Taxonomy and abundance of microbial cells (phytoplankon and heterotrophic bacteria) during a deployment of the Environmental Sample Processor (ESP) in Fall, 2014 in Monterey Bay, CA

Website: https://www.bco-dmo.org/dataset/662653
Data Type: Other Field Results
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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Methods & Sampling

Dilutions to the sample due to preservative, dyes and run volume:
PFA = 0.95
Hoechst = 0.98
Run Volume = 0.10
Correction Factor = 0.82

For methodology details, see:
Varaljay, V., et al. Single-taxon field measurements of bacterial gene regulation controlling DMSP fate. The ISME Journal (2015), 1-10. doi:10.1038/ismej.2015.23

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
- re-formatted date from m/d/yyyy to yyyy-mm-dd

- added lat and lon of ESP mooring for mapping purposes

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Data Files

File
cell_counts.csv (Comma Separated Values (.csv), 4.37 KB) MD5:1556087b8cbd057ef324394116e499e8 Primary data file for dataset ID 662653

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Parameters

Parameter	Description	Units
listmode_id	sample identification	unitless
date	sampling date	year-month=day
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
T	the sample day (0 is the first sample collection day, up to the 13th collection day	days
Num	replicate	unitless
syn_ml	Synechococcus abundance	cells/milliliter
peuk_ml	photosynthetic eukaryotes abundance (distinguished based on Chlorophyll and Scatter signatures)	cells/milliliter
HiPE_phyto_mL	abundance of cells with very high Phycoerythrin and very high Chlorophyll content	cells/milliliter
Hbact_mL	abundance of non-pigmented bacteria (distinguished based on DNA content (Hoechst stain) and scatter signatures)	cells/milliliter
Syn_num	Synechococcus cell count	cells
Peuk_num	photosynthetic eukaryote cell count	cells
HiPE_Phyto_num	high Phycoerythrin and Chlorophyll content cell count	cells
HBact_num	non-pigmented bacteria cell count	cells
Pro_Mean_FS	Prochlorococcus mean forward scatter from flow cytometer	unitless
Pro_Mean_SS	Prochlorococcus mean side scatter from flow cytometer	unitless
Pro_Mean_Chl	Prochlorococcus chlorophyll mean content from flow cytometer	unitless
Pro_Mean_DNA	Prochlorococcus mean DNA content from flow cytometer	unitless
Syn_Mean_FS	Synechococcus mean forward scatter from flow cytometer	unitless
Syn_Mean_SS	Synechococcus mean side scatter from flow cytometer	unitless
Syn_Mean_Chl	Synechococcus chlorophyll mean content from flow cytometer	unitless
Syn_Mean_DNA	Synechococcus mean DNA content from flow cytometer	unitless
Peuk_Mean_FS	photosynthetic eukaryote mean forward scatter from flow cytometer	unitless

Peuk_Mean_SS	photosynthetic eukaryote mean side scatter from flow cytometer	unitless
Peuk_Mean_Chl	photosynthetic eukaryote chlorophyll mean content from flow cytometer	unitless
Peuk_Mean_DNA	photosynthetic eukaryote mean DNA content from flow cytometer	unitless
HiPE_Phyto_Mean_FS	high Phycoerythrin and Chlorophyll cell mean forward scatter from flow cytometer	unitless
HiPE_Phyto_Mean_SS	high Phycoerythrin and Chlorophyll cell mean side scatter from flow cytometer	unitless
HiPE_Phyto_Mean_Chl	high Phycoerythrin and Chlorophyll cell chlorophyll mean content from flow cytometer	unitless
HiPE_Phyto_Mean_DNA	high Phycoerythrin and Chlorophyll cell mean DNA content from flow cytometer	unitless
HBact_Mean_FS	non-pigmented bacteria mean forward scatter from flow cytometer	unitless
HBact_Mean_SS	non-pigmented bacteria mean side scatter from flow cytometer	unitless
HBact_Mean_DNA	non-pigmented bacteria mean DNA content from flow cytometer	unitless

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Instruments

Dataset-specific Instrument Name	Beckman Coulter Altra flow
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	Simultaneously detects Hoechst stain (DNA), cell pigments, and forward and side (90 degrees) scatter.
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)

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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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