NCBI GenBank with links to accessions pages.

Related Dataset:
Cyanophage abundance: includes physical data and nutrients from samples collection sites

Methods & Sampling

Cyanomyoviruses were isolated on *Synechococcus* sp. WH7803 or WH8101 from surface seawater samples collected from Southern California (n=19) between 2008 and 2010; Padilla Bay, Washington (n=3) in August 2010; and Narragansett Bay, Rhode Island (n=108) from 1999 to 2015 as described in Clasen et al. (2013) and Marston et al. (2013).

Plaque-purified isolates were removed from 4°C storage and regrown on *Synechococcus* sp. WH7803 liquid culture. Phage genomic DNA was extracted as described in Henn et al. (2010). A genomic DNA library was prepared for Illumina sequencing as described in the “Low Sample (LS) Protocol” of the Illumina TruSeq DNA

sample prep kit. Samples were sequenced on an Illumina HiSeq2000 sequencer (single read, paired-end with 100 cycles) at the UCI Genomics High-throughput Facility or on a Illumina MiSeq at the Rhode Island Genomics and Sequencing Center at the University of Rhode Island.

Related references:

Clasen, J., Hanson, C., Ibrahim, Y., Weihe, C., Marston, M., Martiny, J., 2013. Diversity and temporal dynamics of Southern California coastal marine cyanophage isolates. Aquat Microb Ecol 69, 17-31.

Henn, M.R., Sullivan, M.B., Stange-Thomann, N., Osburne, M.S., Berlin, A.M., Kelly, L., Yandava, C., Kodira, C., Zeng, Q., Weiand, M., Sparrow, T., Saif, S., Giannoukos, G., Young, S.K., Nusbaum, C., Birren, B.W., Chisholm, S.W., 2010. Analysis of high-throughput sequencing and annotation strategies for phage genomes. PLoS ONE 5, e9083.

Marston, M. F., Taylor, S., Sme, N., Parsons, R., Noyes, T. J. E., and Martiny, J. B. H. (2013). Marine cyanophages exhibit local and regional biogeography. Environ. Microbiol. 15, 452–1463. doi: 10.1111/1462-2920.12062.

Data Processing Description

Genome assembly of paired-end reads was performed with CLC Genomics Workbench 6.0.2 software using the default software parameters or with the Geneious software package. Genome coverage (nucleotide redundancy) ranged from 2,000x – 8,000x. ORF calling and primary annotation of protein coding sequences (CDS) and transfer RNAs were performed using RAST.

BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date
- renamed parameters to BCO-DMO standard
- created links to NCBI accession pages
- added lat, lon, and site name

BCO-DMO data manager processing notes

* Version 2 (2021-06-10) replaces version 1 (2016-10-24). There was an unsupported character in the source file after accession URLs in the hyperlinks. Converted to utf-8 which resolved the problem.

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Data Files

File
cyanomyovirus_access.csv (Comma Separated Values (.csv), 22.10 KB) MD5:4ad0479c092bab4a90a76aa32ca3291b Primary data file for dataset ID 658729

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Parameters

Parameter	Description	Units
viral_isolate_name	viral isolate identification	unitless
Genbank_accession	NCBI GenBank accession number	unitless
site_code	collection site code	unitless
site_name	collection site name	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
isolation_date	isolation date	month-year

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina HiSeq2000 sequencer (single read, paired-end with 100 cycles) at the UCI Genomics High-throughput Facility or Illumina MiSeq at the Rhode Island Genomics and Sequencing Center at the University of Rhode Island.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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Deployments

lab_UCIrvine_Martiny

Website	https://www.bco-dmo.org/deployment/59027
Platform	Unknown Platform
Start Date	2007-11-15
End Date	2012-12-19
Description	Laboratory study: Abundance (estimated number of infecting particles per ml seawater and standard error) of cyanophages infecting laboratory strains of Synechococcus at three southern California locations. Four Synechococcus hosts were used at one site (Newport Beach), whereas only one host (WH7803) was used at two additional sites (Seal Beach and Crystal Cove). Date and time of sampling is recorded, along with various abiotic parameters including salinity, water temperature ("temp"), pH, air temperature, and nutrients (PO4, SiO4, NO2, NO3+NO2, NH4).

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Project Information

Evolutionary ecology of marine cyanophages (Cyanophage Evolutionary Ecology)

Website: http://jmartiny.bio.uci.edu/

Coverage: Pacific and Atlantic coasts of North America

ABSTRACT

The evolutionary ecology of virus-host interactions are key to understanding viral-induced mortality rates in marine ecosystems, as the pattern and dynamics of virus-host interactions will ultimately determine the influence of viruses on nutrient cycling. Recent studies suggest that the diversity and composition of marine viruses appears to vary over time and space. The goal of this research is to move beyond simply documenting biogeographic patterns in marine viruses and to begin to ask why the genetic composition of marine viruses varies over time and space. Part of the challenge in doing this is that little is known about how the genetic diversity of a marine virus relates to its phenotype. To address this challenge, the PIs are taking an isolation approach, using lytic cyanophages that infect marine *Synechococcus* as a model system. In this way they can compare the genotype and phenotype of each virus isolate.

There are three specific goals to do this: (1) Identify genetic markers of cyanophage host range (the particular hosts that a phage can infect); (2) Conduct a time-series study of cyanophage isolates from the Pacific and Atlantic coasts of North America; and (3) Using isolates from the time series, characterize cyanophage phenotypes.

Relevant References:

Marston, M., S. Taylor, N. Sme, R. Parsons, T. Noyes, J.B.H. Martiny. "Marine cyanophages exhibit local and regional biogeography," Environmental Microbiology, v.15, 2013, p. 1452.

Clasen J.L.*, C.A. Hanson*, Y. Ibrahim, C. Weihe, M.F. Marston, and J.B.H. Martiny. "Diversity and temporal dynamics of southern California coastal marine cyanophage isolates," Aquatic Microbial Ecology, v.69, 2013, p. 17.

Marston, M.F., F.J. Pierciey, A. Shepard, G. Gearin, J. Qi, C. Yandava, S.C. Schuster, M.R. Henn, J.B.H. Martiny. "Rapid diversification of coevolving marine Synechococcus and a virus," Proceedings of the National Academy of Sciences, v.109, 2012, p. 4544.

Hanson, C.A., J.A. Fuhrman, M.C. Horner-Devine, J.B.H. Martiny. "Beyond biogeographic patterns: processes shaping the microbial landscape," Nature Reviews Microbiology, v.10, 2012, p. 497.

Cyanophage-Synechococcus interactions in complex communities (Cyanophage-Synechococcus interactions)

Coverage: coastal locations in CA and RI

Description from NSF award abstract:
Viral-induced mortality of marine microorganisms alters the quantity and quality of pools of dissolved organic matter in the oceans, shuttling organic matter back into the microbial loop and away from the larger marine food web. A major hindrance to understanding the role of viruses in biogeochemical cycling is that we know surprisingly little about which viruses infect which bacteria in the marine environment. In this project, a network-based framework will be used to investigate marine phage-bacteria interactions in complex, multispecies communities. The research focuses on cyanophages, viruses that infect Synechococcus, an ecologically important cyanobacterium in the oceans. There are three parts of the project. The first part will identify genetic signatures of cyanophage-Synechococcus interactions by using laboratory evolution experiments and genomic sequencing. The second part will examine the temporal and spatial diversity of these candidate interaction genes in natural cyanophage populations, by comparing the full genome sequences of hundreds of isolates previously collected over many years. The third part will adapt the new method of viral-tagging to natural host populations to characterize cyanophage-Synechococcus interaction networks in the environment.

The role of viruses in global marine biogeochemical cycles depends on viral-induced mortality rates, which have been estimated to vary widely. The pattern and dynamics of who infects whom are central to our understanding of these rates as well as the role viruses play in marine nutrient cycling. This project will also contribute generally to our knowledge about viral diversity. The vast majority of marine viral sequences are not similar to any known diversity, and it is reasonable to conclude that many of these genes have to do with host recognition and infection. Finally, this project will develop a method of characterizing phage-bacteria interactions in natural, diverse microbial communities, thereby opening avenues for similar studies of viruses in other environments.

Note: This is an NSF Collaborative Research Project supported by OCE-1332740 (Lead PI Jennifer Martiny) and OCE-1332782 (Lead PI Marica Marston).

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Funding

Funding Source	Award
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NSF Division of Ocean Sciences (NSF OCE)	OCE-1332782

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