Microbial community composition from 16s V4 region amplicon sequencing of the methane Seep at the Cinder Cones Cold Seep site, Nov 2016

Website: https://www.bco-dmo.org/dataset/756997

Data Type: Other Field Results

Version: 1

Version Date: 2019-02-25

Project

» EAGER: Elucidating the Antarctic Methane Cycle at the Cinder Cones Reducing Habitat (Cinder Cone Seep)

Contributors	Affiliation	Role
Thurber, Andrew	Oregon State University (OSU-CEOAS)	Principal Investigator
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

This dataset includes microbial community composition from 16s V4 region amplicon sequencing on 151 marine sediment community samples collected from the Cinder Cones Cold Seep site [-77.8, 166.666] in the Ross Sea region, Antarctica in November 2016. Data are uploaded to the NCBI Sequence Read Archive under submission SUB2655615 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA387720] with a subset of the data from that archive originating from this project.

Table of Contents

Coverage

Spatial Extent: **Lat**:-77.8 **Lon**:166.666

Temporal Extent: 2016-11-03 - 2016-11-15

Dataset Description

This dataset includes details on 151 marine sediment community samples collected from the Cinder Cones Cold Seep site [-77.8, 166.666] in the Ross Sea region, Antarctica in November 2016. Data are uploaded to the NCBI Sequence Read Archive under submission SUB2655615 [https://www.ncbi.nlm.nih.gov/bioproject/PRJNA387720] with a subset of the data from that archive originating from this project.

Acquisition Description

Sediment cores were collected from the Cinder Cones site including a methane seep habitat and vertically sectioned into cm intervals with the exterior of the cores discarded to avoid vertical smearing. Sediments were placed in whirlpack bags and kept at -80 until DNA was extracted.

Between 0.25 and 0.5 grams of frozen sediment had DNA extracted using the MoBio (now Qiagen) PowerSoil kits. Primers and amplification procedures follow 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 if 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.

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

Processing Description

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- re-formatted date from m/d/yyyy to yyyy-mm-dd
- split lat and lon into separate columns; converted lat to negative degrees

[table of contents | back to top]

Related Publications

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

[table of contents | back to top]

Parameters

Parameter	Description	Units
accession	NCBI accession number for the archive	unitless
sample_name	reference file name used in NCBI	unitless
organism	type of organism analyzed: all are marine sediment whose microbial community has been extracted	unitless
host	host type: these are environmental samples rather than from individual organisms	unitless
collection_date	Date sample was collected formatted as yyyy-mm-dd	unitless
geo_loc_name	location sampled	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
Replicate	Individual identifier for the core	unitless
Sediment_Depth_cm	depth range from which microbial community was analyzed	centimeters
Habitat	Whether the sample was from an area of active methane seepage or sampled as a control for this habitat.	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA Sequencer
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	
Generic Instrument Name	PCR Thermal Cycler
Generic Instrument Description	General term for a laboratory apparatus commonly used for performing polymerase chain reaction (PCR). 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. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

[table of contents | back to top]

Project Information

EAGER: Elucidating the Antarctic Methane Cycle at the Cinder Cones Reducing Habitat (Cinder Cone Seep)

Coverage: Ross Sea, Antarctica (78 S, 166 E)

NSF abstract: Methane is a potent greenhouse gas that is naturally emitted into the oceans by geologic seeps and microbial production. Based on studies of persistent deep-sea seeps at mid- and northern latitudes, researchers have learned that bacteria and archaea can create a "sediment filter" that oxidizes methane prior to its release. Antarctica is thought to contain large reservoirs of organic carbon buried beneath its ice which could a quantity of methane equivalent to all of the permafrost in the Arctic and yet we know almost nothing about the methane oxidizing microbes in this region. How these microbial communities develop and potentially respond to fluctuations in methane levels is an under-explored avenue of research. A bacterial mat was recently discovered at 78 degrees south, suggesting the possible presence of a methane seep, and associated microbial communities. This project will explore this environment in detail to assess the levels and origin of methane, and the nature of the microbial ecosystem present. An expansive bacterial mat appeared and/or was discovered at 78 degrees south in 2011. This site, near McMurdo Station Antarctica, has been visited since the mid-1960s, but this mat was not observed until 2011. The finding of this site provides an unusual opportunity to study an Antarctic marine benthic habitat with active methane cycling and to examine the dynamics of recruitment and community succession of seep fauna including bacteria, archaea, protists and metazoans. This project will collect the necessary baseline data to facilitate further studies of Antarctic methane cycling. The concentration and source of methane will be determined at this site and at potentially analogous sites in McMurdo Sound. In addition to biogeochemical characterization of the sites, molecular analysis of the microbial community will quantify the time scales on which bacteria and archaea respond to methane input and provide information on rates of community development and succession in the Southern Ocean. Project activities will facilitate the training of at least one graduate student and results will be shared at both local and international levels. A female graduate student will be mentored as part of this project and data collected will form part of her dissertation. Lectures will be given in K-12 classrooms in Oregon to excite students about polar science. National and international audiences will be reached through blogs and presentations at a scientific conference. The PI's previous blogs have been used by K-12 classrooms as part of their lesson plans and followed in over 65 countries.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Office of Polar Programs (formerly NSF PLR) (NSF OPP)	OPP-1642570

[table of contents | back to top]