

Bacterial 16S rRNA sequences from inactive sulfide chimneys from R/V Atlantis cruise AT11-20 in the North East Pacific Rise in November 2004

Website: <https://www.bco-dmo.org/dataset/654352>

Data Type: Cruise Results

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Project

» [Ridge2000 Integrated Studies at 9degN East Pacific Rise: Establishing a Role for Fe and S Microbial Metabolism in Ocean Crust Weathering](#) (Backwards)

Program

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

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Table of Contents

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

Dataset Description

Bacterial 16S rRNA sequences from inactive sulfide chimneys sampled in the East Pacific Rise on R/V Atlantis/Alvin Voyage 11 Leg 20 (AT11-20), Alvin Dives 4053, 4057 and 4059.

Related references:

Sylvan JB, Toner BM, Edwards KJ. 2012. Life and death of deep-sea vents: bacterial diversity and ecosystem succession on inactive hydrothermal sulfides. *mBio* 3(1): e00279-11. doi:[10.1128/mBio.00279-11](https://doi.org/10.1128/mBio.00279-11)

Methods & Sampling

Hydrothermal chimneys are a globally dispersed habitat on the seafloor associated with mid-ocean ridge (MOR) spreading centers. Active, hot, venting sulfide structures from MORs have been examined for microbial diversity and ecology since their discovery in the mid-1970s, and recent work has also begun to explore the microbiology of inactive sulfides—structures that persist for decades to millennia and form moderate to massive deposits at and below the seafloor.

The investigators studied bacterial diversity on inactive hydrothermal sulfide chimney samples from 9°N on the East Pacific Rise to learn their bacterial community composition, potential ecological roles, and succession from

active venting to inactive chimneys. The investigators used tag pyrosequencing of the V6 region of the 16S rRNA and full-length 16S rRNA sequencing on inactive hydrothermal sulfide chimney samples from 9°N on the East Pacific Rise to learn their bacterial composition, metabolic potential, and succession from venting to nonventing (inactive) regimes. Many bacteria on inactive sulfide chimneys are closely related to lineages involved in sulfur, nitrogen, iron, and methane cycling, and two common groups found on active chimneys are nearly absent from inactive vents, where they were replaced by groups likely involved in the elemental cycling mentioned above. Alpha-, beta-, delta-, and gammaproteobacteria and members of the phylum Bacteroidetes dominate all inactive sulfides. Greater than 26% of the V6 tags obtained are closely related to lineages involved in sulfur, nitrogen, iron, and methane cycling. Epsilonproteobacteria represent <4% of the V6 tags recovered from inactive sulfides and 15% of the full-length clones, despite their high abundance in active chimneys. Members of the phylum Aquificae, which are common in active vents, were absent from both the V6 tags and full-length 16S rRNA data sets. In both analyses, the proportions of alphaproteobacteria, betaproteobacteria, and members of the phylum Bacteroidetes were greater than those found on active hydrothermal sulfides. These shifts in bacterial population structure on inactive chimneys reveal ecological succession following cessation of venting and also imply a potential shift in microbial activity and metabolic guilds on hydrothermal sulfides, the dominant biome that results from seafloor venting.

Data Processing Description

Full-length 16S rRNA sequences were chimera checked with Bellerophon. For V6 16S rRN sequences obtained through 454 sequencing, sequences <50 bp were eliminated, as were sequences that contained any mismatches to the PCR primers or that contained one or more undetermined nucleotides (N's).

In addition to NCBI, data have been deposited in the Marine Biological Laboratory's (MBL) VAMPS system (<https://vampls.mbl.edu/>): Dataset KCK_SBF_Bv6, samples 4053_M2_D3_DF, 4053_M3_O_DF03, 4053_M3_O_DF4wt, 4057_M2_DF04, 4059_M3_O_DF02, 4059_M4_I_DF02, 4059_M4_O_DF02 and 4059_M4_sph

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

Data Files

File
EPR_9N_Inactive_Sulfides.csv (Comma Separated Values (.csv), 162.37 KB) MD5:e6f3fc6c454289511eddba49beaec8c9
Primary data file for dataset ID 654352

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

Parameters

Parameter	Description	Units
cruise_id	Cruise identifier	unitless
location	Sampling location	unitless
lat_start	Starting latitude of range of sampling	decimal degrees
lat_end	Ending latitude of range of sampling	decimal degrees
lon	Longitude of sampling	decimal degrees
depth	Depth at which sample was collected	meters
description	Description of the sequence	unitless
accession_num	NCBI accession number	unitless
accession_link	Link to NCBI for the accession number	unitless
popset_id	NCBI PopSet ID number	unitless
popset_link	Link to NCBI for the PopSet ID	unitless

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

Instruments

Dataset-specific Instrument Name	Applied Biosystems
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Automated DNA Sequencer, Applied Biosystems and Roche 454 GS20 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

AT11-20

Website	https://www.bco-dmo.org/deployment/654275
Platform	R/V Atlantis
Start Date	2004-11-05
End Date	2004-11-26
Description	More information is available from the Rolling Deck to Repository (R2R).

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

Project Information

Ridge2000 Integrated Studies at 9degN East Pacific Rise: Establishing a Role for Fe and S Microbial Metabolism in Ocean Crust Weathering (Backwards)

Coverage: East Pacific Rise, 9 degrees North

Hydrothermal chimneys are a globally dispersed habitat on the seafloor associated with mid-ocean ridge (MOR) spreading centers. Active, hot, venting sulfide structures from MORs have been examined for microbial diversity and ecology since their discovery in the mid-1970s, and recent work has also begun to explore the microbiology of inactive sulfides—structures that persist for decades to millennia and form moderate to massive deposits at and below the seafloor. The investigators studied bacterial diversity on inactive hydrothermal sulfide chimney samples from 9°N on the East Pacific Rise to learn their bacterial community composition, potential ecological roles, and succession from active venting to inactive chimneys. The investigators used tag pyrosequencing of the V6 region of the 16S rRNA and full-length 16S rRNA sequencing on inactive hydrothermal sulfide chimney samples from 9°N on the East Pacific Rise to learn their bacterial composition, metabolic potential, and succession from venting to nonventing (inactive) regimes. Many bacteria on inactive sulfide chimneys are closely related to lineages involved in sulfur, nitrogen, iron, and methane cycling, and two common groups found on active chimneys are nearly absent from inactive vents, where they were replaced by groups likely involved in the elemental cycling mentioned above. Alpha-, beta-, delta-, and gammaproteobacteria and members of the phylum Bacteroidetes dominate all inactive sulfides. Greater than 26% of the V6 tags obtained are closely related to lineages involved in sulfur, nitrogen, iron, and methane cycling. Epsilonproteobacteria represent <4% of the V6 tags recovered from inactive sulfides and 15% of the full-length clones, despite their high abundance in active chimneys. Members of the phylum Aquificae, which are common in active vents, were absent from both the V6 tags and full-length 16S rRNA data sets. In both analyses, the proportions of alphaproteobacteria, betaproteobacteria, and members of the phylum Bacteroidetes were greater than those found on active hydrothermal sulfides. These shifts in bacterial population structure on inactive chimneys reveal ecological succession following cessation of venting and also imply a potential shift in microbial activity and metabolic guilds on hydrothermal sulfides, the dominant biome that results from seafloor venting.

Note: This project was supported by NSF award OCE-0241791 as add-on work to the original proposal. The [proposal abstract is available from NSF](#).

[[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

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0939564
NSF Division of Ocean Sciences (NSF OCE)	OCE-0241791
Gordon and Betty Moore Foundation (GBMF)	GBMF1609

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