

Sample accession numbers for raw metagenome and metatranscriptome Illumina HiSeq 2500 sequencing from an Fe mat sampled during cruise TN293 to Loihi Seamount, Hawaii on 03/25/2013

Website: <https://www.bco-dmo.org/dataset/719770>

Data Type: Other Field Results

Version: 20 November 2017

Version Date: 2017-11-20

Project

» [Ecology of microbial mats at seamount associated Fe-rich hydrothermal vent systems](#) (Ecology of Vent Mats)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: Lat:18.901418 Lon:-155.258191

Temporal Extent: 2013-03-25

Dataset Description

This dataset includes accession numbers and links to NCBI SRA for metagenomic and metatranscriptomic reads from BioProject PRJNA412510. Samples were collected during the R/V Thomas G. Thompson cruise TN293 at Loihi Seamount. A single Fe mat was sampled (J2-674-BM1-C123456) at Pohaku (Mkr #57), with syringe J2-674-BM1-C3 used for metagenomic sequencing and syringe J2-674-BM1-C6 used for metatranscriptomic sequencing. Latitude: 18.901418 N; Longitude: 155.258191 W; Depth: 1179.43 meters below sea level.

Further details on sequencing are available on the [NCBI BioProject page](#).

Methods & Sampling

Microbial mat samples were acquired with sub-centimeter sampling resolution from the seafloor using a novel microbial mat sampling device (see Breier, et al. 2012 for details) operated by the ROV Jason 2. Microbial mat samples were collected at the seafloor with RNALater within each collection syringe, fixing RNA activity on collection (in situ RNA expression profiles). On return to the ship, samples were allowed to settle, and the settled floc was stored at -80 degrees C until extraction and analysis.

Data Processing Description

DNA and RNA were extracted as described in Chan et al. (2018). Raw metagenomic sequences were quality controlled, assembled, and binned (metagenome-assembled genomes [MAGs]), after which quality controlled RNA sequences were recruited to MAGs to estimate gene expression.

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Data Files

File
Fe_mat_accessions_Chan.csv (Comma Separated Values (.csv), 308 bytes) MD5:4b81965ae165b96ee8e06fffa641d5b9
Primary data file for dataset ID 719770

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Related Publications

Breier, J. A., Gomez-Ibanez, D., Reddington, E., Huber, J. A., & Emerson, D. (2012). A precision multi-sampler for deep-sea hydrothermal microbial mat studies. *Deep Sea Research Part I: Oceanographic Research Papers*, 70, 83–90. doi:[10.1016/j.dsr.2012.10.006](https://doi.org/10.1016/j.dsr.2012.10.006)
Methods

Chan, C., McAllister, S. M., Garber, A., Hallahan, B. J., & Rozovsky, S. (2018). Fe oxidation by a fused cytochrome-porin common to diverse Fe-oxidizing bacteria. doi:[10.1101/228056](https://doi.org/10.1101/228056)
Methods

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Parameters

Parameter	Description	Units
accession_id	Accession number at NCBI	unitless
accession_link	Link to accession at NCBI	unitless
lat	Latitude where sample was collected; N = positive.	decimal degrees
lon	Longitude where samples were collected. E = positive.	decimal degrees

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Instruments

Dataset-specific Instrument Name	ROV Jason 2
Generic Instrument Name	ROV Jason
Generic Instrument Description	The Remotely Operated Vehicle (ROV) Jason is operated by the Deep Submergence Laboratory (DSL) at Woods Hole Oceanographic Institution (WHOI). WHOI engineers and scientists designed and built the ROV Jason to give scientists access to the seafloor that didn't require them leaving the deck of the ship. Jason is a two-body ROV system. A 10-kilometer (6-mile) fiber-optic cable delivers electrical power and commands from the ship through Medea and down to Jason, which then returns data and live video imagery. Medea serves as a shock absorber, buffering Jason from the movements of the ship, while providing lighting and a bird's eye view of the ROV during seafloor operations. During each dive (deployment of the ROV), Jason pilots and scientists work from a control room on the ship to monitor Jason's instruments and video while maneuvering the vehicle and optionally performing a variety of sampling activities. Jason is equipped with sonar imagers, water samplers, video and still cameras, and lighting gear. Jason's manipulator arms collect samples of rock, sediment, or marine life and place them in the vehicle's basket or on "elevator" platforms that float heavier loads to the surface. More information is available from the operator site at URL.

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Deployments

TN293

Website	https://www.bco-dmo.org/deployment/659705
Platform	R/V Thomas G. Thompson
Start Date	2013-03-16
End Date	2013-04-01
Description	For Jason data/information from this cruise, please visit the Jason Virtual Control Van: http://4dgeo.who.edu/webdata/virtualvan/html/VV-tn293/index.html (This link includes all navigational data, images, and sample collection metadata and comments for the cruise. Data can be downloaded with export viewer.) Additional cruise information and original data are available from the NSF R2R data catalog.

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Project Information

Ecology of microbial mats at seamount associated Fe-rich hydrothermal vent systems (Ecology of Vent Mats)

Website: <http://oceanexplorer.noaa.gov/explorations/14fire/welcome.html>

Coverage: Loihi Seamount, Hawaii; and Mariana Arc and Backarc Hydrothermal Systems

Description from NSF award abstract:

A grand challenge in microbial ecology is to understand what drives the structure of microbial communities. A recently discovered novel class of Proteobacteria, the Zetaproteobacteria, are associated with microbial mats at iron rich hydrothermal vents at submarine volcanoes deep in the ocean. These bacteria only grow using iron as an energy source and fix carbon dioxide. Within iron rich microbial mats, Zetaproteobacteria are the

dominant bacterial population; however they are rare in most other deep-sea or marine habitats, suggesting they may be restricted to specific niches characterized by gradients of oxygen and iron. Recent discoveries have expanded their range to fluids collected from deep ocean crust boreholes, iron deposits in coastal saltmarshes, and with steel associated bio-corrosion, demonstrating that marine Zetaproteobacteria are cosmopolitan. A unique property of these marine iron oxidizing bacteria is that they produce morphologically distinct iron oxide structures in the form of filamentous sheaths or stalk-like structures. These structures are easily recognized by light microscopy, and electron microscopy is beginning to reveal subtle differences among them that may be diagnostic of different populations of iron oxidizing bacteria. Another unusual aspect of iron oxidizing bacteria is that they produce large quantities of oxides with relatively little bacterial biomass. As a result, the oxides form a matrix that influences water and nutrient flow in the microbial mats where they grow, and in turn, may influence the growth of other groups of bacteria and archaea that live in the mats. In an ecological context, the PIs believe this makes them a keystone species that form the predominant structural matrix of the mat, and engineer an environment conducive for growth of specific bacterial populations within the mat ecosystem. The PIs propose to use high resolution mat sampling techniques to investigate the architecture of mat ecosystems and couple these with modern molecular methods (i.e., single-cell metagenomics) and geochemical measurements of the vent fluid to couple morphological and functional diversity to phylogenetic and physiological diversity. Because the Zetaproteobacteria are ancient, have unique metabolic and morphological attributes, and appear to be restricted to a well-defined habitat, they offer an interesting model for understanding fundamental ecological concepts that drive microbial diversity and evolution.

A better understanding of iron oxidizing bacteria that include Zetaproteobacteria is of fundamental interest to scientists interested in areas of earth science and oceanography because they illustrate how microbes can fundamentally influence geochemical cycling and mineral deposition. Furthermore, morphological structures similar to those produced by Zetaproteobacteria can still be identified hundreds of millions (and possibly billions) of years back in the geological record, making them of paleontological, and potentially of exobiological, interest. As knowledge of extant populations grow, it is possible they will also help to inform us of environmental change in past Earth history. A wealth of educational and outreach opportunities will be made possible by this work, including graduate and postdoctoral education, research experiences for undergraduates, and teacher training. In addition the participating scientists are involved in a number of programs to make the general public aware of the process of how scientific research is conducted, and how discoveries of a fundamental nature can ultimately benefit humankind.

Additional information/resources:

TN293 (Loihi 2013)

[Loihi Summit Map \(PDF\)](#)

Cruise blog: <https://zetahunters.wordpress.com/>

Jason Virtual Control Van: <http://4dgeo.who.edu/webdata/virtualvan/html/VV-tn293/index.html>

Related Publications:

Fullerton, H., K. W. Hager, S. M. McAllister, and C. L. Moyer. 2017. Hidden diversity revealed by genome-resolved metagenomics of iron-oxidizing microbial mats from Lō'ihi Seamount, Hawai'i. *ISMEJ* 11:1900–1914. doi:[10.1038/ismej.2017.40](https://doi.org/10.1038/ismej.2017.40)

Emerson, D., J. J. Scott, A. Leavitt, E. Fleming, and C. L. Moyer. 2016. In situ estimates of iron-oxidation and accretion rates for iron-oxidizing bacterial mats at Loihi Seamount. *bioRxiv* 095414. doi:[10.1101/095414](https://doi.org/10.1101/095414)

Scott, J. J., B. T. Glazer, and D. Emerson. 2017. Bringing microbial diversity into focus: high-resolution analysis of iron mats from the Lō'ihi Seamount. *Environmental Microbiology* 19:301–316. doi:[10.1111/1462-2920.13607](https://doi.org/10.1111/1462-2920.13607)

Chan, C.S., S.M. McAllister, A.H. Leavitt, B.T. Glazer, S.T. Krepiski, and D. Emerson. 2016. The architecture of iron microbial mats reflects the adaptation of chemolithotrophic iron oxidation in freshwater and marine environments. *Frontiers in Microbiology* 7:796. doi:[10.3389/fmicb.2016.00796](https://doi.org/10.3389/fmicb.2016.00796)

Fullerton, H., K. W. Hager, and C. L. Moyer. 2015. Draft genome sequence of *Mariprofundus ferrooxydans* strain JV-1, isolated from Loihi Seamount, Hawaii. *Genome announcements* 3:e01118-15. doi:[10.1128/genomeA.01118-15](https://doi.org/10.1128/genomeA.01118-15)

Field, E.K., A. Sczyrba, A.E. Lyman, C.C. Harris, T. Woyke, R. Stepanauskas, and D. Emerson. 2015. Genomic insights into the uncultivated marine Zetaproteobacteria at Loihi Seamount. *ISMEJ* 9:857–870. doi:[10.1038/ismej.2014.183](https://doi.org/10.1038/ismej.2014.183)

Jesser, KJ, Fullerton H, Hager KW, Moyer CL. 2015. Quantitative PCR analysis of functional genes in iron-rich microbial mats at an active hydrothermal vent system (Lō'ihi Seamount, Hawai'i). *Appl Environ Microbiol* 81:2976–2984. doi:[10.1128/AEM.03608-14](https://doi.org/10.1128/AEM.03608-14). ([PDF](#))

RR1413 (Mariana 2014)

[RR1413 Cruise Report](#) (5.2 MB PDF)

[Urushima to Rota Map \(PDF\)](#)

Jason Virtual Control Van website: <http://4dgeo.who.edu/webdata/virtualvan/html/VV-rr1413/index.html>

Related Publications:

Hager, K. W., H. Fullerton, D. A. Butterfield, and C. L. Moyer. 2017. Community structure of lithotrophically-driven hydrothermal microbial mats from the Mariana Arc and Back-Arc. *Frontiers in Microbiology* 8:1578. doi:[10.3389/fmicb.2017.01578](https://doi.org/10.3389/fmicb.2017.01578)

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1155290

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