Bulk water cell abundance of samples taken aboard the R/V Endeavor EN638, May 2019 in the Northern Atlantic

Website: https://www.bco-dmo.org/dataset/820961
Data Type: Cruise Results
Version: 1
Version Date: 2020-08-14

Project
» A mechanistic microbial underpinning for the size-reactivity continuum of dissolved organic carbon degradation (Microbial DOC Degradation)

Contributors	Affiliation	Role
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Abstract
Bulk water cell abundance of samples taken aboard the R/V Endeavor EN638, May 2019 in the Northern Atlantic

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Coverage

Spatial Extent: **N**:42.83954 **E**:-53.3949 **S**:34.50102 **W**:-75.67819
Temporal Extent: 2019-05-15 - 2019-05-25

Dataset Description

Measurements of bulk water cell abundance from RV/Endeavor EN638, May 2019 in the Northern Atlantic.

Acquisition Description

For each depth, 20-30 ml of 1% formaldehyde (FA) fixed sample were filtered through a 0.2 µm pore size poly-carbonate filter, applying a maximum vacuum of 200 mbar. Nucleic acids of filtered cells were counterstained with 4',6-diamidino-2-phenylindole (DAPI) and mounted using a Citifluor/VectaShield (4:1) solution. Cell abundance was measured on a fully automated epifluorescence microscope as described by Bennke *et al.,* 2016, with a minimum of 45 fields of view (FOV) per sample were acquired using a 63x

magnification oil immersion plan apochromatic objective with a numerical aperture of 1.4 (Carl Zeiss). Validation of the automated counts was done by manual cell counting.

Processing Description

Cell counting was performed with a fully automated epifluorescence microscope as described by Bennke et al., 2016 and image analysis software ACMETOOL (http://www.technobiology.ch and Max Planck Institute for marine microbiology, Bremen). Excel

BCO-DMO processing note:

- Adjusted column names to comply with database requirements
- Added ISO_DateTine_UTC column
- Converted data to ISO format (yyyy-mm-dd)

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Related Publications

Bennke, C. M., Reintjes, G., Schattenhofer, M., Ellrott, A., Wulf, J., Zeder, M., & Fuchs, B. M. (2016). Modification of a High-Throughput Automatic Microbial Cell Enumeration System for Shipboard Analyses. Applied and Environmental Microbiology, 82(11), 3289–3296. doi:10.1128/aem.03931-15
https://doi.org/10.1128/AEM.03931-15
Methods

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Parameters

Parameter	Description	Units
deployment	Cruise ID	unitless
station	Station number for cruise	unitless
longitude	Longitude, south is negative	decimal degrees
latitude	Latitude, west is negative	decimal degrees
date	Date of sample collection in ISO format (yyyy-mm-dd), US Eastern Time (UTC-05:00)	unitless
time	Time of sample collection in ISO format (hh:mm:ss), US Eastern Time (UTC-05:00)	unitless
cast_number	Cast number (refers to cast of CTD/Niskin bottles on cruise)	unitless
depth_sequence	Sequence of depths sampled (1 is surface; higher numbers at greater depths)	unitless
depth_actual	Actual depth at which water was collected	meters (m)
sample_type	Sample from bulk water or Large Volume incubation	unitless
unammended_ammended	Whether high molecular weight thalassiosira weissflogii extract was added or not; A, B, C refers to incubation depth, and the following number corresponds to incubation replicate.	unitless
cell_count	Number of cells per mL	cells per mL
ISO_DateTime_UTC	Datetime of sample collection in ISO format in UTC timezone (yyyy-mm-dd:hh:mm:ssZ)	yyyy-MM-dd'T'HH:mm:ss'Z'

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Instruments

Dataset-specific Instrument Name	Cooled charged-coupled-device camera (AxioCam MRm)
Generic Instrument Name	Camera
Dataset-specific Description	An automated epifluorescence microscope (Zeiss AxioImager.Z2 microscope stand, Carl Zeiss Jena, Gemany) equipped with a cooled charged-coupled-device (CCD) camera (AxioCam MRm + Colibri LED light source, Carl Zeiss), a light-emitting diode for DAPI (UV-emitting LED, 365 nm) and a HE-62 multi filter module with a triple emission filter (425/50 nm, 527/54 nm, LP 615 nm, including a triple beam splitter of 395/495/610, Carl Zeiss).
Generic Instrument Description	All types of photographic equipment including stills, video, film and digital systems.

Dataset-specific Instrument Name	Zeiss Axio Imager Epifluorescence microscope
Generic Instrument Name	Fluorescence Microscope
Dataset-specific Description	An automated epifluorescence microscope (Zeiss AxioImager.Z2 microscope stand, Carl Zeiss Jena, Gemany) equipped with a cooled charged-coupled-device (CCD) camera (AxioCam MRm + Colibri LED light source, Carl Zeiss), a light-emitting diode for DAPI (UV-emitting LED, 365 nm) and a HE-62 multi filter module with a triple emission filter (425/50 nm, 527/54 nm, LP 615 nm, including a triple beam splitter of 395/495/610, Carl Zeiss)
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.

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Deployments

EN638

Website	https://www.bco-dmo.org/deployment/820578
Platform	R/V Endeavor
Start Date	2019-05-15
End Date	2019-05-30

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Project Information

A mechanistic microbial underpinning for the size-reactivity continuum of dissolved organic carbon degradation (Microbial DOC Degradation)

Coverage: Northern Atlantic, Southern Indian Ocean, Svalbard

NSF Award Abstract: Marine dissolved organic matter (DOM) is one of the largest actively-cycling reservoirs of organic carbon on the planet, and thus a major component of the global carbon cycle. The high molecular weight (HMW) fraction of DOM is younger in age and more readily consumed by microbes than lower molecular weight (LMW) fractions of DOM, but the reasons for this difference in reactivity between HMW DOM and LMW DOM are unknown. Two factors may account for the greater reactivity of HMW DOM: (i) targeted uptake of HMW DOM by specific bacteria, a process the PI and her collaborators at the Max Planck Institute for Marine Microbiology (MPI) recently identified in surface ocean waters; and (ii) a greater tendency of HMW DOM to aggregate and form gels and particles, which can be colonized by bacteria that are well-equipped to breakdown organic matter. Scientists and students from the University of North Carolina (UNC) - Chapel Hill will collaborate with researchers at the MPI for Marine Microbiology (Bremen, Germany) to investigate this breakdown of HMW DOM by marine microbial communities. These investigations will include a field expedition in the North Atlantic, during which HMW DOM degradation rates and patterns will be compared in different water masses and under differing conditions of organic matter availability. DOM aggregation potential, and degradation rates of these aggregates, will also be

assessed. Specialized microscopy will be used in order to pinpoint HMW DOM uptake mechanisms and rates. The work will be complemented by ongoing studies of specific bacteria that breakdown HMW DOM, their genes, and their proteins. Graduate as well as undergraduate students will participate as integral members of the research team in all aspects of the laboratory and field work; aspects of the project will also be integrated into classes the scientist teaches at UNC. The existence of a size-reactivity continuum of DOM - observations and measurements showing that HMW DOM tends to be younger and more reactive than lower MW DOM - has been demonstrated in laboratory and field investigations in different parts of the ocean. A mechanistic explanation for the greater reactivity of HMW DOM has been lacking, however. This project will investigate the mechanisms and measure rates of HMW DOM degradation, focusing on identifying the actors and determining the factors that contribute to rapid cycling of HMW DOM. Collaborative work at UNC and MPI-Bremen recently identified a new mechanism of HMW substrate uptake common among pelagic marine bacteria: these bacteria rapidly bind, partially hydrolyze, and transport directly across the outer membrane large fragments of HMW substrates that can then be degraded within the periplasmic space, avoiding production of LMW DOM in the external environment. This mode of substrate processing has been termed selfish, since targeted HMW substrate uptake sequesters resources away from other members of microbial communities. Measurements and models thus must account for three modes of substrate utilization in the ocean: selfish, sharing (external hydrolysis, leading to low molecular weight products), and scavenging (uptake of low molecular weight hydrolysis products without production of extracellular enzymes). Using field studies as well as mesocosm experiments, the research team will investigate the circumstances and locations at which different modes of substrate uptake predominate. A second focal point of the project is to determine the aggregation potential and microbial degradation of aggregated HMW DOM. Preliminary studies have demonstrated that particle-associated microbial communities utilize a broader range of enzymatic capabilities than their free-living counterparts. These capabilities equip particle-associated communities to effectively target a broad range of complex substrates. The project will thus focus on two key aspects of HMW DOM - the abilities of specialized bacteria to selectively sequester HMW substrates, as well as the greater potential of HMW substrates to aggregate ? and will quantify these factors at different locations and depths in the ocean. The project will thereby provide a mechanistic underpinning for observations of the DOC size-reactivity continuum, an essential part of developing an overall mechanistic understanding of organic matter degradation in the ocean.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1736772

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