Paired metagenomic and metatranscriptomic data from R/V Atlantic Explorer AE1006, AE1024, Bermuda Atlantic Time Series Station (BATS), Sargasso Sea, Mar and Aug 2010 (Active bacteria in surface waters project)

Website: https://www.bco-dmo.org/dataset/512782
Version: 2014-04-23

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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Methods & Sampling

A combination of pyrosequencing and QPCR approaches were used to examine rRNA:rDNA ratios, BrdU incorporating cells, and transcript types and amounts in the metatranscriptome of Sargasso Sea surface water. The investigators also used Micro-FISH to examine incorporation of thymidine, leucine, and PO4. Samples were collected in 2010 during the spring phytoplankton bloom when heterotrophic bacterial production is lowest and during the peak of bacterial production in summer.

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Data Files

File
bact_accessions.csv (Comma Separated Values (.csv), 1.54 KB) MD5:cd54d62accbb1c53a93efa0587b7385c Primary data file for dataset ID 512782

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Parameters

Parameter	Description	Units
cruise_id	cruise identification; AE is Atlantic Explorer	unitless
date	date of collection	mm/dd/yyyy
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
depth	depth of sample	meters
accession_number	NCBI accession number	unitless

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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.

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Deployments

AE1006

Website	https://www.bco-dmo.org/deployment/58903
Platform	R/V Atlantic Explorer
Start Date	2010-03-23
End Date	2010-03-27

AE1024

Website	https://www.bco-dmo.org/deployment/506345
Platform	R/V Atlantic Explorer
Start Date	2010-08-19
End Date	2010-08-23

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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
NSF Division of Ocean Sciences (NSF OCE)	OCE-0824981

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