Metal quotas (ratios of Metal:P) of the polar diatom Chaetoceros sp. RS19 in +Zn and +Co incubation studies from January 2020 (MM Saito project)

Website: https://www.bco-dmo.org/dataset/859211
Data Type: experimental
Version: 1
Version Date: 2021-08-30

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

Program
» Marine Microbiology Initiative (MMI)

Contributors	Affiliation	Role
Saito, Mak A.	Woods Hole Oceanographic Institution (WHOI)	Principal Investigator
Kellogg, Riss	Massachusetts Institute of Technology (MIT)	Student, Contact
Newman, Sawyer	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Metal quotas (ratios of Metal:P) of the Ross Sea diatom isolate Chaetoceros RS19 measured via ICP-MS after growth in +Zn+Co media amendments.

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Coverage

Spatial Extent: **Lat**:-76.48338 **Lon**:177.12379
Temporal Extent: 2020-01 - 2020-01

Dataset Description

Metal quotas (ratios of Metal:P) of the Ross Sea diatom isolate Chaetoceros RS19 measured via ICP-MS after growth in +Zn+Co media amendments.

Acquisition Description

Methodology:

Sampling and analytical procedures:

Metal quotas

Cellular metal quotas were measured by inductively coupled plasma mass spectrometry (ICP-MS). Biomass from replicate 25 mL double addition cultures of *Chaetoceros* RS19 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. Half of the remaining cell pellet was acidified in 800 mL of 5% nitric acid (Optima) containing 1 ppb indium for at least seven days while the other half was retained for proteomic analysis. 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 (0.7 nmol L-1 and 0.1 nmol L-1, respectively).

Processing Description

BCO-DMO Processing Notes:

- Renamed fields to meet BCO-DMO naming conventions

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Related Publications

Kellogg, M.M., Moran, D.M., McIlvin, M.R., Subhas, A.V., Allen, A.E., Saito, M.A. Lack of a Zn/Co substitution ability in the polar diatom Chaetoceros RS19.
Results

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Related Datasets

IsRelatedTo

Kellogg, R., Saito, M. A. (2021) **Growth rates of the polar diatom Chaetoceros RS19 under various +Zn and +Co conditions from September 2019 (MM Saito project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-08-31 http://lod.bco-dmo.org/id/dataset/858743 [view at BCO-DMO]

Kellogg, R., Saito, M. A. (2021) **Metal uptake rates of the polar diatom Chaetoceros RS19 in +Zn**

and +Co incubation studies from January 2020 (MM Saito project). Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-08-30 http://lod.bco-dmo.org/id/dataset/859581 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
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)
Growth_rate_average	Average growth rate of replicates A and B	per day (d-1)
FE_to_P_avg	Average ratio of iron (Fe) in millmoles to phosphorous (P) in moles. Fe (mmol):P(mol) quota.	unitless
MN_to_P_avg	Average ratio of manganese (Mn) in millmoles to phosphorous (P) in moles. Mn (mmol):P(mol) quota.	unitless
NI_to_P_avg	Average ratio of nickel (Ni) in millmoles to phosphorous (P) in moles. Ni (mmol):P(mol) quota.	unitless
CU_to_P_avg	Average ratio of copper (Cu) in millmoles to phosphorous (P) in moles. Cu (mmol):P(mol) quota.	unitless
ZN_to_P_avg	Average ratio of zinc (Zn) in millimoles to phosphorous (P) in moles. Zn (mmol):P(mol) quota.	unitless
CD_to_P_avg	Average ratio of cadmium (Cd) in micromoles to phosphorous (P) in moles. Cd (umol):P(mol) quota.	unitless
CO_to_P_avg	Average ratio of cobalt (Co) in millimoles to phosphorous (P) in moles. Co (mmol):P(mol) quota.	unitless

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Instruments

Dataset-specific Instrument Name	Thermo ICAP-Q plasma mass spectrometer
Generic Instrument Name	Inductively Coupled Plasma Mass Spectrometer
Dataset-specific Description	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.
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	Centrifuge
Generic Instrument Name	Centrifuge
Dataset-specific Description	Biomass from replicate 25 mL double addition cultures of Chaetoceros RS19 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. Half of the remaining cell pellet was acidified in 800 mL of 5% nitric acid (Optima) containing 1 ppb indium for at least seven days while the other half was retained for proteomic analysis. Solids were removed by centrifugation.
Generic Instrument Description	A machine with a rapidly rotating container that applies centrifugal force to its contents, typically to separate fluids of different densities (e.g., cream from milk) or liquids from solids.

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Project Information

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.

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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.

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Funding

Funding Source	Award
Gordon and Betty Moore Foundation: Marine Microbiology Initiative (MMI)	GBMF3782
NSF Division of Ocean Sciences (NSF OCE)	OCE-1657766
NSF Division of Ocean Sciences (NSF OCE)	OCE-1658030
NSF Division of Ocean Sciences (NSF OCE)	OCE-1736599
NSF Division of Ocean Sciences (NSF OCE)	OCE-1850719

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