Metal quotas of NE Pacific and Altantic diatom isolates measured via ICP-MS after growth in zinc and cobalt media amendments in experiments with cultures collected from R/V Thomas G. Thompson cruise TN280, along Line P in the NE Pacific, in May of 2012

Website: https://www.bco-dmo.org/dataset/807299
Data Type: experimental, Cruise Results
Version: 1
Version Date: 2020-03-31

Project
» US GEOTRACES PMT: Cobalt Biogeochemical Cycling and Connections to Metalloenzymes in the Pacific Ocean (PMT Cobalt and Metalloenzymes)
» Marine Microbial Investigator Award: Investigator Mak Saito (MM Saito)

Program
» Marine Microbiology Initiative (MMI)

Contributors	Affiliation	Role
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Abstract
Metal quotas of two NE Pacific Line P diatom isolates and one Atlantic diatom isolate measured via ICP-MS after growth in zinc and cobalt media amendments. Experiments with cultures collected from the GeoMICS expedition on the R/V Thomas G. Thompson (cruise TN280), along Line P in the NE Pacific, in May of 2012.

Table of Contents

Coverage

Spatial Extent: **N**:54 **E**:-4 **S**:40.756 **W**:-128.666
Temporal Extent: 2012-05-17 - 2012-05-22

Dataset Description

Metal quotas of two NE Pacific Line P diatom isolates and one Atlantic diatom isolate measured via ICP-MS after growth in zinc and cobalt media amendments. Experiments with cultures collected from the GeoMICS expedition on the R/V Thomas G. Thompson (cruise TN280), along Line P in the NE Pacific, in May of 2012.

Methods & Sampling

Location: Cultures collected from Northeast Pacific Line P Transect 48.8167 N 128.667 W

Metal quotas
Cellular metal quotas were measured by inductively coupled plasma mass spectrometry (ICP-MS). Biomass from replicate 25 mL matrix cultures of P. tricornutum CCMP632, P. delicatissima UNC1205, and Thalassiosira UNC1203 were pooled upon entering stationary phase and were centrifuged at 11,000 RPM (14,610 x g) for 40 minutes at 4°C. The cell pellet was resuspended in ~1 mL media and transferred to an acid-cleaned microcentrifuge tube. Cultures were centrifuged again for 30 min at 14,100 RPM (13,336 x g) at 4°C before the supernatant was discarded. The remaining cell pellet was acidified in 800 L of 5% nitric acid (Optima) containing 1 ppb indium for at least seven days. Solids were removed by centrifugation. No attempt was made to remove extracellular metals by washing cells with additional metal chelators in order to minimize processing blanks. Quota determinations therefore include contributions from both intracellular and extracellular pools. Process blank digestions containing acid but no cells were performed in parallel. Digests were diluted by a factor of 9 with 5% nitric acid 1 ppb indium solution before being analyzed in duplicate on a Thermo ICAP-Q plasma mass spectrometer calibrated to a multi-element standard curve (Spex Certiprep) over a range of 1 – 20 ppb. Samples were analyzed in KED mode after an 85s sample uptake window and element mass windows were scanned 3 times during measurements. The 1 ppb indium internal standard was used to correct for variation in sample delivery and plasma suppression between samples. Process blanks were subtracted from measured concentrations. Phosphorus concentrations were also measured by ICP-MS simultaneously and were calibrated to a standard curve ranging from 100 – 3,200 ppb using a 1 ppm certified P stock (Alfa Aesar Specpure). The seawater media base used for all growth experiments was similarly analyzed via ICP-MS using a 1:10 dilution of media base into 5% nitric acid 1 ppb indium and analyzed as above to determine background media concentrations of total Zn and Co (0.9 nmol L-1 and 0.1 nmol L-1, respectively).

Missing data identifiers in this dataset include:
* "nd" indicating no data
* Below Detection
* "contam" indicating the sample was contaminated

Isolation sources and locations
* Pseudonitzschia delicatissima UNC1205 and Thalassiosira UNC1203 were isolated from station P8 of the Line P transect, 48.817□N 128.666□W
* Phaeodactylum tricornutum CCMP632 was ordered from Bigelow, the strains original location of isolation was 54□N 4□W
* Thalassiosira pseudonana CCMP1335 was also from Bigelow, original location of isolation was 40.756° N 72.82° W

Data Processing Description

BCO-DMO Data Manager Processing Notes:
* Combined three tables in sheet "Metal Quotas" in originally submitted excel file "BCO-DMO LineP Metal Quotas.xlsx" and extracted to csv format.
* Column "culture" added to capture information in the title of each of the three original tables (P. delicatissima UNC1205, Thalassiosira UNC1203, P. tricornutum CCMP632)
* added a conventional header with dataset name, PI name, version date
* Missing data identifier in original data "NA" is displayed by default as "nd" in the bco-dmo data system.
* modified parameter names to conform with BCO-DMO naming conventions (only letters, numbers, and underscores)

[table of contents | back to top]

Parameters

Parameter	Description	Units
Culture	Culture name (e.g. Thalassiosira UNC12032)	unitless
Added_Zn	Total amount of added zinc (Zn) to incubation.	nanomoles per liter (nmol/L)
Added_Co	Total amount of added cobalt (Co) to incubation.	nanomoles per liter (nmol/L)
Total_Zn	Total zinc (Zn). Added Zn and background media Zn.	nanomoles per liter (nmol/L)
Total_Co	Total cobalt (Co). Added Co and background media Co.	nanomoles per liter (nmol/L)
log_Zn2plus	Log of calculated free Zn2+ ion concentration in media. [Zn2+]	moles per liter (mol/L)
log_Co2plus	Log of calculated free Co2+ ion concentration in media. [Co2+]	moles per liter (mol/L)
CO_to_P_avg	Average ratio of cobalt (Co) in millimoles to phosphorous (P) in moles. Co (mmol):P(mol) quota.	dimensionless
ZN_to_P_avg	Average ratio of zinc (Zn) in millimoles to phosphorous (P) in moles. Zn (mmol):P(mol) quota.	dimensionless
CD_to_P_avg	Average ratio of cadmium (Cd) in micromoles to phosphorous (P) in moles. Cd (umol):P(mol) quota.	dimensionless
MN_to_P_avg	Average ratio of manganese (Mn) in millmoles to phosphorous (P) in moles. Mn (mmol):P(mol) quota.	dimensionless
FE_to_P_avg	Average ratio of iron (Fe) in millmoles to phosphorous (P) in moles. Fe (mmol):P(mol) quota.	dimensionless
NI_to_P_avg	Average ratio of nickel (Ni) in millmoles to phosphorous (P) in moles. Ni (mmol):P(mol) quota.	dimensionless
CU_to_P_avg	Average ratio of copper (Cu) in millmoles to phosphorous (P) in moles. Cu (mmol):P(mol) quota.	dimensionless
MO_to_P_avg	Average ratio of molybdenum (Mo) in millmoles to phosphorous (P) in moles. Mo (mmol):P(mol) quota.	dimensionless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Thermo ICAP-Q plasma mass spectrometer
Generic Instrument Name	Mass Spectrometer
Generic Instrument Description	General term for instruments used to measure the mass-to-charge ratio of ions; generally used to find the composition of a sample by generating a mass spectrum representing the masses of sample components.

[table of contents | back to top]

Deployments

TN280

Website	https://www.bco-dmo.org/deployment/664928
Platform	R/V Thomas G. Thompson
Start Date	2012-05-16
End Date	2012-05-22

[table of contents | back to top]

Project Information

US GEOTRACES PMT: Cobalt Biogeochemical Cycling and Connections to Metalloenzymes in the Pacific Ocean (PMT Cobalt and Metalloenzymes)

Coverage: Laboratory Study and Cultures from Northeast Pacific Line P Transect 48.8167 N 128.667 W

NSF abstract:

Cobalt is important for many forms of marine life, yet it is one of the scarcest nutrients in the sea. Cobalt's oceanic abundance and distribution, along with other scarce nutrients, can influence the growth of microscopic plants (phytoplankton). This in turn can influence carbon cycles in the ocean and atmosphere. Therefore, knowledge of the controls on cobalt's abundance and chemical forms in seawater is a valuable component of our ability to understand the ocean's influence on global carbon cycling. Within phytoplankton and other marine microbes, metals such as cobalt, iron, nickel, and copper are used as critical components of enzymes responsible for key cellular reactions. Since these enzymes require metals to work, they are named metalloenzymes. Participating in a Pacific Ocean cruise from Alaska to Tahiti, this project will study the oceanic distributions of dissolved cobalt and the cellular content of a group of metalloenzymes known to influence biogeochemical cycles. The project will provide scientific impact by creating new knowledge about oceanic micronutrients in regions of economic interest with regard to fisheries and deep-sea mining. Measurement of proteins in the North Pacific will provide data of broad biological and chemical interest and will be made available through a new NSF-funded "EarthCube Ocean Protein Portal" data base. Educational impact will stem from participation of a graduate student and two young technicians, as well as the PI's development of a high school chemistry curriculum for use in two local high schools, thus allowing teachers to include real oceanic and environmental data at their first introduction to chemistry.

Cobalt has a complex biogeochemical cycle. Both its inorganic and organic forms are used by biology in the upper ocean and it is removed from solution by being scavenged in the intermediate and deep ocean. This scavenging removal results in cobalt having the smallest oceanic inventory of any biologically utilized element. Recent studies, however, have found that large dissolved cobalt plumes occur in major oxygen minimum zones due to a combination of less scavenging and additions from sedimentary and remineralization fluxes. The GP15 US GEOTRACES Pacific Meridional Transect (PMT) provides an opportunity to examine the influence of oxygen depletion on cobalt chemistry. Moreover, the study of the protein component of microbial communities using new proteomic techniques will provide evidence of how different major microorganisms respond to the chemical environment (e.g. through transporter production for specific nutrients and micronutrients) as well as the biochemical basis for metal requirements related to the use of specific metalloenzymes. Specifically, the PMT provides an opportunity to confirm that the Pacific oxygen minimum zones contain a large amount of cobalt and to test the hypotheses that simultaneous zinc scarcity could induce wide-scale biochemical substitution of cobalt for zinc in the North Pacific Ocean.

Marine Microbial Investigator Award: Investigator Mak Saito (MM Saito)

In support of obtaining deeper knowledge of major biogeochemically relevant proteins to inform a mechanistic understanding of global marine biogeochemical cycles.

[table of contents | back to top]

Program Information

Marine Microbiology Initiative (MMI)

Website: https://www.moore.org/initiative-strategy-detail?initiativeId=marine-microbiology-initiative

A Gordon and Betty Moore Foundation Program.

Forging a new paradigm in marine microbial ecology:

Microbes in the ocean produce half of the oxygen on the planet and remove vast amounts of carbon dioxide, a greenhouse gas, from the atmosphere. Yet, we have known surprisingly little about these microscopic organisms. As we discover answers to some long-standing puzzles about the roles that marine microorganisms play in supporting the ocean's food webs and driving global elemental cycles, we realized that we still need to learn much more about what these organisms do and how they do it—including how they evolved and contribute to our ocean's health and productivity.

The Marine Microbiology Initiative seeks to gain a comprehensive understanding of marine microbial communities, including their diversity, functions and behaviors; their ecological roles; and their origins and evolution. Our focus has been to enable researchers to uncover the principles that govern the interactions among microbes and that govern microbially mediated nutrient flow in the sea. To address these opportunities, we support leaders in the field through investigator awards, multidisciplinary team research projects, and efforts to create resources of broad use to the research community. We also support development of new instrumentation, tools, technologies and genetic approaches.

Through the efforts of many scientists from around the world, the initiative has been catalyzing new science through advances in methods and technology, and to reduce interdisciplinary barriers slowing progress. With our support, researchers are quantifying nutrient pools in the ocean, deciphering the genetic and biochemical bases of microbial metabolism, and understanding how microbes interact with one another. The initiative has five grant portfolios:

Individual investigator awards for current and emerging leaders in the field.
Multidisciplinary projects that support collaboration across disciplines.
New instrumentation, tools and technology that enable scientists to ask new questions in ways previously not possible.
Community resource efforts that fund the creation and sharing of data and the development of tools, methods and infrastructure of widespread utility.
Projects that advance genetic tools to enable development of experimental model systems in marine microbial ecology.
We also bring together scientists to discuss timely subjects and to facilitate scientific exchange.

Our path to marine microbial ecology was a confluence of new technology that could accelerate science and an opportunity to support a field that was not well funded relative to potential impact. Around the time we began this work in 2004, the life sciences were entering a new era of DNA sequencing and genomics, expanding possibilities for scientific research – including the nascent field of marine microbial ecology. Through conversations with pioneers inside and outside the field, an opportunity was identified: to apply these new sequencing tools to advance knowledge of marine microbial communities and reveal how they support and influence ocean systems.

After many years of success, we will wind down this effort and close the initiative in 2021. We will have invested more than $250 million over 17 years to deepen understanding of the diversity, ecological activities and evolution of marine microbial communities. Thanks to the work of hundreds of scientists and others involved with the initiative, the goals have been achieved and the field has been profoundly enriched; it is now positioned to address new scientific questions using innovative technologies and methods.

[table of contents | back to top]

Funding

Funding Source	Award
Gordon and Betty Moore Foundation: Marine Microbiology Initiative (MMI)	GBMF3782
NSF Division of Ocean Sciences (NSF OCE)	OCE-1736599

[table of contents | back to top]