NCBI accession numbers describing nifH 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/863192
Data Type: Cruise Results
Version: 1
Version Date: 2021-10-13

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

Contributors	Affiliation	Role
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Abstract

These data are raw, demultiplexed nifH amplicon sequences generated from Illumina MiSeq for the investigation of potential diazotroph diversity along a continental margin transect. Raw Illumina MiSeq 2×250 bp sequence data can be accessed in the NCBI SRA database under accession numbers ERP130242 and ERP120468 and BioProject accession numbers PRJEB46054 and PRJEB37167. Data under accession number ERP120468 and BioProject accession number PRJEB37167 were published in Kapili and Dekas, 2021. The generation of these data was completed on June 29, 2021.

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Coverage

Spatial Extent: **N**:37.134378 **E**:-122.544233 **S**:35.68905 **W**:-124.92211

Methods & Sampling

Sediment samples were collected using a multicorer on board the R/V Oceanus (March 2017) and sample aliquots were immediately stored at -80°C until DNA extraction. DNA was extracted in the laboratory using an RNeasy PowerSoil DNA elution kit (Qiagen, catalog no. 12867-25) after RNA was extracted using an RNeasy PowerSoil Total RNA kit. (Qiagen, catalog no. 12866-25).

nifH sequences were amplified using the PCR primers described in Mehta et al., 2003 and amplicons were prepared for 2×250 bp sequencing on an Illumina MiSeq platform following the protocol described in Kapili et al., 2020.

Data Processing Description

Data Processing:
Samples were demultiplexed at the UC Davis DNA Technologies Core facility.

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

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Data Files

File
nifH_amplicons.csv(Comma Separated Values (.csv), 62.29 KB) MD5:bb978997ab2d8ebe08aa42663aadd333 Primary data file for dataset ID 863192

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Related Publications

Kapili, B. J., & Dekas, A. E. (2021). PPIT: an R package for inferring microbial taxonomy from nifH sequences. Bioinformatics, 37(16), 2289–2298. doi:10.1093/bioinformatics/btab100
Results

Kapili, B. J., Barnett, S. E., Buckley, D. H., & Dekas, A. E. (2020). Evidence for phylogenetically and catabolically diverse active diazotrophs in deep-sea sediment. The ISME Journal, 14(4), 971–983. doi:10.1038/s41396-019-0584-8
Methods

Mehta, M. P., Butterfield, D. A., & Baross, J. A. (2003). Phylogenetic Diversity of Nitrogenase (nifH) Genes in Deep-Sea and Hydrothermal Vent Environments of the Juan de Fuca Ridge. Applied and Environmental Microbiology, 69(2), 960–970. doi:10.1128/aem.69.2.960-970.2003
Methods

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Related Datasets

IsRelatedTo

STANFORD UNIVERSITY. PPIT: an R package for inferring microbial taxonomy from nifH sequences. 2020/09. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJEB37167. NCBI:BioProject: PRJEB37167

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Parameters

Parameter	Description	Units
BioProject	BioProject accession	unitless

BioSample	BioSample accession	unitless
SRA_study	SRA study accession	unitless
Assay_Type	Assay type	unitless
Sequencing_platform	Squencing platform	unitless
Instrument_model	Illumina model	unitless
Library_layout	Library layout	unitless
File_name_1	File name of forward reads	unitless
File_name_2	File name of reverse reads	unitless
File_type	File type	unitless
Sequencing_method	Sequencing method	unitless
Library_selection	Library selection	unitless
PCR_primers	PCR primer sequences	unitless
Sequencing_adapters	Illumina adapter sequences	unitless
Geographic_location	Sampling location	unitless
Sample_type	Environmental sample type	unitless
Sample_name	Sample name	unitless
Sample_latitude	Sampling latitude	decimal degrees North
Sample_longitude	Sampling longitude	decimal degrees East
Deployment_number	Deployment number	unitless

Multicore_number	Mulitcore number	unitless
Seawater_depth	Seawater depth	meters below sea surface
Sediment_depth	Sediment depth	centimeters below sediment surface

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq platform
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	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.

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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

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