Environmental data collected during a deployment of the Environmental Sample Processor (ESP) in Fall, 2014 in Monterey Bay, CA

Website: https://www.bco-dmo.org/dataset/753267
Data Type: Other Field Results
Version: 0
Version Date: 2019-01-22

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

Program
» Dimensions of Biodiversity (Dimensions of Biodiversity)

Contributors	Affiliation	Role
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Coverage

Temporal Extent: 2014-09-22 - 2014-10-13

Methods & Sampling

The Environmental Sample Processor (ESP) filtered seawater sequentially through 0.2 um pore size polyethersulfone filters. Seawater was evacuated from filters and followed twice with a 2 minute incubation with 1 ml of RNAlater™. RNAlater was evacuated, and filters were stored in the ESP until they were transferred to -80 C upon instrument recovery.

Filters were processed for DNA using the phenol-chloroform extraction method of Crump et al. (2003) after placing the filters into 1 ml of DNA extraction buffer. Extracted DNA was sheared ultrasonically to ~350 bp fragments, and library preparation was performed at the Georgia Genomics and Bioinformatics Core (GGBC) facility. Single-end 250 bp sequencing was performed using an Illumina HiSeq Rapid Run at Hudson Alpha Genomic Services Laboratory (Huntsville, AL, USA).

Single-cell sequencing: Seawater was transferred directly from the Niskin bottle to a 50 ml Falcon tube and placed on ice until brought back to lab. Each sampling day, 3 x 1 ml of seawater was preserved in cryovials using 100 ul of glyTe (5 ml glycerol, 3 ml Milli-Q H2O, 1 ml 100 x TE pH 8.0, 0.2 um filter sterilized after mixing the above, and stored in -20 C freezer). Preserved samples were then placed in a -80 C freezer. Samples were processed and sequenced at Bigelow Single Cell Genomics Center (Stepanauskas and Sieracki, 2007).

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
- reformatted date from Mon-DD (Oct-04) to YYYYMMDD (20141004)
- transposed the table to have field labels as columns headers

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Related Publications

Crump, B. C., Kling, G. W., Bahr, M., & Hobbie, J. E. (2003). Bacterioplankton Community Shifts in an Arctic Lake Correlate with Seasonal Changes in Organic Matter Source. Applied and Environmental Microbiology, 69(4), 2253–2268. doi:10.1128/aem.69.4.2253-2268.2003 https://doi.org/10.1128/AEM.69.4.2253-2268.2003
Methods

Stepanauskas, R., & Sieracki, M. E. (2007). Matching phylogeny and metabolism in the uncultured marine bacteria, one cell at a time. Proceedings of the National Academy of Sciences, 104(21), 9052–9057. doi:10.1073/pnas.0700496104
Methods

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Parameters

Parameter	Description	Units
date	date samples were collected	unitless
DMSPt	total DMSP concentration	nanoMoles (nM)
DMSPd_consumption_rate	dissolved DMSP consumption rate	nanoMole per day (nM/day)
DMSPd	dissolved DMSP concentration	nanoMole (nM)
chl_a	chlorophyll a concentration	microgram per liter (ug/L)

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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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