soxB gene sequence data from microbial mats; collected on R/V Atlantis cruise AT18-08 at the Axial Seamount, Juan de Fuca Ridge in 2011

Website: https://www.bco-dmo.org/dataset/636540
Data Type: Cruise Results
Version: 26 Jan 2016
Version Date: 2016-01-26

Project
» Function, activity, and adaptation of microbial communities in geochemically diverse subseafloor habitats (AXIAL)

Contributors	Affiliation	Role
Huber, Julie	Marine Biological Laboratory (MBL)	Principal Investigator
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Table of Contents

Dataset Description

soxB gene sequence data from microbial mats at Axial Seamount, 2011. Sample collected on cruise AT18-08.

Methods & Sampling

Diffuse fluids were collected from newly discovered snowblower vents at Axial Seamount in late July 2011 with the ROV Jason II using the hydrothermal fluid and particle sampler (Butterfield et al., 2004). White and orange flocculent materials were collected on the subsequent University Of Washington Visions' 11 cruise, in support of the Regional Scale Nodes component of the Ocean Observatories Initiative in August 2011. White flocculent material was collected from the orifice of the Subway snowblower vent on dives R1467 (White Floc 1) and R1472 (White Floc 2) and orange flocculent material was collected on the seafloor distal to Marker 33 during dive R1472 where it coated freshly deposited basalt. All of the fluid and floc samples analyzed in this study are from a small area in the south rift zone at the southeastern edge of Axial Caldera, with the exception of background seawater which was collected outside of the caldera.

Total genomic DNA was extracted from Sterivex filters as previously described (Sogin et al., 2006) with the minor modifications described by Akerman et al. (2013). Total genomic DNA was extracted from 20 to 30mg of wet flocculent material using a MoBio UltraClean® Soil DNA Isolation Kit.

We targeted the amplification of the soxB gene in Epsilonproteobacteria to assess the diversity of sulfur oxidizers in white floc vs. orange floc samples. The soxB gene was amplified in one white flocculent sample (White Floc 2) and in the orange flocculent sample, using the newly designed primers and conditions described by Akerman et al. (2013). The PCR reaction mixture consisted of 1X buffer (Promega), 4 mM MgCl2, 0.2 mM of each deoxynucleoside triphosphate (dNTP), 0.6 uM of each primer, 1U GoTaq polymerase (Promega), 1 ul DNA template, and DEPC H2O to 25 ul. Thermocycling conditions on an Eppendorf thermal cycler consisted of an initial denaturation step at 94 degrees C for 3 min, followed by 35 cycles of 94 degrees C for 30s, 46

degrees C for 45 s, and 72 degrees C for 1 min, followed by a final extension at 72 degrees C for 5 min. The primers used in this study were sox527F (5'-TGGTWGGWCAYTGGGAATTTA-3') and sox1198R (5'-AGAANGTATCTCKYTTATAAAG-3'). These primers target the genera Sulfurovum, Sulfurimonas, and Nitratiruptor. The soxB gene in members of the Epsilonproteobacterial genera Arcobacter and Nitratifractor are more like sequences in Gammaproteobacteria and are not expected to amplify with this primer set. Successfully amplified soxB PCR products were cleaned with a Qiagen MinElute PCR purification kit and run on a 0.8% agarose gel. Bands in the expected size range were gel excised, purified with the MinElute kit, cloned, and sequenced as previously described (Huber et al., 2009).

Related references:
Meyer, J.L., Akerman, N.H., Proskurowski, G. and J.A. Huber. 2013. Microbiological characterization of post-eruption "snowblower" vents at Axial Seamount, Juan de Fuca Ridge. Frontiers in Microbiology. 4:153. doi: 10.3389/fmicb.2013.00153

Data Processing Description

Nucleotide sequences were translated into amino acids using EMBOSS Transeq (Rice et al., 2000) and phylogenetic relationships were analyzed using MEGA5 (Tamura et al., 2011). Sequences are deposited in GenBank under Accession numbers KC793341-KC793425.

BCO-DMO Processing:
- modified parameter names to conform with BCO-DMO naming conventions;
- removed "m" (meters) in depth column;
- changed format of date to YYYYmmdd;
- replaced commas with semi-colons;
- Added cruise_id field.

[table of contents | back to top]

Data Files

File	
Snowblower_soxBSequences.csv	(Comma Separated Values (.csv), 866 bytes) MD5:06582ae153c31ba219cafaff9ccc2c97
Primary data file for dataset ID 636540	

[table of contents | back to top]

Parameters

Parameter	Description	Units
cruise_id	Cruise identifier.	dimensionless
collection_date	Year, month, and day of sample collection.	YYYYmmdd
organism	Organism.	dimensionless
env_feature	Environmental feature.	dimensionless
env_material	Environmental material.	dimensionless
env_biome	Biome.	dimensionless
geo_loc_name	Geographic location name.	dimensionless
sample_name	Sample name.	dimensionless
vent_name	Vent name.	dimensionless
sample_title	Sample title.	dimensionless
accession_number_range	NCBI accession numbers.	dimensionless
depth	Depth of sample collection.	meters (m)
lat	Latitude of sample collection.	decimal degrees
lon	Longitude of sample collection.	decimal degrees
NCBI_PopSet_ID	NCBI PopSet ID number.	dimensionless
NCBI_PopSet_link	Hyperlink to NCBI PopSet.	dimensionless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	ROV Jason
Generic Instrument Description	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 URL.

Dataset-specific Instrument Name	
Generic Instrument Name	Thermal Cycler
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

[table of contents | back to top]

Deployments

AT18-08

Website	https://www.bco-dmo.org/deployment/568087
Platform	R/V Atlantis
Report	http://dmoserv3.whoi.edu/data_docs/C-DEBI/cruise_reports/AT18-08_nemo11-cruise-report.pdf
Start Date	2011-07-19
End Date	2011-08-01
Description	Data expected from C-DEBI investigator, Julie Huber. Additional cruise information and original data are available from the NSF R2R data catalog.

[table of contents | back to top]

Project Information

Function, activity, and adaptation of microbial communities in geochemically diverse subseafloor habitats (AXIAL)

Website: http://www.pmel.noaa.gov/vents/index.html

Coverage: NE Pacific Ocean, Juan de Fuca Ridge, Axial Seamount

Collaborative Research: Function, activity, and adaptation of microbial communities in geochemically diverse subseafloor habitats

The integration of both laboratory and field-based chemical and microbiological measurements into a quantitative predictive framework is crucial to understanding the microbial ecology of marine systems. This project work will provide a quantitative assessment of the functional diversity, activity, and physiological adaptation of microbial communities in geochemically diverse subseafloor habitats. Results will guide development of models for linking biogeochemical processes with particular microbial communities at deep-sea hydrothermal vents, with implications for other marine habitats as well. The focus of the effort is at Axial Seamount, a well-studied, active, deep-sea hydrothermal seamount in the NE Pacific Ocean. Samples already collected from Axial, along with a field program in Year 2, will serve as the foundation for the three objectives, which are to:

1. Determine and quantify the functional diversity and activity (expression) of key subseafloor microbial lineages at Axial Seamount.

2. Determine physiological adaptations to the subseafloor habitat by quantifying the growth response of Axial Seamount isolates to in-situ geochemical parameters.

3. Develop a quantitative predictive framework for linking particular types of geochemical vent conditions with specific microbial functional groups and activities at Axial Seamount.

Specific outcomes of this project include the creation of a comprehensive quantitative microbiological and chemical dataset on diffuse and adjacent high-temperature vents within Axial Seamount. This database will include chemical measurements (gases, nutrients, metals, isotopes, and calculated Gibbs free energies) relevant to microbial metabolic processes that can be compared to microbiological data (abundance and activity of microbial lineages and functional genes, growth rates of subseafloor isolates at relevant environmental conditions) using statistical analysis to identify how specific microbial activity is linked to the geochemical environment. This project builds on previous studies of microbial population structure and geochemical measurements at Axial Seamount and addresses critical gaps in current knowledge and understanding that are impeding progress of modeling hydrothermal systems. Results will increase understanding of deep-sea hydrothermal ecosystems as well as provide new insights into controls on the distribution and activity of marine microbial communities throughout the world's oceans.

NeMO10 TN253 Cruise Report

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0929167

[table of contents | back to top]