

Physical and chemical metadata for microbiological samples from R/V New Horizon cruises GoCAL1, GoCAL2, GoCAL3 in the Guaymas Basin, Gulf of California from 2004-2005 (Guaymas plumes project)

Website: <https://www.bco-dmo.org/dataset/543286>

Data Type: Cruise Results

Version: 1

Version Date: 2014-12-19

Project

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

Contributors	Affiliation	Role
Dick, Gregory J.	University of Michigan	Principal Investigator
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

This dataset includes physical and chemical metadata for microbiological samples from R/V New Horizon cruises GoCAL1, GoCAL2, GoCAL3 in the Guaymas Basin, Gulf of California from 2004-2005.

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Coverage

Spatial Extent: N:27.506 E:-110.72388 S:26.37925 W:-111.4109

Temporal Extent: 2004-07-11 - 2005-02-05

Dataset Description

Physical and chemical metadata (sal, Mn, O₂, temp, etc.) for microbiological samples from Guaymas Basin plumes.

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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1038/ismej.2012.63)

Methods & Sampling

Hydrothermal plumes were detected by turbidity anomalies as measured by an air-calibrated transmissometer (WetLabs) on a CTD rosette (Sea-Bird). Water samples were collected in 10-L niskin bottles by CTD Rosette (Sea-Bird).

Samples were transferred from niskin bottles to acidwashed 50 mL polypropylene tubes. Samples for dissolved Mn (dMn) were filtered through 0.2 μ m acid-washed nucleopore polycarbonate filters within 1 h of collection. Filtrate (dMn) and unfiltered total Mn samples (tMn) were stabilized by acidification with Optima grade nitric acid to a pH of <2 and stored at 4 degrees C until analysis. All shipboard manipulations were performed in a laminar flow hood with clean techniques. Mn concentrations were determined on a Thermoquest Finnigan Element 2 double focusing, single collector, magnetic sector inductively coupled plasma mass spectrometer (ICP-MS) at the SIO unified laboratory analytical facility. ICP-MS was done at low resolution following instrument and induction parameters described previously (Field et al., 1999). Samples were diluted 1:50 in 2% nitric acid in quartz-distilled (QD) water prior to analysis. A calibration curve was prepared as described previously (Rodushkin and Ruth, 1998) using matrix-matched external standards made with 2% natural seawater stripped of metals by precipitation with Optima ammonium hydroxide. Indium (1 ppb) was used as an internal standard in all standards and samples. Standard additions (Willard et al., 1965) were used to rule out a matrix effect. To confirm analytical accuracy, reference waters CASS-4 and NASS-5 (Verplank et al., 2001) were included in the analysis as samples. Our experimentally determined average Mn concentration for CASS was 56 ± 10 nM (reported to be 51 nM) and for NASS-5 it was 16 ± 8 nM (reported to be 17 nM). Six samples from station 1 were collected, processed and analyzed in duplicate. The average standard deviation was 8 nM, which includes variation due to both sampling and analytical error.

Data Processing Description

BCO-DMO processing:

- modified parameter names to conform with BCO-DMO naming conventions;
- formatted date to mm/dd/yyyy; added separate month, day, and year columns;
- converted lat and lon to decimal degrees.

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Data Files

File**Guymas_metadata.csv**(Comma Separated Values (.csv), 834 bytes)

MD5:dee8c0bbf3b75d76659b5d7598e86536

Primary data file for dataset ID 543286

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Related Publications

Anantharaman, K., Breier, J. A., Sheik, C. S., & Dick, G. J. (2012). Evidence for hydrogen oxidation and metabolic plasticity in widespread deep-sea sulfur-oxidizing bacteria. *Proceedings of the National Academy of Sciences*, 110(1), 330–335. doi:[10.1073/pnas.1215340110](https://doi.org/10.1073/pnas.1215340110)

General

Anantharaman, K., Duhaime, M. B., Breier, J. A., Wendt, K. A., Toner, B. M., & Dick, G. J. (2014). Sulfur Oxidation Genes in Diverse Deep-Sea Viruses. *Science*, 344(6185), 757–760. doi:[10.1126/science.1252229](https://doi.org/10.1126/science.1252229)

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Baker, B. J., Lesniewski, R. A., & Dick, G. J. (2012). Genome-enabled transcriptomics reveals archaeal populations that drive nitrification in a deep-sea hydrothermal plume. *The ISME Journal*, 6(12), 2269–2279. doi:[10.1038/ismej.2012.64](https://doi.org/10.1038/ismej.2012.64)

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Baker, B. J., Sheik, C. S., Taylor, C. A., Jain, S., Bhasi, A., Cavalcoli, J. D., & Dick, G. J. (2013). Community transcriptomic assembly reveals microbes that contribute to deep-sea carbon and nitrogen cycling. *The ISME Journal*, 7(10), 1962–1973. doi:[10.1038/ismej.2013.85](https://doi.org/10.1038/ismej.2013.85)

General

Dick, G. J., Anantharaman, K., Baker, B. J., Li, M., Reed, D. C., & Sheik, C. S. (2013). The microbiology of deep-sea hydrothermal vent plumes: ecological and biogeographic linkages to seafloor and water column habitats. *Frontiers in Microbiology*, 4. doi:[10.3389/fmicb.2013.00124](https://doi.org/10.3389/fmicb.2013.00124)

General

Lesniewski, R. A., Jain, S., Anantharaman, K., Schloss, P. D., & Dick, G. J. (2012). The metatranscriptome of a deep-sea hydrothermal plume is dominated by water column methanotrophs and lithotrophs. *The ISME Journal*, 6(12), 2257–2268. doi:[10.1038/ismej.2012.63](https://doi.org/10.1038/ismej.2012.63)

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Li, M., Jain, S., Baker, B. J., Taylor, C., & Dick, G. J. (2013). Novel hydrocarbon monooxygenase genes in the metatranscriptome of a natural deep-sea hydrocarbon plume. *Environmental Microbiology*, 16(1), 60–71. doi:[10.1111/1462-2920.12182](https://doi.org/10.1111/1462-2920.12182)

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Li, M., Toner, B. M., Baker, B. J., Breier, J. A., Sheik, C. S., & Dick, G. J. (2014). Microbial iron uptake as a mechanism for dispersing iron from deep-sea hydrothermal vents. *Nature Communications*, 5(1). doi:[10.1038/ncomms4192](https://doi.org/10.1038/ncomms4192)

General

Sheik, C. S., Jain, S., & Dick, G. J. (2013). Metabolic flexibility of enigmatic SAR324 revealed through metagenomics and metatranscriptomics. *Environmental Microbiology*, 16(1), 304–317. doi:[10.1111/1462-2920.12165](https://doi.org/10.1111/1462-2920.12165)

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Parameters

Parameter	Description	Units
sample	Sample identification number.	unitless
sample_type	Type of sample.	text
month	2-digit month.	mm (01-12)
day	2-digit day of month.	dd (01-31)
year	4-digit year	YYYY
date	Date formatted as month/day/year.	mm/dd/yyyy
cast	Cast identification number.	unitless
lat	Latitude. Positive values = North.	decimal degrees
lon	Longitude. Negative values = West.	decimal degrees
depth_w	Depth of the water.	meters (m)
depth	Sample depth.	meters (m)
sal	Salinity.	parts per million (ppm)
Mn_tot	Total Manganese (Mn) concentration.	nanomolar (nM)
Mn_diss	Dissolved Manganese (Mn) concentration.	nanomolar (nM)
O2	Oxygen (O2) concentration.	micromolar (um)
temp	Temperature.	degrees Celsius (C)
filter_type	Type of filter.	text
filter_pore_size	Pore size of the filter.	micrometers (um)

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Instruments

Dataset-specific Instrument Name	CTD Sea-Bird
Generic Instrument Name	CTD Sea-Bird
Dataset-specific Description	Hydrothermal plumes were detected by turbidity anomalies as measured by an air-calibrated transmissometer (WetLabs) on a CTD rosette (Sea-Bird). Water samples were collected in 10-l niskin bottles by CTD Rosette (Sea-Bird).
Generic Instrument Description	Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics, no specific unit identified. This instrument designation is used when specific make and model are not known. See also other SeaBird instruments listed under CTD. More information from Sea-Bird Electronics.

Dataset-specific Instrument Name	Thermoquest Finnigan Element 2
Generic Instrument Name	Inductively Coupled Plasma Mass Spectrometer
Dataset-specific Description	Mn concentrations were determined on a Thermoquest Finnigan Element 2 double focusing, single collector, magnetic sector inductively coupled plasma mass spectrometer (ICP-MS) at the SIO unified laboratory analytical facility.
Generic Instrument Description	An ICP Mass Spec is an instrument that passes nebulized samples into an inductively-coupled gas plasma (8-10000 K) where they are atomized and ionized. Ions of specific mass-to-charge ratios are quantified in a quadrupole mass spectrometer.

Dataset-specific Instrument Name	Niskin bottle
Generic Instrument Name	Niskin bottle
Dataset-specific Description	Water samples were collected in 10-l niskin bottles by CTD Rosette (Sea-Bird). Samples were transferred from niskin bottles to acidwashed 50 ml polypropylene tubes.
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

Dataset-specific Instrument Name	Transmissometer
Generic Instrument Name	Transmissometer
Dataset-specific Description	Hydrothermal plumes were detected by turbidity anomalies as measured by an air-calibrated transmissometer (WetLabs) on a CTD rosette (Sea-Bird).
Generic Instrument Description	A transmissometer measures the beam attenuation coefficient of the lightsource over the instrument's path-length. This instrument designation is used when specific manufacturer, make and model are not known.

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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 Prah 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 Prah 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 Prah 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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