Experimental data: El Nino virus abundance from Southern California and Rhode Island coast from 2007-2013 (El Nino and virus diversity project, Cyanophage Evolutionary Ecology project)

Website: https://www.bco-dmo.org/dataset/3507
Version: 2
Version Date: 2021-06-08

Project
» El Nino and the controls of marine virus diversity (El Nino and virus diversity)
» Evolutionary ecology of marine cyanophages (Cyanophage Evolutionary Ecology)

Contributors	Affiliation	Role
Marston, Marcia	Roger Williams University (RWU)	Principal Investigator
Martiny, Jennifer B.H.	University of California-Irvine (UC Irvine)	Principal Investigator
Hughes, Bradley	University of California-Irvine (UC Irvine)	Co-Principal Investigator
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

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Coverage

Spatial Extent: **N**:41.6853 **E**:-71.2568 **S**:33.5735 **W**:-118.1078
Temporal Extent: 2007-11-15 - 2013-11-05

Dataset Description

Abundance (estimated number of infecting particles per ml seawater and standard error) of cyanophages infecting laboratory strains of *Synechococcus* at four southern California and three Rhode Island coastal locations. In California, four *Synechococcus* hosts were used at one site (Newport Beach), whereas only one host (WH7803) was used the other sites. In Rhode Island, *Synechococcus* WH7803 was used. Date and time of sampling is recorded, along with various abiotic parameters including salinity, water temperature, pH, air temperature, and nutrients (PO4, SiO4, NO2, NO3+NO2, NH4).

Related Dataset:
Cyanomyovirus genome sequences

Methods & Sampling

Viral abundance was estimated by Most Probable Number (MPN) assay as described in Marston and Sallee (2003) for the RI samples and Clasen et al (2013) for the CA samples. For the RI samples, the abundance of

cyanophages capable of infecting *Synechococcus* sp. WH7803 was estimated. For the CA samples, the abundance of cyanophages capable of infecting *Synechococcus* sp. WH7803, WH8012, WH8018, WH 8101 was estimated. A subsample (60ml) of each replicate seawater sample was centrifuged to remove large particles and bacteria, and the supernatant was serially diluted with sterile natural seawater media (SN media (Waterbury et al. 1986)). A 100µl aliquot of this diluted seawater was added to 100µl of exponentially a growing *Synechococcus* strain in each well of 48-well microtiter plates (except control wells which received no seawater). After a 30 - 60 min incubation at room temperature, 500 ul of sterile SN media was added to each well. Plates were then incubated for two weeks at 25°C on a 14:10 hr day:night cycle at 19µE m-2 s-1 light intensity. After 14 days, the plates were visually monitored for lysis (wells with less visible pigmentation than control host-only wells), and the total number of lysed wells was recorded. Estimates of the concentration of infectious cyanophages were determined using MPN Calculator software.

Nutrient samples were filtered and sent to UC Santa Barbara's Marine Science Institute for analysis. Values are the mean of two samples. Nutrient detection limits: Phosphate 0.10; Silicate 1.00; Nitrite 0.10; Nitrite+Nitrate 0.20; Ammonia 0.10; all units are micromolar.

Seawater was collected from the shore surf zone.

Metadata taken prior to March 2009 are scattered and may be unreliable.

Salinity measured using a handheld refractometer and may be high.

Most Probable Numbers of cyanophage abundance are based on 3 dilutions and an MPN calculator (e.g., http://www.i2workout.com/mcuriale/mpn/index.html).

For the CA sites, the MPN estimate is the average estimate calculated separately for the three replicates (using 48 wells for each of three dilutions), and standard errors for the mean value are reported.

For the RI sites, the MPN estimate is calculated by combining the results of all three replicates (a total of 30 wells for each of three dilutions), and the 95% CIs (as estimated by the MPN calculator) are reported.

Detection limits for nutrients are indicated at top of the file. Nutrient values are average of two replicates, and may include values that are below detection limits.

Related files and references:

Clasen, J.L., C.A. Hanson, Y. Ibrahim, C. Weihe, M.F. Marston, & J.B.H. Martiny (2013) Diversity and temporal dynamics of Southern California coastal marine cyanophage isolates. Aquatic Microbial Ecology, 69:17-31.

Marston and Sallee (2003) Applied and Environmental Microbiology 69: 4639-4647.

Data Processing Description

BCO-DMO data manager processing notes
* Version 2 (2021-06-08) replaces version 1 (2014-06-17). There was an unsupported character in the source file. Converted to utf-8 and made the following correction to the comment for readability. Also added parameter info for column yrday_local which was missing in version 1.

Corrected comment "Overcast��_still; findlly sunny at 9am" to :
Pacific NP 33.598372 -117.901203 2010 17-Nov-10 0830 11 17 320.3458 40 16.6 8.3 16.1 0.16 1.68 0.22 0.28 1.97 cyano_wh7803 91.67 24.25 nd nd Overcast still; finally sunny at 9am

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Data Files

File
virus_2014.csv (Comma Separated Values (.csv), 162.33 KB) MD5:3c07cbc31dcb23b2fe2bc3b09b229214 Primary data file for dataset ID 3507

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Parameters

Parameter	Description	Units
site	location of samples collection: BI=Balboa Island; SB=Seal Beach; NP=Newport Pier; CC=Crystal Cove	text
lat	latitude; postive is North	decimal degrees
lon	longitude; negative is West	decimal degrees
strain	bacterial strain of Synecoccus	text
year	year of sampling	YYYY
date_local	local date of sampling	dd-mmm-yy
time_local	local time of sampling	HH:MM
sal	salinity	parts per thousand
temp	temperature	degrees Celsius
pH_sw	seawater pH	pH scale
temp_air	air temperature	degrees Celsius
PO4	phosphate	micromoles/liter
SiO4	silicate	micromoles/liter
NO2	nitrite	micromoles/liter
NO3_NO2	nitrate plus nitrite	micromoles/liter
NH4	ammonia	micromoles/liter
comments	weather observations	text
abundance	Cyanophages infecting Syn strain	number per milliliter
std_err	standard error of abundance values	number
month_local	month of sampling, local time	
day_local	sampling day of month in local time	
basin	ocean basin where samples were collected	unitless
lower95bound	lower bound of the 95% confidence range	unitless
upper95bound	upper bound of the 95% confidence range	unitless
yrday_local	Yearday (local). Decimal day of the year.	

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Instruments

Dataset-specific Instrument Name	Refractometer
Generic Instrument Name	Refractometer
Dataset-specific Description	hand held, not highly accurate.
Generic Instrument Description	A refractometer is a laboratory or field device for the measurement of an index of refraction (refractometry). The index of refraction is calculated from Snell's law and can be calculated from the composition of the material using the Gladstone-Dale relation. In optics the refractive index (or index of refraction) n of a substance (optical medium) is a dimensionless number that describes how light, or any other radiation, propagates through that medium.

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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).

RWU_Marston_2014

Website	https://www.bco-dmo.org/deployment/516975
Platform	Marston_RI
Start Date	2009-06-30
End Date	2013-12-27

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Project Information

El Nino and the controls of marine virus diversity (El Nino and virus diversity)

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

In July 2009, the NOAA National Weather Service Climate Prediction Center announced the arrival of El Niño, an episode of abnormal warming of sea surface temperature (SST) in the equatorial Pacific that occurs every 3-8

years. This project will investigate the impact of El Niño on marine virus communities, using cyanophages that infect the cyanobacterium Synechoccocus as a model system. The upcoming El Niño presents an opportunity to advance research on the fundamental question of what drives temporal variability in cyanophage diversity.

The goals of this project are: (1) to disentangle various abiotic factors that influence cyanophage diversity and (2) to test the mechanisms behind temporal variability in cyanophage diversity, by comparing the evolutionary processes by which cyanophages adapt to temperature and host composition. To meet these objectives, ~150 cyanophage will be isolated monthly from three coastal sites in the Southern California Bight. The purified isolates will be characterized by sequencing their g20 gene. Phenotypic assays will be carried out on a selection of these isolates and isolates from the previous non-El Niño years.

The environmental variability that El Niño will provide is crucial to both parts of this project. It will help to disentangle the effect of covarying factors on in situ cyanophage composition. For instance, in Southern California, El Niño should provide higher-than-normal SST during months of relatively low UV intensity (fall and winter). It will also permit isolation of a broader genetic diversity of cyanophages from a wider array of environmental conditions, providing crucial statistical power to the laboratory experiments. The project will further our mechanistic understanding of the controls of marine virus diversity.

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.

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