19 Metagenomes and 7 metatranscriptomes from sediment samples collected offshore of San Francisco, Califronia, USA

Website: https://www.bco-dmo.org/dataset/862731
Data Type: Cruise Results
Version: 1
Version Date: 2021-10-11

Project
» Nitrogen Fixation in Deep-Sea Sediments (Deep Sediment N Fix)

Contributors	Affiliation	Role
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Abstract
This dataset includes metadata and NCBI accession numbers describing 19 metagenomes and 7 metatranscriptomes from sediment samples collected offshore of San Francisco, Califronia, USA in March 2017 on R/V Oceanus cruise OC1703A. The generation of these data was completed on May 7, 2021.

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Coverage

Spatial Extent: **N**:37.13 **E**:-121.03 **S**:35.69 **W**:-123.08
Temporal Extent: 2017-03-14 - 2017-03-21

Methods & Sampling

Sediment was collected with an MC-800 multicorer aborad the R/V Oceanus (expedition 1703A) approximately 0-300 km off the coast of San Francisco, CA, USA. Cores were stored at 4C until extrusion and sectioning within 24h of collection. Cores were sectioned into 2.5-5cm vertical horizons, and approximately 2g of sediment were sampled from each horizon with a cut-off syringe, flash frozen in liquid nitrogen, and stored at -80C until extraction of nucleic acids. DNA was extracted with an RNeasy PowerSoil DNA elution kit (Qiagen, cat. no 12867-25) in combination with an RNeasy PowerSoil Total RNA kit (Qiagen, cat. no 12866-25). The manufacturer's protocol was modified to include a bead-beating step of 5.5 m/s for 2x45s with a FastPrep-24 instrument. DNA and RNA were eluted in 100 microliters of DNAse and RNAse-free water or 1xTE and stored at -80C. Total RNA was treated with DNAse (Thermo Fisher Scientific,cat. no AM1907). Three DNA samples were additionally processed for long-read sequencing by size-selection with the BluePippin instrument targeting the size range of 10-50kb and a library was prepared for sequencing with the 10x Genomics Chromium system according to manufacturer's protocol and described in Bishara et al. (2018, https://doi.org/10.1038/nbt.4266). Chromium libraries were sequenced with 2 x 151bp sequencing on an HiSeq 4000 instrument (Illumina). All other samples were processed by the Joint Genome Institute (Department of Energy). DNA was sheared to approximately 300bp using a Covaris LE220 ultrasonicator and size selected

with SPRI beads and libraries prepared and barcoded using Kapa Biosystems library preparation kit. Total RNA was treated with Ribo-Zero rRNA removal kit (Illumina) and cDNA libraries generated using the Illumina Truseq Stranded mRNA Library Prep kit. The rRNA depleted RNA was fragmented and reversed transcribed using random hexamers and SSII (Invitrogen) followed by second strand synthesis. The fragmented cDNA was treated with end-pair, A-tailing, adapter ligation, and 10 cycles of PCR. DNA and cDNA were sequenced with 2 x 151bp sequencing on a Nova Seq S4 (Illumina) instrument.

Data Processing Description

BCO-DMO Processing:
- replaced "na" with "nd" (no data)

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Related Publications

Bishara, A., Moss, E. L., Kolmogorov, M., Parada, A. E., Weng, Z., Sidow, A., … Bhatt, A. S. (2018). High-quality genome sequences of uncultured microbes by assembly of read clouds. Nature Biotechnology, 36(11), 1067–1075. doi:10.1038/nbt.4266
Methods

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Parameters

Parameter	Description	Units
BioProject	BioProject accession	unitless
BioSample	BioSample accession	unitless
SRA_run_ID	SRA run accession	unitless
SRA_run_link	Hyperlink to SRA run	unitless
SRA_study_ID	SRA study accession	unitless
SRA_title	SRA title	unitless
library_strategy	Sequence library type	unitless
library_source	Source of nucleic acids	unitless
library_selection	Library selection	unitless
library_layout	Library layout	unitless
platform	Sequencing platform	unitless
instrument_model	Sequencer model	unitless
design_description	Sampling design	unitless
elevation	Depth from sea level surface	meters (m)
depth	Depth from seafloor	centimeters (cm)
latitude	Sampling latitude	decimal degrees North
longitude	Sampling longitude	decimal degrees East
collection_date	Date sample collected; format: YYYY-MM-DD	unitless

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Instruments

Dataset-specific Instrument Name	Illumina NovaSeq 6000
Generic Instrument Name	Automated DNA Sequencer
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.

Dataset-specific Instrument Name	Illumina HiSeq 4000
Generic Instrument Name	Automated DNA Sequencer
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.

Dataset-specific Instrument Name	Sea-Bird Scientific CTD
Generic Instrument Name	CTD Sea-Bird
Dataset-specific Description	provided real-time collection of depth, temperature, salinity
Generic Instrument Description	Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics, no specific unit identified. This instrument designation is used when specific make and model are not known. See also other SeaBird instruments listed under CTD. More information from Sea-Bird Electronics.

Dataset-specific Instrument Name	MC-800
Generic Instrument Name	Multi Corer
Generic Instrument Description	The Multi Corer is a benthic coring device used to collect multiple, simultaneous, undisturbed sediment/water samples from the seafloor. Multiple coring tubes with varying sampling capacity depending on tube dimensions are mounted in a frame designed to sample the deep ocean seafloor. For more information, see Barnett et al. (1984) in Oceanologica Acta, 7, pp. 399-408.

Dataset-specific Instrument Name	BluePippin
Generic Instrument Name	Sage Science BluePippin DNA size selection device
Generic Instrument Description	An automated DNA size selection instrument, with pulsed-field electrophoresis for resolving and collecting high molecular weight DNA. The instrument is used to automatically extract DNA fragments of a user selected size for downstream technologies such as miRNA isolation, DNA sequencing, RNA-seq, genotyping, DNA sequencing, ChIP-seq, and Long-read sequencing. The instrument uses electrophoresis along with laser detection or other imaging technology to determine when to start collecting DNA based on size ranges entered by the user. Once the DNA is no longer in the desired size range, collection ceases. The instrument has electrophoresis voltage options: 25V, 100V or 150V constant, or 100V pulsed field. The optical detection wavelength is 470 nm excitation, and 525 nm emission. The instrument can run up to 5 samples/gel cassettes at a time, with no possibility of cross contamination.

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Deployments

OC1703A

Website	https://www.bco-dmo.org/deployment/717423
Platform	R/V Oceanus
Start Date	2017-03-14
End Date	2017-03-23
Description	See additional cruise information from the Rolling Deck to Repository (R2R): https://www.rvdata.us/search/cruise/OC1703A

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Project Information

Nitrogen Fixation in Deep-Sea Sediments (Deep Sediment N Fix)

Coverage: California Shelf (36,-123)

NSF Award Abstract:

Life requires nitrogen for growth. Atmospheric nitrogen (N2) is the most abundant form of nitrogen on the surface of the planet, but most organisms cannot assimilate N2 directly. Habitats can therefore be nitrogen limited, meaning the demand for "bioavailable" nitrogen exceeds the supply, and its availability controls the overall growth and productivity of the community. A small subset of microorganisms, termed diazotrophs, convert N2 to bioavailable forms of nitrogen, including ammonium and nitrogenous organic matter, in a process known as N2 fixation. Diazotrophs are the largest natural source of bioavailable nitrogen on the planet, and the rate at which they fix N2 can control the rates at which other important microbial processes occur, such as the production and consumption of greenhouse gases. Understanding diazotrophs in the environment - their identity, distribution, activity levels, and biogeochemical controls - is therefore essential to understanding overall microbial community activity and biogeochemical cycling. The goal of this project is to characterize N2 fixation in deep-sea sediments, a generally understudied but expansive habitat, covering nearly two thirds of our planet. The project will have broader impacts via educational outreach, support and training of early career scientists, and scientific impact: since rates of marine methane, carbon dioxide, and nitrous oxide cycling are affected by nitrogen availability, the results will inform our understanding of greenhouse gas cycling in the marine environment, and therefore climate stability, a topic central to global security.

N2 fixation is a critical and intensely studied metabolism in the marine photic zone. Much less is known about N2 fixation in deep-sea sediments, but it could be an important factor in both benthic productivity and ocean-scale elemental cycling. Several observations have suggested or directly detected N2 fixation at localized areas of enhanced productivity on the seafloor (e.g., methane seeps and hydrothermal vents), raising the possibility that deep-sea N2 fixation is widespread. However, few measurements of N2 fixation have been made outside of these anomalous areas, and thus little is known about N2 fixation in the vast majority of the deep ocean floor. Preliminary data suggest N2 fixation does occur in typical deep marine sediment, and is mediated by a diverse set of yet unidentified microorganisms. This project will combine techniques from molecular biology and geochemistry to systematically investigate N2 fixation in representative deep-sea sediments collected along a depth profile (500 to 4500 m water depth) offshore California. The project will determine the (1) rates and distribution of N2 fixation (2) abundance, diversity, and distribution of genes and transcripts associated with N2 fixation (nif) (3) phylogenetic identity of the biological mediators (diazotrophs) and (4) physiochemical controls on diazotrophic community structure and activity. For context, the activity of the non-diazotrophic bacterial community will also be characterized. The results may lead to upward revisions of the estimates of new nitrogen production in the seafloor, and therefore change our understanding of the current balance of the marine nitrogen cycle. Together, this hypothesis-driven characterization of N2 fixation in deep-sea sediments will shed light on an expansive, climatically important, and traditionally understudied habitat, and facilitate more accurate extrapolation of the rates and distribution of N2 fixation on the whole seafloor as well as the metabolic response of the seafloor community to environmental change.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1634297
US Department of Energy - Joint Genome Institute (DOE-JGI)	504079

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