

Genome sequence for the virus ANMV-1 from the R/V Atlantis AT15-53 cruise in the Santa Monica Basin during 2009 (Viruses in Methanotrophic Marine Ecosystems project)

Website: <https://www.bco-dmo.org/dataset/633022>

Version: 19 January 2016

Version Date: 2016-01-19

Project

» [Dimensions: The Role of Viruses in Structuring Biodiversity in Methanotrophic Marine Ecosystems](#) (Viruses in Methanotrophic Marine Ecosystems)

Program

» [Dimensions of Biodiversity](#) (Dimensions of Biodiversity)

Contributors	Affiliation	Role
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Dataset Description

Assembled genome sequence for the virus, ANMV-1, from marine sediments at a methane seep in the Santa Monica Basin and with a putative archaeal host.

Location:

Pacific Ocean: Santa Monica Basin, offshore California; Depth 820m; Lat. 33.799N, Long. 118.646W

Related files and references:

Henn, M. R., Sullivan, M. B., Stange-Thomann, N., Osburne, M. S., Berlin, A. M., Kelly, L., ... Chisholm, S. W. (2010). Analysis of High-Throughput Sequencing and Annotation Strategies for Phage Genomes. PLoS ONE, 5(2), e9083. doi:10.1371/journal.pone.0009083

Paul, B. G., Bagby, S. C., Czornyj, E., Arambula, D., Handa, S., Sczyrba, A., ... Valentine, D. L. (2015). Targeted diversity generation by intraterrestrial archaea and archaeal viruses. Nature Communications, 6(1). doi:10.1038/ncomms7585

Methods & Sampling

Sampling and Analytical Methodology:

Metagenomic sequencing was performed at the Broad Institute on 454-FLX plates, as part of the Gordon and Betty Moore Marine Phage Metagenome Initiative (Henn et al. 2010). Detailed methods on processing of metagenomic sequences, assembly, and genome annotation are described in Paul et al. (2015).

Data Processing Description

Data Processing:

Sediment metagenome ANM1 consists of raw reads from 454-FLX sequencing. To procure the ANMV-1 genome, metagenomic reads were first preprocessed, then assembled as described in Paul et al. (2015).

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Data Files

File
ANMV-1.csv (Comma Separated Values (.csv), 388 bytes) MD5:51e5a187c5f6493692185691ddf54208
Primary data file for dataset ID 633022

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Related Publications

Henn, M. R., Sullivan, M. B., Stange-Thomann, N., Osburne, M. S., Berlin, A. M., Kelly, L., ... Chisholm, S. W. (2010). Analysis of High-Throughput Sequencing and Annotation Strategies for Phage Genomes. PLoS ONE, 5(2), e9083. doi:[10.1371/journal.pone.0009083](https://doi.org/10.1371/journal.pone.0009083)

Results

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Methods

Paul, B. G., Bagby, S. C., Czornyj, E., Arambula, D., Handa, S., Sczyrba, A., ... Valentine, D. L. (2015). Targeted diversity generation by intraterrestrial archaea and archaeal viruses. Nature Communications, 6(1).

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Results

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Methods

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Parameters

Parameter	Description	Units
CruiseId	Official UNOLS Cruise Id	text
Site	Site Id	text
Site_Description	Site Description	text
Collection_Date	Collection Date	DD-Mon-YYYY
Latitude	Latitude (South is negative)	decimal degrees
Longitude	Longitude (West is negative)	decimal degrees
Depth	Depth	meters
Description	Sample Description	text
Accession	Accession Id	text
Version	Version	text
Link	Link to Accession in Genbank	text

Deployments

AT15-53

Website	https://www.bco-dmo.org/deployment/632876
Platform	R/V Atlantis
Start Date	2009-09-13
End Date	2009-09-29

Project Information

Dimensions: The Role of Viruses in Structuring Biodiversity in Methanotrophic Marine Ecosystems (Viruses in Methanotrophic Marine Ecosystems)

Marine methanotrophic ecosystems are responsible for consuming around 75 Tg of methane annually, preventing this potent greenhouse gas from entering the atmosphere. These microbial ecosystems thus play a vital role in the global climate system. The nature of these communities depends on the presence or absence of oxygen: methanotrophy is a bacterial lifestyle in aerobic shallow sediments, but in deeper anaerobic sediments it is the exclusive province of archaea, in syntrophy with sulfate-reducing bacteria. It is known which phyla are most commonly found in methanotrophic environments. However, because of these environments' physical inaccessibility and because nearly all microbes from these systems have resisted cultivation, understanding of these communities lags far behind their importance. The cultivation-resistance of microbial hosts from these systems has additionally prevented the use of classical methods to study the viral community. Thus, to date science is largely unable to fill in the broad outlines of marine methanotrophic biodiversity, to fully describe the microbial communities or determine what shapes them.

This project seeks to define the importance of viruses in structuring functional, genetic, and taxonomic diversity in methanotrophic marine ecosystems. The underlying assertion is that viruses structure the diversity of archaeal and bacterial communities in these ecosystems by causing both mortality and horizontal gene transfer. To establish viral contributions to biodiversity of aerobic and anaerobic marine methanotrophic ecosystems, this project combines biogeochemical, genomic, and metagenomic approaches, in both field and laboratory settings.

The project first seeks to assess viral activity in situ by extending established stable isotope probing techniques to quantify rates of viral production at sea floor methane seeps. The same techniques will be used to track the flow of carbon from methane to microbes to viruses and to isolate genetic material from just those organisms that actively cycle methane-derived carbon, enabling the production of microbial and viral metagenomes that are anchored in ecosystem function. Comparisons among these metagenomes will reveal any functional sequences in transit between organisms, providing the basis for an evaluation of the relationships between functional and genetic diversity. At the same time, single-cell whole-genome amplification will pinpoint individual cells for comparison with the microbial and viral assemblages, permitting assessment of the relationships between taxonomic and genetic diversity. Last, the comparison of genomic and metagenomic data both within and across distinctive marine methanotrophic ecosystems will enable analysis of the relationship between functional and taxonomic diversity.

Program Information

Dimensions of Biodiversity (Dimensions of Biodiversity)

Website: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446

Coverage: global

(adapted from the NSF Synopsis of Program)

Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [\[MORE from NSF\]](#)

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1046144

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