Metagenomic data from site U1382B at North Pond (IODP 336), western flank of the mid-Atlantic Ridge from core samples collected in November of 2011

Website: https://www.bco-dmo.org/dataset/809862
Data Type: Cruise Results
Version: 1
Version Date: 2020-04-22

Project
» Potential phosphorus uptake mechanisms of the deep sedimentary biosphere (Deep sea sediments)

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

Contributors	Affiliation	Role
Paytan, Adina	University of California-Santa Cruz (UCSC)	Principal Investigator
Defforey, Delphine	University of California-Santa Cruz (UCSC)	Co-Principal Investigator
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Abstract
Metagenomic data from site U1382B at North Pond (IODP 336), western flank of the mid-Atlantic Ridge from core samples collected on 2011-11-08. These data were published in Defforey, D. (2016). Metagenomic sequences are available at the National Center for Biotechnology Information SRA database: https://www.ncbi.nlm.nih.gov/sra/?term=SRP096133, BioProject: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA360271.

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Coverage

Spatial Extent: **Lat**:22.75589 **Lon**:-46.08125
Temporal Extent: 2011-11-08

Dataset Description

Metagenomic data from site U1382B at North Pond (IODP 336), western flank of the mid-Atlantic Ridge from core samples collected on 2011-11-08. These data were published in Defforey, D. (2016).

Metagenomic sequences are available at the National Center for Biotechnology Information SRA database: https://www.ncbi.nlm.nih.gov/sra/?term=SRP096133,
BioProject: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA360271.

Additional award information:

* NSF C-DEBI subaward # 156246 to Adina Paytan
* NSF C-DEBI subaward # 157598 to Delphine Defforey

Methods & Sampling

Location: North Atlantic, western flank of the mid-Atlantic Ridge 22.75589 N 46.08125 W

DNA was extracted using the method described in (Mills et al. 2012) as modified by B. K. Reese for nucleic acids in low biomass open ocean sediments. The interior of the whole-round core for sample U1382B 7H-5 was subsampled using sterile techniques and was divided into 25 splits, each weighing ~0.5 g. Initial cell lysis was achieved using five cycles of freeze (liquid nitrogen), thaw (55oC water bath) and vortex steps while stabilizing nucleic acids in a Tris–EDTA–glucose buffer. This step was followed by the addition of lysozyme to the buffer and incubation at 30oC for 10 minutes. Samples were then treated twice with buffered phenol, chloroform and isoamyl alcohol (25:24:1; pH 8.0), and sodium dodecyl sulfate to dissolve the cell membrane and solubilize both high and low molecular weight proteins. Nucleic acids within the aqueous layer above the phenol–chloroform layer were then precipitated in an ethanol and sodium acetate solution. The ethanol solution was decanted following centrifugation of samples at 4°C. Lastly, DNA pellets were resuspended in sterile water, combined into one sample. We quantified the DNA content using a Quibit fluorometer (Thermo Scientific, Waltham, MA, USA) and assessed its quality on a NanoDrop 1000 Spectrophotometer (Thermo Scientific, Waltham, MA, USA) prior to sequencing at the Marine Biological Laboratory Keck facility (Woods Hole, MA, USA). Extraction blanks were included with each sample extraction and yielded no measurable DNA.

Data Processing Description

Raw reads were quality controlled using cutadapt (v1.7.1) and Trimmomatic (v0.33). The QCed sequences were searched for SSU rRNA fragments using Meta-RNA (v.H3). SSU rRNA fragments were assembled using EMIRGE (v.1.3) utilizing SILVA SSU as the reference database using the SINA web portal aligner (Ludwig et al. 2004; Capella-Gutiérrez et al. 2009; Pruesse et al. 2012).

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Related Publications

Capella-Gutierrez, S., Silla-Martinez, J. M., & Gabaldon, T. (2009). trimAl: a tool for automated alignment trimming in large-scale phylogenetic analyses. Bioinformatics, 25(15), 1972–1973. doi:10.1093/bioinformatics/btp348
Methods

Defforey, D. (2016). Phosphorus cycling in the deep sedimentary subseafloor environment. PhD Thesis, UC Santa Cruz. https://escholarship.org/uc/item/85p2s7dx
Results

Edwards, K.J., Bach, W., Klaus, A., et al. (2012). Expedition 336 summary. Proc. IODP, 336: Tokyo (Integrated Ocean Drilling Program Management International, Inc.). doi:10.2204/iodp.proc.336.101.2012
Methods

Ludwig, W. (2004). ARB: a software environment for sequence data. Nucleic Acids Research, 32(4), 1363–1371. doi:10.1093/nar/gkh293
Methods

Martin, M. (2011). Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnet.journal, 17(1), 10. doi:10.14806/ej.17.1.200
Software

Mills, H. J., Reese, B. K., & Peter, C. S. (2012). Characterization of Microbial Population Shifts during Sample Storage. Frontiers in Microbiology, 3. doi:10.3389/fmicb.2012.00049
Methods

Paytan, A., Marine Biological Laboratory, and UC Santa Cruz (2017). Marine sediment metagenome: North Pond site U1382 metagenome. National Library of Medicine (US), National Center for Biotechnology Information.

Available from: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA360271. NCBI:BioProject: PRJNA360271.
References

Pruesse, E., Peplies, J., & Glöckner, F. O. (2012). SINA: Accurate high-throughput multiple sequence alignment of ribosomal RNA genes. Bioinformatics, 28(14), 1823–1829. doi:10.1093/bioinformatics/bts252
Methods

cutadapt. (n.d.). Version 1.7.1. Retrieved from https://cutadapt.readthedocs.io/en/v1.7.1/
Software

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Parameters

Parameters for this dataset have not yet been identified

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Instruments

Dataset-specific Instrument Name	Quibit fluorometer (Thermo Scientific, Waltham, MA, USA)
Generic Instrument Name	Fluorometer
Generic Instrument Description	A fluorometer or fluorimeter is a device used to measure parameters of fluorescence: its intensity and wavelength distribution of emission spectrum after excitation by a certain spectrum of light. The instrument is designed to measure the amount of stimulated electromagnetic radiation produced by pulses of electromagnetic radiation emitted into a water sample or in situ.

Dataset-specific Instrument Name	NanoDrop 1000 Spectrophotometer (Thermo Scientific, Waltham, MA, USA)
Generic Instrument Name	Spectrophotometer
Generic Instrument Description	An instrument used to measure the relative absorption of electromagnetic radiation of different wavelengths in the near infra-red, visible and ultraviolet wavebands by samples.

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Deployments

JRES-336

Website	https://www.bco-dmo.org/deployment/628214
Platform	R/V JOIDES Resolution
Report	http://dmoserv3.whoi.edu/data_docs/C-DEBI/cruise_reports/336PR.pdf
Start Date	2011-09-16
End Date	2011-11-16
Description	More information is available from the IODP website: http://iodp.tamu.edu/scienceops/expeditions/midatlantic_ridge_microbio.html

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Project Information

Potential phosphorus uptake mechanisms of the deep sedimentary biosphere (Deep sea sediments)

Coverage: Mid-Atlantic Ridge flank

The goal of this project is to explore potential microbial P uptake mechanisms in marine sediments beneath the North Atlantic Gyre and their effects on the relative distribution of organic P compounds as a function of burial depth and changing redox conditions. We use a combination of metagenomic analyses and solution 31P nuclear magnetic resonance spectroscopy (31P NMR) to investigate (1) the presence of microbial functional genes pertaining to P uptake and metabolism and (2) the possible P substrates for the deep biosphere in these oligotrophic sediments.

NSF C-DEBI Award #156246 to Dr. Adina Paytan

NSF C-DEBI Award #157598 to Dr. Delphine Defforey

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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

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