Bacterial production of bulk water and large volume samples taken aboard the R/V Endeavor EN638, May 2019 in the Northern Atlantic.

Website: https://www.bco-dmo.org/dataset/820556
Data Type: Cruise Results
Version: 1
Version Date: 2020-08-12

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
Bacterial production or bulk water and large volume 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: 2019-05-14 - 2019-06-10

Dataset Description

Bacterial production was estimated from 3H-leucine incorporation by heterotrophic bacteria using a cold trichloroacetic acid (TCA) and microcentrifuge extraction method (Kirchman, 2001). All work and incubations were performed in a UNOLS isotope lab.

Methods & Sampling

Samples were collected in one of two ways:

- Bulk water from each station was collected by combining equal portions from three niskin bottles triggered at each depth into an acid washed glass media bottle.
- After shaking, large volume (mesocosm) incubations were sampled by pouring into 500 mL acid washed glass media bottles.

Data Processing Description

To 1.5ml triplicate subsamples and one 100% (w/v) TCA -killed control 23 uL of L-[3,4,5-3H(N)]-Leucine (PerkinElmer, NET460250UC) was added and incubated between 10 and 40 hours at near in situ temperature. Live samples were then killed with 89 uL of 100% (w/v) TCA and centrifuged (10,000 rpm at 4°C for 10 min) to pelletize cell material. The supernatant liquid was removed and 1 mL of 5% (w/v) TCA solution was added followed by vortex mixing and centrifugation. Supernatant removal, mixing, and centrifugation were repeated using 1 mL of 80% ethanol solution. Again, the supernatant liquid was removed and each sample was left to dry in a hood overnight. After drying, 1 mL of scintillation cocktail (ScintiSafe 30% Cocktail, Fisher SX23-5) was added and incorporated radioactivity was measured using a PerkinElmer Tri-Carb 2910TR LSA scintillation counter for bulk, and PerkinElmer Tri-Carb 3110TR LSA for large volume (mesocosm) samples. Radioactivity was compared to 1 mL of scintillation cocktail spiked with 23 uL of L-[3,4,5-3H(N)]-Leucine radioactivity and divided by incubation time to calculate.

Data processing was done using excel.

BCO-DMO processing notes:

- 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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Data Files

File
bulk_water_leucine.csv (Comma Separated Values (.csv), 22.64 KB) MD5:361ff35bf513078da9baea7a1f624b89 Primary data file for dataset ID 820556

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Related Publications

Kirchman, D. (2001). Measuring bacterial biomass production and growth rates from leucine incorporation in natural aquatic environments. Marine Microbiology, 227–237. doi:10.1016/s0580-9517(01)30047-8
https://doi.org/10.1016/S0580-9517(01)30047-8
Methods

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Parameters

Parameter	Description	Units
deployment	Cruise ID	unitless
station	Station number for cruise	unitless

latitude	Latitude, west is negative	decimal degrees
longitude	Longitude, south 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
substrate	[3H] Leucine substrate added for measurement of bacterial productivity	unitless
timepoint	sampling point (0, 1, 2, ...) post-incubation	unitless
time_elapsed	Incubation time	hours (hrs)
incorporation_rate	Average 3H-Leu (pM) incorporation/hr	pmol L-1 h-1
incorporation_rate_std_dev	Deviation of incorporation rates	pmol L-1 h-1
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	PerkinElmer Tri-Carb 2910TR LSA, PerkinElmer Tri-Carb 3110TR LSA
Generic Instrument Name	Liquid Scintillation Counter
Generic Instrument Description	Liquid scintillation counting is an analytical technique which is defined by the incorporation of the radiolabeled analyte into uniform distribution with a liquid chemical medium capable of converting the kinetic energy of nuclear emissions into light energy. Although the liquid scintillation counter is a sophisticated laboratory counting system used the quantify the activity of particulate emitting (ß and a) radioactive samples, it can also detect the auger electrons emitted from 51Cr and 125I samples. Liquid scintillation counters are instruments assaying alpha and beta radiation by quantitative detection of visible light produced by the passage of rays or particles through a suitable scintillant incorporated into the sample.

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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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