MEDEA-II stations for catalyzed reporter deposition fluorescence in situ hybridization (CARD FISH) samples collected on RV/Pelagia 64PE356i June-July 2012 (Eukaryote Microbes NAtl project)

Website: https://www.bco-dmo.org/dataset/658765
Data Type: Cruise Results
Version: 1
Version Date: 2016-09-16

Project
» Ecology of eukaryote microbes in the deep North Atlantic (Eukaryote Microbes NAtl)

Contributors	Affiliation	Role
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Abstract
Station depth, water mass and the volume of water filtered for catalyzed reporter deposition fluorescence in situ hybridization (CARD FISH) samples

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Coverage

Spatial Extent: **N**:67.35 **E**:-2.69 **S**:50.86 **W**:-40.07
Temporal Extent: 2012-06-23 - 2012-07-23

Methods & Sampling

Samples were derived during the Medea 2 research expedition on the RV Pelagia (Royal Netherlands Institute for Sea Research (NIOZ)) to the north-temperate, subpolar and polar North Atlantic and the Norwegian Sea. The RV Pelagia traveled from the Porcupine Plains west to the Charlie Gibbs Fracture Zone (CGFZ), then turned northeast, and crossed over the Faroe Ridge into the Norwegian Sea.

Data Processing Description

BCO-DMO Processing:
- added conventional header with dataset name, PI name, version date, reference information
- renamed parameters to BCO-DMO standard

- transformed Word doc table to flat files
- added lat and lon columns

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Data Files

File
CARD_FISH_stations.csv (Comma Separated Values (.csv), 686 bytes) MD5:53a3c1e914f022bace361e97a0f81237 Primary data file for dataset ID 658765

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Related Datasets

IsSupplementTo

Bochdansky, A. B. (2021) **CARD FISH Eukaryote, Fungi, Labyrinthomycete, Kinetoplastid counts from MEDEA-II R/V Pelagia 64PE356 in the North Atlantic: Galway, Ireland to Reykjavik, Iceland from June to July 2012.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2016-09-16 doi:10.26008/1912/bco-dmo.658821.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
station	station number	unitless
lat	latitude; north is positive	decimal degrees
lon	longitude; east is positive	decimal degrees
depth	depth	meters
water_mass	water mass name:	unitless
vol_filt	volume of water filtered	liters

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Instruments

Dataset-specific Instrument Name	
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

64PE356

Website	https://www.bco-dmo.org/deployment/565135
Platform	R/V Pelagia
Start Date	2012-06-23
End Date	2012-07-23
Description	Cruise for the MEDEA II project

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Project Information

Ecology of eukaryote microbes in the deep North Atlantic (Eukaryote Microbes NAtl)

Coverage: Temparate, subarctic Atlantic and Arctic Ocean

Description from NSF award abstract:
In the microbial realm, one of the three domains of life -- the Eukarya -- has received little attention in deep-sea research. This stands in contrast to the fact that in all known aquatic environments, and measured by the amount of material and energy transferred, the link between prokaryotic and eukaryotic cells is one of the most significant trophic interactions on Earth. In terms of volume, the deep sea is the largest biome, and despite its tremendous role in long-term biogeochemical cycles, it has largely been neglected. Biological activity in the deep sea is neither negligible nor homogeneous in space and time. Recent data suggest that biological activity in the dark ocean (as evidenced by respiration rates, bacterial secondary production and a variety of other metrics) is much higher than anticipated from all known organic carbon fuel sources combined (i.e., POC flux, DOC convection, in situ production and active transport by zooplankton). Water masses in the deep ocean represent highly-diverse biogeographic regions with distinct communities and particle distributions. Moreover, because of feeding thresholds, cold temperatures, extreme pressures and unique adaptations that deep-sea microbes exhibit, biological activity rules cannot simply be extrapolated from laboratory cultures and from experiments with surface-dwelling microbes. This study focuses on the fundamental role of eukaryotic microbial communities in deep-sea ecology with the overarching hypothesis that protists represent sensitive biological indicators of utilizable organic carbon. There is good reason to believe that microbial eukaryotes and their activities are better indicators of "new" sources of organic carbon than particle inventories, sediment traps, isotope ratios, or models based on surface production and theoretical flux attenuation. For these new biological indicators to work, however, one needs to separate live from the moribund and dead cells, the bacterivores from saprotrophs, the inactive resting stages from those actively feeding on prokaryotes, the gametes and zoospores from vegetative and feeding stages, and those located on particles from the ones

freely suspended in the water column. Each of these groups represents different levels of per-cell energy and carbon requirements.

This study determines the ecological role of eukaryotic microbes in the deep North Atlantic over large geographic regions. The research incorporates two fundamentally different experimental designs that capitalize on different time scales: 1) Short-term incubations (~72 hours) of respiratory activity and bacterivory combined with a high resolution sampling of abundances across large geographic regions performed from a research vessel, and 2) Long-term incubations (=/> 4 weeks) measuring colonization of sinking particles and growth of eukaryotic microbes using free-falling (untethered) vehicles representing the first attempt of physiological rate measurements directly in the deep sea. Methods include new tracers for bacterivory, incubations for single-cell respiration, taxonomic identification using fluorescence in situ hybridization, single-cell genomics, and the first of its kind deep-sea holographic microscope capturing images to a maximum depth of 6000 m at 5 micrometer resolution.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1235169

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