

Bacterial 16S rRNA sequences from seafloor rocks (silicates and sulfides) collected on R/V Thomas G. Thompson cruise TN235 in the Eastern Lau Spreading Center from May to June 2009

Website: <https://www.bco-dmo.org/dataset/658175>

Data Type: Cruise Results

Version: 24 Aug 2016

Version Date: 2016-08-24

Project

» [Lau Basin low temperature geomicrobiology](#) (Lau Basin Geomicrobio)

Program

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

Contributors	Affiliation	Role
Sylvan, Jason Brent	Texas A&M University (TAMU)	Principal Investigator
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Dataset Description

Bacterial 16S rRNA sequences from seafloor rocks (silicates and sulfides) sampled on R/V Thomas G. Thompson cruise TN235 in the Lau Basin.

Related references:

Sylvan, JB, Sia, TY, Haddad, AG, Briscoe, LJ, Toner, BM, Girguis, PR and Edwards KJ. 2013. Low temperature geomicrobiology follows host rock composition along a geochemical gradient in Lau Basin. *Frontiers in Microbiology*, 4:61. doi:[10.3389/fmicb.2013.00061](https://doi.org/10.3389/fmicb.2013.00061)

Methods & Sampling

Samples were taken from the following locations and depths:

Kilo Moana (~2600 m water depth),

ABE (~2100 m water depth),

Tui Malila (~1875 m water depth), and

Mariner (~1900 m water depth) hydrothermal vent fields

The East Lau Spreading Center (ELSC) and Valu Fa Ridge (VFR) comprise a ridge segment in the southwest Pacific Ocean where rapid transitions in the underlying mantle chemistry manifest themselves as gradients in seafloor rock geochemistry. The investigators studied the geology and microbial diversity of three silicate rock samples and three inactive sulfide chimney samples collected, from north to south, at the vent fields Kilo

Moana, ABE, Tui Malila, and Mariner. This is the first study of microbial populations on basaltic andesite, which was sampled at Mariner vent field. Silicate rock geochemistry exhibits clear latitudinal trends that are mirrored by changes in bacterial community composition. Alphaproteobacteria, Epsilonproteobacteria, and Bacteroidetes are most common on a silicate collected from Kilo Moana and their proportions decrease linearly on silicates collected further south. Conversely, a silicate from Mariner vent field hosts high proportions of a unique lineage of Chloroflexi unrelated (<90% sequence similarity) to previously recovered environmental clones or isolates, which decrease at ABE and are absent at Kilo Moana. The exteriors of inactive sulfide structures are dominated by lineages of sulfur oxidizing Alphaproteobacteria, Gammaproteobacteria, and Epsilonproteobacteria, while the interior of one chimney is dominated by putative sulfur-reducing Deltaproteobacteria. A comparison of bacterial communities on inactive sulfides from this and previous studies reveals the presence of a clade of uncultured Bacteroidetes exclusive to sulfidic environments, and a high degree of heterogeneity in bacterial community composition from one sulfide structure to another. In light of the heterogeneous nature of bacterial communities observed here and in previous studies of both active and inactive hydrothermal sulfide structures, the presence of numerous niches may be detected on these structures in the future by finer scale sampling and analysis.

Data Processing Description

Chimera were checked with Bellerophon.

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Data Files

File
Lau_Basin_sequences.csv (Comma Separated Values (.csv), 127.75 KB) MD5:b6c1dc348316d3a269437959c0d63993 Primary data file for dataset ID 658175

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Parameters

Parameter	Description	Units
cruise_id	Cruise identifier	unitless
description	Description of the sequence	unitless
sample	Sample name	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
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	Automated DNA Sequencer
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Applied Biosystems
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	Inductively Coupled Plasma mass spectrometer
Generic Instrument Name	Inductively Coupled Plasma Mass Spectrometer
Dataset-specific Description	Thermo Scientific XSERIES 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.

Dataset-specific Instrument Name	Inductively Coupled Plasma Optical Emission Spectrophotometer
Generic Instrument Name	Inductively Coupled Plasma Optical Emission Spectrometer
Dataset-specific Description	Thermo Scientific iCAP 6500
Generic Instrument Description	Also referred to as an Inductively coupled plasma atomic emission spectroscopy (ICP-AES). These instruments pass nebulised samples into an inductively-coupled gas plasma (8-10000 K) where they are atomised and excited. The de-excitation optical emissions at characteristic wavelengths are spectroscopically analysed. It is often used in the detection of trace metals.

Dataset-specific Instrument Name	X-Ray Diffractometer
Generic Instrument Name	X-ray diffractometer
Dataset-specific Description	Siemens D-500
Generic Instrument Description	Instruments that identify crystalline solids by measuring the characteristic spaces between layers of atoms or molecules in a crystal.

Deployments

TN235

Website	https://www.bco-dmo.org/deployment/654455
Platform	R/V Thomas G. Thompson
Start Date	2009-05-16
End Date	2009-06-08
Description	More information is available from the Rolling Deck to Repository (R2R).

Project Information

Lau Basin low temperature geomicrobiology (Lau Basin Geomicrobio)

Coverage: Lau Basin hydrothermal vent fields

The East Lau Spreading Center (ELSC) and Valu Fa Ridge (VFR) comprise a ridge segment in the southwest Pacific Ocean where rapid transitions in the underlying mantle chemistry manifest themselves as gradients in seafloor rock geochemistry. The investigators studied the geology and microbial diversity of three silicate rock samples and three inactive sulfide chimney samples collected, from north to south, at the vent fields Kilo Moana, ABE, Tui Malila, and Mariner. This is the first study of microbial populations on basaltic andesite, which was sampled at Mariner vent field. Silicate rock geochemistry exhibits clear latitudinal trends that are mirrored by changes in bacterial community composition. Alphaproteobacteria, Epsilonproteobacteria, and Bacteroidetes are most common on a silicate collected from Kilo Moana and their proportions decrease linearly on silicates collected further south. Conversely, a silicate from Mariner vent field hosts high proportions of a unique lineage of Chloroflexi unrelated (<90% sequence similarity) to previously recovered environmental clones or isolates, which decrease at ABE and are absent at Kilo Moana. The exteriors of inactive sulfide structures are dominated by lineages of sulfur oxidizing Alphaproteobacteria, Gammaproteobacteria, and Epsilonproteobacteria, while the interior of one chimney is dominated by putative sulfur-reducing Deltaproteobacteria. A comparison of bacterial communities on inactive sulfides from this and previous studies reveals the presence of a clade of uncultured Bacteroidetes exclusive to sulfidic environments, and a high degree of heterogeneity in bacterial community composition from one sulfide structure to another. In light of the heterogeneous nature of bacterial communities observed here and in previous studies of both active and inactive hydrothermal sulfide structures, the presence of numerous niches may be detected on these structures in the future by finer scale sampling and analysis.

Note: This project was supported by NSF award OCE-0732369 as add-on work to the original proposal. The [proposal abstract is available from NSF](#).

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
Gordon and Betty Moore Foundation (GBMF)	GBMF1609
NSF Division of Ocean Sciences (NSF OCE)	OCE-0732369

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