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

Website: https://www.bco-dmo.org/dataset/658821
Data Type: Other Field Results
Version: 1
Version Date: 2016-09-16

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

Contributors	Affiliation	Role
Bochdansky, Alexander B.	Old Dominion University (ODU)	Principal Investigator
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Abstract
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.

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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

For methodology, see Bochdansky, A. B., M. A. Clouse, G. J. Herndl (2016). (exerpt: PDF)
For Medea 2 Oligonucleotide probe sequences and evaluation details, see Supplemental Files. (PDF)

Raw lengths were converted into micrometers using a calibration curve with relative object distance. The calibration equation is =uncorrected length/(1+0.00893*(object distance/1000)).

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_30um_filter.csv (Comma Separated Values (.csv), 3.28 KB) MD5:68f3362ec738fae4340a46eea9ae5888 Primary data file for dataset ID 658821

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Supplemental Files

File
Medea 2 Oligonucleotide probe sequences and evaluation details filename: MEDEA_II_cardfish_Oligonucleotide_probe_sequences_eval.pdf (Portable Document Format (.pdf), 155.38 KB) MD5:17521da3260bebaf8c8f2c387695ea1d

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Related Publications

Bochdansky, A. B., Clouse, M. A., & Herndl, G. J. (2016). Eukaryotic microbes, principally fungi and labyrinthulomycetes, dominate biomass on bathypelagic marine snow. The ISME Journal, 11(2), 362–373. doi:10.1038/ismej.2016.113
Methods

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Related Datasets

IsSupplementedBy

Bochdansky, A. B. (2021) **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).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2016-09-16 doi:10.26008/1912/bco-dmo.658765.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
filter_name	Sample label (filter name) indicating the station and pore size of filter	unitless

station	Station number	unitless
lat	Latitude; north is positive	decimal degrees
lon	Longitude; east is positive	decimal degrees
pore_size	Filter pore size	micrometers (um)
EKD_NEN	Normalized eukaryote numbers (NEN); number of eukaryotes counted using the EKD probes combined divided by the number of prokaryotes counted using DAPI counter stain	ratio
EKD_RER	Relative enrichment ratios (RER) of eukaryotes over prokaryotes on the 30 micrometer pore-size filters versus 0.2 micrometer pore-size filters; mathematically: NEN on the 30 micron filter divided by the NEN on the 0.2 micron filters for all eukaryotes	ratio
Kin_NEN	Normalized eukaryote numbers (NEN); number of kinetoplastids counted using the KIN516 probe divided by the number of prokaryotes counted using DAPI counter stain	ratio
Kin_RER	Relative enrichment ratios (RER) of kinetoplastids over prokaryotes on the 30 micrometer pore-size filters versus 0.2 micrometer pore-size filters; mathematically: NEN on the 30 micron filter divided by the NEN on the 0.2 micron filters for kinetoplastids	ratio
LabY_NEN	Normalized eukaryote numbers (NEN); number of labyrithulomycetes counted using the LabY probe divided by the number of prokaryotes counted using DAPI counter stain	ratio
LabY_RER	Relative enrichment ratios (RER) of labyrithulomycetes over prokaryotes on the 30 micrometer pore-size filters versus 0.2 micrometer pore-size filters; mathematically: NEN on the 30 micron filter divided by the NEN on the 0.2 micron filters for labyrithulomycetes	ratio
PF2_NEN	Normalized eukaryote numbers (NEN); number of fungi counted using the PF2 probe divided by the number of prokaryotes counted using DAPI counter stain	ratio
PF2_RER	Relative enrichment ratios (RER) of fungi over prokaryotes on the 30 micrometer pore-size filters versus 0.2 micrometer pore-size filters; mathematically: NEN on the 30 micron filter divided by the NEN on the 0.2 micron filters for fungi	ratio

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Fluorescence Microscope
Dataset-specific Description	Olympus BX51 epifluorescence microscope, U-LH100HG APO mercury burner, 100 x UPlanSApo objective lens, and 20 x ocular magnification.
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	
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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