Cell abundance, nutrient and DMSP concentrations measured during a mesocosm study of the effect of phytoplankton composition on bacterial DMSP transformation (OceanSulfurFluxBact project)

Website: https://www.bco-dmo.org/dataset/662681
Data Type: experimental
Version:
Version Date: 2016-10-25

Project
» Bacterial Taxa that Control Sulfur Flux from the Ocean to the Atmosphere (OceanSulfurFluxBact)

Program
» Dimensions of Biodiversity (Dimensions of Biodiversity)

Contributors	Affiliation	Role
Moran, Mary Ann	University of Georgia (UGA)	Principal Investigator
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Coverage

Spatial Extent: **Lat**:36.835 **Lon**:-121.901

Methods & Sampling

Cell counts: Ruegeria pomeroyi, Thalassiosira pseudonana, and Alexandrium tamarense cells were measured using a flow cytometer.

DIN: Cadmium reduction method; Nitrate is measured by reducing it to nitrite in an alkaline-buffered solution passing through a column of copper-cadmium metal filings and then measuring nitrite by diazotizing with sulfanilamide and coupling with N-(1-naphthyl)-ethylenediamine dihydrochloride to form a pink colored azo dye which is measured colorimetrically. Instrument: Alpkem and Astoria-Pacific Autoanalyzers

DIP: Orthophosphate method; PO4 is measured colorimetrically as an antimony-phospho-molybdate complex (APHA 4500-P F) that is reduced to an intensely blue-colored complex by ascorbic acid. Instrument: Alpkem and Astoria-Pacific Autoanalyzers

DOC: Combustion method; Total dissolved carbon and dissolved inorganic carbon are determined by combustion of an unacidified and acidified 0.2 micron filtered subsamples. DOC concentration is calculated by subtracting the DIC concentration from the TDC concentration. Instrument: Shimadzu TOC-5000A Total Organic Carbon Analyzer

TOC: Combustion method; Total organic carbon is determined by combustion of an unacidified and unfiltered sample. Instrument: Shimadzu TOC-5000A Total Organic Carbon Analyzer

DMSP: See: Rellinger, A., et al. Occurrence and turnover of DMSP and DMS in deep waters of the Ross Sea, Antarctica. Deep-Sea Research I 56 (2009) 686–702. doi:10.1016/j.dsr.2008.12.010

Data Processing Description

BCO-DMO Processing notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- replaced commas with underscores

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Data Files

File
switch.csv (Comma Separated Values (.csv), 4.08 KB) MD5:b14b9daa3d22d826e12a20df8e8d386d Primary data file for dataset ID 662681

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Parameters

Parameter	Description	Units
timepoint	Time point	unitless
cubitainer	Cubitainer identification: treatment and replicate number	unitless
Ruegeria_pomeroyi	Number of bacterial cells per ml of culture; determined by flow cytometry	cells/milliliter
Thalassiosira_pseudonana	Number of diatom cells per ml of culture; determined by flow cytometry	cells/milliliter
Alexandrium_tamarense	Number of dinoflagellate cells per ml of culture; determined by flow cytometry	cells/milliliter
DIN	Concentrations of dissolved inorganic nitrogen; infered from the measurements of nitrate and nitrite concentrations.	micromoles/liter of culture
DIP	Concentrations of dissolved inorganic phosphorus; infered from the measurements of phosphate concentrations.	micromoles/liter of culture
DOC	Concentrations of dissolved organic carbon	micromoles/liter of culture
TOC	Concentrations of total organic carbon	micromoles/liter of culture
DMSP_total	Total dimethylsufoniopropionate concentrations	nanomoles/liter of culture
DMSP_diss	Dissolved dimethylsufoniopropionate concentrations	nanomoles/liter of culture

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Instruments

Dataset-specific Instrument Name	flow cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	To measure abundance of cells.
Generic Instrument Description	Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm)

Dataset-specific Instrument Name	Shimadzu GC-2014 gas chromatograph equipped with a Chromosil 330 column and a flame photometric detector for quantification
Generic Instrument Name	Gas Chromatograph
Dataset-specific Description	To measure DMSP concentrations
Generic Instrument Description	Instrument separating gases, volatile substances, or substances dissolved in a volatile solvent by transporting an inert gas through a column packed with a sorbent to a detector for assay. (from SeaDataNet, BODC)

Dataset-specific Instrument Name	Alpkem and Astoria-Pacific Autoanalyzers
Generic Instrument Name	Nutrient Autoanalyzer
Dataset-specific Description	To measure DIN and DIP
Generic Instrument Description	Nutrient Autoanalyzer is a generic term used when specific type, make and model were not specified. In general, a Nutrient Autoanalyzer is an automated flow-thru system for doing nutrient analysis (nitrate, ammonium, orthophosphate, and silicate) on seawater samples.

Dataset-specific Instrument Name	Shimadzu TOC-5000A Total Organic Carbon Analyzer
Generic Instrument Name	Total Organic Carbon Analyzer
Dataset-specific Description	To measure DOC and TOC
Generic Instrument Description	A unit that accurately determines the carbon concentrations of organic compounds typically by detecting and measuring its combustion product (CO2). See description document at: http://bcodata.whoi.edu/LaurentianGreatLakes_Chemistry/bs116.pdf

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Deployments

Moran_Monterey_2014

Website	https://www.bco-dmo.org/deployment/662989
Platform	Univ_Georgia
Start Date	2014-09-08
End Date	2014-09-08
Description	Microbial collections and environmental data collected by moored ESP and CTD.

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Project Information

Bacterial Taxa that Control Sulfur Flux from the Ocean to the Atmosphere (OceanSulfurFluxBact)

Surface ocean bacterioplankton preside over a divergence point in the marine sulfur cycle where the fate of dimethylsulfoniopropionate (DMSP) is determined. While it is well recognized that this juncture influences the fate of sulfur in the ocean and atmosphere, its regulation by bacterioplankton is not yet understood. Based on recent findings in biogeochemistry, bacterial physiology, bacterial genetics, and ocean instrumentation, the microbial oceanography community is poised to make major advances in knowledge of this control point. This research project is ascertaining how the major taxa of bacterial DMSP degraders in seawater regulate DMSP transformations, and addresses the implications of bacterial functional, genetic, and taxonomic diversity for global sulfur cycling.

The project is founded on the globally important function of bacterial transformation of the ubiquitous organic sulfur compound DMSP in ocean surface waters. Recent genetic discoveries have identified key genes in the two major DMSP degradation pathways, and the stage is now set to identify the factors that regulate gene expression to favor one or the other pathway during DMSP processing. The taxonomy of the bacteria mediating DMSP cycling has been deduced from genomic and metagenomic sequencing surveys to include four major groups of surface ocean bacterioplankton. How regulation of DMSP degradation differs among these groups and maps to phylogeny in co-occurring members is key information for understanding the marine sulfur cycle and predicting its function in a changing ocean. Using model organism studies, microcosm experiments (at Dauphin Island Sea Lab, AL), and time-series field studies with an autonomous sample collection instrument (at Monterey Bay, CA), this project is taking a taxon-specific approach to decipher the regulation of bacterial DMSP degradation.

This research addresses fundamental questions of how the diversity of microbial life influences the

geochemical environment of the oceans and atmosphere, linking the genetic basis of metabolic potential to taxonomic diversity. The project is training graduate students and post-doctoral scholars in microbial biodiversity and providing research opportunities and mentoring for undergraduate students. An outreach program is enhance understanding of the role and diversity of marine microorganisms in global elemental cycles among high school students. Advanced Placement Biology students are participating in marine microbial research that covers key learning goals in the AP Biology curriculum. Two high school students are selected each year for summer research internships in PI laboratories.

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Program Information

Dimensions of Biodiversity (Dimensions of Biodiversity)

Website: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446

Coverage: global

(adapted from the NSF Synopsis of Program)
Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [MORE from NSF]

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1342694

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