

# McMurdo Spiophanes beds 16s V4 region community composition from sediment cores at McMurdo Station, Antarctica on Sept 9th, 2012 (McMurdo Benthos project)

**Website:** <https://www.bco-dmo.org/dataset/716443>

**Data Type:** Other Field Results

**Version:**

**Version Date:** 2017-10-10

## Project

» [Microbe - Metazoan Interactions in an Antarctic Infaunal Community](#) (McMurdo Benthos)

Contributors	Affiliation	Role
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## Coverage

**Spatial Extent:** Lat:-77.846 Lon:166.639

**Temporal Extent:** 2012-09-09

## Dataset Description

This dataset includes accession numbers for raw genetic sequence reads from sediment cores of McMurdo Station Spiophanes beds to investigate 16s V4 region community composition.

The accession numbers in this dataset are part of the BioProject titled [16S Amplicon Data from an Antarctic Cold Seep \(PRJNA387720\)](#) at the National Center for Biotechnology Information (NCBI).

Sediment cores at McMurdo Station were taken at "The Jetty", Hutt Point, Ross Sea, Antarctica at a depth of 20m.

## Methods & Sampling

### Methodology:

Sediment cores were collected from the Spiophanes beds at the "Jetty" dive location and vertically sectioned into cm intervals with the exterior of the cores discarded to avoid vertical smearing. Sediment were placed in whirlpack bags and kept at -80 until DNA was extracted.

### Sampling and analytical procedures:

Between 0.25 and 0.5 grams of frozen sediment had DNA extracted using the MoBio (now Qiagen) PowerSoil kits. rDNA and amplification follows the Earth Microbiome Project Protocol (<http://www.earthmicrobiome.org/protocols-and-standards/16s/>) using the updated primers in Apprill et al (2015) following Caporaso et al. (2011). In short, triplicate PCRs were run using the 515FB and the 806RB primers that copy the V4 region of the 16S rRNA gene. These primers were barcoded allowing later in silico separation of pooled samples. Controls and all samples were run on a gel to check for contamination. DNA was cleaned up using the MoBio UltraClean PCR Clean-Up Kit, samples were pooled into equal molar concentrations and submitted for sequencing.

Sequencing was performed on the Illumina MiSeq platform using the V.2 chemistry at the Center for Genome Research and Biocomputing at Oregon State University.

## Data Processing Description

Data processing: Data were de-multiplexed and primers trimmed. No other data manipulation has been performed.

BCO-DMO Data Manager Processing Notes:

- \* added a conventional header with dataset name, PI name, version date
- \* modified parameter names to conform with BCO-DMO naming conventions
- \* blank values replaced with no data value 'nd' for "no data" so they are recognized in our system
- \* Latitude and Longitude converted to decimal degrees
- \* added ISO Date format generated from Date and Time values
- \* changed date format to yyyy-mm-dd
- \* updated coordinates in data for hutt point sample site based on correspondence with data contributor.

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## Data Files

File
<b>Spiophanes_Microbial.csv</b> (Comma Separated Values (.csv), 3.55 KB) MD5:af5f1f443c558afcf746dd0513422ac
Primary data file for dataset ID 716443

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## Related Publications

16S Illumina Aplicon Protocol (Earth Microbiome Project) <http://www.earthmicrobiome.org/protocols-and-standards/16s/>

*Methods*

Apprill, A., McNally, S., Parsons, R., & Weber, L. (2015). Minor revision to V4 region SSU rRNA 806R gene primer greatly increases detection of SAR11 bacterioplankton. *Aquatic Microbial Ecology*, 75(2), 129–137. doi:[10.3354/ame01753](https://doi.org/10.3354/ame01753)

*Methods*

Caporaso, J. G., Lauber, C. L., Walters, W. A., Berg-Lyons, D., Lozupone, C. A., Turnbaugh, P. J., ... Knight, R. (2010). Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proceedings of the National Academy of Sciences*, 108(Supplement\_1), 4516–4522. doi:[10.1073/pnas.1000080107](https://doi.org/10.1073/pnas.1000080107)

*Methods*

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## Parameters

Parameter	Description	Units
accession	BioSample (a description of the biological source material) accession number at the National Center for Biotechnology Information (NCBI). An associated raw genetic accession in the Sequence Read Archive (SRA) is associated with this BioSample and can be found at NCBI	unitless
sample_name	reference file name used in NCBI	unitless
organism	All are marine sediment whose microbial community has been extracted	unitless
host	These are environmental samples; not from individual organisms.	unitless
collection_date	Date sample was collected	unitless
geo_loc_name	location sampled	unitless
lat_lon	specific location of collection	Latitude and longitude in format decimal degrees with cardinal direction
lat	Latitude	decimal degrees
lon	Longitude	decimal degrees
Replicate	Individual identifier for the core (all 1s are from one core; 2 from another; etc).	unitless
Sediment_Depth	Sediment depth range below seafloor from which microbial community was analyzed.	centimeters
accession_link	Link to the BioSample (a description of the biological source material) accession page at the National Center for Biotechnology Information (NCBI). An associated raw genetic accession in the Sequence Read Archive (SRA) is associated with this BioSample and can be found at NCBI	unitless

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## Deployments

### Thurber\_Hutt\_Point\_2012

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/716447">https://www.bco-dmo.org/deployment/716447</a>
<b>Platform</b>	Ross Island

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## Project Information

### Microbe - Metazoan Interactions in an Antarctic Infaunal Community (McMurdo Benthos)

**Coverage:** Ross Sea, 78 S 167 E

The biota of the world's seafloor is fueled by bursts of seasonal primary production. For food-limited sediment communities to persist, a balance must exist between metazoan consumption of and competition with bacteria, a balance which likely changes through the seasons. Polar marine ecosystems are ideal places to study such complex interactions due to stark seasonal shifts between heterotrophic and autotrophic communities, and temperatures that may limit microbial processing of organic matter. The research will test the following hypotheses: 1) heterotrophic bacteria compete with macrofauna for food; 2) as phytoplankton populations decline macrofauna increasingly consume microbial biomass to sustain their populations; and 3) in

the absence of seasonal photosynthetic inputs, macrofaunal biodiversity will decrease unless supplied with microbially derived nutrition. Observational and empirical studies will test these hypotheses at McMurdo Station, Antarctica, where a high-abundance macro-infaunal community is adapted to this boom-and-bust cycle of productivity. The investigator will mentor undergraduates from a predominantly minority-serving institution, in the fields of invertebrate taxonomy and biogeochemistry. The general public and young scientists will be engaged through lectures at local K-12 venues and launch of an interactive website. The results will better inform scientists and managers about the effects of climate change on polar ecosystems and the mechanisms of changing productivity patterns on global biodiversity.

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## Funding

Funding Source	Award
<a href="#">NSF Office of Polar Programs (formerly NSF PLR) (NSF OPP)</a>	<a href="#">OPP-1103428</a>

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