Accession numbers of viral metagenomes from samples collected in the Eastern Tropical North Pacific oxygen minimum zone region (ETNP OMZ) on R/V New Horizon cruise NH1315 during June 2013

Website: https://www.bco-dmo.org/dataset/823295
Data Type: Cruise Results
Version: 1
Version Date: 2020-09-04

Project
» Ecology and biogeochemical impacts of viruses in marine oxygen minimum zones (OMZ Viruses)

Contributors	Affiliation	Role
Brum, Jennifer R.	University of Arizona (UA)	Principal Investigator
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Accession numbers of viral metagenomes from samples collected in the Eastern Tropical North Pacific oxygen minimum zone region (ETNP OMZ) on R/V New Horizon cruise NH1315 from 13-28 June 2013.

Table of Contents

Coverage

Spatial Extent: **N**:18.92018 **E**:-104.88952 **S**:18.91944 **W**:-108.79926
Temporal Extent: 2013-06-19 - 2013-06-22

Dataset Description

Accession numbers of viral metagenomes from samples collected in the Eastern Tropical North Pacific oxygen minimum zone region (ETNP OMZ) on R/V New Horizon cruise NH1315 from 13-28 June 2013.

Acquisition Description

Detailed protocols, including suggestions from the scientific community, are published on the lab website at https://u.osu.edu/viruslab/protocols/ and maintained on protocols.io at https://www.protocols.io/workspaces/sullivan-lab.

Samples were collected from the Eastern Tropical North Pacific oxygen minimum zone region (ETNP OMZ) during the OMZ Microbial Biogeochemistry Expedition cruise (R/V NewHorizon,13-28 June 2013). Seawater was collected from 16 depths spanning the mixed layer, oxycline, OMZ core, and below the OMZ. Collections were made using Niskin bottles on a rosette. Samples were preserved with EM-grade glutaraldehyde (2% final concentration), flash-frozen in liquid nitrogen and stored between -72 °C and -80 °C until analysis.

After resuspension in ascorbic-EDTA buffer (0.1 M EDTA, 0.2 M Mg, 0.2 M ascorbic acid, pH 6.0), viral particles were concentrated using Amicon Ultra 100-kD cen- trifugal devices (Millipore), treated with DNase I (100 U/mL) followed by the addition of 0.1 M EDTA and 0.1 M EGTA to halt enzyme activity, and extracted. Viral particle suspensions were treated with Wizard Polymerase Chain Reaction Preps DNA Purification Resin (Promega, Fitchburg, WI, USA) at a ratio of 0.5 ml sample to 1 ml resin, and eluted with TE buffer (10 mM Tris, pH 7.5, 1 mM EDTA) using Wizard Minicolumns. Extracted DNA was Covaris-sheared and size-selected to 160 to 180 bp, followed by amplification and ligation per the standard Illumina protocol. Sequencing was done on a HiSEq 2000 system at the DOE Joint Genome Institute.

[table of contents | back to top]

Related Publications

Brum, J. (2015). Concentrating Viruses with an Amicon or Nanosep Centrifugal Ultrafiltration Device v1. Protocols.io. doi:10.17504/protocols.io.c54y8v
Methods

John, S. G., Mendez, C. B., Deng, L., Poulos, B., Kauffman, A. K. M., Kern, S., … Sullivan, M. B. (2010). A simple and efficient method for concentration of ocean viruses by chemical flocculation. Environmental Microbiology Reports, 3(2), 195–202. doi:10.1111/j.1758-2229.2010.00208.x
Methods

[table of contents | back to top]

Parameters

Parameter	Description	Units
SAMPLE	unique sample identification	unitless
JGI_Project_Id	JGI project ID number	unitless
IMG_Genome_ID	IMG genome ID number	unitless
LAT	latitude	degrees North
LONG	longitude	degrees East

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Niskin bottles
Generic Instrument Name	Niskin bottle
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

Dataset-specific Instrument Name	Illumina HiSEq 2000
Generic Instrument Name	Automated DNA Sequencer
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.

[table of contents | back to top]

Deployments

NH1315

Website	https://www.bco-dmo.org/deployment/628427
Platform	R/V New Horizon
Start Date	2013-06-13
End Date	2013-06-28
Description	Oxygen Minimum Zone Microbial Biogeochemistry Expedition (OMZoMBiE) Proposed Sampling Stations Cruise information and original data are available from the NSF R2R data catalog.

[table of contents | back to top]

Project Information

Ecology and biogeochemical impacts of viruses in marine oxygen minimum zones (OMZ Viruses)

NSF Award Abstract: Marine oxygen minimum zones (OMZs) are regions of the world's oceans that have low or no oxygen. Often referred to as "dead zones" because of their lack of larger organisms, OMZs actually support specific microbial communities adapted to survive in these low-oxygen regions. These microbes perform metabolic processes that produce greenhouse gases such as methane, and significantly alter global nitrogen budgets. In turn, viruses can alter every aspect of microbial communities by causing mortality and altering microbial functions; yet we know little regarding how viruses affect OMZ ecosystems, which is limiting our ability to predict future changes to the Earth system as these OMZs expand over time. This proposed research seeks to fill this knowledge gap by examining the types of viruses that are present in OMZs, as well as how they alter microbial communities and their impact on global processes. In the broader perspective, this proposed work will provide extensive datasets for 7 marine OMZ regions that can be interrogated through publically-available analysis tools, thus enabling environmental science for both research and educational purposes including real-world research experience in undergraduate classes to strengthen scientific education. One postdoc, two graduate students, and undergraduate students will be trained and mentored during this project. Furthermore, the work will facilitate international collaboration with leading microbial oceanographers from across the world. This project will use recent advances in quantitative environmental viral analysis to rapidly enhance our knowledge of OMZ viral communities through examination of 100s of samples from 7 globally-distributed marine OMZ regions with varying levels of oxygen depletion. The specific aims of the project are to (i) gain a basic understanding of viral abundances, viral-induced microbial mortality, and viral community structure, as well as the environmental conditions that drive differences in these parameters, and (ii) assess the effects of viruses on nutrient and gas cycling in OMZs. These aims will be accomplished through analyzing viral metagenomes to assess how viral communities differ among the 7 diverse OMZ regions, and how they diverge from communities in oxygenated waters. Further, the viral metagenomes will be coupled with microbial metagenomes to assess virus-host dynamics and the effects of viral-induced mortality on microorganisms performing key metabolic functions. Finally, the abundance and expression of viral-encoded metabolic genes will be used to perform gene-based biogeochemical modeling to determine the extent of viral influences in OMZ biogeochemical cycling.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1658040

[table of contents | back to top]