Accession numbers for raw sequence reads; samples collected on R/V Roger Revelle cruise KNOX02RR in the South Pacific Gyre from 2006-2007 (Microbial Diversity SPG project)

Website: https://www.bco-dmo.org/dataset/626263
Version: 10 November 2015
Version Date: 2015-11-10

Project
» Deep phylogenetic and metagenomic analysis of microbial diversity associated with ferromanganese nodules collected from the South Pacific Gyre (Microbial Diversity SPG)

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

Contributors	Affiliation	Role
Heidelberg, John	University of Southern California (USC-WIES)	Principal Investigator
Tully, Benjamin	University of Southern California (USC)	Student, Contact
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Table of Contents

- Dataset Description
  - Methods & Sampling
  - Data Processing Description
- Data Files
- Parameters
- Instruments
- Deployments
- Project Information
- Program Information
- Funding

Dataset Description

Accession numbers from the NCBI SRA for 16S amplicons; samples collected on KNOX02RR.

Methods & Sampling

All methodology can be located in the reference:
Tully and Heidelberg 2013. Microbial communities associated with ferromanganese nodules and the surrounding sediments. Frontiers in Microbiology. 4(161). doi:10.3389/fmicb.2013.00161

In summary (refer to publication above for complete description of methodology):
Sediment and FeMn nodules were collected during Expedition Knox-02RR (December 2006–January 2007 aboard the R/V *Roger Revelle*). Extraction of DNA from nodules proceeded using a modified phenol-chloroform extraction method. Due to low yield using the described phenol-chloroform method, extraction of DNA from sediment samples was performed using the MoBio PowerLyzer PowerSoil DNA kit following the manufacturer's protocol. All samples with >0.1 ng/uL final DNA concentration were cleaned and concentrated and samples were resuspended in 20 uL of sterile, DNase-free H2O. Samples were amplified using PCR, targeting the V4 region of the 16S rRNA gene. All amplifications were performed using the FastStart High Fidelity PCR System (Roche). Initial PCR products were pooled and the PCR product (~550 bp) was gel excised using the Qiagen Gel Extraction Kit (Qiagen) following the manufacturer's protocol. Excised DNA products were amplified in duplicate to generate sufficient material for pyrosequencing. PCR products were pooled and cleaned using the AMPure Bead XP (Agencourt) kit, following the manufacturer's protocol. Samples were quantified using

PicoGreen and visualized using Agilent Bioanalyzer using the High Sensitivity (Agilent) chip.

Data Processing Description

Data processing can be located in the reference:
Tully and Heidelberg 2013. Microbial communities associated with ferromanganese nodules and the surrounding sediments. Frontiers in Microbiology. 4(161). doi:10.3389/fmicb.2013.00161

[table of contents | back to top]

Data Files

File
SPG_accession_nums.csv (Comma Separated Values (.csv), 14.48 KB) MD5:905a5b13024519aebc38cafe265653de Primary data file for dataset ID 626263

[table of contents | back to top]

Parameters

Parameter	Description	Units
cruise_id	Cruise identification number.	dimensionless
bioproject_ID	NCBI BioProject ID number.	dimensionless
SRA_ID	NCBI SRA ID number.	dimensionless
strategy	16S rRNA hypervariable gene amplification.	dimensionless
source	Various samples collected via multicore instrument.	dimensionless
selection	Available aseptic samples.	dimensionless
primer	Primer used. FU515-GTGY CAGCMGCCGCGGTA & RU1048-CGRCRCCATGYANCWC	dimensionless
bioproject_URL	Hyperlink to NCBI BioProject.	dimensionless
SRA_URL	Hyperlink to NCBI SRA.	dimensionless
accession_ID	NCBI accession number.	dimensionless

accession_URL	Hyperlink to NCBI accession.	dimensionless
sample_name	Sample identifer.	dimensionless
sample_name2	Sample identifer.	dimensionless
sample_description	Description of the sample: Surface sediments and ferromanganese nodules.	dimensionless
sample_location	Location of sampling: South Pacific Ocean, central gyre.	dimensionless
lat	Latitude of sample collection.	decimal degrees
lon	Longitude of sample collection.	decimal degrees
sample_depth	Depth at which sample was collected.	meters
method	DNA extraction method; via phenol:chloroform method	dimensionless
barcode	DNA barcode.	dimensionless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Qubit 1.0
Generic Instrument Name	Fluorometer
Dataset-specific Description	Samples were then quantified using the Qubit 1.0 fluorometer and the Qubit dsDNA HS Assay Kit (Life Technologies).
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	PCR
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	Samples were amplified using PCR, targeting the V4 region of the 16S rRNA gene. All amplifications were performed using the FastStart High Fidelity PCR System (Roche).
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

KNOX02RR

Website	https://www.bco-dmo.org/deployment/567923
Platform	R/V Roger Revelle
Start Date	2006-12-17
End Date	2007-01-27

[table of contents | back to top]

Project Information

Deep phylogenetic and metagenomic analysis of microbial diversity associated with ferromanganese nodules collected from the South Pacific Gyre (Microbial Diversity SPG)

Coverage: Central South Pacific Gyre (39.3103S, 139.8006 W)

Project description obtained from C-DEBI:
The importance of microbial mediation in the biogeochemical cycles of the ocean is well documented. A major source of marine metallic minerals exists as ferromanganese (polymetallic) nodules in the deep ocean (4,000-5,000 m deep). Composed predominantly of iron, manganese, copper, nickel, and zinc, these nodules play a key role in governing the biogeochemical availability of many of these metals in the global ocean. While it is assumed that microorganisms mediate some of the processes that form nodules, it is poorly constrained as to which organisms mediate these processes or how these processes in turn may support microbial metabolisms. We propose using fingerprinting and sequencing methods to examine the microbial community diversity of organism associated with ferromanganese nodule collected from the South Pacific Gyre. Further, because many of the microbial organisms present in the deep-sea are novel and uncultivated, we plan to perform metagenomic analysis to link phylogenetic identity with physiology, with the goal of generating (near-)complete environmental genomes. The proposed research will be the first attempt to determine how the microbiology of deep oceanic nodules shape and are shaped by the environment.

This project was funded by a C-DEBI Graduate Student Fellowship.

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0939564

[table of contents | back to top]