Cruise schedule summary from R/V Cape Henlopen BAMS-multi in the Chesapeake Bay from 2001-2004 (BAMS project)

Website: https://www.bco-dmo.org/dataset/2915
Data Type: document
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Project
» Biocomplexity of Aquatic Microbial Systems (BAMS)

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Dataset Description

BAMS - Cruise schedule summary

Methods & Sampling

BAMS cruise summary data compiled from general cruise information provided by Bess Ward in the cruise metadata form and from the UNOLS yearly schedules for the R/V Cape Henlopen for the years 2000-2004.

Data Processing Description

Prepared by BCO-DMO staff

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Parameters

Parameters for this dataset have not yet been identified

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Deployments

BAMS-multi

Website	https://www.bco-dmo.org/deployment/57844
Platform	R/V Cape Henlopen
Start Date	2001-04-04
End Date	2004-10-06
Description	Multiple year sampling at sites in the Chesapeake Bay, one of its branches, the Choptank River,and the open ocean of the Sargasso Sea. **Methods & Sampling** BAMS cruise summary data compiled from general cruise information provided by Bess Ward in the cruise metadata form and from the UNOLS yearly schedules for the R/V Cape Henlopen for the years 2000-2004. **Processing Description** Prepared by BCO-DMO staff

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Project Information

Biocomplexity of Aquatic Microbial Systems (BAMS)

Website: http://geoweb.princeton.edu/research/biocomplexity/index.html

Coverage: Chesapeake Bay, one of its branches, the Choptank River, and the open ocean of the Sargasso Sea

NSF: Collaborative Research: Biocomplexity of Aquatic Microbial Systems: Relating Diversity of Microorganisms to Ecosystem Function

The "Biocomplexity of Aquatic Microbial Systems: Relating Diversity of Microorganisms to Ecosystem Function" Project was funded by the US NSF in 2000 as one of several collaborative research initiatives comprising the NSF Biocomplexity program. Microbial biogeochemical cycling of the elements regulates a dynamic environment in which the cycles of different elements are linked through the physiology of microorganisms. While a certain degree of understanding can be gained through physical/chemical approaches to measurement and modeling of the net transformations, these approaches necessarily rely on gross simplifications about the role and regulation of the various functional groups (guilds) involved. The nutrient elements, such as carbon , nitrogen, phosphorous and several important metals, occur in ecosystems in many different forms (e.g., organic carbon and carbon dioxide; nitrate, nitrite, nitrous oxide, organic nitrogen and nitrogen gas, etc.). The transformations between different forms, and the distributions of the various compounds, are largely controlled by microbes. Thus the physiology of bacteria and phytoplankton is largely responsible for the chemistry of natural systems, through what we call microbial biogeochemical cycling.

Our present understanding of elemental cycling is partly derived from measurements and modeling of the distribution of chemical compounds, and the measurement of the rates of transfer of compounds from one form to another. This approach has led to an appreciation of the overwhelming importance of microbes in regulating ecosystem biogeochemistry. But they still represent a great oversimplification of the complexities of microbial processes. Recent advances in molecular microbial ecology have shown the microbial world to contain immense diversity and complexity at every level: redundancy and duplication of functional genes within a single organism; molecular diversity among functional genes that encode the same process in different organisms; large genetic diversity among different organisms apparently engaged in the same biogeochemical function within single communities; great variability in the species composition of different communities that apparently perform equally well.

The goal of this project is to investigate the functional relationship between complexity in microbial communities and the physical/chemical environment at a range of biological and ecological scales. Previously, such analysis was technologically limited by the inability to assay large numbers of samples simultaneously for a large

number of genes and phylotypes. Using gene array technology, the researchers will be able to detect the distribution and differential expression of functional genes in natural systems.

The results of this study constitute the first step towards application of DNA chip technology for gene expression of "exotic" (i.e., not of biomedical importance) processes and organisms in the environment. The gene arrays, along with a full suite of ecosystem process measurements, were applied and assessed along a transect that spans the eutrophic - oligotrophic gradient from the inland waters of the Chesapeake Bay out to the Sargasso Sea. The study area included sites in the Chesapeake Bay, one of its branches, the Choptank River, and the open ocean of the Sargasso Sea, which is the major ocean basin into which water from the Chesapeake Bay flows. Experiments and functional gene studies focused on key transformations in the carbon and nitrogen cycles (C fixation, N fixation, nitrification, denitrification, urea assimilation). The diversity of guilds are being interpreted in terms of ecosystem function, assessed using geochemical data and tracer experiments. In addition to field studies designed to investigate and dissect the natural system, the group of collaborating scientists also performed perturbation experiments using mesocosms. The goal of these experiments was to determine how microbial species diversity affects the major energy and nutrient flows within ecosystems, and to assess the degree of stability or instability associated with changes in redundancy within guilds of microorganisms responsible for major nitrogen and carbon pathways.

The complexity of microbial guilds and microbial processes and the attendant diversity of functional genes and organisms were represented in two parallel investigative themes:

1.Diversity of functional genes: Previously, such analysis was technologically limited by the inability to assay large numbers of samples simultaneously for a large number of genes and organisms. Using gene array technology , we were able to detect the distribution and differential expression of functional genes in natural systems. The results of this study constitutes the first step towards application of DNA chip technology for gene expression of processes and organisms in the natural environment.

2.Rates of biogeochemical processes: Studies focused on key transformations in the carbon and nitrogen cycles (C fixation, N fixation, nitrification, denitrification, urea assimilation). The diversity of microbial guilds were interpreted in terms of ecosystem function, assessed using the physical/chemical data mentioned above and tracer experiments to estimate actual transformation rates.

Station Identifications, locations, and sample depths
Location ID Latitude Longitude Shallow (m) Deep (m)
Upper Choptank CT100 N 38° 48.356' W 75° 54.625' 1 5
Lower Choptank CT200 N 38° 37.215' W 76° 08.189' 1 8
Upper Bay CB100 N 39° 20.9' W 76° 10.9' 1 10
Mid Bay CB200 N 38° 34.1' W 76° 26.6' 1 21
Lower Bay CB300 N 37° 16.1' W 76° 09.0' 1 12
Plume PL100 N 36° 52' W 75° 55' 1 14
Sargasso SS100 N 36° 24' W 72° 00' 1 2000+

Bacterial Productivities: Leucine incorporation (Kirchman, et al. 1985. Appl. Environm. Microbiol. 49: 599-607)

Photosynthesis: Carbon-14 incorporation (1 hr incubation) in Photosynthetron light gradient. Alpha and Pmax determined from hyperbolic curve fit.

Data supplied by Todd Kana, Horn Point Laboratory, Cambridge, MD.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-9981482
NSF Division of Ocean Sciences (NSF OCE)	OCE-9981617

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