# Polysaccharide hydrolysis rates from bulk water incubations from waters taken aboard the R/V Thomas G. Thompson in the Southern Indian Ocean during the research cruise TN362 from November and December, 2018

**Website**: https://www.bco-dmo.org/dataset/996032
**Data Type**: Cruise Results
**Version**: 1
**Version Date**: 2026-04-06

**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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| Brown, Sarah Allison | University of North Carolina at Chapel Hill (UNC-Chapel Hill) | Student |
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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 HMW (high-molecular-weight) DOM tends to be younger and more reactive than lower MW (molecular-weight) 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 the measurement of polysaccharide hydrolase activities from samples taken from bulk water incubations from various stations and depths aboard the R/V Thomas G. Thompson in the Southern Indian Ocean during the research cruise TN362 in November and December, 2018.

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## Coverage

**Location**: Southern Indian Ocean, Various stations from approximately 30 to 42 South and 78 to 110 East. Sampling depths varied from 3 to 5090 meters.
**Spatial Extent**: **N**:-31.482 **E**:110.004 **S**:-41.646 **W**:96.55
**Temporal Extent**: 2018-11-09 - 2018-11-18

### Methods & Sampling

Water was collected via Niskin bottles mounted on a rosette, 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 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. Polysaccharide substrate was added at 3.5 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 µm pore size syringe filter, and stored frozen until processing.

Molecular weight distributions were determined by sequential size-exclusion chromatography using a Bio-Rad Econo-Column packed with ~20 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 nm, respectively) controlled by 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 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 CSV file "20251212_FlaRates_TN362_071922_Corrected_Final_BCO-DMO.csv" with header row 1; missing values coded as empty string, "nd", or "NA"
- Converted field "date" from "%Y.%m.%d" format (UTC) to ISO "%Y-%m-%d" datetime format (UTC)
- Renamed 12 fields replacing dot notation with underscores: rate.x.nM.hr → rate_x_nM_hr, rate.1.nM.hr → rate_1_nM_hr, rate.2.nM.hr → rate_2_nM_hr, rate.3.nM.hr → rate_3_nM_hr, mean.rate.nM.hr → mean_rate_nM_hr, sd.rate.nM.hr → sd_rate_nM_hr, kcrate.x.nM.hr → kcrate_x_nM_hr, kcrate.1.nM.hr → kcrate_1_nM_hr, kcrate.2.nM.hr → kcrate_2_nM_hr, kcrate.3.nM.hr → kcrate_3_nM_hr, mean.kcrate.nM.hr → mean_kcrate_nM_hr, sd.kcrate.nM.hr → sd_kcrate_nM_hr
- Exported file as "996032_v1_fla_rates_tn362.csv"

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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*
,
*Software*

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| deployment | Cruise ID | unitless |
| Station | Station number 3, 6, 13, 18, 31 | 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 | Sequence of depths sampled (1 is surface; higher numbers at greater depths) | unitless |
| depth_actual | Actual depth at which water was collected | m |
| sample_type | Sample from bulk water (bulk) or Large Volume incubation (LV) | unitless |
| Incubation_temp | Temperature of incubation. RT = Room Temperature (~20 C) | degrees Celsius |
| unamended_amended | Whether high molecular weight organic matter was added or not; U for unamended | 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, pul = pullulan, xyl = xylan | unitless |
| rate_x_nM_hr | The hydrolysis rate for the kill-control | nmol L-1 hr-1 |
| rate_1_nM_hr | The hydrolysis rate for the first replicate | nmol L-1 hr-1 |

| | | |
|---|---|---|
| rate_2_nM_hr | The hydrolysis rate for the second replicate | nmol L-1 hr-1 |
| rate_3_nM_hr | The hydrolysis rate for the third replicate | nmol L-1 hr-1 |
| mean_rate_nM_hr | The average hydrolysis rate for all replicates | nmol L-1 hr-1 |
| sd_rate_nM_hr | The standard deviation of the hydrolysis rates for all replicates | nmol L-1 hr-1 |
| kcrate_x_nM_hr | The kill-corrected hydrolysis rate for the kill-control | nmol L-1 hr-1 |
| kcrate_1_nM_hr | The kill-corrected hydrolysis rate for the first replicate | nmol L-1 hr-1 |
| kcrate_2_nM_hr | The kill-corrected hydrolysis rate for the second replicate | nmol L-1 hr-1 |
| kcrate_3_nM_hr | The kill-corrected hydrolysis rate for the third replicate | nmol L-1 hr-1 |
| mean_kcrate_nM_hr | The average kill-corrected hydrolysis rate for all replicates | nmol L-1 hr-1 |
| sd_kcrate_nM_hr | The standard deviation of the kill-corrected hydrolysis rates for all replicates | nmol L-1 hr-1 |

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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** | HPLC system with Hitachi fluorescence detectors (L-7485, L-2485, Chromaster - 5440) |
| **Generic Instrument Name** | High-Performance Liquid Chromatograph |
| **Dataset-specific Description** | Methods Description: Molecular weight distributions were determined by sequential size-exclusion chromatography using a Bio-Rad Econo-Column packed with ~20 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 nm, respectively) controlled by EZStart software. Instruments 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. |

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|---|---|
| **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

**TN362**

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/996056 |
| **Platform** | R/V Thomas G. Thompson |
| **Start Date** | 2018-11-07 |
| **End Date** | 2018-12-19 |
| **Description** | Project: Indian Ocean coring |

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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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