Bacterial 16S rRNA sequences from hydrothermal plume particles sampled at 9 degrees North, East Pacific Rise, depth 2500m, on R/V Atlantis cruise AT15-06 in July 2006.

Website: https://www.bco-dmo.org/dataset/654298
Data Type: Cruise Results
Version: 18 Aug 2016
Version Date: 2016-08-16

Project
» EPR 9 North Plume Particles (RESET06)

Program
» Center for Dark Energy Biosphere Investigations (C-DEBI)

Contributors	Affiliation	Role
Sylvan, Jason Brent	Texas A&M University (TAMU)	Principal Investigator
Edwards, Katrina	University of Southern California (USC)	Co-Principal Investigator
German, Christopher R.	Woods Hole Oceanographic Institution (WHOI)	Co-Principal Investigator
Pyenson, Benjamin C.	Arizona State University (ASU)	Co-Principal Investigator
Rouxel, Olivier	Universite de Brest	Co-Principal Investigator
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

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Dataset Description

Bacterial 16S rRNA sequences from hydrothermal plume particles sampled at 9 degrees North, East Pacific Rise, depth 2500m, on R/V Atlantis cruise AT15-06 in July 2006.

Related references:

Sylvan, JB, BC Pyenson, O. Rouxel, GR German and KJ Edwards. 2012. Time series analysis of two hydrothermal plumes at 9˚50'N East Pacific Rise reveals distinct, heterogeneous bacterial populations. Geobiology, 10: 178-192. doi:10.1111/j.1472-4669.2011.00315.x

Methods & Sampling

The investigators deployed sediment traps adjacent to two active hydrothermal vents at 9°50'N on the East Pacific Rise (EPR) to assess the variability in bacterial community structure associated with plume particles on the timescale of weeks to months, to determine whether an endemic population of plume microbes exists, and to establish ecological relationships between bacterial populations and vent chemistry. Automated rRNA intergenic spacer analysis (ARISA) indicated that there are separate communities at the two different vents and

temporal community variations between each vent. Correlation analysis between chemistry and microbiology indicated that shifts in the coarse particulate (>1 mm) Fe/(Fe+Mn+Al), Cu, V, Ca, Al, 232Th, and Ti as well as fine-grained particulate (<1 mm) Fe/(Fe+Mn+Al), Fe, Ca, and Co are reflected in shifts in microbial populations. 16S rRNA clone libraries from each trap at three time points revealed a high percentage of Epsilonproteobacteria clones and hyperthermophilic Aquificae. There is a shift toward the end of the experiment to more Gammaproteobacteria and Alphaproteobacteria, many of whom likely participate in Fe and S cycling. The particle-attached plume environment is genetically distinct from the surrounding seawater. While work to date in hydrothermal environments has focused on determining the microbial communities on hydrothermal chimneys and the basaltic lavas that form the surrounding seafloor, little comparable data exist on the plume environment that physically and chemically connects them. By employing sediment traps for a time-series approach to sampling, the investigators show that bacterial community composition on plume particles changes on timescales much shorter than previously known.

Data Processing Description

Chimera were checked with Bellerophon.

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Data Files

File
EPR_9_North_Plume_Particles.csv (Comma Separated Values (.csv), 142.63 KB) MD5:643eed95fb84bb0254ef1fa4fd65b13d Primary data file for dataset ID 654298

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Parameters

Parameter	Description	Units
cruise_id	Cruie identifier	unitless
location	Sampling location	unitless
lat	Latitude 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

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Applied Biosystems Automated 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.

Dataset-specific Instrument Name	Thermo-Electron Element 2
Generic Instrument Name	Inductively Coupled Plasma Mass Spectrometer
Dataset-specific Description	Inductively Coupled Plasma Mass Spectrometer (ICP Mass Spec) - Thermo-Electron Element 2
Generic Instrument Description	An ICP Mass Spec is an instrument that passes nebulized samples into an inductively-coupled gas plasma (8-10000 K) where they are atomized and ionized. Ions of specific mass-to-charge ratios are quantified in a quadrupole mass spectrometer.

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Deployments

AT15-06

Website	https://www.bco-dmo.org/deployment/654285
Platform	R/V Atlantis
Start Date	2006-06-18
End Date	2006-07-07
Description	More information is available from Rolling Deck to Repository (R2R).

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Project Information

EPR 9 North Plume Particles (RESET06)

Coverage: East Pacific Rise, 9 degrees N

The investigators deployed sediment traps adjacent to two active hydrothermal vents at 9°50'N on the East Pacific Rise (EPR) to assess the variability in bacterial community structure associated with plume particles on the timescale of weeks to months, to determine whether an endemic population of plume microbes exists, and to establish ecological relationships between bacterial populations and vent chemistry. Automated rRNA intergenic spacer analysis (ARISA) indicated that there are separate communities at the two different vents and temporal community variations between each vent. Correlation analysis between chemistry and microbiology indicated that shifts in the coarse particulate (>1 mm) Fe/(Fe+Mn+Al), Cu, V, Ca, Al, 232Th, and Ti as well as fine-grained particulate (<1 mm) Fe/(Fe+Mn+Al), Fe, Ca, and Co are reflected in shifts in microbial populations. 16S rRNA clone libraries from each trap at three time points revealed a high percentage of Epsilonproteobacteria clones and hyperthermophilic Aquificae. There is a shift toward the end of the experiment to more Gammaproteobacteria and Alphaproteobacteria, many of whom likely participate in Fe and S cycling. The particle-attached plume environment is genetically distinct from the surrounding seawater. While work to date in hydrothermal environments has focused on determining the microbial communities on hydrothermal chimneys and the basaltic lavas that form the surrounding seafloor, little comparable data exist on the plume environment that physically and chemically connects them. By employing sediment traps for a time-series approach to sampling, the investigators show that bacterial community composition on plume particles changes on timescales much shorter than previously known.

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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
NSF Division of Ocean Sciences (NSF OCE)	OCE-0424953
Gordon and Betty Moore Foundation (GBMF)	GBMF1609

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