Accession numbers for sequences generated from hydrothermal plume samples collected on R/V New Horizon cruises GoCAL1, GoCAL2, GoCAL3 in the Guaymas Basin, Gulf of California from 2005-2014 (Guaymas plumes project)

Website: https://www.bco-dmo.org/dataset/544279
Version: 12 Jan 2015
Version Date: 2015-01-12

Project
» Linking biogeochemistry and microbial community dynamics in deep-sea hydrothermal plumes (Guaymas plumes)

Contributors	Affiliation	Role
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Dataset Description

Accession numbers and links are provided for DNA sequence data. Samples were collected in the Guaymas and Carmen Basins, Gulf of California.

The following publications are associated with this data:

Anantharaman, K.A., M.B. Duhaime, J.A. Breier, K. Wendt, B.M. Toner, and G.J. Dick (2014). Sulfur oxidation genes in diverse deep-sea viruses. Science 344: 757-760. doi:10.1126/science.1252229

Li, M., B.M. Toner, B.J. Baker, J.A. Breier, C.S. Sheik, and G.J. Dick (2014). Microbial iron uptake as a mechanism for dispersing iron from deep-sea hydrothermal vents. Nature Communications 5: 3192. doi:10.1038/ncomms4192

Li, M., S. Jain, B.J. Baker, C. Taylor, and G.J. Dick (2014). Novel hydrocarbon monooxygenase genes in the metatranscriptome of a natural deep-sea hydrocarbon plume. Environmental Microbiology 16: 60-71. doi:10.1111/1462-2920.12182

Sheik, C.S. 2, S. Jain, and G.J. Dick (2014). Metabolic flexibility of enigmatic SAR324 revealed through metagenomics and metatranscriptomics. Environmental Microbiology 16: 304-317. doi:10.1111/1462-2920.12165

Baker, B.J., C.S. Sheik, C.A. Taylor, S. Jain, A. Bhasi, J.D. Cavalcoli, and G.J. Dick (2013). Community transcriptomic assembly reveals microbes that contribute to deep-sea carbon and nitrogen cycling. The ISME Journal 7: 1962-1973. doi:10.1038/ismej.2013.85

Dick, G.J., K. Anantharaman, B.J. Baker, M. Li, D.C. Reed, and C.S. Sheik (2013). Hydrothermal vent plume microbiology: ecological and biogeographic linkages to seafloor and water column habitats. Frontiers in Microbiology 4: 124. doi:10.3389/fmicb.2013.00124

Anantharaman, K., J.A. Breier, C.S. Sheik, and G.J. Dick (2013). Evidence for hydrogen oxidation and metabolic plasticity in widespread deep-sea bacteria. Proceedings of the National Academy of Sciences 110: 330-335. doi:10.1073/pnas.1215340110

Baker, B.J., R.A. Lesniewski, and G.J. Dick. Genome-enabled transcriptomics reveals archaeal populations that drive nitrification in a deep-sea hydrothermal plume (2012). The ISME Journal 6: 2269-2279. doi:10.1038/ismej.2012.64

Lesniewski, R.A., S. Jain, P.D. Schloss, K. Anantharaman,and G.J. Dick (2012). The metatranscriptome of a deep-sea hydrothermal plume is dominated by water column methanotrophs and chemolithotrophs. The ISME Journal 6: 2257-2268. doi:10.1038/ismej.2012.63

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Data Files

File
sequence_accessions.csv (Comma Separated Values (.csv), 4.92 KB) MD5:d867552be05bf3939490b1ea5baf70fc Primary data file for dataset ID 544279

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Parameters

Parameter	Description	Units
database	Name of the database/repository where the sequence data are located.	text
accession_num	Sequence accession number (or Taxon Object ID for DOE JGI-IMG/MER).	alphanumeric
description	Description of the type of sequence.	text
URL	Hyperlink to the database/repository for the accession number.	text

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Deployments

GoCAL1

Website	https://www.bco-dmo.org/deployment/543276
Platform	R/V New Horizon
Start Date	2014-07-07
End Date	2014-07-23
Description	GoCAL1 Cruise. Guaymas Basin, Gulf of California. San Diego, CA to San Diego, CA. July 7 – 23, 2004. R/V New Horizon Chief Scientists: Fred Prahl and Brian Popp OCE-0094329

GoCAL2

Website	https://www.bco-dmo.org/deployment/543280
Platform	R/V New Horizon
Start Date	2005-01-25
End Date	2005-02-09
Description	GoCAL2 Cruise. Guaymas Basin, Gulf of California. San Diego, CA to San Diego, CA. January 25 – February 9, 2005. R/V New Horizon Chief Scientists: Fred Prahl and Brian Popp OCE-0326573

GoCAL3

Website	https://www.bco-dmo.org/deployment/543283
Platform	R/V New Horizon
Start Date	2005-07-23
End Date	2005-08-13
Description	GoCAL3 Cruise. Guaymas Basin, Gulf of California. San Diego, CA to San Diego, CA. July 23 – August 13, 2005. R/V New Horizon Chief Scientists: Fred Prahl and Brian Popp OCE-0326573

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Project Information

Linking biogeochemistry and microbial community dynamics in deep-sea hydrothermal plumes (Guaymas plumes)

Website: http://www.earth.lsa.umich.edu/geomicrobiology/Guaymas.html

Coverage: Guaymas Basin and Carmen Basin, Gulf of California

Description from NSF award abstract:
Deep-sea hydrothermal vent plumes are globally distributed along the 60,000-km mid-ocean ridge system and are hot spots of microbial biogeochemistry in the deep oceans. These plumes play host to important interactions between microbial communities and hydrothermal inputs; hydrothermal energy sources stimulate enhanced microbial activity and productivity, and microorganisms mediate the flux of elements and energy from deep-sea hydrothermal vents into the oceans. This hydrothermal flux is a significant source of two key micronutrients, iron and manganese, for the oceans. Despite this importance, microbial communities in deep sea-hydrothermal plumes have been understudied relative to those inhabiting near-vent and subsurface environments. The overall goal of this project is to reveal the microbial community dynamics responsible for enhanced microbial activities and mediation of geochemical processes that has been observed in deep-sea hydrothermal plumes. This research project is focused on plumes in the Guaymas Basin (Gulf of California), where previous results showed dramatic enhancement of microbial activity and enzymatic manganese (II) oxidation relative to the ambient deep sea. Cutting-edge DNA sequencing technologies will be utilized to characterize the microbial diversity, metabolic potential and physiological state of plume versus background communities through metagenomics and metatranscriptomics. The specific objectives are:
(1) to utilize hundreds of thousands of rRNA gene sequences available from DNA and RNA to compare community structure and population-specific activity in plumes versus background;
(2) to reconstruct composite genomes from the most abundant deep-sea microbial populations and evaluate their metabolic capabilities and nutritional needs; and
(3) to quantitatively compare gene content and expression profiles in plume and background, with a focus on uncovering metabolic shifts towards chemolithoautotrophy.

Overall, results are expected to shed light on the nature of microbial players and processes in plumes: is plume biogeochemistry mediated by indigenous deep-sea microorganisms that have been stimulated by hydrothermal inputs, or by plume-specific groups that were entrained from near-vent environments?

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1029242
Gordon and Betty Moore Foundation (GBMF)	GBMF2609

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