Dilution batch-culture bioassay (remineralization) experiments from SBDOM11 project cruise from R/V Point Sur PS1103 in the Santa Barbara Channel, May 2011 (SBDOM project, SBC LTER project)

Website: https://www.bco-dmo.org/dataset/718117
Data Type: experimental
Version: 1
Version Date: 2017-10-30

Project
» Mechanisms controlling the production and fate of DOM during diatom blooms (SBDOM)

Contributors	Affiliation	Role
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Abstract
This dataset includes results from dilution batch-culture bioassay experiments reporting bacterial abundance, growth rates, barcode sequences and DOC were from the SBDOM 11 cruise in May 2011.

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Coverage

Spatial Extent: **Lat**:34.3 **Lon**:-120.2
Temporal Extent: 2011-05-11 - 2011-07-24

Dataset Description

This dataset includes results from dilution batch-culture bioassay experiments reporting bacterial abundance, growth rates, barcode sequences and DOC were from the SBDOM 11 cruise in May 2011.

Methods & Sampling

Dilution batch-culture bioassay experiments were established 11 May 2011 - 15 May 2011 on the SBDOM 11 cruise using water samples collected from the upper 8m of the water column. Water was gravity-filtered from the sampling Niskin bottle through two mixed cellulose ester filters (1.2 µm and 0.2 µm). Duplicate 500 mL polycarbonate bottles were filled with 375 mL 0.2 µm filtrate (filter sterilized media) and 125 mL 1.2 µm filtrate (bacterial inoculum) collected from the same cast. Bottles were incubated in the dark at 11degrees C for 10 weeks. Samples for bacterial abundance, DOM, and community composition by DNA were collected by decanting from the bottle at specified intervals.

DOC was quantified by high-temperature combustion on a modified Shimadzu TOC-V. We used 1.5 µM DOC as a detection limit for these experiments.

Bacterial abundance was measured using a BD LSRII flow cytometer with an autosampler attachment. Samples were preserved in sterile cryovials with 0.2% final concentration paraformaldehyde, then stored frozen until analysis. Samples were stained with SYBR Green I for enumeration.

DNA was collected from duplicate bottles combined (to conserve volume); 125 mL from each bottle was vacuum-filtered onto a 0.2 µm polyethersulfone filter and frozen. Samples were lysed in sucrose lysis buffer with 1% w/v sodium dodecyl sulfate and 0.2 mg mL-1 proteinase-K, and genomic DNA was extracted using a Qiagen DNEasy silica centrifugation kit. DNA was used to conduct multiplex amplicon pyrosequencing using primers 8F and 338R, following the protocol of Nelson et al. (2014; doi: 10.1111/1462-2920.12241). Sequence analysis was conducted in mothur (Schloss et al. 2009; doi: 10.1128/AEM.01541-09) using a non-redundant subset of the SILVA SSU Ref 16S alignment database (v111) curated as in Nelson et al. (2014).

Data Processing Description

DOC concentrations at timepoints 0, 3, and 7 were corrected for bacterial biomass by subtracting bacterial abundance multiplied by a standard conversion factor of 10 fg C cell-1 (Fukuda et al. 1998).

µ: µ was calculated as the rate of change of the natural log of bacterial cell abundance during exponential growth, defined here as extending from the end of lag phase to the start of stationary phase and/or to the maximum biomass observed (with additional abundance measurements from the lag and stationary phases averaged when available to increase robustness of estimates). Linear growth was assumed.

BGE: BGE was calculated as the rate of change in bacterial cell biomass [bacterial abundance multiplied by a standard conversion factor of 10 fg C cell-1 (Fukuda et al. 1998)] divided by the slope of the DOC drawdown from experiment initiation to one week, then multiplied by 100 to format as a percent. BGE values > 70, or those resulting from a change in DOC of < 1.5 µM, were considered invalid.

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- blank cells were replaced by 'nd' (no data)

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Data Files

File	
SBDOM11_mini_remins.csv	(Comma Separated Values (.csv), 23.76 KB) MD5:7eb14133629a81c3705bd637e01e1a20
Primary data file for dataset ID 718117	

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Related Publications

Nelson, C. E., Carlson, C. A., Ewart, C. S., & Halewood, E. R. (2013). Community differentiation and population enrichment of Sargasso Sea bacterioplankton in the euphotic zone of a mesoscale mode-water eddy.

Environmental Microbiology, 16(3), 871–887. doi:10.1111/1462-2920.12241
Methods

Schloss, P. D., Westcott, S. L., Ryabin, T., Hall, J. R., Hartmann, M., Hollister, E. B., … Weber, C. F. (2009). Introducing mothur: Open-Source, Platform-Independent, Community-Supported Software for Describing and Comparing Microbial Communities. Applied and Environmental Microbiology, 75(23), 7537–7541. doi:10.1128/aem.01541-09 https://doi.org/10.1128/AEM.01541-09
Software

Wear, E. K., Carlson, C. A., James, A. K., Brzezinski, M. A., Windecker, L. A., & Nelson, C. E. (2015). Synchronous shifts in dissolved organic carbon bioavailability and bacterial community responses over the course of an upwelling-driven phytoplankton bloom. Limnology and Oceanography, 60(2), 657–677. doi:10.1002/lno.10042
Results

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Parameters

Parameter	Description	Units
Sample	Internal experiment ID; A/B = replicate bottles	unitless
sta_id	station where water for experiment was collected	unitless
bottle	rosette bottle from which water for experiment was drawn	unitless
Initiation_date	local date when experiment was begun	unitless
Initiation_time	local time when experiment was begun	unitless
Timepoint	sampling timepoint; from 0 (post-initiation) through 8	unitless
Date	local date on which timepoint was sampled	unitless
DOC_sampling_time	local time at which DOC was sampled	unitless
DOC_Bottle_A	DOC concentration in Bottle A at specified timepoint (nd missing data = failed QC)	micromol/liter
DOC_A_st_dev	standard deviation between injections on Shimadzu instrument while measuring DOC in Bottle A at specified timepoint	micromol/liter
DOC_Bottle_B	DOC concentration in Bottle B at specified timepoint (nd missing data = failed QC)	micromol/liter

DOC_B_st_dev	standard deviation between injections on Shimadzu instrument while measuring DOC in Bottle B at specified timepoint	micromol/liter
Bact_abun_sampling_time	local time at which bacterial abundance was sampled	unitless
Bact_abun_A	Bacterial abundance in Bottle A at specified timepoint	cells/liter
Bact_abun_B	Bacterial abundance in Bottle B at specified timepoint	cells/liter
DNA_sampling_time	local time at which DNA was sampled	unitless
Pyrosequencing_barcode	multiplexing barcode corresponding to this sample; in the combined dataset available under SRA accession number SRR1222603	unitless
mu_growth_A	specific growth rate of bacterial cells in Bottle A; calculated over the exponential growth phase of the experiment	cells/day
mu_growth_B	specific growth rate of bacterial cells in Bottle B; calculated over the exponential growth phase of the experiment	cells/day
BGE_A	bacterial growth efficiency (percent) in Bottle A; calculated over the exponential growth phase	unitless
BGE_B	bacterial growth efficiency (percent) in Bottle B; calculated over the exponential growth phase	unitless

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	used to conduct multiplex amplicon pyrosequencing
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	BD LSRII flow cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	BD LSRII flow cytometer with an autosampler attachment used to obtain bacterial abundance.
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	modified Shimadzu TOC-V
Generic Instrument Name	Shimadzu TOC-V Analyzer
Dataset-specific Description	Used to measure dissolved organic carbon concentrations
Generic Instrument Description	A Shimadzu TOC-V Analyzer measures DOC by high temperature combustion method.

Dataset-specific Instrument Name	
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	used to conduct multiplex amplicon pyrosequencing
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

PS1103

Website	https://www.bco-dmo.org/deployment/517703
Platform	R/V Point Sur
Report	http://dmoserv3.whoi.edu/data_docs/SBDOM/SBDOM11_cruise_plan.doc
Start Date	2011-05-07
End Date	2011-05-20
Description	Triaxus and CTD operations within the Santa Barbara Channel. Collected samples for particulates and dissolved constituents. Made determinations of phytoplankton productivity using 14C, 15NO3 and 32Si incorporation using on-deck incubator. Measurements of microbial activity, biomass and DNA. 3H-Leucine will be used to assess bacterial production. Conducted deck board incubation experiments. See information on PS1103 in the R2R Cruise Catalog.

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Project Information

Mechanisms controlling the production and fate of DOM during diatom blooms (SBDOM)

Coverage: Pacific California, Santa Barbara Channel

This project is also affiliated with the Plumes and Blooms project.

Data:
The following data files have been submitted to BCO-DMO but are not yet available online. Data are restricted until June 2016. Please contact the PI for access prior to public availability:
-- SBDOM10 and SBDOM11 CTD and Niskin bottle data.

The following are available online (see 'Datasets' heading below):
-- SBDOM10 and SBDOM11 cruise plans (available online on deployment pages: PS1009, PS1103)
-- SBDOM10 and SBDOM11 event logs (available online; see 'Datasets' below)
-- Laboratory-based Bloom in a Bottle (BIB) Experiment
-- Laboratory-based Remineralization Experiments
-- SBDOM10 and SBDOM11 data summaries (including CTD data, nutrients, and bacterial production)

Project Description from NSF Award Proposal and Abstract:
Diatom blooms are known to produce prodigious quantities of DOM upon entering nutrient stress with a chemical composition that varies with the type of nutrient limitation (Si or N). This variable composition likely influences the nutritional value of DOM to microbes driving species successions towards functional groups of heterotrophic prokaryotes that are best able to metabolize particular forms of DOM. To date each side of this coupled system of production/consumption has been examined independently. A few studies have examined how limitation by different limiting nutrients affects the chemical character of the DOM produced by phytoplankton, while others have focused on the fate of DOM without detailed understanding of the mechanisms influencing its initial chemical composition.

We propose to investigate the mechanisms determining the character and fate of DOM produced during temperate diatom blooms. Specifically we will investigate how physiological stress on diatoms induced by different limiting nutrients influences the production, chemical composition of DOM and the microbial community structure that respond to it to better understand the mechanisms driving the accumulation and persistence of DOM in marine systems. The research will involve both laboratory and field experiments. The novel aspects of this work are:
1) We will investigate how limitation by either N or Si impacts the quantity and chemical composition of the DOM released by diatoms.
2) Assess how the differences in the chemical composition of the DOM produced under N or Si limitation affect its lability by examining the productivity, growth efficiency and community structure of heterotrophic bacterioplankton responding to the release of substrates.
3) Predicted DOM dynamics based on (1) and (2) will be tested in the field during diatom blooms in the Santa Barbara Channel, California.

While experiments investigating aspects of either 1 or 2 have been conducted successfully in the past (Lancelot, 1983; Billen and Fontigny, 1987; Goldman et al., 1992; Carlson et al.,1999; Cherrier and Bauer, 2004; Conan et al., 2007) ours will be the first study to combine these approaches in an integrated assessment of the mechanisms governing both the production and fate of DOM produced by diatom blooms experiencing limitation by different nutrients.

References:

Lancelot, C. (1983). Factors affecting phytoplankton extracellular release in the Southern Bight of the North Sea. Marine Ecology Progress Series 12: 115-121.

Billen, G. and A. Fontigny (1987). Dynamics of a Phaeocystis -dominated spring bloom in Belgian coastal waters. II. Bacterioplankton dynamics. Mar. Ecol. Prog. Ser. 37: 249-257.

Goldman, J.C., D.A. Hansell and M.R. Dennett (1992). Chemical characterization of three large oceanic diatoms: potential impact on water column chemistry. Marine Ecology Progress Series 88: 257-270.

Carlson, C.A., N.R. Bates, H.W. Ducklow and D.A. Hansell (1999). Estimation of bacterial respiration and growth efficiency in the Ross Sea, Antarctica. Aquatic Microbial Ecology 19: 229-244.

Cherrier, J. and J.E. Bauer (2004). Bacterial utilization of transient plankton-derived dissolved organic carbon and nitrogen inputs in surface ocean waters. Aquatic Microbial Ecology 35(3): 229-241.

Conan, P., M. Sondegaard, T. Kragh, F. Thingstad, M. Pujo-Pay, P.J.l.B. Williams, S. Markager, G. Cauwet, N.H. Borch, D. Evans and B. Rieman (2007). Partitioning of organic production in marine plankton communities: The effects of inorganic nutrient ratios and community composition on new dissolved organic matter. Limnology and Oceanography 52(2): 753-765.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0850857

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