Accession numbers for metagenome-assembled genomes (MAGs) from samples collected in 2018 on R/V Thompson cruise TN350 at the Upper and Lower Cones, Upper Caldera Wall and NW Caldera, Brothers Volcano

Website: https://www.bco-dmo.org/dataset/868323
Data Type: Cruise Results
Version: 1
Version Date: 2022-01-19

Project
» Collaborative Research: Hydrothermal and Microbiological Investigations of the Active Brothers Volcano in the Kermadec Arc (Brothers Volcano Microbiology)

Contributors	Affiliation	Role
Reysenbach, Anna-Louise	Portland State University (PSU)	Principal Investigator
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Abstract
Accession numbers for metagenome-assembled genomes (MAGs) from the Upper and Lower Cones, Upper Caldera Wall and NW Caldera, Brothers Volcano. Published in Reysenbach & St. John et al., 2020. Sequence data is available in NCBI Genbank under BioProject accession PRJNA546572.

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Coverage

Spatial Extent: **N**:-34.8579131 **E**:179.071443 **S**:-34.8823655 **W**:179.051933
Temporal Extent: 2018-03 - 2018-03

Methods & Sampling

Water samples and hydrothermal vent deposits were collected as described in Reysenbach & St. John et al., 2020. Samples were collected with remotely operated vehicle ROV Jason. Water samples were obtained using major water samplers. Hydrothermal deposits were placed in sealed bioboxes in the ROV sampling basket to restrict flushing of samples by surrounding seawater during the ascent. Once shipboard, 1L of water samples were filtered through a 0.2-µm Sterivex filter (Merck). For the hydrothermal deposits, the outer few millimeters (up to approximately 5 mm) was subsampled for DNA extraction. These exterior samples were homogenized and stored in cryovials at -80 degrees C for subsequent DNA extraction. For the water samples, the DNA was

extracted from the sterivex filters as previously described by R. E. Anderson et al. (2017). The DNA was extracted from the homogenized hydrothermal depot samples using the DNeasy PowerSoil kit (Qiagen) All purified environmental DNA was stored at -80 degrees C. After DNA extraction and library preparation, metagenomes were sequenced using the Illumina HiSeq 3000.

Data Processing Description

Data Processing:
Metagenome reads were trimmed using Trimmomatic, and assembled into contigs with MEGAHIT. Reads were then mapped back to the contigs with Bowtie2 and SAMtools. Metagenome-assembled genomes were binned using MetaBAT, followed by curation of key genomes using Emergent Self Organizing Maps.

Software:
Trimmomatic v.0.36: Trimming software for read processing.

MEGAHIT v.1.1.1-2-g02102e1: Assembly software used to generate contigs from reads.

Bowtie2 v.2.2.9 and SAMtools v.1.3.1: Software used to map reads back to contigs and parse results of the mapping.

MetaBAT v.0.32.4: Binning software, used to group contigs into metagenome-assembled genomes (MAGs).

Emergent Self Organizing Maps (ESOM): manual binning software used to curate genomes of interest.

BCO-DMO Processing:
- removed commas from Collection_location column;
- removed directional letters from the Latitude and Longitude columns and made Latitude values negative to indicate South;
- converted Collection_date field to YYYY-MM format.

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Data Files

File
accessions.csv(Comma Separated Values (.csv), 127.20 KB) MD5:daaeddac8c48edc050062d9bfa67034c Primary data file for dataset ID 868323

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Related Publications

A. Ultsch, F. Mörchen. (2005). "ESOM-Maps: Tools for clustering, visualization, and classification with Emergent SOM" (Technical Report, Dept. of Mathematics and Computer Science, University of Marburg, Marburg, Germany).
Software

Anderson, R. E., Reveillaud, J., Reddington, E., Delmont, T. O., Eren, A. M., McDermott, J. M., Seewald, J. S., & Huber, J. A. (2017). Genomic variation in microbial populations inhabiting the marine subseafloor at deep-sea hydrothermal vents. Nature communications, 8(1), 1114. https://doi.org/10.1038/s41467-017-01228-6
Methods

Bolger, A. M., Lohse, M., & Usadel, B. (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics, 30(15), 2114–2120. doi:10.1093/bioinformatics/btu170
Software

Kang, D. D., Froula, J., Egan, R., & Wang, Z. (2015). MetaBAT, an efficient tool for accurately reconstructing single genomes from complex microbial communities. PeerJ, 3, e1165. doi:10.7717/peerj.1165

Software

Langmead, B., & Salzberg, S. L. (2012). Fast gapped-read alignment with Bowtie 2. Nature Methods, 9(4), 357–359. doi:10.1038/nmeth.1923
Software

Li, D., Luo, R., Liu, C.-M., Leung, C.-M., Ting, H.-F., Sadakane, K., … Lam, T.-W. (2016). MEGAHIT v1.0: A fast and scalable metagenome assembler driven by advanced methodologies and community practices. Methods, 102, 3–11. doi:10.1016/j.ymeth.2016.02.020
Software

Li, H. (2011). A statistical framework for SNP calling, mutation discovery, association mapping and population genetical parameter estimation from sequencing data. Bioinformatics, 27(21), 2987–2993. doi:10.1093/bioinformatics/btr509
Software

Reysenbach, A.-L., St. John, E., Meneghin, J., Flores, G. E., Podar, M., Dombrowski, N., … Bach, W. (2020). Complex subsurface hydrothermal fluid mixing at a submarine arc volcano supports distinct and highly diverse microbial communities. Proceedings of the National Academy of Sciences, 117(51), 32627–32638. doi:10.1073/pnas.2019021117
Results

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Related Datasets

IsRelatedTo

Portland State University. hydrothermal vent metagenome, Brothers Volcano 16S rRNA gene amplicon sequencing and metagenome-assembled genomes (MAGs) sequencing and assembly. 2020/11. 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/PRJNA546572. NCBI:BioProject: PRJNA546572.

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Parameters

Parameter	Description	Units
Sample	Sample identifier	unitless
MAG	Metagenome-assembled genome (MAG) identifier	unitless
Repository	Public database where data is deposited	unitless
Biosample_accession	Genbank Biosample accession number	unitless
WGS_accession	Genbank whole genome sequence accession number	unitless
Organism	Genbank-compatable organism name	unitless
Collection_location	Geographic location of collection	unitless
Collection_date	Collection date; format: YYYY-MM	unitless
Latitude	Collection latitude	decimal degrees North
Longitude	Collection longitude	decimal degrees East
Depth	Depth	meters
Sequencing_technology	Technology used to sequence metagenomes	unitless
Assembly_program	Software used to assemble contigs from metagenome reads	unitless
Binning_program	Software used to bin MAGs from contigs	unitless

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq 3000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina HiSeq 3000: Sequencing platform used to generate metagenome reads
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.

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Deployments

TN350

Website	https://www.bco-dmo.org/deployment/868364
Platform	R/V Thomas G. Thompson
Start Date	2018-03-03
End Date	2018-03-28
Description	See additional cruise information from R2R: https://www.rvdata.us/search/cruise/TN350

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Project Information

Collaborative Research: Hydrothermal and Microbiological Investigations of the Active Brothers Volcano in the Kermadec Arc (Brothers Volcano Microbiology)

Coverage: Brothers volcano, NE of New Zealand on the Kermadec arc (34.88, 179.08)

NSF Award Abstract:
Nearly one third, or 22,000 km of Earth's submarine volcanic activity, occurs along intraoceanic volcanic arcs. The volcanos and seafloor spreading centers in these areas host significant numbers of hydrothermal systems that vent hot, mineral-charged waters into the oceans and support unique micro- and macrobiological communities that are found nowhere else on Earth. The chemistry of hydrothermal systems found along interoceanic arcs differ substantially from those located at mid-ocean ridges, with arc systems exhibiting strong magmatic signatures. This unique chemistry, coupled with the shallow depths at which the calderas of many of these arc volcanoes occur, result in highly acidic and volatile-enriched fluids that are the precursors to economically metal-rich mineral deposits. Because these systems are difficult to detect unless they are come upon by accident, these systems are relatively unstudied and have unexplored microbiological communities.

This research will undertake a 20-day oceanographic research expedition and shore-based laboratory studies of the samples that are collected to characterize one of these unique volcanoes: Brothers Volcano in the Kermadec Arc in the Western Pacific Ocean. This volcano has also been selected as a potential ocean drilling site with science focused on the development of a better understanding of active seafloor hydrothermal systems and their circulation pathways. Goals of the present research program include using remotely operated vehicles to survey and sample the rocks, vent fluids, and microbes in the Brothers Volcano caldera. It also includes an extensive heat flow survey to identify areas of fluid recharge and discharge. Broader impacts of the research include establishing collaborations with New Zealand scientists, graduate student training, support of two investigators whose genders are under-represented in the sciences, and public outreach through the Woods Hole Oceanographic Institution's award-winning Dive and Discover website. Presentations will also be made to the public as opportunities present themselves. There is also the potential for the discovery of new microbiological species with unusual metabolic pathways or enzymes which may have natural products and/or pharmacological utility. The work also has the ability to help us understand the formation of hydrothermal vent related sulfide deposits which commonly are rich in copper, gold, and molybdenum. This research also complements the science agenda of the NSF-funded International Ocean Discovery Program and provides a critical site survey upon which seafloor drilling legs can be based.

This research is focused on documenting and understanding the geology, heat flow, hydrothermal, and microbial characteristics of the Brothers Volcano edifice in the Kermadec Arc in the Western Pacific Ocean. A 20-day sample collection cruise will take place in the caldera of the Brothers Volcano and will be followed up by onshore laboratory geochemical and microbiological work. The research project will test five hypotheses related to hydrothermal circulation at Brothers volcano. Work will include documenting the heat and chemical fluxes coming from the caldera; the role of low pH in these systems; and the influence of magmatic volatile-rich hydrothermal fluids on rock alteration. Research will also involve determining mechanisms and the extent of fluid-rock interaction and mass transfer of carbon, sulfur, metals and metalloids into the ocean; the subseafloor distribution of metals and associated mineral deposits; and the diversity and extent of microbial life in an arc volcano hydrothermal environment. Brothers volcano is ideally suited for such studies because it harbors two different styles of hydrothermal vents within its caldera: (1) high-temperature black smoker-type fluids discharging from Cu-Au-rich sulfide chimneys; and (2) moderate temperature, gassy, acid-sulfate waters where native sulfur chimneys and extensive Fe-oxyhydroxide crusts occur. During the cruise a mapping, sampling, and observational program will take place, consisting of a series of dives by a remotely operated vehicle to four distinct hydrothermal fields within Brothers caldera. Thermal blankets will be deployed in the caldera around the hydrothermal vents to measure heat flow and fluid recharge and discharge zones. Coexisting minerals and fluids associated with the vents and the surrounding caldera will be collected and geochemically analyzed. This research and the resulting caldera survey complements other observational and analytical work carried out over the past decade by NOAA, the National Ocean and Atmospheric Administration, and its corresponding agency associated with the government of New Zealand. One important goal of the survey work is to identify potential sites for ocean drilling for further understanding of seafloor arc volcanic systems.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1558795
NSF Division of Ocean Sciences (NSF OCE)	OCE-1558356

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