Rates of water column nitrification determined from bottle incubations with 15N tracers (15NH4Cl); samples collected on METZYME cruise.

Website: https://www.bco-dmo.org/dataset/647792
Data Type: Cruise Results
Version: 27 May 2016
Version Date: 2016-05-27

Project
» Connecting Trace Elements and Metalloenzymes Across Marine Biogeochemical Gradients (GPc03) (MetZyme)
» Gene content, gene expression, and physiology in mesopelagic ammonia-oxidizing archaea (AmoA Archaea)

Program
» U.S. GEOTRACES (U.S. GEOTRACES)

Contributors	Affiliation	Role
Santoro, Alyson E.	University of California-Santa Barbara (UCSB)	Principal Investigator
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Dataset Description

Rates of water column nitrification determined from bottle incubations with 15N tracers (15NH4Cl); sample collected on METZYME cruise (KM1128).

Related references:

Santoro, A.E., Casciotti, K.L., and C.A. Francis. 2010. Activity, abundance,and diversity of nitrifying archaea and bacteria in the central California Current. Environmental Microbiology 12: 1989-2006. doi:10.1111/j.1462-2920.2010.02205.x

Santoro, A.E., Saito, M.A., Goepfert, T.J., Lamborg, C.H., Dupont, C.L., G.R. DiTullio. Thaumarchaeal ecotype distributions across the equatorial Pacific and their potential roles in nitrification and sinking flux attenuation. Submitted to *Limnology & Oceanography, April 2016*.

Methods & Sampling

Nitrification rate incubations were conducted at Stations 1, 3, and 5 at four depths and followed procedures described in Santoro et al. 2010, Environ. Micro. Timecourse samples of d15NNOx were analyzed by isotope ratio mass spectrometer using the 'denitrifier method.' Complete methods specific to the MetZyme cruise dataset deposited here are described in Santoro et al., submitted to L&O.

Rates for Station 1 were initiated from the ship's rosette; Stations 3 and 5 used a trace metal clean rosette.

Data Processing Description

The MATLAB script ‘metzyme_rates.m’ was used with the raw data files ('initials…' and ‘data…'). Compiled rates were deposited in a tab-delimited text file.

MATLAB scripts: (click to view files or right-click to save)
metzyme_rates.m
nitr_rate_rev.m

Raw data: (click to view files or right-click to save)
initials_mzst1.csv
initials_mzst3.csv
initials_mzst5.csv
data_mzst1.csv
data_mzst3.csv
data_mzst5.csv

BCO-DMO Processing:
- Modified paramter names to conform with BCO-DMO naming conventions;
- Added cruise ID.

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Data Files

File
nitrification.csv (Comma Separated Values (.csv), 1.52 KB) MD5:d34184aae27d752c3715acd6f3f4a7ab Primary data file for dataset ID 647792

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Parameters

Parameter	Description	Units
cruise	Cruise identifier.	unitless
cast	Cast number. TMR = Trace Metal Rosette. CTD = Ship's CTD.	unitless
station	Station number.	unitless
lon	Longitude east.	decimal degrees
lat	Latitude north.	decimal degrees
depth	Sample depth.	meters (m)
bottle	Incubation bottle number (1,2 = experimental bottles; 3 = no addition control)	unitless
nitr_rate	Nitrification rate.	nanomoles per liter per day (nmol L-1 d-1)
nitr_rate_SE	Standard error of the rate fit.	nanomoles per liter per day (nmol L-1 d-1)

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Deployments

KM1128

Website	https://www.bco-dmo.org/deployment/59053
Platform	R/V Kilo Moana
Start Date	2011-10-01
End Date	2011-10-25
Description	This is a MetZyme project cruise. The original cruise data are available from the NSF R2R data catalog.

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Project Information

Connecting Trace Elements and Metalloenzymes Across Marine Biogeochemical Gradients (GPc03) (MetZyme)

Coverage: Tropical North Pacific along 150 degrees West from 18 degrees North to the equator

MetZyme project researchers will determine the role of enzymatic activity in the cycling of trace metals. Specifically the research will address the following questions: (1) degradation of sinking particulate organic material in the Tropical North Pacific can be influenced by the ability of microbes to synthesize zinc proteases, which in turn is controlled by the abundance or availability of zinc, and (2) methylation of mercury is controlled, in part, by the activity of cobalt-containing enzymes, and therefore the supply of labile cobalt to the corrinoid-containing enzymes or co-factors responsible for methylation. To attain their goal, they will collect dissolved and particulate samples for trace metals and metalloenzymes from three stations along a biogeochemical gradient in the Tropical North Pacific (along 150 degrees West from 18 degrees North to the equator). Sinking particles from metal clean sediment traps will also be obtained. The samples will also be used to carry out shipboard incubation experiments using amendments of metals, metal-chelators, B12, and proteases to examine the sensitivity and metal limitation of heterotrophic, enzymatic degradation of organic matter within the oceanic "Twilight Zone" (100-500 m). This study will result in a novel metaproteomic/metalloenzyme datasets that should provide insights into the biogeochemical cycling of metals, as well as co-limitation of primary productivity and controls on the export of carbon from the photic zone. In addition to the final data being contributed to BCO-DMO, an online metaproteomic data server will be created so the community has access to the raw data files generated by this research.

Gene content, gene expression, and physiology in mesopelagic ammonia-oxidizing archaea (AmoA Archaea)

Coverage: Epipelagic and mesopelagic, Equatorial Pacific

NSF award abstract:

Intellectual Merit. How organisms respond to their physical and chemical and environment is a central question in marine ecology. For microbes living in the mesopelagic - the ocean's "twilight zone" - an efficient response is particularly important to capitalize on the intermittent delivery of organic and inorganic compounds sinking from the surface ocean. These organisms must have a suite of metabolic and regulatory strategies used to cope with environmental variability, but these strategies are largely unknown. Understanding when and why metabolic genes are expressed is critical to our understanding of nutrient remineralization in the ocean. Marine group 1 (MG1) archaea are ubiquitous, abundant microbes in the meso- and bathypelagic and promising model organisms for investigating these questions. MG1 archaea are chemolithoautotrophs that oxidize ammonia for energy and fix carbon for biomass, and as such, play a central role in the ocean's coupled carbon and nitrogen cycles. Though MG1 have historically eluded cultivation, recent efforts have been successful at bringing representative MG1 archaea from the open ocean into culture and demonstrating their importance in the

production of the greenhouse gas nitrous oxide. This project takes advantage of unique MG1 cultures and the recently sequenced draft genome of one of the organisms - strain CN25 - to investigate the physiological and transcriptional responses of MG1 archaea to variations in their chemical environment, specifically:

1. Comparative transcriptomics of CN25 cells grown under a range of energy availability and nitrosative stress will identify select genes that can be used to diagnose the physiological state of natural populations

2. Improvements in the genomic and transcriptomic knowledge of MG1 archaea will facilitate a thorough reinterpretation of existing metagenomic and metatranscriptomic datasets, as well as provide a better contextual understanding in future studies

The investigators will conduct comparative transcriptomics of CN25 cells harvested in mid-exponential growth and stationary phase versus starved cells. Transcriptomes of cells grown at high nitrate concentrations and low pO2 with those grown in standard conditions will be characterized. A strand-specific, high-density RNAseq approach will be used to examine the expression of putative ORFs, polycistronic operons, and small RNAs, which, in addition to gene expression profiling, has the ancillary benefit of improving genome annotation. Finally, the investigators will sequence the genomes of two additional MG1 strains isolated from the open ocean, as well as single cells from environmental surveys, and leverage the combination with the CN25 genome to reanalyze available metagenomic and metatranscriptomic datasets. The results will define the transcriptional response of a model mesopelagic microbe to a range of chemical environments, and show how the physicochemical environment induces changes in gene expression and gene content that result in greenhouse gas production. This work will rapidly generate new knowledge of how some of the most ubiquitous, yet heretofore elusive, microorganisms respond to geochemical variability and shape our evolving understanding of the marine nitrogen cycle.

Broader Impacts. The scientific and societal impact of the project will be to elucidate the mechanisms of greenhouse gas production in a model marine organism that is of broad interest to biological and chemical oceanographers. Transcriptome sequencing will improve the assembly of the CN25 genome, the first genome of an MG1 archaeon from the open ocean. Both the genome and transcriptomes will be important references for researchers using metagenomics, metatranscriptomics, and metaproteomics in the ocean, as these techniques are reliant on a knowledgebase composed of both DNA sequence and physiology. Thus, the results add value to both existing and future studies. The proposed research will advance education, teaching, and training for the next generation of marine scientists by providing support for two early-career investigators, one postdoctoral researcher, and a secondary school teacher.

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Program Information

U.S. GEOTRACES (U.S. GEOTRACES)

Website: http://www.geotraces.org/

Coverage: Global

GEOTRACES is a SCOR sponsored program; and funding for program infrastructure development is provided by the U.S. National Science Foundation.

GEOTRACES gained momentum following a special symposium, S02: Biogeochemical cycling of trace elements and isotopes in the ocean and applications to constrain contemporary marine processes (GEOSECS II), at a 2003 Goldschmidt meeting convened in Japan. The GEOSECS II acronym referred to the Geochemical Ocean Section Studies To determine full water column distributions of selected trace elements and isotopes, including their concentration, chemical speciation, and physical form, along a sufficient number of sections in each ocean basin to establish the principal relationships between these distributions and with more traditional hydrographic parameters;

* To evaluate the sources, sinks, and internal cycling of these species and thereby characterize more completely the physical, chemical and biological processes regulating their distributions, and the sensitivity of these processes to global change; and

* To understand the processes that control the concentrations of geochemical species used for proxies of the past environment, both in the water column and in the substrates that reflect the water column.

GEOTRACES will be global in scope, consisting of ocean sections complemented by regional process studies. Sections and process studies will combine fieldwork, laboratory experiments and modelling. Beyond realizing the scientific objectives identified above, a natural outcome of this work will be to build a community of marine scientists who understand the processes regulating trace element cycles sufficiently well to exploit this knowledge reliably in future interdisciplinary studies.

Expand "Projects" below for information about and data resulting from individual US GEOTRACES research projects.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1031271
NSF Division of Ocean Sciences (NSF OCE)	OCE-1260006

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