Culture-independent identification of bacteria present in the pressure-retaining seawater (PRS) sampler deployed during Leggo drop 1 from R/V Falkor cruise FK141215 in the Challenger Deep, Mariana Trench in December 2014

Website: https://www.bco-dmo.org/dataset/684362
Data Type: Cruise Results
Version: 1
Version Date: 2017-03-13

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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Abstract
Culture-independent identification of bacteria present in the pressure-retaining seawater (PRS) sampler deployed during Leggo drop 1.

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Coverage

Spatial Extent: **Lat**:11.36639 **Lon**:142.432555
Temporal Extent: 2014-12-16

Dataset Description

Culture-independent identification of bacteria present in the pressure-retaining seawater (PRS) sampler deployed during Leggo drop 1.

Methods & Sampling

This data set is associated with PI Douglas Bartlett (NSF OCE-1536776) and Schmidt Ocean Institute R/V Falkor cruise FK141215. The cruise occurred December 15-21, 2014 in the Challenger Deep within the territorial waters of the Federated States of Micronesia. During this cruise the Leggo lander was deployed multiple times and drops 1 and 3 recovered seawater samples that were analyzed. 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/

Leggo Lander Drop 1:
Time (in Guam) deployed/recovered: December 16, 9:00/19:26.
Position at deployment: 11° 21.9836 N 142° 25.9533 E, middle section of the Challenger Deep.
Greatest depth of dive: approximately ~10,900 m.
In situ temperature on seafloor: 2.6°C.
Notes: This drop recovered seawater samples from about a meter off the seafloor. This included a 3 L Niskin bottle of seawater and ~ 150 mls of seawater collected in a pressure-retaining seawater sampler. The PRS sampler held more than 81% of the in situ pressure.

PRS data:
The culture independent identification of the bacteria present in the pressure-retaining seawater (PRS) sampler deployed during Leggo drop 1. This involved cell sorting, multiple displacement amplification, and 16S rRNA gene PCR and sequencing. More complete details are described in:

Leon-Zayas, R., Novotny, M., Podell, S., Shepard, C. M., Berkenpas, E., Nikolenko, S., Pevzner, P., Lasken, R. S. and Bartlett, D. H. 2015. Single cells within the Puerto Rico Trench suggest hadal adaptation of microbial lineages. Appl. Environ. Microbiol. 81: 8265-8276. doi:10.1128/AEM.01659-15

Colony Identification:
Data from the identification of bacteria cultured from the Leggo drop 1 and 3 Niskin bottles are available as a supplemental file (.txt). These identifications were performed using standard methods associated with PCR amplification of the 16S rRNA gene followed by dideoxy sequencing at Retrogen Inc.

Data Processing Description

The only processing of the data is that the 16S rRNA gene sequences has been examined using BLAST: https://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome

BCO-DMO Processing:
-modified parameter names to conform with BCO-DMO naming conventions;
-replaced spaces with underscores;
-replaced '-' with 'nd' (no data);
-added dates, times, locations from metadata form.

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Data Files

File
PRS.csv (Comma Separated Values (.csv), 1.76 KB) MD5:f599a4ffb24202f010809440edb4d846 Primary data file for dataset ID 684362

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Supplemental Files

File
Colony Identification filename: colony_identification.txt (Plain Text, 24.35 KB) MD5:f7053b28b2a33c7861b298d45d4304d2 The identification of bacteria cultured from the Leggo drop 1 and 3 Niskin bottles

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Parameters

Parameter	Description	Units
SILVA_classification	SILVA classification	unitless
partial_16S_seq	Partial 16S rRNA gene sequence	unitless

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	Cells were sorted using a flow cytometer
Generic Instrument Description	Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm)

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	
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	Multiple displacement amplification and 16S rRNA gene PCR and sequencing were performed
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)

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Deployments

FK141215

Website	https://www.bco-dmo.org/deployment/684236
Platform	R/V Falkor
Report	http://dmoserv3.whoi.edu/data_docs/Mariana_Perspectives/Bartlett-final-FK141215-cruise-report.pdf
Start Date	2014-12-15
End Date	2014-12-21
Description	During this cruise the Leggo lander was deployed multiple times and drops 1 and 3 recovered seawater samples that were analyzed. 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-2.... More information is available in the post-cruise and final expedition reports (PDF). Original cruise data are available from the NSF R2R data catalog

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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.

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Funding

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

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