Experimental results and survey of biogeochemical and microbial data collected on the R/V Atlantic Explorer (AE1516) at the Bermuda Atlantic Time-series study site during 2015 (Bacterial DOC cycling project)

Website: https://www.bco-dmo.org/dataset/616269
Data Type: experimental
Version: 1
Version Date: 2015-10-23

Project
» Dissolved Organic Carbon Cycling by SAR11 Marine Bacteria (Bacterial DOC cycling)

Contributors	Affiliation	Role
Giovannoni, Stephen	Oregon State University (OSU)	Principal Investigator
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Abstract
This dataset is a log of samples collected on AE1516 at the Bermuda Atlantic Time-series study site (BAT) Hydrostation S. The samples were analyzed for microbial diversity, dissolved organic carbon (DOC), total DOC, single celled genomics, and an osmolyte inculation experiment.

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Coverage

Spatial Extent: **N**:32.4011 **E**:-64.48 **S**:32.078 **W**:-64.719
Temporal Extent: 2015-07 - 2015-07

Dataset Description

This dataset is a log of samples collected on AE1516 at the Bermuda Atlantic Time-series study site (BAT) Hydrostation S. The samples were analyzed for microbial diversity, dissolved organic carbon (DOC), total DOC, single celled genomics, and an osmolyte inculation experiment.

Methods & Sampling

Methodology References:

Tangential flow filtration methods are described in Giovannoni, et al (1990).
Methods for DOM oxidation measurements are described in Sun, et al (2011).
Methods for rRNA gene diversity analysis are described in Vergin, et al (2013).
Methods for DOM analysis are described in Carini, et al (2014).

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Data Files

File
sample_log_AE1516.csv (Comma Separated Values (.csv), 4.49 KB) MD5:80944ab03045916340b24031cc6b50a9
Primary data file for dataset ID 616269

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Related Publications

Carini, P., Campbell, E. O., Morré, J., Sañudo-Wilhelmy, S. A., Cameron Thrash, J., Bennett, S. E., … Giovannoni, S. J. (2014). Discovery of a SAR11 growth requirement for thiamin's pyrimidine precursor and its distribution in the Sargasso Sea. The ISME Journal, 8(8), 1727–1738. doi:10.1038/ismej.2014.61
Methods

Giovannoni, S. J., DeLong, E. F., Schmidt, T. M., & Pace, N. R. (1990). Tangential flow filtration and preliminary phylogenetic analysis of marine picoplankton. Applied and environmental microbiology, 56(8), 2572-2575.
Methods

Sun, J., Steindler, L., Thrash, J. C., Halsey, K. H., Smith, D. P., Carter, A. E., … Giovannoni, S. J. (2011). One Carbon Metabolism in SAR11 Pelagic Marine Bacteria. PLoS ONE, 6(8), e23973. doi:10.1371/journal.pone.0023973
Methods

Vergin, K. L., Beszteri, B., Monier, A., Cameron Thrash, J., Temperton, B., Treusch, A. H., … Giovannoni, S. J. (2013). High-resolution SAR11 ecotype dynamics at the Bermuda Atlantic Time-series Study site by phylogenetic placement of pyrosequences. The ISME Journal, 7(7), 1322–1332. doi:10.1038/ismej.2013.32
Methods

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Parameters

Parameter	Description	Units
cruise_id	cruise identification	unitless
sample_descrip	samples taken for this purpose	unitless
date	date in yyyy-mm-dd format.	unitless
time	time; UTC or local?	hh:mm
person	person who handles the sample	unitless
depth	sample collection depth	meters
sample_id	sample identification (date and depth); taken with PPL cartridge	unitless
filtrand_id	filtrand identification (date and depth); from Sterivex filter	unitless
TOC_id	total organic carbon sample id (date_time_depth); given to Craig Carlson for analysis	unitless
sample_volume	sample volume filtered	milliliters
filter_size	filter pore size and membrane type	unitless
preservation	preservative/buffer used	unitless
incubation	incubation period	hours
temp_stored	temperature at which samples were stored	degrees Celsius

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Deployments

AE1516

Website	https://www.bco-dmo.org/deployment/616266
Platform	R/V Atlantic Explorer
Report	http://dmoserv3.bco-dmo.org/data_docs/Bacterial_DOC_cycling/Cruise_Report_Giov_AE15.pdf
Start Date	2015-07-01
End Date	2015-07-03
Description	Objectives: 1. TFF surface water samples to collect cells for two metabolite oxidation experiments: A) osmolytes, B) 14C-dimethylarsenate. 80 L surface sample to 600 ml, expecting ~10^7 cells ml. This collection plan executed --- times over two days (late afternoon and morning, each day; (Giovannoni/Halsey experiments; Landry, Giovannoni on TFF). 2. TFF surface water samples to collect cells single cell genomics by FACS at JGI. After concentration by TFF cells will be filtered through 0.45 um Nuclepore filters, and cryopreserved in SCGC glycine betaine cryopreservation buffer. 3. TFF 100 m water samples to collect cells for Ib, IIa, IIIa, IV or Vb ecotypes, TFF cell concentrates from will be filtered through 0.45 um Nuclepore filters, and cryopreserved in SCGC glycerol cryopreservation buffer. 4. DOM and nucleic acid water profile for chemistry and amplicon sequencing. Surface to 300 m (surface, 40, 80, 120, 160, 200, 250, 300 m), all samples that will be first filtered through 0.2 µm Sterivex cartridges and then A) 300 ml will frozen at -80 (or -20, in a pinch) in polypropylene or teflon bottles; for chemistry, or B) 3.7 liter will be concentrated with PPL cartridges and stored at -20 in the bound state (sealed and store PPLs). Add SLP to Sterivex cartridges and freeze at -80 C. DOC samples, collected in ashed EPA vials, will be collected for every DOM sample. Cruise information and original data are available from the NSF R2R data catalog.

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Project Information

Dissolved Organic Carbon Cycling by SAR11 Marine Bacteria (Bacterial DOC cycling)

Coverage: Western Sargasso Sea, Bermuda Atlantic Time Series Site: Hydrostation S

SAR11 (Pelagibacterales) are the most abundant group of bacterioplankton in the oceans. Globally, they are estimated to oxidize to carbon dioxide (CO2) between 5 and 22% of all the organic carbon produced by photosynthesis each day. The activities of bacterioplankton such as SAR11 determine the residence times of different forms of organic carbon, and ultimately shape the composition of dissolved organic pools in the oceans, which rival atmospheric CO2 in mass. Accurate and detailed information about the oceanic carbon cycle is used in models that are valued for their potential to predict and understand future changes in ocean ecosystems. This grant supports analyses of genomic data that predict the carbon oxidation functions of SAR11 cells, and supports experiments with cells in culture, where high-resolution mass spectrometry technology is applied to discover new organic carbon oxidation biochemistry. To assess the importance of SAR11 carbon oxidation functions in ocean ecosystems, this project includes four short oceanographic cruises to the Bermuda Atlantic Time-series Study (BATS) site, in the western Sargasso Sea. On these cruises the concentrations and oxidation rates of organic compounds will be measured, and linked to variation in planktonic SAR11 populations.

It is a paradox that SAR11 cells are the most abundant in the oceans, but also have among the smallest genomes known. The central goal of this proposal is to understand what types of dissolved organic matter (DOM) are oxidized to CO2 by SAR11. Implicit to this approach is the perspective that some abundant chemoheterotrophic bacterioplankton taxa, particularly those with small genomes, have evolved specialist strategies for oxidizing organic matter. Understanding these strategies can lead to a more detailed and accurate understanding of the biological processes that recycle biological production to CO2. Major project aims are: 1) investigate SAR11 genomes and assay cells in culture with high-resolution mass spectrometry approaches and isotopic labeling to identify the range of compounds these cells can oxidize to CO2; 2) at BATS, measure biological oxidation rates of DOM compounds used by SAR11; 3) link spatiotemporal SAR11 genome variation to patterns of DOM oxidation in the ocean surface layer (0-300 m). This projects includes four short cruises to BATS that target the four microbial plankton community types at this site: upper euphotic zone, deep chlorophyll maximum, spring bloom and upper mesopelagic. Products of this activity will include new information about variation in labile DOM oxidation across the surface layer, and specific links to genome features that will improve the accuracy of interpretation of global ocean metagenomic data.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1436865

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