Cell abundance in HMW-DOM amended mesocosm incubations from water collected in the Western North Atlantic during the research cruise EN638 in May 2019 aboard R/V Endeavor

Website: https://www.bco-dmo.org/dataset/994900
Data Type: Cruise Results
Version: 1
Version Date: 2026-03-17

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
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 existence of a size-reactivity continuum of DOM - observations and measurements showing that high molecular weight (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. Here we investigated the potential of seawater microbial communities from different water masses and under differing conditions of organic matter availability to hydrolyze six high-molecular-weight polysaccharides (arabinogalactan, chondroitin sulfate, fucoidan, laminarin, pullulan, and xylan). Samples were taken from incubation experiments of DCM, OMZ, and bottom waters aboard R/V Endeavor (EN638), May 2019 in the Northern Atlantic. This dataset includes the measurement of cell abundance from samples taken from mesocosm incubations after the addition of HMW DOM.

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Coverage

Location: Western North Atlantic, Stn. 18 at approximately 37 degrees 30 N, 72 degrees 0 W, Stn. 19 at approximately 42 degrees 50 N, 53 degrees 23 W, and stn 20 at approximately 34 degrees 38 N, 53 degrees 58 W
Spatial Extent: **N**:42.83954 **E**:-53.3949 **S**:34.6369 **W**:-72.0021
Temporal Extent: 2019-05-15 - 2019-05-30

Methods & Sampling

Water was collected via Niskin bottles mounted on a rosette, equipped with a CTD.

For mesocosm (large volume) incubation experiments (referred to as “LV” incubations), seawater was transferred to 20 L carboys that were rinsed three times with water from the sampling depth and then filled with seawater from a single Niskin bottle, using silicone tubing that had been acid washed then rinsed with distilled water prior to use. Four carboys were filled at each depth from bottom water, water from the depth at which oxygen showed a minimum, and deep chlorophyll maximum (DCM) water, according to the CTD. Triplicate 20L carboys were amended with ca. 500 mg (exact mass was recorded for each addition) of HMW *Thalassiosira*; unamended single carboys were used for controls. All mesocosms were incubated in the dark at near in-situ temperatures. Mesocosms were sub-sampled at the start of incubation (0 days), and then after at approximately 2 days, 6 or 7 days, 11 days, and 16 days for multiple assays including total cell abundance.

Total cell abundance was quantified following Giljan et al. (2023). In brief, 25-50 mL of water was fixed with a final concentration of 1% formaldehyde and subsequently filtered onto 0.2 µm polycarbonate filters (Millipore). The DNA of filtered cells were simultaneously counterstained and mounted using a 1 ng/µL working solution of 4’,6-diamidin-2-phenylindol (DAPI) mixed with Citifluor/VectaShield (4:1) solution. A minimum of 45 microscopic images were acquired per sample using an automated imaging system (Zeiss AxioImager.Z2 microscope stand; 63x magnification oil immersion plan apochromatic objective with 1.4 NA, Carl Zeiss). Final cell abundance was determined using ACMETOOL 3 (http://www.tchnobiology.ch and Max Planck Institute of Marine Microbiology, Bremen). Quantification of DAPI-stained cells (signal:background > 1.5) is reported as total cell abundance. Note that for the amended mesocosms, in many cases the cells were too dense to count automatically. For these samples, 15 microscopic images were manually counted using the ACMETOOL 3 software; a minimum of 12 of 4510 images are needed to accurately capture the total cell abundance per filter. In some cases, moreover, there were not enough cells to calculate total cell abundance or the filters needed to determine cell abundance were not available (i.e., samples were lost during transit; some filters were dropped during experimental subsampling), so the data presented for each timepoint in several cases originates from different replicate mesocosms during the time course of incubation.

Data Processing Description

Image analysis was performed with ACMETOOL (Zeder, M. 2005-2021, Software for Biology, http://www.technobiology.ch and Max Planck Institute for marine microbiology, Bremen, version 3) and Zen software package (Carl Zeiss).

BCO-DMO Processing Description

- Loaded CSV file "20251114_EN638_CellCounts_Processed_BCODMO.csv" with header row 1; treated empty strings and "nd" as missing values
- Extracted non-numeric values from cell_abundance into a new flag field cell_abundance_flag, to capture symbols that were present in the "cell_abundance" values ("-" indicating lost samples or missing images, "*" indicating too few cells to quantify) without corrupting the numeric column
- Applied find/replace to time_sampled to normalize timestamps lacking seconds by appending ":00" to values matching the pattern m/d/yyyy h:mm
- Converted time_sampled from format "%m/%d/%Y %H:%M:%S" to ISO 8601 format "%Y-%m-%dT%H:%M" as a string field
- Renamed field "in-situ_temp" to "in_situ_temp" to remove the hyphen
- Exported file as "994900_v1_en638_lv_cell_counts.csv"

Problem Description

In some cases, there were not enough cells to calculate total cell abundance or the filters needed to determine cell abundance were not available (i.e., samples were lost during transit; some filters were dropped during experimental subsampling), so the data presented for each timepoint in several cases originates from different replicate mesocosms during the time course of incubation.

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Related Publications

Giljan, G., Brown, S., Lloyd, C. C., Ghobrial, S., Amann, R., & Arnosti, C. (2023). Selfish bacteria are active throughout the water column of the ocean. ISME Communications, 3(1). https://doi.org/10.1038/s43705-023-00219-7
Methods

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Parameters

Parameter	Description	Units
Deployment	Cruise ID	unitless
Station	Station number for cruise: 18, 19, or 20	unitless
latitude	Latitude, south is negative	decimal degrees
longitude	Longitude, west is negative	decimal degrees
time_sampled	Date and time of sample collection	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_m	Actual depth at which water was collected	meters
in_situ_temp	Temperature of bulk water at depth at time of collection	degrees Celsius
incub_temp	Temperature of mesocosm incubation	degrees Celsius
sample_type	Sample from bulk water (Bulk) or Large Volume (LV) incubation	unitless
unamended_amended	Refers to whether high molecular weight *Thalassiosira Weissflogii* extract was added to the incubation or was left unamended	unitless
timepoint_number	Timepoint number of sample collection (t0, t1, t2, t3, or t4)	unitless
time_elapsed_days	Incubation time elapsed at sample collection in days	days
cell_abundance	Total cell abundance from mesocosm experiments subsampled at each timepoint	cells/mL
cell_abundance_flag	Flags for cell_abundance: - indicates where no data are available because samples were lost or images were not acquired due to technical difficulties; * indicates that there were too few cells to accurately quantify	unitless

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Instruments

Dataset-specific Instrument Name	CTD
Generic Instrument Name	CTD Sea-Bird SBE 911plus
Dataset-specific Description	Water was collected via Niskin bottles mounted on a rosette, equipped with a CTD.
Generic Instrument Description	The Sea-Bird SBE 911 plus is a type of CTD instrument package for continuous measurement of conductivity, temperature and pressure. The SBE 911 plus includes the SBE 9plus Underwater Unit and the SBE 11plus Deck Unit (for real-time readout using conductive wire) for deployment from a vessel. The combination of the SBE 9 plus and SBE 11 plus is called a SBE 911 plus. The SBE 9 plus uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3 plus and SBE 4). The SBE 9 plus CTD can be configured with up to eight auxiliary sensors to measure other parameters including dissolved oxygen, pH, turbidity, fluorescence, light (PAR), light transmission, etc.). more information from Sea-Bird Electronics

Dataset-specific Instrument Name	Zeiss AxioImager.Z2
Generic Instrument Name	Fluorescence Microscope
Dataset-specific Description	A minimum of 45 microscopic images were acquired per sample using an automated imaging system (Zeiss AxioImager.Z2 microscope stand; 63x magnification oil immersion plan apochromatic objective with 1.4 NA, 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.

Dataset-specific Instrument Name	Niskin bottles
Generic Instrument Name	Niskin bottle
Dataset-specific Description	Water was collected via Niskin bottles mounted on a rosette, equipped with a CTD.
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

EN638

Website	https://www.bco-dmo.org/deployment/820578
Platform	R/V Endeavor
Start Date	2019-05-15
End Date	2019-05-30
Description	Underway datasets (and their DOIs) provided by R2R are the following. Click the cruise DOI for more general information ADCP: 10.7284/134159 Anemometer: 10.7284/134174 Anemometer: 10.7284/134176 CTD: 10.7284/134160 GNSS: 10.7284/134158 GNSS: 10.7284/134167 GNSS: 10.7284/134168 GNSS: 10.7284/134170 Gyrocompass: 10.7284/134161 Gyrocompass: 10.7284/134162 Met Station: 10.7284/134166 Radiometer: 10.7284/134163 Radiometer: 10.7284/134164 Singlebeam Sonar: 10.7284/134172 Speed Log: 10.7284/134169 Time Server: 10.7284/134171 TSG: 10.7284/134165 TSG: 10.7284/134173 Winch: 10.7284/134175

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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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