Virioplankton abundance using FISH probe at BATS site in the western Sargasso Sea from 2000-2011 (Ocean Microbial Observatory project)

Website: https://www.bco-dmo.org/dataset/543828
Data Type: Cruise Results
Version: 1
Version Date: 2020-05-04

Project
» Transitions in the Surface Layer and the Role of Vertically Stratified Microbial Communities in the Carbon Cycle - An Oceanic Microbial Observatory (Ocean Microbial Observatory)

Contributors	Affiliation	Role
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Abstract
Virioplankton abundances were measured from samples collected from January 2000 to December 2011 as part of the larger BATS program aboard the R/V Weatherbird II or the R/V Atlantic Explorer. Supporting data provided by the BATS time-series program and are available at (http://bats.bios.edu/). This dataset reports abundances quantified using FISH (Fluorescence in situ hybridization).

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Coverage

Spatial Extent: **Lat**:31.67 **Lon**:-64.17
Temporal Extent: 2003-01-23 - 2005-12-09

Dataset Description

Virioplankton abundances were measured from samples collected from January 2000 to December 2011 as part of the larger BATS program aboard the R/V Weatherbird II or the R/V Atlantic Explorer. Supporting data provided by the BATS time-series program and are available at (http://bats.bios.edu/). This dataset reports abundances quantified using FISH (Fluorescence *in situ* hybridization).

Methods & Sampling

The probe and hybridization protocol for members of the SAR11 clade are described in Morris et al. (2002).

Study site and sample collection:
Samples were collected aboard the RV Weatherbird II or the RV Atlantic Explorer at the BATS site (31° 40′ N, 64°10′ W). All cruises were conducted as part of the larger BATS program and sampled at least monthly with biweekly sampling between February and April. This sampling strategy has been successful in revealing the major temporal microbial and biogeochemical patterns at this site (Carlson and Ducklow, 1996; Steinberg et al., 2001; Morris et al., 2005; Carlson et al., 2009; Treusch et al., 2009; Lomas et al., 2010). A broader assessment of the BATS biogeochemical data is presented in Deep Sea Research II in 1996 (volume 43, issues 2–3) and 2001 (volume 48, issues 8–9).

Samples for virioplankton (0, 20, 40, 60, 80, 100, 140, 160, 200, 250 and 300 m) and bacterioplankton (0, 10, 20, 40, 60, 80, 100, 120, 140, 160, 200, 250 and 300 m) were collected at the BATS site from January 2000 to December 2009 via conductivity, temperature, depth profiling rosette equipped with 12 l Niskin bottles. The 120 m virioplankton sample was added after October 2007. Throughout the entire time-series, all virioplankton samples were fixed with 0.02 µm filtered formalin (1% final concentration), placed in 5 ml cryovials and flash frozen in liquid nitrogen (Wen et al., 2004) until processing (within 12 weeks of collection). Samples for bacterioplankton abundance were fixed with 0.2 µm filtered gluteraldehyde (1% final concentration) and stored at either 4 °C for 72 h or flash frozen and subsequently stored at −80 °C for up to 6 months until processing as described in Steinberg et al (2001). Storage tests demonstrated no appreciable loss of virioplankton or bacterioplankton abundance when stored in liquid nitrogen for periods up to 6 months (unpublished data). Picophytoplankton samples were collected at the same depths through 250 m from October 2001 to December 2009 (Casey et al., 2007). Samples for fluorescence in situ hybridization (FISH) of specific heterotrophic bacterioplankton lineages were collected from the upper 300 m from January 2003 to December 2005 (Carlson et al., 2009).

Biogeochemical and physical data collected at the BATS site are available at http://bats.bios.edu. The MLD was determined as the depth where potential density (sigma-t) of the water was equal to sea surface sigma-t plus the equivalent in sigma-t to a 0.2 °C decrease in temperature (Sprintall and Tomczak, 1992). Contour plots were created in Ocean Data View (R Schlitzer, http://odv.awi.de/) with VG Gridding and linear mapping adjusted to the median of each data set. Statistics (Pearson's correlation and two-tailed Student's t-test for unequal variances), ratios and percent contributions were determined using Microsoft Excel.

Fluorescence in situ hybridization:
FISH was used to quantify the abundance of members of the SAR11 and Rhodobacteraceae clades. The probe and hybridization protocol for members of the SAR11 clade are described in Morris et al. (2002). The probe for Rhodobacteraceae (5′-CAACGCTAACCCCCTCCG-3′) was used at a final concentration of 2 ng µl−1 in hybridization buffer (0.9 moll−1 NaCl, 35% formamide, 20 mmoll−1 Tris-HCl (pH 7.4) and 0.01% (w/v) sodium dodecyl sulfate). The hybridization wash temperature was 52 °C. Washes were conducted in buffer containing 20 mmoll−1 Tris-HCl (pH 7.4), 70 mmoll−1 NaCl, 5 mmoll−1 EDTA and 0.01% sodium dodecyl sulfate. Filters were mounted with 20 µl of 1.67 µg ml−1 DAPI (SIGMA-Aldrich) in citiflour solution (Ted Pella Inc., Redding, CA, USA) and sealed with nail polish. Image analysis was performed using Cy3 and DAPI filter sets as described by Carlson et al (2009).

Data Processing Description

BCO-DMO Processing:

- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard
- converted longitudes to negative values to represent degrees West

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Data Files

File
probe.csv (Comma Separated Values (.csv), 36.31 KB) MD5:7e962de8bb52d521c8eb9e241bff5e75 Primary data file for dataset ID 543828

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Related Publications

Morris, R. M., Rappé, M. S., Connon, S. A., Vergin, K. L., Siebold, W. A., Carlson, C. A., & Giovannoni, S. J. (2002). SAR11 clade dominates ocean surface bacterioplankton communities. Nature, 420(6917), 806–810. doi:10.1038/nature01240
Methods

Parsons, R. J., Breitbart, M., Lomas, M. W., & Carlson, C. A. (2011). Ocean time-series reveals recurring seasonal patterns of virioplankton dynamics in the northwestern Sargasso Sea. The ISME Journal, 6(2), 273–284. doi:10.1038/ismej.2011.101
Methods

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Parameters

Parameter	Description	Units
station	BATS cruise number during which sample was collected	unitless
cruise_ID	BATS cruise ID for the sample that matches the BATS sample collected from the same niskin	unitless
date_in	date of collection at the time of CTD entry year month day	unitless
decyear	decimal year	unitless
lat_in	Latitude at the time of CTD entry in degrees N	decimal degrees
lon_in	Longitude at the time of CTD entry in degrees W	decimal degrees
depth	the actual depth in meters	meters
depth_nom	bottle target depths in meters	meters
depth_mixed	mixed layer depth in meters; MLD was determined as the depth where potential density (sigma-t) of the water was equal to sea surface sigma-t plus the equivalent in sigma-t to a 0.2 1C decrease in temperature (Sprintall and Tomczak 1992).	meters
abund_Probe_Bact	Abundance of Bacteria and Archaea as determined by DAPI staining and microscopy counts using the same filter as the probe data	10^8 cells/liter
abund_Probe_Bact_sd	standard deviation of Bacteria and Archaea abundance	10^8 cells/liter
abund_Eubac	Abundance of Bacteria as determined by the Eubacteria prob	10^8 cells/liter
abund_Cyano	Abundance of Cyanobacteria mainly Synechococcus as determined by microscopy	10^7 cells/liter
abund_SAR11	Abundance of SAR11 bacterioplankton; FISH Probe = Morris et al. 2002	10^8 cells/liter
abund_Cyt	Abundance of Bacteriodetes bacterioplankton; FISH Probe = CF319a; CF319b	10^7 cells/liter
abund_Rose	Abundance of Rhodobacteraceae bacterioplankton; FISH Probe = 536R	10^7 cells/liter

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Instruments

Dataset-specific Instrument Name	CTD
Generic Instrument Name	CTD - profiler
Generic Instrument Description	The Conductivity, Temperature, Depth (CTD) unit is an integrated instrument package designed to measure the conductivity, temperature, and pressure (depth) of the water column. The instrument is lowered via cable through the water column. It permits scientists to observe the physical properties in real-time via a conducting cable, which is typically connected to a CTD to a deck unit and computer on a ship. The CTD is often configured with additional optional sensors including fluorometers, transmissometers and/or radiometers. It is often combined with a Rosette of water sampling bottles (e.g. Niskin, GO-FLO) for collecting discrete water samples during the cast. This term applies to profiling CTDs. For fixed CTDs, see https://www.bco-dmo.org/instrument/869934.

Dataset-specific Instrument Name	Flow Cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	Becton Dickenson (Franklin Lakes, NJ, USA; formerly Cytopeia) high speed jet-in-air InFlux flow cytometer, using a 488 nm blue excitation laser, appropriate Chl-a (692±20 nm) and phycoerythrin (580±15 nm) bandpass filters.
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. Description from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm

Dataset-specific Instrument Name	Epifluorescence Microscope
Generic Instrument Name	Fluorescence Microscope
Dataset-specific Description	Olympus AX70 microscope (Olympus, Tokyo, Japan) equipped with a Toshiba CCD video camera (Irvine, CA, USA)
Generic Instrument Description	Instruments that generate enlarged images of samples using the phenomena of fluorescence and phosphorescence instead of, or in addition to, reflection and absorption of visible light. Includes conventional and inverted instruments.

Dataset-specific Instrument Name	Niskin bottle
Generic Instrument Name	Niskin bottle
Dataset-specific Description	12 liter Niskin bottles
Generic Instrument Description	A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc.

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Deployments

BATS_cruises

Website	https://www.bco-dmo.org/deployment/58883
Platform	Multiple Vessels
Report	http://bats.bios.edu/bats-data/
Start Date	1988-10-20
Description	Bermuda Institute of Ocean Science established the Bermuda Atlantic Time-series Study with the objective of acquiring diverse and detailed time-series data. BATS makes monthly measurements of important hydrographic, biological and chemical parameters throughout the water column at the BATS Study Site, located at 31 40N, 64 10W.

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Project Information

Transitions in the Surface Layer and the Role of Vertically Stratified Microbial Communities in the Carbon Cycle - An Oceanic Microbial Observatory (Ocean Microbial Observatory)

Website: http://www.bios.edu/research/projects/oceanic-microbial-observatory/

Coverage: Bermuda Atlantic Time-Series study site

(*Adapted from the NSF award abstract*)

The premise of this project is that stratified bacterioplankton clades engage in specialized biogeochemical activities that can be identified by integrated oceanographic and microbiological approaches. Specifically, the objective of this project is to assess if the mesopelagic microbial community rely on diagenetically altered organic matter and subcellular fragments that are produced by microbial processes in the euphotic zone and delivered into the upper mesopelagic by sinking or mixing. In past efforts this microbial observatory had greater success cultivating members of the euphotic zone microbial community, and revealed an unanticipated growth requirement for reduced sulfur compounds in alphaproteobacteria of the SAR11 clade. Genomic information showed that intense competition for substrates imposes trade-offs on bacterioplankton - there are regions of N dimensional nutrient space where specialists win. We postulate that specific growth requirements

may explain some the regular spatial and temporal patterns that have been observed in upper mesopelagic bacterioplankton communities, and the difficulties of culturing some of these organisms.

The specific objectives of this project are: 1) to produce 13C and 15N labeled subcellular (e.g., soluble, cell wall, and membrane) and DOM fractions from photosynthetic plankton cultures and use stable isotope probing to identify specific clades in the surface and upper mesopelagic microbial community that assimilate fractions of varying composition and lability. 2) to use fluorescence in situ hybridization approaches to monitor temporal and spatial variability of specific microbial populations identified from the SIP and HTC experiments. To increase resolution we will use CARD-FISH protocols. 3) to measure the proteomes of bacterioplankton communities to identify highly translated genes in the surface layer and upper mesopelagic, and community responses to seasonal nutrient limitation. 4) and, to cultivate these organisms via high throughput culturing (HTC) by pursuing the hypothesis that they require specific nutrient factors and/or diagenetically altered organic substrates. Complete genome sequences from key organisms will be sought and used as queries to study patterns of natural variation in genes and populations that have been associated with biogeochemically important functions.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0802004

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