515F-926R 16S rRNA gene sequencing accessions from seawater and sediment samples from R/V Falkor FK141109 and R/V Thompson TN309 from the Mariana and Kermadec trenches, 2014 (Mariana Perspectives project)

Website: https://www.bco-dmo.org/dataset/720916
Data Type: Cruise Results
Version:
Version Date: 2017-12-13

Project
» Patterns of Microbial Community Structure Within and Between Hadal Environments (Mariana Perspectives)

Contributors	Affiliation	Role
Bartlett, Douglas	University of California-San Diego (UCSD-SIO)	Principal Investigator
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Table of Contents

Coverage

Spatial Extent: **N**:12.7306 **E**:-170 **S**:-37.7337 **W**:145
Temporal Extent: 2014-04-10 - 2014-12-09

Dataset Description

This dataset includes links to 515F-926R 16S rRNA gene sequencing accessions archived at NCBI and associated collection data from seawater and sediment samples from the Mariana and Kermadec trenches from April and November 2014.

For those accessions with a status of 'not yet available' at NCBI, they will be made available once the paper has been published, likely by mid-2018. Please check back for them then or contact the PI.

Methods & Sampling

This data set is associated with PI Douglas Bartlett (NSF OCE-1536776) and R/V Thomas G. Thompson from Apr. 10 - May 20 to the Kermadec Trench adjacent to New Zealand and Schmidt Ocean Institute R/V Falkor cruise FK141109 from Nov. 9 - Dec. 9, 2014, to the Mariana Trench. During the cruises, sediment and water samples were collected. Additional details can be found at: https://schmidtocean.org/cruise/expanding-mariana-trench-perspectives/ and https://scripps.ucsd.edu/labs/dbartlett/contact/challenger-deep-cruise-2014/

Seawater (40-120 L per sample) was serially filtered through 3.0 (47 mm diameter), 0.2 (47 mm or Sterivex), and 0.1 µm (142 mm) polycarbonate filters using a peristaltic pump. Filters were then placed into a sucrose

buffer (Rusch et al., 2007) and frozen at -80°C. DNA was extracted from whole filters using a protocol previously described (Fuhrman et al., 1988; Tarn et al., 2016). Negative controls using blank filters were extracted in concomitance with every extraction performed.

DNA from sediment (5 g wet-weight) samples was extracted using a modified version of Lysis Protocol II described by Lever et al. (2015). 2.5 V of lysis solution (30 mM EDTA, 30 mM Tris-HCl, 800 mM guanidine hydrochloride, 0.5% Triton X-100, final pH 10) and 500 µmol pyrophosphate was added to each sample and the mixture briefly vortexed. Samples were then subjected to two 15 minute freeze-thaw cycles at -80°C, followed by incubation at 50°C with shaking at 150 rpm for one hour. Samples were centrifuged and the supernatant was treated twice with 1 V chloroform isoamyl alcohol. DNA was precipitated using 5 M NaCl and ethanol for two hours at room temperature and resuspended in nuclease-free water. Extracted DNA was cleaned again using a Quick-gDNA MiniPrep kit (Zymo Research, Irvine, CA). Negative control blanks, consisting of all reagents but no sediment material, were performed in concomitance with every extraction.

The V4-V5 16S rRNA gene region between 515f-926R was amplified (Parada et al., 2015) and tagged with Illumina barcodes using a secondary PCR procedure. Samples were pooled at equimolar concentrations and sent for sequencing on an Illumina Miseq at the Institute for Genomic Medicine Genomics Center (University of California, San Diego, La Jolla, CA).

Data Processing Description

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- split lat and lon into separate columns and rounded to 4 decimal places
- removed blank spaces in 3 sample names.

[table of contents | back to top]

Data Files

File
accessions.csv (Comma Separated Values (.csv), 55.54 KB) MD5:005ac80dc77e7a594d52c107a8b9681e Primary data file for dataset ID 720916

[table of contents | back to top]

Related Publications

Fuhrman JA, Comeau DE, Hagstrom A, Chan AM. Extraction from natural plankton microorganisms of DNA suitable for molecular biological studies. Appl Environ Microbiol. 1988;54: 1426-1429.
Methods

Lever, M. A., Torti, A., Eickenbusch, P., Michaud, A. B., Å antl-Temkiv, T., & JÃ¸rgensen, B. B. (2015). A modular method for the extraction of DNA and RNA, and the separation of DNA pools from diverse environmental sample types. Frontiers in Microbiology, 6. doi:10.3389/fmicb.2015.00476
Methods

Parada, A. E., Needham, D. M., & Fuhrman, J. A. (2015). 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

Rusch, D. B., Halpern, A. L., Sutton, G., Heidelberg, K. B., Williamson, S., Yooseph, S., … Venter, J. C. (2007). The Sorcerer II Global Ocean Sampling Expedition: Northwest Atlantic through Eastern Tropical Pacific. PLoS Biology, 5(3), e77. doi:10.1371/journal.pbio.0050077
Methods

Tarn, J., Peoples, L. M., Hardy, K., Cameron, J., & Bartlett, D. H. (2016). Identification of Free-Living and Particle-Associated Microbial Communities Present in Hadal Regions of the Mariana Trench. Frontiers in Microbiology, 7. doi:10.3389/fmicb.2016.00665
Methods

[table of contents | back to top]

Parameters

Parameter	Description	Units
Sample_name	sample identifier	unitless
Sample_title	NCBI sample title	unitless
Collection_date	sample collection date	unitless
Depth	sample deplth	meters
Type	sample type: seawater or sediment	unitless
Location	collection location: ocean and trench name	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
filter_size	filter size fractions	microns
status	whether access to NCBI pages are public or not	unitless
Bioproject_link	NCBI BioProject accession number and link to associated NCBI web page	unitless
Biosample_link	NCBI BioSample accession number and link to associated NCBI web page	unitless
sediment_depth	sediment core depth of the sample	centimeters

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina Miseq
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Sequencing was performed at the Institute for Genomic Medicine Genomics Center (University of California, San Diego, La Jolla, CA).
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	Rock grabber
Generic Instrument Name	Bottom Sediment Grab Samplers
Generic Instrument Description	These samplers are designed to collect an accurate representative sample of the sediment bottom. The bite of the sampler should be deep enough so all depths are sampled equally. The closing mechanism is required to completely close and hold the sample as well as prevent wash-out during retrieval. Likewise, during descent the sampler should be designed to minimize disturbance of the topmost sediment by the pressure wave as it is lowered to the bottom.

Dataset-specific Instrument Name	
Generic Instrument Name	CTD - profiler
Generic Instrument Description	The Conductivity, Temperature, Depth (CTD) unit is an integrated instrument package designed to measure the conductivity, temperature, and pressure (depth) of the water column. The instrument is lowered via cable through the water column. It permits scientists to observe the physical properties in real-time via a conducting cable, which is typically connected to a CTD to a deck unit and computer on a ship. The CTD is often configured with additional optional sensors including fluorometers, transmissometers and/or radiometers. It is often combined with a Rosette of water sampling bottles (e.g. Niskin, GO-FLO) for collecting discrete water samples during the cast. This term applies to profiling CTDs. For fixed CTDs, see https://www.bco-dmo.org/instrument/869934.

Dataset-specific Instrument Name	
Generic Instrument Name	HROV Nereus
Generic Instrument Description	Nereus is an efficient, multi-purpose “hybrid” vehicle that can explore and operate in the crushing pressures of the greatest ocean depths. An unmanned vehicle, Nereus operates in two complementary modes. It can swim freely as an autonomous underwater vehicle (AUV) to survey large areas of the depths, map the seafloor, and give scientists a broad overview. When Nereus locates something interesting, the vehicle’s support team can bring the vehicle back on board the ship and transforms it into a remotely operated vehicle (ROV) tethered to the ship via a micro-thin, fiber-optic cable. Through this tether, Nereus can transmit high-quality, real-time video images and receive commands from skilled pilots on the ship to collect samples or conduct experiments with a manipulator arm. Technical specifications: Weight on land: 2,800 kg Payload capacity: 25 kg Maximum speed: 3 knots Batteries: rechargable lithium ion, 15 kilowatt hours in two pressure housings Thrusters: 2 fore and aft, 2 vertical, 1 lateral (ROV mode) 2 fore and aft, 1 vertical (AUV mode) Lights: variable output LED array, strobes Manipulator arm: Kraft TeleRobotics 7-function hydraulic manipulator Sonar: scanning sonar, forward look and profile, 675 KHz Sensors: magnetometer, CTD (to measure conductivity, temperature, and depth) Nereus supports a variety of science operations: Push coring, measuring heat flow, geotechnical and geochemical sensing, rock sampling and drilling, biological sampling, water sampling, high resolution acoustic bathymetry, and optical still and video imagery. More information is available from the operator site at URL.

Dataset-specific Instrument Name	
Generic Instrument Name	Leggo Lander
Generic Instrument Description	The "Leggo Lander" is a lander system that primarily relies on syntactic foam for buoyancy and uses iridium GPS, radio signal, strobe light and flag for surface recovery, and acoustics for underwater monitoring and instrument control. The lander has a timer with 5 control settings for various operations. It routinely measures pressure (depth) throughout its dive and temperature on the seafloor. The lander payloads include a pressure-retaining seawater sampler plus 2 liter Niskin bottle, and a camera/battery/light system that also includes a 30 liter Niskin bottle and a sea cucumber trap. With the camera payload it travels down or up the water column at about 39 meters per minute (~ 4.5 hours for a descent to the Challenger Deep at ~10,920 m). (Description obtained from the R/V Falkor FK141215 post-cruise report (PDF))

Dataset-specific Instrument Name	Niskin bottle
Generic Instrument Name	Niskin bottle
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	UW
Generic Instrument Name	Pump - Surface Underway Ship Intake
Dataset-specific Description	The underway system used to collect samples aboard the Falkor.
Generic Instrument Description	The 'Pump-underway ship intake' system indicates that samples are from the ship's clean water intake pump. This is essentially a surface water sample from a source of uncontaminated near-surface (commonly 3 to 7 m) seawater that can be pumped continuously to shipboard laboratories on research vessels. There is typically a temperature sensor near the intake (known as the hull temperature) to provide measurements that are as close as possible to the ambient water temperature. The flow from the supply is typically directed through continuously logged sensors such as a thermosalinograph and a fluorometer. Water samples are often collected from the underway supply that may also be referred to as the non-toxic supply. Ideally the data contributor has specified the depth in the ship's hull at which the pump is mounted.

Dataset-specific Instrument Name	Free vehicle coring respirometer (FVCR)
Generic Instrument Name	Respirometer
Dataset-specific Description	The Free Vehicle Coring Respirometer (FVCR) is deployed from the ship and sinks slowly to the seafloor. After landing on a targeted soft bottom it slowly inserts four megacore tubes into the mud and retracts them using a drive motor, which closes the lids and seals the core. Each tube is equipped with an oxygen optode and water mixing pump to measure sediment community oxygen consumption in each core. Each core is trapped by a standard megacore core catching device and returned to the surface with the lander. The instrument also includes an oxygen sensor to measure the ambient bottom water. Data and a video of the coring operation are stored inside the titanium pressure housing. Samples from this instrument are designated with 'CR##'.
Generic Instrument Description	A device that measures the rate of respiration by a living organism or organic system by measuring its rate of exchange of oxygen and/or carbon dioxide.

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

FK141109

Website	https://www.bco-dmo.org/deployment/629311
Platform	R/V Falkor
Report	https://datadocs.bco-dmo.org/d3/data_docs/Mariana_Perspectives/FK141109_Cruise_Report_JDC_2015-01-12.pdf
Start Date	2014-11-09
End Date	2014-12-09
Description	The very deepest reaches of the sea are one of the planet's last true frontiers. That's mostly because a lack of support for needed technological advancements and vehicles has severely limited access to depths beyond 7,000 meters. But the situation is finally beginning to change, and SOI is helping push the process forward. In November, the institute collaborated with a group of biologists and geologists working aboard R/V Falkor to conduct a new study of one of the deepest places in the world. The team deployed SOI's new full-ocean-depth landers—frames equipped with cameras, sensors and sample collection devices that return to the surface automatically after a set time on the seafloor—as well as three other landers, in the Mariana Trench's Sirena Deep, near Guam. The work, at depths down to almost 11,000 meters, will help answer enduring questions about the biology of such alien zones, including who lives there and how they survive the massive pressure. The research should also improve understanding of the processes that control earthquake and tsunami formation, among others geological goals. Original cruise data are available from the NSF R2R data catalog (Cruise DOI: 10.7284/900733)

TN309

Website	https://www.bco-dmo.org/deployment/536488
Platform	R/V Thomas G. Thompson
Start Date	2014-04-10
End Date	2014-05-20
Description	Original data are available from the NSF R2R data catalog

[table of contents | back to top]

Project Information

Patterns of Microbial Community Structure Within and Between Hadal Environments (Mariana Perspectives)

Coverage: Challenger Deep, Mariana Trench

Award Abstract from NSF:
The deepest portion of the ocean is present in ocean trenches, whose steep walls descend from approximately 4 miles down to depths that in some cases are close to 7 miles below the seawater surface. At these locations Earth's crust is recycled. Perhaps not surprisingly given their remoteness, deep ocean trenches are the least understood habitats in the ocean. The researchers participating in this project are working to characterize the microbes present in two of the deepest trenches present on Earth, both in the Pacific Ocean, the Kermadec Trench located north of New Zealand, and the Mariana Trench, located east and south of the island of Guam. Most of the Mariana Trench is located within the United States Mariana Trench Marine National Monument. Relatively little is known about the diversity and adaptations of the microorganisms in deep ocean trenches. An unknown fraction of the microbes present have descended from shallow waters above and are unlikely to participate in any nutrient cycles in the deep sea. Others are adapted to near freezing temperatures and up to pressures greater than 10e7 kilograms per square meter (16,000 pounds per square inch). These latter microbes perform important roles recycling organic matter. But who are they? This project is contributing to the training of diverse undergraduate and graduate students participating in research, additional

undergraduate students learning about microbes inhabiting extreme environments in a web-based class, and additional graduate students and postdoctoral scientists participating in an advanced training course being offered in Antarctica.

Experiments being performed include direct counts of prokaryotes and viruses in seawater and sediments, analyses of the abundance and phylogenetic breadth of culturable heterotrophic bacteria at a range of pressures, measurements of bacterial community species diversity and richness both within and across seawater and sediment samples, as well as within and across the two trench systems, measurements of microbial activity as a function of pressure and the identification of high pressure-active cells. The data generated from these analyses are being integrated into the results of additional chemical, geological and biological measurements performed by others as a part of the National Science Foundation funded Hadal Ecosystems Studies Project. Two of the working hypotheses are that prokaryote numbers and diversity are generally positively correlated with surface productivity and proximity to the trench axis and that bacterial taxa exist which are endemic to specific trenches, present in multiple trenches and more widely distributed in deep-sea environments.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1536776

[table of contents | back to top]