

Dilution batch-culture bioassay (rem Mineralization) 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)

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|-------------------------------------|---|---------------------------|
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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_remains.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.

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](https://doi.org/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 |

Instruments

| | |
|---|--|
| Dataset-specific Instrument Name | |
| Generic Instrument Name | Automated DNA Sequencer |
| Dataset-specific Description | used to conduct multiplex amplicon pyrosequencing |
| Generic Instrument Description | General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step. |

| | |
|---|--|
| 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 ¹⁴ C, ¹⁵ NO ₃ and ³² Si incorporation using on-deck incubator. Measurements of microbial activity, biomass and DNA. ³ H-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.I.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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