Sequence read accession (SRA) numbers for bacterial and archaeal 16S rRNA gene amplicons from the DeepCCZ and Abyssline programs

Website: https://www.bco-dmo.org/dataset/861683
Data Type: Cruise Results
Version: 1
Version Date: 2023-10-25

Project
» DeepCCZ (DeepCCZ)

Contributors	Affiliation	Role
Church, Matthew J.	University of Montana	Principal Investigator
Drazen, Jeffrey C.	University of Hawaii at Manoa (SOEST)	Co-Principal Investigator
Smith, Craig R.	University of Hawaii at Manoa (SOEST)	Co-Principal Investigator
Wear, Emma	University of Montana	Scientist, Contact
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This dataset includes sequence read accession (SRA) numbers for bacterial and archaeal 16S rRNA gene amplicons from the DeepCCZ and Abyssline programs.

Table of Contents

Coverage

Spatial Extent: **N**:19.4724 **E**:-116.4598 **S**:4.8879 **W**:-153.7464
Temporal Extent: 2013-10-08 - 2018-06-13

Dataset Description

This sample set includes 16S rRNA gene amplicon sequences from both samples newly collected on the DeepCCZ cruise in the western Clarion-Clipperton Zone and re-sequenced, archival samples from the Abyssline01 and Abyssline02 cruises in the northeastern Clarion-Clipperton Zone.

Methods & Sampling

On the DeepCCZ cruise, benthic samples (sediments and nodules) were collected using the ROV Lu'ukai, using

push corers and the ROV's manipulator arm. On the Abyssline cruises, benthic samples were collected with box corers and megacorers. On both cruises, water samples were collected with Niskin bottles mounted on a sampling rosette.

Sediment samples were sectioned into depth horizons and stored frozen at -80 degrees Celsius (C). Nodules were rinsed with 0.2-µm-filtered seawater and frozen whole at -80C. On DeepCCZ, seawater was sequentially collected on 3 µm and 0.2 µm pore-size filters; on the Abyssline cruises, seawater was collected on 0.2 micrometer (µm) pore-size filters. Filters were stored frozen at -80C.

Genomic DNA was extracted from seawater filters using a DNeasy Plant Mini Kit (Qiagen) with modifications as described in Shulse et al. (2017; doi: 10.1002/mbo3.428). Genomic DNA was extracted from subsamples of sediments and nodules using the FastDNA Spin Kit for Soil, modified as described in Shulse et al. (2017). gDNA was concentrated using the Zymo Clean & Concentrator-5 kit.

The V4-V5 region of the 16S rRNA gene was amplified using primers 515F-Y and 926R as recommended by Parada et al. (2016; doi: 10.1111/1462-2920.13023), with a multiplexing index on the forward primer following the design of the Earth Microbiome Project (https://earthmicrobiome.org/protocols-and-standards/16s/). Triplicate amplifications were combined and cleaned with an ENZA Cycle Pure Kit (Omega Bio-Tek) and then pooled at approximately equimolar proportions into two libraries. Libraries were sequenced at the University of Montana on an Illumina MiSeq using paired-end 250 v2 chemistry. Samples were demultiplexed by the sequencing facility.

Problem Report:
On DeepCCZ, sediments were not collected from the seamount in APEI 1 due to ROV constraints.

Data Processing Description

Data Processing:
Demultiplexing was conducted by the sequencing facility.

BCO-DMO Processing Description

- Imported original file named "DeepCCZ_DNA_metadata_for_BCODMO_v2.xlsx" into the BCO-DMO system.
- Changed date format to YYYY-MM-DD.
- Converted longitude from positive degrees west to negative degrees east.
- Replaced mu symbol with u.
- Saved the final file as "861683_v1_sra.csv".

[table of contents | back to top]

Data Files

File	
861683_v1_sra.csv	(Comma Separated Values (.csv), 151.32 KB) MD5:816205c2eaed6b6e1fd3c92853c66793
Primary data file for dataset ID 861683, version 1.	

[table of contents | back to top]

Related Publications

Lindh, M. V., Maillot, B. M., Shulse, C. N., Gooday, A. J., Amon, D. J., Smith, C. R., & Church, M. J. (2017). From the Surface to the Deep-Sea: Bacterial Distributions across Polymetallic Nodule Fields in the Clarion-Clipperton Zone of the Pacific Ocean. Frontiers in Microbiology, 8. doi:10.3389/fmicb.2017.01696

Methods

Shulse, C. N., Maillot, B., Smith, C. R., & Church, M. J. (2016). Polymetallic nodules, sediments, and deep waters in the equatorial North Pacific exhibit highly diverse and distinct bacterial, archaeal, and microeukaryotic communities. MicrobiologyOpen, 6(2), e00428. doi:10.1002/mbo3.428
Methods

Wear, E. K., Church, M. J., Orcutt, B. N., Shulse, C. N., Lindh, M. V., & Smith, C. R. (2021). Bacterial and Archaeal Communities in Polymetallic Nodules, Sediments, and Bottom Waters of the Abyssal Clarion-Clipperton Zone: Emerging Patterns and Future Monitoring Considerations. Frontiers in Marine Science, 8. doi:10.3389/fmars.2021.634803
Methods

[table of contents | back to top]

Related Datasets

IsRelatedTo

University of Montana. DeepCCZ bacterial and archaeal 16S rRNA gene community surveys from Clarion-Clipperton Zone APEIs. 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/PRJNA660809. NCBI:BioProject: PRJNA660809.

[table of contents | back to top]

Parameters

Parameter	Description	Units
bioproject_accession	NCBI SRA BioProject accession number	unitless
sample_name	sample name	unitless
SRA_run_ID	NCBI SRA run ID	unitless
design_description	basic description of how sequences were generated	unitless
Cruise	name of cruise on which sample was collected	unitless
Isolation_Source	physical substrate from which DNA was sequenced	unitless
latitude	latitude, in degrees north	decimal degrees North
longitude	longitude (negative values = West)	decimal degrees East
CCZ_region	administrative region where sample was collected, following the terminology of the International Seabed Authority	unitless
benthic_structure	bathymetric feature where sample was collected	unitless
bottom_depth	total depth of water column where sample was collected	m
sample_depth	depth where sample was collected (seawater samples: depth in water column in m; sediment and nodule samples: depth (range) in sediments where collected)	m or cm or descriptive
date_collected	date sample was collected from the field (UTC); format: YYYY-MM-DD	unitless
filter_size_range	size range of filter cut-offs on which DNA was collected (water column samples only)	um
sample_size	amount of sample collected from the environment (seawater samples: volume filtered in L; sediment: volume frozen in mL)	L or mL or descriptive
sample_size_extracted	volume or mass of sample from which DNA was extracted (large nodules were extracted multiple times and resulting gDNA was combined with weighting by extraction mass)	L or g

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	box corers
Generic Instrument Name	Box Corer
Generic Instrument Description	General description of a box corer: A box corer is a marine geological tool that recovers undisturbed soft surface sediments. It is designed for minimum disturbance of the sediment surface by bow wave effects. Traditionally, it consists of a weighted stem fitted to a square sampling box. The corer is lowered vertically until it impacts with the seabed. At this point the instrument is triggered by a trip as the main coring stem passes through its frame. While pulling the corer out of the sediment a spade swings underneath the sample to prevent loss. When hauled back on board, the spade is under the box. (definition from the SeaVox Device Catalog) Box corers are one of the simplest and most commonly used types of sediment corers. The stainless steel sampling box can contain a surface sediment block as large as 50cm x 50cm x 75cm with negligible disturbance. Once the sediment is recovered onboard, the sediment box can be detached from the frame and taken to a laboratory for subsampling and further analysis. The core sample size is controlled by the speed at which the corer is lowered into the ocean bottom. When the bottom is firm, a higher speed is required to obtain a complete sample. A depth pinger or other depth indicator is generally used to determine when the box is completely filled with sediment. Once the core box is filled with sediment, the sample is secured by moving the spade-closing lever arm to lower the cutting edge of the spade into the sediment, until the spade completely covers the bottom of the sediment box. (definition from Woods Hole Oceanographic Institution).

Dataset-specific Instrument Name	megacorers
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	Niskin bottle
Generic Instrument Name	Niskin bottle
Dataset-specific Description	Water samples were collected with Niskin bottles mounted on a sampling rosette.
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

Dataset-specific Instrument Name	push corers
Generic Instrument Name	Push Corer
Generic Instrument Description	Capable of being performed in numerous environments, push coring is just as it sounds. Push coring is simply pushing the core barrel (often an aluminum or polycarbonate tube) into the sediment by hand. A push core is useful in that it causes very little disturbance to the more delicate upper layers of a sub-aqueous sediment. Description obtained from: http://web.whoi.edu/coastal-group/about/how-we-work/field-methods/coring/

Dataset-specific Instrument Name	ROV Lu'ukai
Generic Instrument Name	Remotely Operated Vehicle
Dataset-specific Description	See: https://www.soest.hawaii.edu/UMC/cms/Luukai.php SOEST took delivery of the ROV Lu'ukai in 2013. It is a two-part, "top hat" system, consisting of the vehicle itself, performing science operations on the seabed or in the water column, and a Tether Management System (TMS) which hovers above the working vehicle and relays power and data to and from the support ship on the surface. The two components are launched, recovered and transported to the ocean floor as a stacked unit. Upon arrival at the work site, the ROV vehicle is "undocked" from the TMS and piloted to the seabed to commence a mission. Upon completion of the mission, the vehicle is docked to the TMS and the "stack" is then recovered to deck.
Generic Instrument Description	Remotely operated underwater vehicles (ROVs) are unoccupied, highly maneuverable underwater robots operated by a person aboard a surface vessel. They are linked to the ship by a group of cables that carry electrical signals back and forth between the operator and the vehicle. Most are equipped with at least a video camera and lights. Additional equipment is commonly added to expand the vehicle’s capabilities. These may include a still camera, a manipulator or cutting arm, water samplers, and instruments that measure water clarity, light penetration, and temperature.

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)

[table of contents | back to top]

Deployments

KM1808

Website	https://www.bco-dmo.org/deployment/857287
Platform	R/V Kilo Moana
Start Date	2018-05-14
End Date	2018-06-16
Description	Additional cruise information is available from the Rolling Deck to Repository (R2R): https://www.rvdata.us/search/cruise/KM1808

MV1313

Website	https://www.bco-dmo.org/deployment/857284
Platform	R/V Melville
Start Date	2013-10-03
End Date	2013-10-27
Description	Additional cruise information is available from the Rolling Deck to Repository (R2R): https://www.rvdata.us/search/cruise/MV1313

TN319

Website	https://www.bco-dmo.org/deployment/857281
Platform	R/V Thomas G. Thompson
Start Date	2015-02-13
End Date	2015-03-25
Description	Additional cruise information is available from the Rolling Deck to Repository (R2R): https://www.rvdata.us/search/cruise/TN319

[table of contents | back to top]

Project Information

DeepCCZ (DeepCCZ)

Website: https://oceanexplorer.noaa.gov/explorations/18ccz/welcome.html

Coverage: Western Clarion-Clipperton Zone of the North Pacific Subtropical Gyre (~5N 142 W to ~11N 154 W)

GBMF Grant Name: Closing Gaps in Knowledge About Biodiversity and Ecology of the Deep Sea to Better Assess the Impacts of Deep-Sea Mining

GBMF Grant Statement: To generate a better understanding of the biodiversity oand ecology of a large deep-sea ecosystem prior to mining

Expected Measurements:

- Shipboard underway data: meteorological data, navigation data, and processed multibeam mapping data,
- processed CTD water-column environmental data (e.g., water temperature, pH, salinity, light),
- raw ROV video records and associated environmental sensor data
- raw free vehicle baited video and still imagery
- specimen capture records (ROV and trap - location, date, time, and all body measurements)
- processed DNA sequence data for captured animal specimens

- processed metagenomic DNA sequence data for microbial assemblages in sediment and water samples
- sediment community respiration and nutrient regeneration data
- isotopic data for sediment infaunal organisms

Anticipated Derived Data Products:

- Biodiversity, abundance, and species composition of benthic megafauna, mobile scavengers, and sediment microbes at each study location
- Sediment community function (respiration, nutrient regeneration, detrital processing) at each study location
- Genetic connectivity at species and population levels for key megafaunal and mobile scavenger species between study locations.

[table of contents | back to top]

Funding

Funding Source	Award
Gordon and Betty Moore Foundation (GBMF)	GBMF5596
National Oceanic and Atmospheric Administration (NOAA)	NA17OAR0110209

[table of contents | back to top]