Microbial abundance, activity, and nutrient concentrations in Delaware Bay from R/V Hugh R. Sharp HRS090706DK in the Delaware Bay from July 2009 (Active bacteria in surface waters project)

Website: https://www.bco-dmo.org/dataset/3866
Version:
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Project
» Are abundant bacteria more active than rare bacteria in the Sargasso Sea? (Active bacteria in surface waters)

Contributors	Affiliation	Role
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Dataset Description

The data set includes salinity, light intensity and attenuation, microbial abundance, microbial heterotrophic activity, and inorganic nutrient concentrations along the salinity gradient of the Delaware estuary in July 2009.

Methods & Sampling

The estuary was sampled with Niskin bottles in a CTD rosette from about 0.5 m. Salinity was taken from the CTD while light intensity at various depths was measured with a Biospherical light meter (model PNF-2102P).

Total microbial abundance and average cell size were determined by epifluorescence microscopy as described previously (Nikrad et al. 2012). The abundance of autotrophic microbes (Synechococcus, picoeukaryotes, and Prochlorococcus) was determined by flow cytometry as previously described (Straza and Kirchman 2011). Incorporation of 3H-leucine was measured in 30 minute incubations using standard methods described elsewhere (Kirchman 2001).

The concentrations of ammonium, nitrate, phosphate, and silicate were measured with a Seal AA3 nutrient autoanalyzer as previously described (Sharp et al. 2009).

Data Processing Description

Light attenuation was calculated from light intensities from linear regression analyses of ln(PAR) vs. depth.

Related files and references:

Kirchman, D. L. 2001. Measuring bacterial biomass production and growth rates from leucine incorporation in natural aquatic environments. Pages 227-237 in J. H. Paul, editor. Marine Microbiology. Academic Press, San Diego.

Nikrad, M. P., M. T. Cottrell, and D. L. Kirchman. 2012. Abundance and Single-Cell Activity of Heterotrophic Bacterial Groups in the Western Arctic Ocean in Summer and Winter. Applied and Environmental Microbiology 78:2402-2409.

Sharp, J. H., K. Yoshiyama, A. E. Parker, M. C. Schwartz, S. E. Curless, A. Y. Beauregard, J. E. Ossolinski, and A. R. Davis. 2009. A biogeochemical view of estuarine eutrophication:Seasonal and spatial trends and correlations in the Delaware Estuary. Estuaries and Coasts 32:1023-1043.

Straza, T. R. A. and D. L. Kirchman. 2011. Single-cell response of bacterial groups to light and other environmental factors in the Delaware Bay, USA. Aquatic Microbial Ecology 62:267-277.

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Data Files

File
active_bact.csv (Comma Separated Values (.csv), 3.49 KB) MD5:d7949f1163a723983e22f6aaa71f598e Primary data file for dataset ID 3866

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Parameters

Parameter	Description	Units
cruise_id	cruise identification; official R2R name	text
cruise_name	cruise identification; project-based name	text
sta	station identifier	text
date_local	local date of sample collection	yyyymmdd
time_local	local time of sample collection	HH:MM:SS
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
temp	temperature	degrees Celsius
sal	salinity	dimensionless
PAR	Photosynthetically Available [Active] Radiation; downwelling irradiance	q/cm2/s
depth_secchi	depth at which a Secchi disk disappears	meters
atten_secchi	light attenuation from Secchi reading	per meter
atten_err	light attenuation standard error	per meter
NO3	nitrate concentration	uM
NO3_sd	nitration standard deviation	uM
PO4	phosphate concentration	uM
PO4_sd	phosphate standard deviation	uM
NH4	ammonium concentration	uM
NH4_sd	ammonium standard deviation	uM
Si	silicate concentration	uM
Si_sd	silicate standard deviation	uM
chl_a	chlorophyl-a concentration	micrograms/liter
chl_a_sd	chlorophyl-a standard deviation	micrograms/liter
bact_cm3	microbial abundance	cells/ml
bact_cm3_sd	microbial abundance standard deviation	cells/ml
cell_size	microbial cell size (volume)	micrometers^3
cell_size_se	microbial cell size standard error	micrometers^3
bact_aap	percent aerobic anoxygenic phototrophic bacteria of total	percent
bact_aap_sd	aerobic anoxygenic phototrophic bacteria standard deviation	percent
Synech	Synechococcus abundance	cells/ml
PicoEuk	picoeukaryotes abundance	cells/ml
Prochlo	Prochlorococcus abundance	cells/ml
leu_incorp	3H-leucine incorporation rate	picoMolar/h
leu_incorp_sd	3H-leucine incorporation standard deviation	picoMolar/h

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Instruments

Dataset-specific Instrument Name	CTD profiler
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
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	Epifluorescence Microscope
Generic Instrument Name	Fluorescence Microscope
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
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.

Dataset-specific Instrument Name	Nutrient Autoanalyzer
Generic Instrument Name	Nutrient Autoanalyzer
Dataset-specific Description	Seal AA3 nutrient autoanalyzer as previously described (Sharp et al. 2009)
Generic Instrument Description	Nutrient Autoanalyzer is a generic term used when specific type, make and model were not specified. In general, a Nutrient Autoanalyzer is an automated flow-thru system for doing nutrient analysis (nitrate, ammonium, orthophosphate, and silicate) on seawater samples.

Dataset-specific Instrument Name	Photosynthetically Available Radiation Sensor
Generic Instrument Name	Photosynthetically Available Radiation Sensor
Dataset-specific Description	Biospherical light meter (model PNF-2102P) Profiling Natural Fluorescence Radiometer: Unlike strobe fluorometers, a natural fluorometer measures fluorescence emitted under the ambient light conditions that are driving photosynthesis in situ.
Generic Instrument Description	A PAR sensor measures photosynthetically available (or active) radiation. The sensor measures photon flux density (photons per second per square meter) within the visible wavelength range (typically 400 to 700 nanometers). PAR gives an indication of the total energy available to plants for photosynthesis. This instrument name is used when specific type, make and model are not known.

Dataset-specific Instrument Name	Secchi Disc
Generic Instrument Name	Secchi Disc
Generic Instrument Description	Typically, a 16 inch diameter white/black quadrant disc used to measure water optical clarity

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Deployments

HRS090706DK

Website	https://www.bco-dmo.org/deployment/58931
Platform	R/V Hugh R. Sharp
Start Date	2009-07-06
End Date	2009-07-08
Description	Cruise information and original data are available from the NSF R2R data catalog.

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Project Information

Are abundant bacteria more active than rare bacteria in the Sargasso Sea? (Active bacteria in surface waters)

Coverage: Coastal Delaware, Delaware Bay, Sargasso Sea

Marine prokaryotic communities are now known to be highly diverse and may be carrying out new types of metabolisms that, if confirmed, could fundamentally alter models of energy and material flow through the oceans. These metabolisms include photoheterotrophic and chemolithotrophic pathways that are entirely novel or were not thought to be occurring in the surface layer of the oceans. The problem is, we do not know which fraction of this diverse community is actually active in biogeochemical processes and whether the metabolic functions, especially the new ones suggested by genomic data, are actually being carried out by marine prokaryotic communities.

This project will address the following questions and hypotheses:

1. What bacteria are most active in open oceanic environments like the Sargasso Sea? The investigators hypothesize that the most abundant bacterioplankton groups are also the most active whereas the rare groups will be less active. This hypothesis will be explored using four indices of activity: i) levels of 16S rRNA vs. 16S rRNA genes; ii) replicating cells as measured by the incorporation of the thymidine analog, BrdU; iii) incorporation of key dissolved compounds by abundant bacterial groups as revealed by microautoradiography combined with fluorescence in situ hybridization (Micro-FISH), and iv) transcript levels of growth-dependent phylogenetic markers other than 16S rRNA (e.g. tuf, rpoB and dnaE). The investigators are especially interested in whether rare bacteria are inactive and are potentially part of a 'seed bank' that serves as the inoculum for future communities.

2. What metabolic processes are represented by the most commonly expressed genes? The investigators hypothesize that the most commonly expressed genes will be those associated with the processing of dissolved organic matter rather than other energy generating mechanisms, including photoheterotrophy and chemolithotrophy. Expression will be examined by pyrosequencing mRNA (metatranscriptome) from the Sargasso Sea. We will map the metatranscriptome onto metagenomic assemblies from the Sargasso Sea and explore which genes called in metagenomic studies are real rather than bioinformatic artifacts.

The project will use a combination of pyrosequencing and QPCR approaches to examine rRNA:rDNA ratios, BrdU incorporating cells, and transcript types and amounts in the metatranscriptome of Sargasso Sea surface water. Pyrosequencing (454) avoids amplification and cloning artifacts and it is cost effective. Preliminary analyses indicate that the sequence length of 454 reads and the proposed number of sequences are ideal for addressing the questions raised here. The investigators will also use Micro-FISH to examine incorporation of thymidine, leucine, and PO4. Samples will be collected twice yearly during the spring phytoplankton bloom when heterotrophic bacterial production is lowest and during the peak of bacterial production in summer.

This project will do much to alter our perception of microbial processes in the oligotrophic ocean by providing answers to long-standing questions about activity and standing stocks of bacterial populations and by linking metabolic processes to the extensive environmental genomic data now becoming available.

The project will support a graduate student and involve underrepresented undergraduates in summer research projects, including at sea field work. The results from this project will be incorporated into an environmental genomics web site and used in courses taught by Kirchman. The Kirchman and Heidelberg labs are featured in lab tours open to the public (~ 1000 visitors per year) and Campbell and Kirchman are also involved in Coast Day, an annual open house that attracts about 10,000 visitors. Finally, the PIs will be involved in K-12 teacher training workshops and other Delaware Center for Critical Zone Research outreach activities

The project is affiliated with the Bermuda Atlantic Time-Series Study (BATS), http://bats.bios.edu.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0825468

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