

# Assessments of bacterial and archaeal diversity from three distinct hydrothermal vents in the Middle Valley vent field along the Juan de Fuca Ridge from R/V Atlantis cruise AT15-67 in the Juan de Fuca Ridge in 2010

**Website:** <https://www.bco-dmo.org/dataset/626625>

**Version:** 17 November 2015

**Version Date:** 2015-11-17

## Project

» [Characterizing the distribution and rates of microbial sulfate reduction at Middle Valley hydrothermal vents](#) (Middle Valley Vents)

## Program

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

Contributors	Affiliation	Role
<a href="#">Girguis, Peter</a>	Harvard University	Principal Investigator
<a href="#">Frank, Kiana</a>	University of Hawai'i at Mānoa (SOEST)	Contact
<a href="#">Rauch, Shannon</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Table of Contents

- [Dataset Description](#)
  - [Methods & Sampling](#)
  - [Data Processing Description](#)
- [Data Files](#)
- [Parameters](#)
- [Deployments](#)
- [Project Information](#)
- [Program Information](#)
- [Funding](#)

## Dataset Description

Assessments of bacterial and archaeal diversity from three distinct hydrothermal vents in the Middle Valley vent field along the Juan de Fuca Ridge. Samples were recovered from actively venting sulfide deposits in the Middle Valley vent field along the Juan de Fuca Ridge at Needles (48.45778, -128.709), Dead Dog (48.45603, -128.71), and Chowder Hill (48.455543, -128.709) vents.

*Analysis and write up of these data can be found at:*

Frank, K.L., Rogers, D. R., Olins, H. C., Vidoudez, C., & Girguis, P. R. 2013. Characterizing the distribution and rates of microbial sulfate reduction at Middle Valley hydrothermal vents. The ISME journal, 7, 1391-1401.

doi:[10.1038/ismej.2013.17](https://doi.org/10.1038/ismej.2013.17)

## Methods & Sampling

**Sampling and Analytical Methodology:** Once on board ship, samples were directly transferred to sterile anaerobic seawater and handled/processed using appropriate sterile microbiological techniques. DNA was extracted from this crushed deposit sample with a protocol modified from (Santelli et al. 2008). Subsamples were washed with 0.1 N HCl, followed by two rinses with a sterile solution containing 10 mM Tris (pH 8.0) and 50 mM EDTA. A known mass of material was added to PowerSoil beadbeating tubes (MoBio Laboratories, Carlsbad CA), incubated at 70 degrees C for 10 minutes, and then amended with 200 ng of poly-A. Subsamples were subjected to beadbeating, followed by three cycles of freeze-thaw steps to further lyse cells.

Nucleic acids were extracted using hot phenol (60 degrees C for 3 min.), followed by two chloroform:isoamyl separations and precipitated with ethanol. DNA was resuspended in TE (pH 8.0) and quantified using the Qubit™ fluorometer (Life Technologies, Grand Island, NY).

## Data Processing Description

**Data Processing:** DNA samples were sequenced using 454 pyrotag methods similar to those described previously (Dowd et al. 2008). All samples were sequenced at the Research and Testing Laboratory (Lubbock, TX) using a 454FLX instrument (Roche Inc.) with Titanium™ reagents. The resulting bacterial and archaeal 16S rRNA (bacterial V1-V3 and archaeal V3-V4 of the 16S rRNA genes; primers are shown in Table 1) as well as dsrB sequences were analyzed via Mothur (Schloss et al. 2009). Sequences were trimmed, quality checked, aligned to the SILVA-compatible alignment database reference alignment (dsrB gene datasets were aligned to a dsrB gene database generated from the Ribosomal Database Project (RDP)), analyzed for chimeras, classified against the Greengenes99 database and clustered in to OTUs. Rarefaction curves were used to examine the number of OTUs as a function of sampling depth. Alpha diversity was assessed by generating values from the Chao1 richness estimators and the inverse Simpson diversity index.

[ [table of contents](#) | [back to top](#) ]

---

## Data Files

File
<b>MV_sequences.csv</b> (Comma Separated Values (.csv), 2.17 KB) MD5:a8736b177b019e4f5af01460dbed2022
Primary data file for dataset ID 626625

[ [table of contents](#) | [back to top](#) ]

---

## Parameters

Parameter	Description	Units
accession_num	NCBI accession number.	dimensionless
sample_name	GenBank sample number.	dimensionless
organism	Organism name/description.	dimensionless
sample	Sample (site) name.	dimensionless
accession_link	Hyperlink to NCBI for the accession number.	dimensionless
description	Description of the sequence.	dimensionless

[ [table of contents](#) | [back to top](#) ]

---

## Deployments

## AT15-67

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/626312">https://www.bco-dmo.org/deployment/626312</a>
<b>Platform</b>	R/V Atlantis
<b>Start Date</b>	2010-07-06
<b>End Date</b>	2010-07-26

[ [table of contents](#) | [back to top](#) ]

---

## Project Information

### Characterizing the distribution and rates of microbial sulfate reduction at Middle Valley hydrothermal vents (Middle Valley Vents)

**Coverage:** Middle Valley vent field along the Juan de Fuca Ridge

This project characterizes rates of microbially mediated sulfate reduction from three distinct hydrothermal vents in the Middle Valley vent field along the Juan de Fuca Ridge, as well as assessments of bacterial and archaeal diversity, estimates of total biomass and the abundance of functional genes related to sulfate reduction, and in situ geochemistry. Maximum rates of sulfate reduction occurred at 90°C in all three deposits. Pyrosequencing and functional gene abundance data reveal differences in both biomass and community composition among sites, including differences in the abundance of known sulfate reducing bacteria. The abundance of sequences for Thermodesulfobrio-like organisms and higher sulfate reduction rates at elevated temperatures, suggests that Thermodesulfobrio-like organisms may play a role in sulfate reduction in warmer environments. The rates of sulfate reduction observed suggest that - within anaerobic niches of hydrothermal deposits - heterotrophic sulfate reduction may be quite common and might contribute substantially to secondary productivity, underscoring the potential role of this process in both sulfur and carbon cycling at vents.

This project was funded, in part, by a C-DEBI Graduate Student Fellowship.

[ [table of contents](#) | [back to top](#) ]

---

## 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 seafloor 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.

[ [table of contents](#) | [back to top](#) ]

---

## **Funding**

<b>Funding Source</b>	<b>Award</b>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1061934</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-0838107</a>
NASA Astrobiology Science & Technology for Exploring Planets (NASA-ASTEP)	<a href="#">NNX09AB78G</a>
NASA Astrobiology Science & Technology for Exploring Planets (NASA-ASTEP)	<a href="#">NNX07AV51G</a>

[ [table of contents](#) | [back to top](#) ]