# Measurement of polysaccharide hydrolysis rates from water samples collected from the Arctic fjord Kongsfjorden near Ny-Ålesund, Svalbard, during April 2018

**Website**: https://www.bco-dmo.org/dataset/1000862
**Data Type**: Cruise Results
**Version**: 1
**Version Date**: 2026-06-11

**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 to hydrolyze six high-molecular-weight polysaccharides: arabinogalactan, chondroitin sulfate, fucoidan, laminarin, pullulan, and xylan. This dataset includes measurement of polysaccharide hydrolase activities obtained from seawater incubations. Seawater samples were collected at various stations and depths in Kongsfjorden, an Arctic fjord near Ny-Ålesund, Svalbard, in April 2018.

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## Table of Contents

- Coverage
- Dataset Description
    - Methods & Sampling
    - Data Processing Description
    - BCO-DMO Processing Description
- Related Publications
- Parameters
- Instruments
- Deployments
- Project Information
- Funding

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## Coverage

**Location**: Kongsfjorden near Ny-Ålesund, Svalbard
**Spatial Extent**: **N**:78.982 **E**:12.267 **S**:78.916 **W**:11.75
**Temporal Extent**: 2018-04-19 - 2018-04-24

### Methods & Sampling

Water samples were collected via Niskin bottles, equipped with a CTD.

From the Niskin bottle, water was dispensed into smaller glass containers that were cleaned and pre-rinsed three times with water from the Niskin bottle prior to dispensing. This water was used to measure the activities

of polysaccharide hydrolases. A separate glass Duran bottle was filled with seawater from the Niskin bottle and sterilized in an autoclave for 20-30 minutes to serve as a killed control for microbial activity measurements.

Polysaccharide hydrolase activity was measured by filling three 50-milliliter (mL) falcon tubes with seawater and one 50 mL falcon tube was filled with autoclaved seawater to serve as a killed control, for each substrate. Fluorescence-labeled polysaccharide substrate was added at 3.5 micromolar (µM) monomer-equivalent concentrations, except for fucoidan, which was added at 5 µM concentrations (a higher concentration was necessary for sufficient fluorescence signal). Two 50 mL falcon tubes – one with seawater and one with autoclaved seawater – with no added substrate served as blank controls. Incubations were stored in the dark at as close to in situ temperature as possible.

Subsamples of the incubations were collected at time zero and at a sequence of subsequent time points. At each time point, 2 mL of seawater was collected from the 50 mL falcon tube using a sterile syringe, filtered through a 0.2-micrometer (µm) pore size syringe filter, and stored frozen until processing.

Molecular weight distributions were determined via sequential size-exclusion chromatography using a Bio-Rad Econo-Column packed with ~20 centimeters (cm) of Sephadex G-50 resin followed by ~18 cm of Sephadex G-75 resin, and quantified on Shimadzu 10ADvp HPLC systems equipped with Hitachi fluorescence detectors (set to excitation and emission wavelengths of 490 and 530 nanometer (nm), respectively) and controlled by Shimadzu EZStart software. Hydrolysis rates were calculated based on the change in molecular weight distribution from higher molecular weight initially to lower molecular weight of the labeled substrate over the course of the incubation time, as described in detail in Arnosti (2003).

### Data Processing Description

Hydrolysis rates were calculated from the change in molecular weight distribution of the substrate over time, as described in detail in Arnosti (2003). Scripts to calculate hydrolysis rates are available in the associated Github repository (Hoarfrost, 2017).

### BCO-DMO Processing Description

- Loaded data from "20260303_Sv18 enz rates complied.xlsx" (first sheet, row 1 as header) into the BCO-DMO processing system.
- Treated "NA" as a missing data value (missing data values are empty/blank in the final CSV file).
- Renamed columns to comply with BCO-DMO naming conventions.
- Converted "date" column from "%Y.%m.%d" format to ISO date format "%Y-%m-%d".
- Saved the final file as "1000862_v1_sv2018_rates.csv".

[ table of contents | back to top ]

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## Related Publications

Arnosti, C. (1996). A new method for measuring polysaccharide hydrolysis rates in marine environments. Organic Geochemistry, 25(1-2), 105–115. doi:10.1016/s0146-6380(96)00112-x https://doi.org/10.1016/S0146-6380(96)00112-X
*Methods*

Arnosti, C. (2003). Fluorescent derivatization of polysaccharides and carbohydrate-containing biopolymers for measurement of enzyme activities in complex media. Journal of Chromatography B, 793(1), 181–191. doi:10.1016/s1570-0232(03)00375-1 https://doi.org/10.1016/S1570-0232(03)00375-1
*Methods*

Hoarfrost, A., Gawarkiewicz, G., & Arnosti, C. (2017, May 15). Ahoarfrost/Shelf1234: Shelf1234 Initial Release. Zenodo. https://doi.org/10.5281/zenodo.580059
*Methods*

[ table of contents | back to top ]

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| deployment | Cruise description | unitless |
| Station | Station number KA, T, F, Tb (resampling of St-T), Gf-T (Gravity filtration of Stn-T bulk water) | unitless |
| latitude | Latitude of sampling site, South is negative | Decimal degrees |
| longitude | Longitude of sampling site, West is negative | Decimal degrees |
| date | Date of sample collection | unitless |
| depth_sequence | 1 - near surface, 2 - deep | unitless |
| depth_actual | Actual depth at which water was collected | meters (m) |
| in_situ_Temp | Temperature at depth water was collected | degrees Celsius (°C) |
| in_situ_Sal | Salinity at depth water was collected | ppt |
| in_situ_chl | Chlorophyll fluorescence at depth water was collected | Fluorescence units |
| sample_type | Sample from bulk water (bulk), Gravity Filtration (GF), or Large Volume incubation (LV) | unitless |
| Incubation_temp | Temperature of incubation. | degrees Celsius (°C) |
| unamended_amended | Whether high molecular weight organic mater was added or not; U for unamended, F, A, T refer to type of organic mater added (Fucodian, Arabinogalactan, Thalassiosira extract), the following number corresponds to amended incubation replicate | unitless |
| Sub_sample_day | The amount of incubation time that has elapsed at each timepoint in days | Days |
| substrate | Polysaccharide used for incubation: ara = arabinogalactan, chn = chondroitin sulfate, fuc = fucoidan, lam = laminarin, man = mannan, pul = pullulan, xyl = xylan | unitless |

| rate_1 | The hydrolysis rate for the first replicate | nanomoles per liter per hour (nmol L-1 hr-1) |
|---|---|---|
| rate_2 | The hydrolysis rate for the second replicate | nanomoles per liter per hour (nmol L-1 hr-1) |
| rate_3 | The hydrolysis rate for the third replicate | nanomoles per liter per hour (nmol L-1 hr-1) |
| avg_rate | The average hydrolysis rate for all replicates | nanomoles per liter per hour (nmol L-1 hr-1) |
| sd_rate | The standard deviation of the hydrolysis rates for all replicates | nanomoles per liter per hour (nmol L-1 hr-1) |

[ table of contents | back to top ]

## Instruments

| **Dataset-specific Instrument Name** | Shimadzu 10ADvp HPLC |
|---|---|
| **Generic Instrument Name** | High-Performance Liquid Chromatograph |
| **Dataset-specific Description** | HPLC system with Hitachi fluorescence detectors (L-7485, L-2485, Chromaster - 5440) set to excitation and emission wavelengths of 490 and 530 nm, respectively. |
| **Generic Instrument Description** | A High-performance liquid chromatograph (HPLC) is a type of liquid chromatography used to separate compounds that are dissolved in solution. HPLC instruments consist of a reservoir of the mobile phase, a pump, an injector, a separation column, and a detector. Compounds are separated by high pressure pumping of the sample mixture onto a column packed with microspheres coated with the stationary phase. The different components in the mixture pass through the column at different rates due to differences in their partitioning behavior between the mobile liquid phase and the stationary phase. |

| **Dataset-specific Instrument Name** | Niskin bottle |
|---|---|
| **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. |

[ table of contents | back to top ]

## Deployments

**Svalbard2018**

| **Website** | https://www.bco-dmo.org/deployment/1000969 |
|---|---|
| **Platform** | MS Teisten |
| **Start Date** | 2018-04-19 |
| **End Date** | 2018-04-24 |

[ table of contents | back to top ]

## 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.

[ table of contents | back to top ]

## Funding

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

[ table of contents | back to top ]