

# Samples sequenced from chemosynthetic biofilm communities in deep-sea hydrothermal vents collected on the R/V Atlantis AT26-10 in the East Pacific Rise, Pacific Ocean from 2013 - 2014 (Microbial Communities at Deep-Sea Vents project)

**Website:** <https://www.bco-dmo.org/dataset/549138>

**Version:** 2015-02-10

## Project

» [An Integrated Study of Energy Metabolism, Carbon Fixation, and Colonization Mechanisms in Chemosynthetic Microbial Communities at Deep-Sea Vents](#) (Microbial Communities at Deep-Sea Vents)

## Programs

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

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

Contributors	Affiliation	Role
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## Dataset Description

This dataset is a sample log of sequenced samples collected by ROV/Jason in the East Pacific Rise, Pacific Ocean. The taxonomic composition of the active microbial community present in biofilm and fluid samples was investigated by sequencing 16S rRNA transcripts.

## Methods & Sampling

Samples were collected at several sites along the East Pacific Rise hydrothermal vent zone. They included ROV/Jason deployments J2-758, J2-759, J2-760, J2-761, J2-762.

About 1 GB of raw sequence data (bacterial ssrRNA) was obtained using the Ion Torrent platform from total RNA extracted from sixteen microbial biofilm samples characterized by different temperature, redox and biological regimes. Samples included background references. Sequence data are currently being analyzed and will be deposited in GenBank prior to publication and will be made available to the scientific community. [2015-02-04]

The use of rRNA transcripts instead of DNA will allow us to identify the fraction of the population actively transcribing *in situ*. Sixteen microbial biofilm samples characterized by different temperature, redox and biological regimes were used. These samples included biofilm formed on experimental colonizers deployed at

selected vents to obtain early stage biofilm. A comparison of early stage and established biofilms will help to understand how the community changes in relation to biofilm age and geochemical regimes.

## Data Processing Description

We have optimized a RNA extraction protocol from biofilm biomass using the RNeasy kit (Qiagen). Following extraction and DNase treatment, we generated cDNA using random primers (SuperScript III First-Strand kit). cDNA from biofilm and fluid samples was used to amplify the 16S rRNA gene with tagged primers and subjected to sequencing. Obtained sequences are currently being analyzed using the QIIME pipeline. The reads are being dereplicated, denoised, screened for chimeric sequences and taxonomically classified using the RDP and GreenGenes databases. Multivariate ordination techniques will be used to discriminate among samples with similar community structures.

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## Data Files

File
<b>AT26-10_samples.csv</b> (Comma Separated Values (.csv), 2.53 KB) MD5:d459044b425e22288c6c1fa6d0bba85
Primary data file for dataset ID 549138

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## Parameters

Parameter	Description	Units
sample_num	sample number	unitless
cruise_id	cruise identification	unitless
dive	Alvin or Jason dive number	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
date	date of collection	yyyy-mm-dd
habitat	habitat at collection site	unitless
site	name of collection site	unitless
sample	sample identification	unitless
sample_description	sample description	unitless
collection_method	how sample was collected	unitless
nucleic_acid	type of nucleic acid measured	unitless
nucleic_acid_conc	total concentration of the nucleic acid	ng/uL
cDNA	concentration of cDNA	ng/uL

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## Instruments

<b>Dataset-specific Instrument Name</b>	Automated Sequencer
<b>Generic Instrument Name</b>	Automated DNA Sequencer
<b>Dataset-specific Description</b>	Ion Torrent next-generation sequencing platform
<b>Generic Instrument Description</b>	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.

<b>Dataset-specific Instrument Name</b>	McLane Pump
<b>Generic Instrument Name</b>	McLane Pump
<b>Dataset-specific Description</b>	Large Volume Pump (LVP): McLane WTS 6-1-142LV
<b>Generic Instrument Description</b>	McLane pumps sample large volumes of seawater at depth. They are attached to a wire and lowered to different depths in the ocean. As the water is pumped through the filter, particles suspended in the ocean are collected on the filters. The pumps are then retrieved and the contents of the filters are analyzed in a lab.

<b>Dataset-specific Instrument Name</b>	ROV Jason
<b>Generic Instrument Name</b>	ROV Jason
<b>Generic Instrument Description</b>	The Remotely Operated Vehicle (ROV) Jason is operated by the Deep Submergence Laboratory (DSL) at Woods Hole Oceanographic Institution (WHOI). WHOI engineers and scientists designed and built the ROV Jason to give scientists access to the seafloor that didn't require them leaving the deck of the ship. Jason is a two-body ROV system. A 10-kilometer (6-mile) fiber-optic cable delivers electrical power and commands from the ship through Medea and down to Jason, which then returns data and live video imagery. Medea serves as a shock absorber, buffering Jason from the movements of the ship, while providing lighting and a bird's eye view of the ROV during seafloor operations. During each dive (deployment of the ROV), Jason pilots and scientists work from a control room on the ship to monitor Jason's instruments and video while maneuvering the vehicle and optionally performing a variety of sampling activities. Jason is equipped with sonar imagers, water samplers, video and still cameras, and lighting gear. Jason's manipulator arms collect samples of rock, sediment, or marine life and place them in the vehicle's basket or on "elevator" platforms that float heavier loads to the surface. More information is available from the operator site at <a href="#">URL</a> .

## Deployments

### AT26-10

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/529031">https://www.bco-dmo.org/deployment/529031</a>
<b>Platform</b>	R/V Atlantis
<b>Report</b>	<a href="http://dmoserv3.bco-dmo.org/data_docs/Microbe_Vent_Communities/AT26-10_Cruise_Report_v2_2015-07-09.pdf">http://dmoserv3.bco-dmo.org/data_docs/Microbe_Vent_Communities/AT26-10_Cruise_Report_v2_2015-07-09.pdf</a>
<b>Start Date</b>	2013-12-29
<b>End Date</b>	2014-01-27
<b>Description</b>	Samples were collected by ROV Jason II at the 9N deep-sea hydrothermal vent field on the East Pacific Rise, Pacific Ocean

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## Project Information

### **An Integrated Study of Energy Metabolism, Carbon Fixation, and Colonization Mechanisms in Chemosynthetic Microbial Communities at Deep-Sea Vents (Microbial Communities at Deep-Sea Vents)**

Deep-sea hydrothermal vents, first discovered in 1977, are poster child ecosystems where microbial chemosynthesis rather than photosynthesis is the primary source of organic carbon. Significant gaps remain in our understanding of the underlying microbiology and biogeochemistry of these fascinating ecosystems. Missing are the identification of specific microorganisms mediating critical reactions in various geothermal systems, metabolic pathways used by the microbes, rates of the catalyzed reactions, amounts of organic carbon being produced, and the larger role of these ecosystems in global biogeochemical cycles. To fill these gaps, the investigators will conduct a 3-year interdisciplinary, international hypothesis-driven research program to understand microbial processes and their quantitative importance at deep-sea vents. Specifically, the investigators will address the following objectives: 1. Determine key relationships between the taxonomic, genetic and functional diversity, as well as the mechanisms of energy and carbon transfer, in deep-sea hydrothermal vent microbial communities. 2. Identify the predominant metabolic pathways and thus the main energy sources driving chemoautotrophic production in high and low temperature diffuse flow vents. 3. Determine energy conservation efficiency and rates of aerobic and anaerobic chemosynthetic primary productivity in high and low temperature diffuse flow vents. 4. Determine gene expression patterns in diffuse-flow vent microbial communities during attachment to substrates and the development of biofilms.

Integration: To address these objectives and to characterize the complexity of microbially-catalyzed processes at deep-sea vents at a qualitatively new level, we will pursue an integrated approach that couples an assessment of taxonomic diversity using cultivation-dependent and -independent approaches with methodologies that address genetic diversity, including a) metagenomics (genetic potential and diversity of community), b) single cell genomics (genetic potential and diversity of uncultured single cells), c) meta-transcriptomics and -proteomics (identification and function of active community members, realized potential of the community). To assess function and response to the environment, these approaches will be combined with 1) measurement of in situ rates of chemoautotrophic production, 2) geochemical characterization of microbial habitats, and 3) shipboard incubations under simulated in situ conditions (hypothesis testing under controlled physicochemical conditions). Network approaches and mathematical simulation will be used to reconstruct the metabolic network of the natural communities. A 3-day long project meeting towards the end of the second year will take place in Woods Hole. This Data Integration and Synthesis meeting will allow for progress reports and presentations from each PI, postdoc, and/or student, with the aim of synthesizing data generated to facilitate the preparation of manuscripts.

Intellectual Merit. Combining the community expression profile with diversity and metagenomic analyses as well as process and habitat characterization will be unique to hydrothermal vent microbiology. The approach will provide new insights into the functioning of deep-sea vent microbial communities and the constraints regulating the interactions between the microbes and their abiotic and biotic environment, ultimately enabling

us to put these systems into a quantitative framework and thus a larger global context.

Broader Impacts. This is an interdisciplinary and collaborative effort between 4 US and 4 foreign institutions, creating unique opportunities for networking and fostering international collaborations. This will also benefit the involved students (2 graduate, several undergraduate) and 2 postdoctoral associates. This project will directly contribute to many educational and public outreach activities of the involved PIs, including the WHOI Dive & Discover program; single cell genomics workshops and Cafe Scientifique (Bigelow); REU (WHOI, Bigelow, CIW); COSEE and RIOS (Rutgers), and others. The proposed research fits with the focus of a number of multidisciplinary and international initiatives, in which PIs are active members (SCOR working group on Hydrothermal energy and the ocean carbon cycle, [http://www.scorint.org/Working\\_Groups/wg135.htm](http://www.scorint.org/Working_Groups/wg135.htm); Deep Carbon Observatory at CIW, <https://dco.gl.ciw.edu/>; Global Biogeochemical Flux (GBF) component of the Ocean Observatories Initiative (OOI), <http://www.who.edu/GBF-OOI/page.do?pid=41475>)

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## Program Information

### Dimensions of Biodiversity (Dimensions of Biodiversity)

**Website:** [http://www.nsf.gov/funding/pgm\\_summ.jsp?pims\\_id=503446](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.

### 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.

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### **Funding**

<b>Funding Source</b>	<b>Award</b>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1136451</a>

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