

Collection information and genetic accession identifiers for Single Amplified Virus Genomes from hydrothermal fluids at IODP HOLE U1362B CORK observatory from R/V Atlantis cruise AT18-07 ROV Jason dives at the Juan de Fuca Ridge Flank in July of 2011

Website: <https://www.bco-dmo.org/dataset/717763>

Data Type: Cruise Results

Version: 2

Version Date: 2022-05-23

Project

» [Viral genetic richness and functions that shape the microbial community at the Juan de Fuca Ridge](#) (Juan de Fuca Viruses)

Program

» [Center for Dark Energy Biosphere Investigations](#) (C-DEBI)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: Lat:47.75833 Lon:-127.76219

Temporal Extent: 2016-03-11

Dataset Description

This dataset contains information related to Single Amplified Virus Genomes originated from hydrothermal fluids collected at a deep-sea subsurface observatory. The accession numbers included in the dataset correspond to genetic sequences at the National Center for Biotechnology Information (NCBI, <https://www.ncbi.nlm.nih.gov/>). Genetic accessions are available at NCBI under BioProject [PRJNA398661](#).

The sampling location was the Integrated Ocean Drilling Program (IODP) Hole U1362B seafloor borehole ("CORK") observatory located at the Juan de Fuca Ridge Flank (47.75833, -127.76219) at a depth of 2658 m (280 m below seafloor). The samples were collected during ROV Jason dives conducted from the R/V Atlantis cruise AT18-07 on July 8th, 2011.

Methods & Sampling

Sampling and Analytical Methodology:

Deep-sea hydrothermal fluid samples were collected from the IODP Hole U1362B CORK observatory using a custom syringe sampler fired in the 'shimmering' effluent of a free-flow chimney connected to the ball valve of the CORK well-head. Upon recovery, fluids for this project were fixed with a glycerol Tris-EDTA buffer for subsequent single virus sorting and genomic analysis. Single virus-like particles were sorted separately by fluorescence activated sorting. DNA was amplified by Multiple Displacement Amplification.

Data Processing Description

BCO-DMO Data Manager Processing Notes:

- * added a conventional header with dataset name, PI name, version date
- * modified parameter names to conform with BCO-DMO naming conventions
- * Since data are now public at NCBI, added columns Sample_Name, BioSample, SRA, Organism and remove Submission identifier.
- * Added columns Lat, Lon to data table from metadata information.

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Data Files

File
viruses.csv (Comma Separated Values (.csv), 2.85 KB) MD5:6a47d8e601385f9fd9fa83e829e212d1 Primary data file for dataset ID 717763

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Related Datasets

IsRelatedTo

Bigelow Laboratory for Ocean Sciences (2017). Viral genetic richness and functions that shape the microbial community at the Juan de Fuca Ridge. NCBI:BioProject: PRJNA398661. 2017/08. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information (NCBI); Available from: <http://www.ncbi.nlm.nih.gov/bioproject/PRJNA398661>

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Parameters

Parameter	Description	Units
Species_Name	Species Name	unitless
Sample_Name	Sample Name	unitless
BioSample	NCBI BioSample accession	unitless
SRA	NCBI Sequence Read Archive Sample accession	unitless
NCBI_BioProject	NCBI BioProject accession	unitless
Types_of_Sequences	Sequence type (e.g. dsDNA genome)	unitless
Location_collected	Geolocation of collection	unitless
Lat	Latitude of collection	decimal degrees
Lon	Longitude of collection	decimal degrees
Date_Collected	Collection date in ISO 8601 format YYYY-MM-DD	unitless
Sequencing_method	Sequencing method	unitless
Analysis_method	Analysis method	unitless
Organism	Organism (e.g. viral metagenome)	unitless
Description	Description	unitless

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Deployments

AT18-07

Website	https://www.bco-dmo.org/deployment/660555
Platform	R/V Atlantis
Start Date	2011-06-29
End Date	2011-07-14

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Project Information

Viral genetic richness and functions that shape the microbial community at the Juan de Fuca Ridge (Juan de Fuca Viruses)

Coverage: IODP Hole U1362B CORK observatory at the Juan de Fuca Ridge (JFR) eastern flank

Project abstract from [C-DEBI](#):

Deep-sea subsurface habitats support novel and abundant microbial life. Recently, several studies have explored the phylogenetic diversity of microorganisms, mostly bacteria and archaea, in those environments. Viruses are key components of microbial assemblages, hence, the need to investigate them to better understand the deep biosphere's ecology. In this study, we performed genomic analysis of 27 targeted flow cytometry-sorted viruses and 3 microbial cells from a one-milliliter hydrothermal fluid sample collected from IODP Hole U1362B CORK observatory at the Juan de Fuca Ridge (JFR) eastern flank. Preliminary results revealed a diverse viral community, as no two sorted viruses were identical to each other. The majority of predicted genes within the partially-sequenced viral genomes had no homology in databases. Phylogenetic analysis of the identified viral genes indicated that the viruses were most similar to large inducible lysogenic myoviruses. Additionally, the discovery of a cell from benthic group E (*Euryarchaeota*), a key member of the microbial community, containing a prophage in its genome supports the hypothesis that lysogeny is likely more pervasive than lytic infections in the deep biosphere. However, these results might reflect inherited flow

cytometry and nucleic acids multiple displacement amplification biases toward large dsDNA viruses (e.g. myoviruses). On the other hand this approach allows investigating larger viruses typically removed by filtration in traditional metagenomics studies, and thus aids in providing a more complete picture of viral assemblages. This exploratory proposal is in line with two of the four C-DEBI research themes: Extent of Life, and Evolution and Survival.

This project was funded by a [C-DEBI Research Grant](#).

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Program Information

Center for Dark Energy Biosphere Investigations (C-DEBI)

Website: <http://www.darkenergybiosphere.org>

Coverage: Global

The mission of the Center for Dark Energy Biosphere Investigations (C-DEBI) is to explore life beneath the seafloor and make transformative discoveries that advance science, benefit society, and inspire people of all ages and origins.

C-DEBI provides a framework for a large, multi-disciplinary group of scientists to pursue fundamental questions about life deep in the sub-surface environment of Earth. The fundamental science questions of C-DEBI involve exploration and discovery, uncovering the processes that constrain the sub-surface biosphere below the oceans, and implications to the Earth system. What type of life exists in this deep biosphere, how much, and how is it distributed and dispersed? What are the physical-chemical conditions that promote or limit life? What are the important oxidation-reduction processes and are they unique or important to humankind? How does this biosphere influence global energy and material cycles, particularly the carbon cycle? Finally, can we discern how such life evolved in geological settings beneath the ocean floor, and how this might relate to ideas about the origin of life on our planet?

C-DEBI's scientific goals are pursued with a combination of approaches:

- (1) coordinate, integrate, support, and extend the research associated with four major programs—Juan de Fuca Ridge flank (JdF), South Pacific Gyre (SPG), North Pond (NP), and Dorado Outcrop (DO)—and other field sites;
- (2) make substantial investments of resources to support field, laboratory, analytical, and modeling studies of the deep subseafloor ecosystems;
- (3) facilitate and encourage synthesis and thematic understanding of submarine microbiological processes, through funding of scientific and technical activities, coordination and hosting of meetings and workshops, and support of (mostly junior) researchers and graduate students; and
- (4) entrain, educate, inspire, and mentor an interdisciplinary community of researchers and educators, with an emphasis on undergraduate and graduate students and early-career scientists.

Note: Katrina Edwards was a former PI of C-DEBI; James Cowen is a former co-PI.

Data Management:

C-DEBI is committed to ensuring all the data generated are publically available and deposited in a data repository for long-term storage as stated in their [Data Management Plan \(PDF\)](#) and in compliance with the [NSF Ocean Sciences Sample and Data Policy](#). The data types and products resulting from C-DEBI-supported research include a wide variety of geophysical, geological, geochemical, and biological information, in addition to education and outreach materials, technical documents, and samples. All data and information generated by C-DEBI-supported research projects are required to be made publically available either following publication of research results or within two (2) years of data generation.

To ensure preservation and dissemination of the diverse data-types generated, C-DEBI researchers are working with BCO-DMO Data Managers make data publicly available online. The partnership with BCO-DMO helps ensure that the C-DEBI data are discoverable and available for reuse. Some C-DEBI data is better served by specialized repositories (NCBI's GenBank for sequence data, for example) and, in those cases, BCO-DMO

provides dataset documentation (metadata) that includes links to those external repositories.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0939564

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