Environmental data from Niskin bottle sampling during the Fall 2016 ESP deployment in Monterey Bay, CA

Website: https://www.bco-dmo.org/dataset/756413
Data Type: Other Field Results
Version: 2
Version Date: 2019-11-08

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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Abstract
Environmental data from Niskin bottle sampling during the Fall 2016 ESP deployment in Monterey Bay, CA. Samples were taken using Niskin bottles that collected seawater at the same depth and location of the Environmental Sample Processor deployed at Station M0 (36.835 N, 121.901W).

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Coverage

Spatial Extent: **Lat**:36.835 **Lon**:-121.901
Temporal Extent: 2016-09-23 - 2016-11-08

Acquisition Description

Grab samples were taken using Niskin bottles that collected seawater at the same depth and location of the Environmental Sample Processor deployed at Station M0 (36.835 N, 121.901W). Water was transferred to a low-density polyethylene cubitainer and maintained at ambient temperature until return to lab within 30 min.

Chlorophyll a: 150 ml of seawater was filtered through a 25 mm GF/F filter in triplicate using a vacuum pump and <5 in Hg pressure. The filter was placed in a glass scintillation vial and 10 ml of 90% acetone was added and placed in -20 freezer for at least 24 hours to extract the pigment. Extracted chlorophyll *a* was quantified using fluorometry (Pennington and Chavez, 2000).

Flow Cytometry: Cubitainer seawater was transferred to a 50 ml Falcon tube using laminar flow. 1.8 ml was then aliquoted to triplicate cryovials and preserved with 200 ul of 5% glutaraldehyde and stored at -80 degrees C. Analysis was run on a Beckman Coulter Altra flow cytometer for detection of DNA, pigments, and forward and side light scatter (Monger and Landry, 1993).

Akashiwo Microscopy Counts: 7 - 14 ml of seawater was preserved to 1% final concentration electron microscopy grade glutaraldehyde and stored at 4 degrees C. Slides were made by filtering the full volume onto a 0.22 um black polycarbonate filter (GE Water & Process Technologies) using a vacuum pump (<5 in Hg), and cells were counted under epifluorescence microscopy.

DMSP concentrations: Immediately upon return to the deck, duplicate samples were collected from the Niskin bottle for in situ dissolved DMSP (DMSPd) (see details below) before seawater transfer to the cubitainer. Upon return to the laboratory, the cubitainer of water was gently mixed by inversion and three replicate 10 ml sub-samples were removed by pipette into individual 15 ml centrifuge tubes (Corning, polypropylene). The samples were immediately acidified with 0.3 ml of 50% concentrated HCl (1.5% final concentration of concentrated HCl) to preserve total DMSP (dissolved plus particulate). These DMSPt samples were closed tightly and stored until analysis (described below) which took place within three months of collection.

DMSPd consumption: To measure the consumption rate of dissolved DMSP, we used the glycine betaine (GBT) inhibition technique (Kiene & Gerard, 1995; Li et al., 2016). Immediately upon return to the laboratory, six 500 ml glass bottles were filled with seawater from the gently-mixed cubitainer. Three of the bottles were treated with 25 ul of a 100 mM GBT anhydrous reagent (Sigma) solution (10 uM final GBT concentration), and three were left untreated as controls. Bottles were incubated in seawater maintained within 1 degree C of the in situ temperature. Immediately after GBT addition, the first time point was collected by simultaneously filtering ~50 ml sub-samples from each bottle through 47 mm Whatman GF/F filters using the small volume gravity drip filtration protocol of Kiene and Slezak (2006). The first 3.5 ml of filtrate from each sample was collected into 15 ml centrifuge tubes (Corning, polypropylene) that contained 100 ul of 50% HCl to immediately preserve any DMSP passing through the GF/F filter, which is defined as dissolved DMSP (DMSPd). Additional time points from each bottle

were collected at 3 and 6 h. The rate of change of DMSPd in no-treatment bottles was subtracted from the rate of change in the +GBT bottles to obtain an estimate of DMSPd consumption rate (Kiene and Gerard, 1995).

< 5 µm DMSPd: The DMSP that was less than 5 µm was measured in water from the cubitainer in the lab, using the drip filtration protocol, as described above for DMSPd, except that a 5.0 µm pore size, track-etched polycarbonate filter was used for the filtration.

DMSP Analysis: DMSP was quantified by proxy as the amount of DMS released from samples after alkaline cleavage (White, 1982). For DMSPt, 0.05 to 0.5 ml of each preserved sample was pipetted into a 14 ml glass serum vial, with the volume being adjusted based on the concentration of DMSPt in the sample. For DMSPd, the volume pipetted was 1.0 to 3.0 ml. Each serum vial was treated with 1 ml of 5 M NaOH and capped with a Teflon-faced serum stopper (Wheaton). After 1 h, the amount of DMS in each vial was quantified by purge and trap gas chromatography with flame photometric detection. Briefly, each vial was attached to the purge system and a flow of helium (90-100 ml per minute) allowed bubbling of the solution. An excurrent needle led to a Nafion dryer and six-port valve (Valco). The DMS in the samples was cryotrapped in a Teflon tubing loop immersed in liquid nitrogen. After a 4 min sparge, during which >99% of the DMS in the samples was removed, hot water replaced the liquid nitrogen to introduce the DMS into the Shimadzu GC-2014 gas chromatograph. Separation of the sulfur gases was achieved with a Chromosil 330 column (Supelco; Sigma) maintained at 60 degrees C with a helium carrier flow of 25 ml per minute. The flame photometric detector was operated in sulfur mode and maintained at 175 degrees C. Minimum detection limits during this study were 0.5 to 1 pmol DMS per sample with minimum detectable concentrations ranging from 0.17 to 10 nM, depending on the volume analyzed. The GC-FPD system was calibrated with a gas stream containing known amounts of DMS from a permeation system.

Problem report: For November chlorophyll a samples, fluorescence after acid addition not measured but estimated from samples with similar total fluorescence (Pennington and Chavez, 2000).

Processing Description

BCO-DMO Processing:
- modified parameter names (removed units; replaced spaces with underscores);
- re-formatted date to yyyy-mm-dd;
- added date/time columns (Local and UTC) in ISO8601 format;
- filled in blank cells with "nd" (no data);
- 2019-11-08: replaced data with version 2.

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Related Publications

Kiene, R. P., & Slezak, D. (2006). Low dissolved DMSP concentrations in seawater revealed by small-

volume gravity filtration and dialysis sampling. Limnology and Oceanography: Methods, 4(4), 80–95. doi:10.4319/lom.2006.4.80

Kiene, R., & Gerard, G. (1995). Evaluation of glycine betaine as an inhibitor of dissolved dimethylsulfoniopropionate degradation in coastal waters. Marine Ecology Progress Series, 128(1/3), 121-131. Retrieved from http://www.jstor.org/stable/24855505

Li, C., Yang, G.-P., Kieber, D. J., Motard-Côté, J., & Kiene, R. P. (2016). Assessment of DMSP turnover reveals a non-bioavailable pool of dissolved DMSP in coastal waters of the Gulf of Mexico. Environmental Chemistry, 13(2), 266. doi:10.1071/EN15052

Monger, B.C. & Landry, M.R. (1993). Flow cytometric analysis of marine bacteria with hoechst 33342. Appl Environ Microbiol 59, 905–911. URL: https://aem.asm.org/content/59/3/905

Timothy Pennington, J., & Chavez, F. P. (2000). Seasonal fluctuations of temperature, salinity, nitrate, chlorophyll and primary production at station H3/M1 over 1989–1996 in Monterey Bay, California. Deep Sea Research Part II: Topical Studies in Oceanography, 47(5-6), 947–973. doi:10.1016/S0967-0645(99)00132-0

White, R. (1982) Analysis of dimethyl sulfonium compounds in marine algae. J Mar Res 40, 529–536.

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Parameters

Parameter	Description	Units
Date	Date. Format: yyyy-mm-dd.	unitless
Time_Pacific	Time (Pacific time zone). Format: HH:MM.	unitless
ISO_DateTime_Local	Date and time (local) formatted to ISO8601 standard.	unitless
Depth	Sampling depth	meters (m)
Chlorophyll_a	Chlorophyll a	micrograms per liter (ug/L)
DMSPd_in_situ	Dissolved DMSP sampled on boat immediately after seawater collection	nanomolar (nM)
DMSPd_lab	Dissolved DMSP sampled after seawater transferred to lab	nanomolar (nM)
DMSPt	Total DMSP	nanomolar (nM)
picophotosynthetic_eukaryotes	Determined by flow cytometry; relative estimate of size; cells with lowest scatter signatures	cells per milliliter (cells/mL)

nanophotosynthetic_eukaryotes	Determined by flow cytometry; relative estimate of size; cells with intermediate scatter signatures	cells per milliliter (cells/mL)
microphotosynthetic_eukaryotes_group_1	Determined by flow cytometry; relative estimate of size; cells with highest scatter and chlorophyll signatures	cells per milliliter (cells/mL)
microphotosynthetic_eukaryotes_group_2	Determined by flow cytometry; relative estimate of size; cells with highest scatter and a bit lower chlorophyll signatures	cells per milliliter (cells/mL)
DMSPd_consumption_rate	Dissolved DMSP consumption rate	nM/d
lt_5_um_DMSPd	Dissolved DMSP concentration of seawater filtered through 5 µm filter	nanomolar (nM)
Photosynthetic_eukaryotes	Determined by flow cytometry	cells per milliliter (cells/mL)
Heterotrophic_bacteria	Determined by flow cytometry	cells per milliliter (cells/mL)
Synechococcus	Determined by flow cytometry	cells per milliliter (cells/mL)
Akashiwo	Determined by microscopy	cells per milliliter (cells/mL)
Chlorophyll_a_stdev	Standard deviation of Chlorophyll_a (n = 3)	micrograms per liter (ug/L)
DMSPd_in_situ_stdev	Standard deviation of DMSPd_in_situ (n = 3)	nanomolar (nM)
DMSPd_lab_stdev	Standard deviation of DMSPd_lab (n =3)	nanomolar (nM)
DMSPt_stdev	Standard deviation of DMSPt (n = 3)	nanomolar (nM)
picophotosynthetic_eukaryotes_stdev	Standard deviation of picophotosynthetic_eukaryotes (n = 2)	cells per milliliter (cells/mL)

nanophotosynthetic_eukaryotes_stdev	Standard deviation of nanophotosynthetic_eukaryotes (n = 2)	cells per milliliter (cells/mL)
microphotosynthetic_eukaryotes_group_1_stdev	Standard deviation of microphotosynthetic_eukaryotes_group_1 (n = 2)	cells per milliliter (cells/mL)
microphotosynthetic_eukaryotes_group_2_stdev	Standard deviation of microphotosynthetic_eukaryotes_group_2 (n = 2)	cells per milliliter (cells/mL)
lt_5_um_DMSPd_stdev	Standard deviation of lt_5_um_DMSPd (n = 3)	nanomolar (nM)
Photosynthetic_eukaryotes_stdev	Standard deviation of Photosynthetic_eukaryotes (n = 2)	cells per milliliter (cells/mL)
Heterotrophic_bacteria_stdev	Standard deviation of Heterotrophic_bacteria (n = 2)	cells per milliliter (cells/mL)
Synechococcus_stdev	Standard deviation of Synechococcus (n = 2)	cells per milliliter (cells/mL)
ISO_DateTime_UTC	Date and time (converted to UTC) formatted to ISO8601 standard.	unitless

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Instruments

Dataset-specific Instrument Name	Turner Designs 10-AU Fluorometer
Generic Instrument Name	Turner Designs Fluorometer -10-AU
Generic Instrument Description	The Turner Designs 10-AU Field Fluorometer is used to measure Chlorophyll fluorescence. The 10AU Fluorometer can be set up for continuous-flow monitoring or discrete sample analyses. A variety of compounds can be measured using application-specific optical filters available from the manufacturer. (read more from Turner Designs, turnerdesigns.com, Sunnyvale, CA, USA)

Dataset-specific Instrument Name	Beckman Coulter Altra
Generic Instrument Name	Flow Cytometer
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
Generic Instrument Name	Gas Chromatograph
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)

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Deployments

Moran_Monterey_2016

Website	https://www.bco-dmo.org/deployment/755677
Platform	Environmental Sample Processor
Start Date	2016-09-23
End Date	2016-11-16

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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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