NCBI accession numbers describing 16S rRNA and 16S rRNA gene amplicon sequences from sediment samples collected offshore of San Francisco, Califronia, USA in March 2017 on R/V Oceanus cruise OC1703A

Website: https://www.bco-dmo.org/dataset/862690
Data Type: Cruise Results
Version: 1
Version Date: 2021-10-07

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 16S rRNA and 16S rRNA gene amplicon sequences from sediment samples collected offshore of San Francisco, Califronia, USA in March 2017 on R/V Oceanus cruise OC1703A.

Table of Contents

- Coverage
- Dataset Description
  - Methods & Sampling
  - Data Processing Description
- Data Files
- Related Publications
- Parameters
- Instruments
- Deployments
- Project Information
- Funding

Coverage

Spatial Extent: **N**:37.134378333333 **E**:-122.54423333333 **S**:35.68905 **W**:-124.92211
Temporal Extent: 2017-03-15 - 2017-03-22

Methods & Sampling

Sediment was collected with an MC-800 multicorer aboard 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 was 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). RNA was then reverse transcribed to cDNA using the SuperScript III First Strand RT PCR kit according to the manufacturer’s instructions (Thermo Fisher Scientific, cat. no 18080-400). DNA and cDNA were amplified wtih universal V4/V5

primers, 515F/926R (Parada et al., 2016). The loci-specific cycling conditions included an initial heating step at 95 C for 180 s, followed by 25 cycles of 95 C for 45 s, 50 C for 45 s, 68 C for 90 s, and a final extension of 68 C for 5 min. Barcodes were added to individual samples by a second PCR step consisting of an initial denaturation step at 95 C for 180 s, followed by 8 cycles of 95 C for 30 s, 55 C for 30 s, 72 C for 30 s and a final extension step at 72 C for 300 s. Sequencing was performed at the UC Davis Genome Center using Illumina MiSeq 2 x 250 bp paired-end technology.

Data Processing Description

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

[table of contents | back to top]

Data Files

File
OC1703A_accessions.csv (Comma Separated Values (.csv), 164.80 KB) MD5:7717025626a8ecc83a4e9bbf8ca962fd Primary data file for dataset ID 862690

[table of contents | back to top]

Related Publications

Parada, A. E., Needham, D. M., & Fuhrman, J. A. (2016). Every base matters: assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. Environmental Microbiology, 18(5), 1403–1414. doi:10.1111/1462-2920.13023
Methods

[table of contents | back to top]

Parameters

Parameter	Description	Units
BioProject	NCBI BioProject accession	unitless
BioSample	NCBI BioSample accession	unitless
SRA_run_ID	NCBI SRA run accession	unitless
SRA_title	NCBI 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
filetype	File type	unitless
filename	File name of forward reads	unitless
filetpe2	File type	unitless
filename2	file name of reverse reads	unitless
depth	Depth from seafloor	centimeters (cm)
elevation	Depth from sea surface level	meters (m)
latitude	Sampling latitude	decimal degrees North
longitude	Sampling longitude	decimal degrees East
collection_date	Date of sample collection in format YYYY-MM-DD	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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	A Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics. This instrument designation is used when specific make and model are not known or when a more specific term is not available in the BCO-DMO vocabulary. Refer to the dataset-specific metadata for more information about the specific CTD used. More information from: http://www.seabird.com/

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.

[table of contents | back to top]

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

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1634297

[table of contents | back to top]