Protist numbers at and below 100 m from R/V Pelagia 64PE280, 64PE325 in the tropical and subtropical N. Atlantic from 2007-2010 (Basin-scale Protists project)

Website: https://www.bco-dmo.org/dataset/471609
Version:
Version Date: 2013-11-13

Project
» Basin-scale distribution and activity of deep-sea protists in the North Atlantic Ocean (Basin-scale Protists)

Program
» Integrated Marine Biogeochemistry and Ecosystem Research -US (IMBER-US)

Contributors	Affiliation	Role
Bochdansky, Alexander B.	Old Dominion University (ODU)	Principal Investigator
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Table of Contents

- Dataset Description
  - Methods & Sampling
  - Data Processing Description
- Data Files
- Parameters
- Instruments
- Deployments
- Project Information
- Program Information
- Funding

Methods & Sampling

Excerpt from Morgan-Smith et al. (2013):

Samples were collected using a rosette sampler fitted with 25 L Niskin bottles. Samples were immediately fixed with 0.2 micron-filtered methanol-stabilized formaldehyde (final concentration ~2%) and kept overnight at room temperature to allow outgassing and prevent bubble formation on filters. Subsamples of 100-250 ml were then filtered under gentle vacuum (-200mbar) onto Millipore 0.2 micron white polycarbonate filters for DAPI-FITC. A pore size of 0.2 micron is preferred for enumeration of total eukaryotes because some smaller eukaryotes are lost through the pores of 0.8 micron filters, leading to underestimation of eukaryote abundance (Morgan-Smith et al., 2011). Filters were washed with phosphate buffered saline (PBS) and ultra-pure water, then immediately stored at -80 C.

DAPI-FITC double staining was used to enumerate total eukaryotes. Pie-shaped slices of approximately 1/16-1/8 of filter were cut and 3-4 of these slices were placed atop a 25 mm diameter, 0.2 micron pore size polycarbonate filter on a glass frit and covered with a 10-ml filter tower, which was then flooded with 1ml FITC staining solution (2.5 ml 0.5 M sodium carbonate buffer, pH 9; 11 ml 0.01 M potassium phosphate buffer, pH 7.2; 11 ml 0.85 % sodium chloride; 10 mg FITC), and incubated for 10 min in the dark. Then vacuum was applied (-200 mbar) and filters were washed twice with 10 ml ice-cold carbonate buffer (0.5M, pH9). Filter sections were mounted on slides using Vectashield mounting medium with DAPI and stored at -20 C until analysis. Samples were counted on Olympus BX51 and BX50 epifluorescence micro scopes.

Data Processing Description

Raw counts were converted into cell numbers per ml using field of view under the microscope, filtered area on the polycarbonate filter, and volume filtered as input variables.

References:

Morgan-Smith D., Clouse M. A., Herndl G. J., Bochdansky A. B. (2013) Diversity and distribution of microbial eukaryotes in the deep tropical and subtropical North Atlantic Ocean. Deep-Sea Res. I: 78: 58-69

Morgan-Smith D., Herndl G. J., van Aken H. M., Bochdansky A. B. (2011) Feature article. Abundance of eukaryotic microbes in the deep subtropical North Atlantic. Aquat. Microb. Ecol. 65.

[table of contents | back to top]

Data Files

File
protists.csv (Comma Separated Values (.csv), 28.36 KB) MD5:e5207d4484c236e6399c7d8f790df2a7 Primary data file for dataset ID 471609

[table of contents | back to top]

Parameters

Parameter	Description	Units
cruise_id	cruise identification	unitless
cruise_name	alternate cruise name	unitless
sta	station number	unitless
date	UTC date	unitless
lat	latitude	decimal degrees
lon	longitude	decimal degrees
depth	depth of sample	meters
vol	volume of water filtered onto 0.2 mm polycarbonate filters (25 mm diam.)	milliliters
split	Epifluorescence counts of a specific nuclear morphotype as detectable with DAPI and described in Morgan-Smith et al. (2011) and Morgan-Smith et al. (2013). See references above	cells
temp	temperature	degrees Celsius
sal	salinity	practical salinity units
O2	oxygen	micromoles per kilogram
FITC_2	Abundance for eukaryotic microbes retained by a 0.2 mm polycarbonate filter	cells per milliliter
FITC_8	Abundance (cells ml-1) for eukaryotic microbes retained by a 0.8 mm polycarbonate filter	cells per milliliter
EUK516	Relative abundance of cells hybridizing with the universal eukaryote probe EUK516	cells
KIN516	Relative abundance of cells hybridizing with probe KIN 516 for Kinetoplastida	cells
LabY	Relative abundance of cells hybridizing with the LabY probe for Labyrinthulomycetes	cells
PF2	Relative abundance of cells hybridizing with the PF2 probe for fungi	cells
Alv01	Relative abundance of cells hybridizing with the Alv01 probe for group II Alveolata	cells
DiploR1792	Relative abundance of cells hybridizing with the DiploR1792 probe for Diplonemids	cells
NS4	Relative abundance of cells hybridizing with the NS4 probe for type 4 Marine Stramenopiles (MAST 4)	cells

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Fluorescence Microscope
Generic Instrument Name	Fluorescence Microscope
Dataset-specific Description	Olympus BX51 and BX50 epifluorescence microscopes
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	25 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.

[table of contents | back to top]

Deployments

64PE280

Website	https://www.bco-dmo.org/deployment/59113
Platform	R/V Pelagia
Report	http://melia.nioz.nl/phptoweb/dmg/melia-codis.php?script=search/bycruise.inc
Start Date	2007-12-19
End Date	2008-01-16
Description	Transect over the subtropical and tropical Atlantic from Brazil to West Africa, and to Cape Verde Islands. The RVPelagia operates out of the Royal Netherlands of Sea Research (NIOZ)

64PE325

Website	https://www.bco-dmo.org/deployment/471613
Platform	R/V Pelagia
Report	http://melia.nioz.nl/phptoweb/dmg/melia-codis.php?script=search/bycruise.inc
Start Date	2010-10-08
End Date	2010-11-04
Description	Cruise leaving Las Palmas (Canary Islands) covered a loop including a transect along the Midatlantic Ridge and returning to Las Palmas

[table of contents | back to top]

Project Information

Basin-scale distribution and activity of deep-sea protists in the North Atlantic Ocean (Basin-scale Protists)

Coverage: Tropical and subtropical Atlantic

ABSTRACT

Little is known about the distribution and ecology of eukaryotic microbes of the deep sea water column. Most of these microbes are small heterotrophic flagellates that feed on bacteria, where biomass in turn is fueled by the input of dissolved and particulate organic material from the surface. This study seeks to understand the distribution of eukaryotic microbes (i.e., protists) in the context of large, basin scale variations in hydrographic and chemical properties. The main hypothesis is that the abundance and taxonomic composition of protists serve as sensitive indicators of the strength and type (particulate or dissolved) of input of organic carbon into the deep ocean system. Samples in vertical profiles targeting major water masses across the North Atlantic will be collected. In addition, deep sea samples will be retrieved under pressure and incubated at in situ pressure and temperature in four newly designed chemostat systems. These cultures will be sub-sampled under pressure and examined for nutrient concentration, as well as for the purpose of monitoring the abundance of both prokaryotes and protists in the chambers. Using the same pressure samplers in short-term incubations, the investigators will explore the activity of deep sea protists by investigating the proportion of actively feeding organisms on fluorescently labeled bacteria. They will enumerate deep sea protists using a combination of fluorescence in situ hybridization and traditional staining methods, and will support taxonomic classifications using electron microscopy. Semi-automated epifluorescence microscopy with image analysis capabilities will be used to scan major filter areas and probe for rare microbes that normally fall below detection limits of other methods. In laboratory experiments, the investigators will use the newly built culture system to study pressure effects of eukaryotic protists while simulating temperature and pressure changes that sinking particles are exposed to when they sink to the abyss.

[table of contents | back to top]

Program Information

Integrated Marine Biogeochemistry and Ecosystem Research -US (IMBER-US)

Website: http://www.imber.info/

Coverage: global

The BCO-DMO database includes data from IMBER endorsed projects lead by US funded investigators. There is

no dedicated US IMBER project or data management office. Those functions are provided by US-OCB and BCO-DMO respectively.

The information in this program description pertains to the Internationally coordinated IMBER research program. The projects contributing data to the BCO-DMO database are those funded by US NSF only. The full IMBER data catalog is hosted at the Global Change Master Directory (GCMD).

IMBER Data Portal: The IMBER project has chosen to create a metadata portal hosted by the NASA's Global Change Master Directory (GCMD). The GCMD IMBER data catalog provides an overview of all IMBER endorsed and related projects and links to datasets, and can be found at URL http://gcmd.nasa.gov/portals/imber/.

IMBER research will seek to identify the mechanisms by which marine life influences marine biogeochemical cycles, and how these, in turn, influence marine ecosystems. Central to the IMBER goal is the development of a predictive understanding of how marine biogeochemical cycles and ecosystems respond to complex forcings, such as large-scale climatic variations, changing physical dynamics, carbon cycle chemistry and nutrient fluxes, and the impacts of marine harvesting. Changes in marine biogeochemical cycles and ecosystems due to global change will also have consequences for the broader Earth System. An even greater challenge will be drawing together the natural and social science communities to study some of the key impacts and feedbacks between the marine and human systems.

To address the IMBER goal, four scientific themes, each including several issues, have been identified for the IMBER project: Theme 1 - Interactions between Biogeochemical Cycles and Marine Food Webs; Theme 2 - Sensitivity to Global Change: How will key marine biogeochemical cycles, ecosystems and their interactions, respond to global change?; Theme 3 - Feedback to the Earth System: What are the roles of the ocean biogeochemistry and ecosystems in regulating climate?; and Theme 4 - Responses of Society: What are the relationships between marine biogeochemical cycles, ecosystems, and the human system?

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0826659

[table of contents | back to top]