16S rRNA gene amplicon sequences from FLOCS experiments at the Juan de Fuca Ridge CORKs during August 2014.

Website: https://www.bco-dmo.org/dataset/754354
Data Type: Cruise Results
Version: 1
Version Date: 2019-02-20

Project
» Collaborative Research: Completing single- and cross-hole hydrgeologic and microbial experiments: Juan de Fuca Flank (JdF Flank)

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

Contributors	Affiliation	Role
Orcutt, Beth N.	Bigelow Laboratory for Ocean Sciences	Principal Investigator
Ramirez, Gustavo	University of Southern California (USC)	Co-Principal Investigator
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Coverage

Spatial Extent: **Lat**:47.45 **Lon**:-127.45
Temporal Extent: 2014-08 - 2014-08

Dataset Description

The DNA data from the Juan de Fuca project are publicly available through NCBI Short Read Archive under BioProject PRJNA472057; BioSample accession numbers: SAMN09228041- SAMN09228055

species: uncultivated marine metagenome

description of the types of sequences: Illumina amplicon sequences of the V1-V3 hypervariable region of the 16S rRNA gene

locations where species were collected: IODP holes U1301A, U1362A, and U1362B on the Juan de Fuca Ridge flank, 47.45N/127.45W

Methods & Sampling

Polished mineral chips were prepared and deployed as described in Fisher et al. 2011 (DOI:

10.2204/iodp.proc.327.107.2011). Mineral colonization experiments were recovered during cruise AT26-18 in August 2014 and processed as described in Orcutt et al. 2011 (DOI: 10.1038/ismej.2010.157). Approximately 6g of each substrate underwent total DNA extraction using the MOBIO PowerSoil® DNA Isolation Kit (MOBIO Laboratories, Inc.) with modification from manufacturer instructions to include a phenol:chloroform:isoamyl alcohol (24:25:1) extraction step. Each batch of samples included procedural blanks. Replicate extracts were pooled and concentrated to 100 µl with vacuum centrifugation (SavantTM DNA SpeedVacTM Concentrator). Concentrated extracts were cleaned with the CleanAll DNA/RNA Clean Up and Concentration Kit (Norgen Biotek Corp, Thorold, Canada) and eluted in 20-50 µl of PCR-grade water. Sequencing of the V1-V3 region of the 16S rRNA gene was performed by Research and Testing Laboratory (Lubbock, TX, USA) using the forward primer 28F (5′- GAG TTT GAT CNT GGC TCA G -3′) and reverse primer 388R (5′- TGC TGC CTC CCG TAG GAG T -3′) for Bacteria using 2 x 300 bp kits on the Illumina MiSeq platform.

Data Processing Description

BCO-DMO Processing Notes:
- Nothing to report

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Related Publications

Fisher, A. T., Wheat, C. G., Becker, K., Cowen, J., Orcutt, B., Hulme, S., … Edwards, K. J. (2011). Design, deployment, and status of borehole observatory systems used for single-hole and cross-hole experiments, IODP Expedition 327, eastern flank of Juan de Fuca Ridge. Proceedings of the IODP. doi:10.2204/iodp.proc.327.107.2011
Methods

Orcutt, B. N., Bach, W., Becker, K., Fisher, A. T., Hentscher, M., Toner, B. M., … Edwards, K. J. (2010). Colonization of subsurface microbial observatories deployed in young ocean crust. The ISME Journal, 5(4), 692–703. doi:10.1038/ismej.2010.157
Methods

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Parameters

Parameters for this dataset have not yet been identified

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Concentrated extracts were cleaned with the CleanAll DNA/RNA Clean Up and Concentration Kit (Norgen Biotek Corp, Thorold, Canada) and eluted in 20-50 µl of PCR-grade water. Sequencing of the V1-V3 region of the 16S rRNA gene was performed by Research and Testing Laboratory (Lubbock, TX, USA) using the forward primer 28F (5′- GAG TTT GAT CNT GGC TCA G -3′) and reverse primer 388R (5'- TGC TGC CTC CCG TAG GAG T -3') for Bacteria using 2 x 300 bp kits on the Illumina MiSeq platform.
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.

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Deployments

AT26-18

Website	https://www.bco-dmo.org/deployment/626369
Platform	R/V Atlantis
Report	http://dmoserv3.whoi.edu/data_docs/C-DEBI/cruise_reports/AT26-18_JFR_Cork_Recovery_Cruise_Report_reduced.pdf
Start Date	2014-08-10
End Date	2014-08-24
Description	Research was conducted on this cruise as part of the C-DEBI project titled "Completing single- and cross-hole hydrogeologic and microbial experiments: Juan de Fuca Flank" (see http://www.bco-dmo.org/project/625989).

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Project Information

Collaborative Research: Completing single- and cross-hole hydrgeologic and microbial experiments: Juan de Fuca Flank (JdF Flank)

Website: http://www.darkenergybiosphere.org/research/juandefuca.html

Coverage: Eastern flank of Juan de Fuca Ridge: 47 N, 128 W

NSF Award Abstract:
In 2010, IODP exp. 327 launched series of experiments based on instrumentation placed in 6 boreholes (Holes 1026B, 1027C, 1301A, 1301B, 1362A, and 1362B) on and near the Juan de Fuca Ridge (JDFR). The experiments were designed to examine hydrological and biological processes in basaltic ocean crust. Major issues to be addressed include overall permeability, the magnitudes, velocity and directions of fluid, solute,and

heat transport,constraints on the fluid storage properties of crust, determining how fluid reservoirs respond to seismic perturbations, and investigating the variability, diversity, and metabolism of resident microbial populations. This project will recover sensors and samplers in the instrumented boreholes(CORKs),access data and samples, collect biological incubators placed at depth within the boreholes, and seal the CORKs. All of these activities are needed for the completion of the JDFR experiments

Once the data and samples are retrieved, the PI's will develop new numerical models for the hydrology (permeability, thickness and extent of permeable zones, connectivity, direction of flow, and anisotropy) of ocean crust based on the results of flow tests. T sensors will enable thermal structure to be determined in conjunction with flow parameters. DNA will be analyzed via 16S ribosomal RNA (rRNA) genes as well as select full-length Sanger-style sequencing and gene fingerprinting techniques. The PI's will look at diversity, shared species, emergence and disappearance of groups. Metagenomic work will be done on some samples.

Broader Impacts include training of 4 shipboard educators, with an emphasis on recruiting underrepresented groups for these positions, teacher workshops, and special training for undergraduate and graduate students and post-docs. Research team includes grads, undergrads, and post-docs

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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-1260697
NSF Division of Ocean Sciences (NSF OCE)	OCE-1536539

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