Bacterial production in microcosm experiments from samples collected by R/V E.O. Wilson in the Gulf of Mexico, Alabama (En-Gen DMSP Cycling project)

Website: https://www.bco-dmo.org/dataset/3872
Data Type: experimental
Version: 1
Version Date: 2012-11-19

Project
» En-Gen: A Functional Genomics Approach to Organic Sulfur Cycling in the Ocean (En-Gen DMSP Cycling)

Contributors	Affiliation	Role
Moran, Mary Ann	University of Georgia (UGA)	Principal Investigator
Kiene, Ronald P.	Dauphin Island Sea Lab (DISL)	Co-Principal Investigator
Whitman, William	University of Georgia (UGA)	Co-Principal Investigator
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Bacterial production measurements from control and experimental microcosms from the Dauphin Island Cubitainer Experiment (DICE).

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Coverage

Spatial Extent: **Lat**:30.05068 **Lon**:-87.99513
Temporal Extent: 2006-10 - 2006-10

Dataset Description

Bacterial production measurements from control and experimental microcosms from the Dauphin Island Cubitainer Experiment (DICE).

Experimental design, methods, and results are further described in:
E. C. Howard, S. Sun, C. R. Reisch, D. A. del Valle, R. P. Kiene, and M. A. Moran (2010). Changes in DMSP Demethylase Gene Assemblages in Response to an Induced Phytoplankton Bloom. Applied and Environmental Microbiology, vol. 77, p. 524. DOI: 10.1128/AEM.01457-10
Rinta-Kanto, H. Burgmann, S. M. Gifford, S. Sun, S. Sharma, R. P. Kiene, and M. A. Moran (2011). Analysis of Sulfur-Related Gene Expression by Roseobacter Communities Using a Taxon-Specific Functional Gene Microarray. Environmental Microbiology, vol. 13, p. 453. DOI: 10.1111/j.1462-2920.2010.02350.x
Vila-Costa, M., J. M. Rinta-Kanto, S. Sun, S. Sharma, R. Poretsky, and M. A. Moran. (2010). Transcriptomic analysis of a marine bacterial community enriched with dimethylsulfoniopropionate. ISME Journal, vol. 4, p. 1410. DOI: 10.1038/ismej.2010.62

Methods & Sampling

See Howard et al. (2010), Rinta-Kanto et al. (2011), and Vila-Coast et al. (2010) for detailed methods, summarized below:

"In October 2006, seawater was collected from surface waters (<1 m deep) in the Gulf of Mexico off the coast of Dauphin Island, AL (lat: 30 03.041N; lon: 87 59.708W). Water was filtered through a 200-um mesh into six 20-liter polyethylene Cubitainers with minimal headspace.

Three microcosms were amended with 10 um sodium nitrate (NaNO3) and 0.6 um potassium phosphate (K2HPO4) to serve as the experimental microcosms. Three microcosms were left untreated to serve as the control. The Cubitainers were maintained at 27 degrees C on a 12-hour light/dark cycle for the duration of the experiment.

Chemical and activity measurements were collected from the microcosms at the beginning of the experiment (Day 0) and every day for the duration of the experiment at the same time. Bacterial production was measured by 3H-leucine incorporation into trichloroacetic acid (TCA) -insoluble material. Incubations were carried out in triplicate in the dark at in situ temperature with additions of 20 nM of 3H-leucine for 4 hours, starting immediately after water collection. One TCA-killed sample was used as a control. Samples were processed by the microcentrifugation method. Bacterial sulfur requirements were estimated through conversion of bacterial heterotrophic production assuming a bacterial C/S molar ratio of 248."

Data Processing Description

BCO-DMO made the following changes:
- Modified parameter names to conform with BCO-DMO naming conventions.
- Replaced blanks with 'nd' to indicate 'no data'.
- Added the site coordinates provided in the publications above.

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Data Files

File
bacterial_production.csv (Comma Separated Values (.csv), 19.28 KB) MD5:9f6d8c0371562d6411638f5ab145d203
Primary data file for dataset ID 3872

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Related Publications

Howard, E. C., Sun, S., Reisch, C. R., del Valle, D. A., Bürgmann, H., Kiene, R. P., & Moran, M. A. (2010). Changes in Dimethylsulfoniopropionate Demethylase Gene Assemblages in Response to an Induced Phytoplankton Bloom. Applied and Environmental Microbiology, 77(2), 524–531. doi:10.1128/aem.01457-10 https://doi.org/10.1128/AEM.01457-10
Methods

Rinta-Kanto, J. M., Bürgmann, H., Gifford, S. M., Sun, S., Sharma, S., del Valle, D. A., … Moran, M. A. (2010). Analysis of sulfur-related transcription by Roseobacter communities using a taxon-specific functional gene microarray. Environmental Microbiology, 13(2), 453–467. doi:10.1111/j.1462-2920.2010.02350.x
Methods

Vila-Costa, M., Rinta-Kanto, J. M., Sun, S., Sharma, S., Poretsky, R., & Moran, M. A. (2010). Transcriptomic analysis of a marine bacterial community enriched with dimethylsulfoniopropionate. The ISME Journal, 4(11), 1410–1420. doi:10.1038/ismej.2010.62

Parameters

Parameter	Description	Units
exp_id	Name of the experiment. DICE = Dauphin Island Cubitainer Experiment.	text
lat	Latitude of the sample collection site. North = Positive.	decimal degree
lon	Longitude of the sample collection. West = Negative.	decimal degree
site_desc	Description of the sample collection site.	text
microcosm	Identifier for the microcosm experiment. C1 and C2 were control microcosms containing Gulf of Mexico seawater. E1 and E2 were experimental microcosms containing Gulf of Mexico seawater amended with inorganic N and P.	text
microcosm_type	Type of microcosm. Experimental or Control.	text
exp_day	Sequential day of the experiment. Day 0 = start of the experiment.	integer
mean	Calculated average of triplicates (including the blank).	dpm
mean_minus_blank	Average corrected for the blank.	dpm
stdev	Standard deviation of the mean.	dpm
coeff_var	Coefficient of variation of the mean.	%
inc_time	Incubation time.	hours
leu_inc_per_h	Measure of bacterial production in nanomoles of radiolabeled leucine incorporated per hour of incubation.	nM Leu per hour
leu_inc_per_d	Measure of bacterial production in nanomoles of radiolabeled leucine incorporated per day of incubation.	nM Leu per day
stdev_calc	Estimated variation about the mean based on % CV in specific activity measurements.	nM Leu per day
bact_prod	Measure of bacterial Carbon production in nanomoles of carbon substrate converted to bacterial biomass each day.	nM Carbon per day
bact_prod_err	Estimated variation about the mean of bacterial production based on % CV in specific activity measurements.	nM Carbon per day
bact_C_demand	Nanomoles of carbon substrate needed by bacteria each day, including bacterial production and bacterial respiration. This assumes a bacterial growth efficiency of 15%.	nM Carbon per day
bact_C_demand_err	Estimated variation about the mean of bacterial carbon demand based on % CV in specific activity measurements.	nM Carbon per day
bact_S_prod	Nanomoles of sulfur substrate needed by bacteria each day. This assumes a C:S ratio of 248 in bacterial biomass.	nM Sulfur per day
replicate	Replicate identifier. a, b, and c are replicate samples from the same treatment. blank is a killed control, with formaldehyde added prior to addition of isotope.	unitless
dpm	Disintegrations per minute (dpm) measured per replicate.	dpm

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Instruments

Dataset-specific Instrument Name	bucket
Generic Instrument Name	bucket
Dataset-specific Description	Water was collected in the field using a clean bucket.
Generic Instrument Description	A bucket used to collect surface sea water samples.

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Deployments

DMSP_Dauphin_Island

Website	https://www.bco-dmo.org/deployment/58888
Platform	R/V E.O. Wilson
Description	October 2006 deployment in the Gulf of Mexico approximately 20 km off the coast of Dauphin Island, AL to collect surface water for the project "En-Gen: A Functional Genomics Approach to Organic Sulfur Cycling in the Ocean". (Latitude: 30°03.041′N, Longitude: 87°59.708′W)

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Project Information

En-Gen: A Functional Genomics Approach to Organic Sulfur Cycling in the Ocean (En-Gen DMSP Cycling)

Coverage: Sapelo Island, GA, USA, 31.4° N Lat, 81.3° W Lon / Dauphin Island, AL, USA, 30.3 ° N Lat, 88.1° W Lon

The recent discovery of key genes that mediate competing pathways at a critical juncture in the marine sulfur cycle has allowed biogeochemists to make rapid advances in understanding where and when sulfur transformations occur in the ocean, and most importantly, what factors regulate them. This project describes an environmental functional genomics project that will rapidly increase our knowledge of the role that bacterioplankton play in dimethylsulfoniopropionate (DMSP) cycling in ocean surface waters, focusing particularly on biological controls of volatile sulfur exchange across the ocean/atmosphere boundary.

The investigators have asked three critical hypotheses to explain the regulation of bacterial DMSP degradation: that involve investigations on the energy constraints of DMSP cycling, the role that DMSP concentration in the oceans plays, and the sulfur requirements for bacterial growth. These research areas serve as the focus for hypothesis-driven laboratory and field studies using functional genomics approaches that will track patterns in gene expression in relation to sulfur metabolism. The hypotheses will be tested with:
1) chemostat systems with a model marine bacterium Silicibacter pomeroyi;
2) microcosm experiments with Gulf of Mexico seawater; and
3) field studies at various sites in the Gulf of Mexico. Marine bacterioplankton play a key role in regulating the flux of DMSP-derived sulfur to the atmosphere, a process of great importance for global climate regulation and marine productivity.

The investigators will also be involved in graduate and undergraduate student education, and two post-doctoral associates will be trained to address multidisciplinary challenges in environmental microbiology. High school biology students in Athens, GA will participate in marine microbial biology research that includes bacterial diversity and discovery studies in coastal Georgia, follow-up training in molecular tools and bioinformatics in

their own classroom, and summer internships at the University of Georgia and Dauphin Island Sea Laboratory. (The description above is from the NSF Award Abstract).

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0724017

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