Illumina sequencing data from sediment strata collected from the cold seeps of Hydrate Ridge, metalliferous sediments of Juan de Fuca Ridge, and organic-rich hydrothermal sediments of Guaymas Basin

Website: https://www.bco-dmo.org/dataset/747948
Data Type: Cruise Results
Version: 1
Version Date: 2018-10-11

Project
» Collaborative Research: The Role of Iron-oxidizing Bacteria in the Sedimentary Iron Cycle: Ecological, Physiological and Biogeochemical Implications (SedimentaryIronCycle)

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

Contributors	Affiliation	Role
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Abstract
Illumina sequencing data (NCBI accession numbers) from sediment strata collected from the cold seeps of Hydrate Ridge, metalliferous sediments of Juan de Fuca Ridge, and organic-rich hydrothermal sediments of Guaymas Basin.

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Coverage

Spatial Extent: **N**:48.45722 **E**:-111.4078 **S**:27.0078 **W**:-128.70861
Temporal Extent: 2013-01-01 - 2014-04-01

Methods & Sampling

This study included cold seep and hydrothermal vent sediments from along the Pacific coast of North America. Sediments were collected via 30 cm long polycarbonate pushcores from a cold methane seep at Hydrate Ridge (44°34'10. 20"N, 125° 8'48. 48"W) at 777 m water depth with the ROV Ropos (Dive 1458); hydrothermal vents at Guaymas Basin, Gulf of California (27°0'27.84"N, 111°24'27.84"W) at 2000 m with the DSV Alvin (Dive 4486); and hydrothermal vents at Middle Valley, Juna de Fuca Ridge (48°27'26.40"N, 128°42'30.60"W) at 2413 m with the DSV Alvin (Dive 4625). For this study, a total of three pushcores were collected from Hydrate Ridge at 4°C, one from Guaymas Basin at 30-35°C, and one from Middle Valley at 5–57°C (Table 4.1). Total genomic DNA was extracted using a phenol-chloroform protocol modified to prevent nucleic acid loss and eliminate

potential inhibitors of downstream PCR, and which has been very successful in studies of low biomass sediments (Adams et al. 2013). PCR amplification was performed with primers designed to be universal to both archaea and bacteria (515F/806R) (Caporaso et al., 2012), containing attached Illumina adaptors and barcodes (Kozich et al., 2013). All DNA extracts were amplified in duplicate with OmniTaq (Taq mutant) polymerase according to the manufacturer's instructions (DNA Polymerase Technologies, St. Louis, MO, USA), with a final concentration of 0.2 µM for each primer. For each PCR, 1 µL template DNA was added to the final reaction mixture for a final volume of 50 µl. Amplification conditions were as follows: 94°C for 3 min to denature DNA; 30 cycles at 94°C for 45 s, 50°C for 60 s, and 72°C for 60 s; and a final extension of 10 min at 72 °C.

Data Processing Description

Raw sequences were first demultiplexed and quality filtered using the QIIME V. 1.8.0 pipeline (Caporaso et al., 2010a). Sequences of poor quality were filtered based on quality scores (< 25), the presence of homopolymers (> 6 nt), and length (< 250 nt). After quality filtering, the sequencing depth was rarified to the least robust sample (4000 nt) for even sub-sampling and maximum rarefaction depth to avoid biases in all downstream analyses (Lundin et al., 2012).

BCO-DMO Processing:
- modified parameter names (replaced spaces with underscores);
- split lat/lon columns into two each; made longitude negative (for West);
- removed degrees, minutes, seconds symbols.

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Data Files

File	
illumina_sequences.csv	(Comma Separated Values (.csv), 1.52 KB) MD5:3a6012d9b5d0855497dce2c8caa4163c
Primary data file for dataset ID 747948	

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Parameters

Parameter	Description	Units
sequence_accession_number	NCBI accession number	unitless
link	URL to NCBI accession	unitless
Species_Names	Description/name of species	unitless
description_of_the_types_of_sequences	Description of the type of sequence	unitless
locations_where_species_were_collected	Location of sample collection	unitless
latitude_dms	Latitude of sample collection in degrees, minutes, and seconds	unitless
longitude_dms	Longitude of sample collection in degrees, minutes, and seconds	unitless
latitude	Latitude of sample collection in decimal degrees; North = positive values	decimal degrees
longitude	Longitude of sample collection in degrees, minutes, and seconds; East = positive values	decimal degrees
Vessel	Name of collection vehicle	unitless
Dive_number	Dive ID number	unitless
sequencing_and_analysis_methods	Description of sequencing and analysis methods	unitless
instrument_and_model	Name of sequencing instruments	unitless
Analysis_methods	Description of analysis methods	unitless

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Instruments

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)

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Project Information

Collaborative Research: The Role of Iron-oxidizing Bacteria in the Sedimentary Iron Cycle: Ecological, Physiological and Biogeochemical Implications (SedimentaryIronCycle)

Coverage: Intertidal coastal river and coastal shelf sediments, mid-coast, Maine, USA; Monteray Bay Canyon, sediments, CA, USA

Iron is a critical element for life that serves as an essential trace element for eukaryotic organisms. It is also able to support the growth of a cohort of microbes that can either gain energy for growth via oxidation of ferrous (Fe(II)) to ferric (Fe(III)) iron, or by utilizing Fe(III) for anaerobic respiration coupled to oxidation of simple organic matter or H2. This coupled process is referred to as the microbial iron cycle. One of the primary sources of iron to the ocean comes from dissolved iron (dFe) that is produced through oxidation and reduction processes in the sediment where iron is abundant. The dFe is transported into the overlaying water where it is an essential nutrient for phytoplankton responsible for primary production in the world's oceans. In fact, iron limitation significantly impacts production in as much as a third of the world's open oceans. The basic geochemistry of this process is understood; however important gaps exist in our knowledge about the details of how the iron cycle works, and how critical a role bacteria play in it.

Intellectual Merit. Conventional wisdom holds that most of the iron oxidation in sediments is abiological, as a result of the rapid kinetics of chemical iron oxidation in the presence of oxygen. This proposal aims to question this conventional view and enhance our understanding of the microbes involved in the sedimentary iron cycle, with an emphasis on the bacteria that catalyze the oxidation of iron. These Fe-oxidizing bacteria (FeOB) utilize iron as a sole energy source for growth, and are autotrophic. They were only discovered in the ocean about forty-five years ago, and are now known to be abundant at hydrothermal vents that emanate ferrous-rich fluids. More recently, the first evidence was published that they could inhabit coastal sediments, albeit at reduced numbers, and even be abundant in some continental shelf sediments. These habitats are far removed from hydrothermal vents, and reveal the sediments may be an important habitat for FeOB that live on ferrous iron generated in the sediment. This begs the question: are FeOB playing an important role in the oxidative part of the sedimentary Fe-cycle? One important attribute of FeOB is their ability to grow at very low levels of O2, an essential strategy for them to outcompete chemical iron oxidation. How low a level of O2 can sustain them, and how this might affect their distribution in sediments is unknown. In part, this is due to the technical challenges of measuring O2 concentrations and dynamics at very low levels; yet these concentrations could be where FeOB flourish. The central hypothesis of this proposal is that FeOB are more common in marine sedimentary environments than previously recognized, and play a substantive role in governing the iron flux from the sediments into the water column by constraining the release of dFe from sediments. A set of experimental objectives are proposed to test this. A survey of near shore regions in the Gulf of Maine, and a transect along the Monterey Canyon off the coast of California will obtain cores of sedimentary muds and look at the vertical distribution of FeOB and putative Fe-reducing bacteria using sensitive techniques to detect their presence and relative abundance. Some of these same sediments will be used in a novel reactor system that will allow for precise control of O2 levels and iron concentration to measure the dynamics of the iron cycle under different oxygen regimens. Finally pure cultures of FeOB with different O2 affinities will be tested in a bioreactor coupled to a highly sensitive mass spectrometer to determine the lower limits of O2 utilization for different FeOB growing on iron, thus providing mechanistic insight into their activity and distribution in low oxygen environments.

Broader Impacts. An important impact of climate change on marine environments is a predicted increase in low O2 or hypoxic zones in the ocean. Hypoxia in association with marine sediments will have a profound influence on the sedimentary iron cycle, and is likely to lead to greater inputs of dFe into the ocean. In the longer term, this increase in dFe flux could alleviate iron-limitation in some regions of the ocean, thereby enhancing the rate of CO2-fixation and draw down of CO2 from the atmosphere. This is one important reason for developing a better understanding of microbial control of sedimentary iron cycle. This project will also provide training to a postdoctoral scientist, graduate students and undergraduates. This project will contribute to a student initiated exhibit, entitled 'Iron and the evolution of life on Earth' at the Harvard Museum of Natural History providing a unique opportunity for undergraduate training and outreach.

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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-1459252

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