# Microbial enzyme activities: glucosidase and peptidase activities of gravity filtered seawater samples from the RV\Sonne cruise SO248 in the South and North Pacific, along 180 W, May, 2016

**Website**: https://www.bco-dmo.org/dataset/743320
**Data Type**: Cruise Results, experimental
**Version**: 1
**Version Date**: 2018-07-31

**Project**
» Latitudinal and depth-related contrasts in enzymatic capabilities of pelagic microbial communities: Predictable patterns in the ocean? (Patterns of activities)



| Contributors | Affiliation | Role |
|---|---|---|
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**Abstract**
This dataset includes MCAMUF (glucosidase and peptidase) hydrolysis rates to measure microbial enzyme activities on particles collected from gravity filtered seawater. Samples were collected on RV/Sonne cruise SO248 in May 2016. Links to archived CTD data are also provided.

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## Coverage

**Spatial Extent**: **N**:58.9 **E**:-179 **S**:-30.0008 **W**:-180
**Temporal Extent**: 2016-05-02 - 2016-05-30

## Dataset Description

This dataset includes MCAMUF (glucosidase and peptidase) hydrolysis rates to measure microbial enzyme activities on particles collected from gravity filtered seawater. Samples were collected on RV/Sonne cruise SO248 in May 2016. Links to archived CTD data are also provided.

### Methods & Sampling

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

Experiments on (operationally defined) particles were carried out by gravity-filtering water through 3 µm pore size filters.  1/12th sections of the 3 µm pore-size filters were submerged in 4 mL artificial seawater in

incubation cuvettes.  Particle-associated peptidase and glucosidase activity assays were set up in 4 mL cuvettes. For live duplicate incubations, two particle-containing filter pieces (each 1/12th of entire filter) were separately submerged in 4 mL of cooled, autoclaved ambient seawater. A single killed control was prepared by submerging a sterile filter piece (1/12th of unused filter) in 4 mL of cooled, autoclaved ambient seawater. Substrates were added to a final concentration of 100 µM. At various timepoints—upon addition of substrate (to), 24 h (t1), 48 (t2), and 72 h (t3)—live duplicates and killed control singleton were subsampled by taking 3 x 200 uL (for technical triplicates) per incubation, and placed in a 96 well plate for fluorescence measurement using the Tecan Plate Reader. Fluorescence values were converted to hydrolysis rates using calibration curves with the MCA and MUF fluorophores, and were  normalized by the volume of filtrate that passed through the 3 µm filter. Two substrates, -glucose and -glucose linked to a 4-methylumbelliferyl (MUF) fluorophore, were used to measure glucosidase activities. Five substrates linked to a 7-amido-4-methyl coumarin (MCA) fluorophore, one amino acid – leucine – and four oligopeptides – the chymotrypsin substrates alanine-alanine-phenylalanine (AAF) and alanine-alanine-proline-phenylalanine (AAPF), and the trypsin substrates glutamine-alanine-arginine (QAR) and phenylalanine-serine-arginine (FSR) – were used to measure exo- and endo-acting peptidase activities, respectively. Hydrolysis rates of the substrates were measured as an increase in fluorescence as the fluorophore was hydrolyzed from the substrate over time [as in Hoppe, 1993; Obayashi and Suzuki, 2005].

a-glu = substrate to measure alpha glucosidase: 4-methylumbelliferyl-a-D-glucopyranoside
b-glu = substrate to measure beta glucosidase: 4-methylumbelliferyl-ß-D-glucopyranoside
L = substrate to measure leucine aminopeptidase (L-leucine-7-amido-4 MCA)
AAF = substrate to measure chymotrypsin activity: ala-ala-phe-MCA
AAPF = substrate to measure chymotrypsin activity: N-succinyl-ala-ala-pro-phe-MCA
QAR = substrate to measure trypsin activity: Boc-gln-ala-arg-MCA
FSR = substrate to measure trypsin activity: N-t-boc-phe-ser-arg-MCA

#### Data Processing Description

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- reduced decimal precision of rate columns from 9 to 6 places; time_elapsed from 7 to 0 places

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## Data Files

| File |
|---|
| **SO248_GF_MCAMUF_joined.csv** (Comma Separated Values (.csv), 50.58 KB) MD5:e66f04f3304944bb113c28ff6e5a0dde<br>Primary data file for dataset ID 743320 |

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## Related Publications

Hoppe, HG. (1993). Use of fluorogenic model substrates for extracellular enzyme activity (EEA) measurement of bacteria, p. 423-431. In P. F. Kemp, B. F. Sherr, E. B. Sherr, and J. J. Cole (ed.), Handbook of methods in aquatic microbial ecology. Lewis Publishers, Boca Raton, FL 978-0873715645
*Methods*

Obayashi, Y., & Suzuki, S. (2005). Proteolytic enzymes in coastal surface seawater: Significant activity of endopeptidases and exopeptidases. Limnology and Oceanography, 50(2), 722–726. doi:10.4319/lo.2005.50.2.0722
*Methods*

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| station_no | refers to station number for cruise | unitless |
| depth_no | sequence of depths sampled (1 is surface; higher numbers at greater depths) | unitless |
| depth_m | actual depth at which water collected | meters |
| cast_no | cast number (refers to cast of CTD/Niskin bottles on cruise) | unitless |
| ISO_DateTime_UTC | date and time in ISO format (yyyy-mm-ddTHH:MM:SS | unitless |
| Latitude | latitude; north is positive | decimal degreed |
| Longitude | longitude; east is postivie | decimal degreed |
| substrate | Substrates for measurement of enzymatic activities:<br>a-glu = substrate to measure alpha glucosidase: 4-methylumbelliferyl-a-D-glucopyranoside<br>b-glu = substrate to measure beta glucosidase: 4-methylumbelliferyl-ß-D-glucopyranoside<br>L = substrate to measure leucine aminopeptidase (L-leucine-7-amido-4 MCA)<br>AAF = substrate to measure chymotrypsin activity: ala-ala-phe-MCA<br>AAPF = substrate to measure chymotrypsin activity: N-succinyl-ala-ala-pro-phe-MCA<br>QAR = substrate to measure trypsin activity: Boc-gln-ala-arg-MCA<br>FSR = substrate to measure trypsin activity: N-t-boc-phe-ser-arg-MCA | unitless |
| timepoint | sampling point post-incubation | unitless |
| time_elapsed_hr | incubation time | hours |
| rep1_rate | replicate 1 hydrolysis rate | nanomoles/liter/hour (nmol L-1 h-1) |
| rep2_rate | replicate 2 hydrolysis rate | nanomoles/liter/hour (nmol L-1 h-1) |
| average | average of hydrolysis rates | nanomoles/liter/hour (nmol L-1 h-1) |

| | | |
|---|---|---|
| std_dev | std deviation of hydrolysis rates | nanomoles/liter/hour (nmol L-1 h-1) |
| filter_um | filter pore size used for gravity filtration | micrometers |

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | CTD - profiler |
| **Generic Instrument Description** | The Conductivity, Temperature, Depth (CTD) unit is an integrated instrument package designed to measure the conductivity, temperature, and pressure (depth) of the water column. The instrument is lowered via cable through the water column. It permits scientists to observe the physical properties in real-time via a conducting cable, which is typically connected to a CTD to a deck unit and computer on a ship. The CTD is often configured with additional optional sensors including fluorometers, transmissometers and/or radiometers. It is often combined with a Rosette of water sampling bottles (e.g. Niskin, GO-FLO) for collecting discrete water samples during the cast. This term applies to profiling CTDs. For fixed CTDs, see https://www.bco-dmo.org/instrument/869934. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | Fluorometer |
| **Generic Instrument Description** | A fluorometer or fluorimeter is a device used to measure parameters of fluorescence: its intensity and wavelength distribution of emission spectrum after excitation by a certain spectrum of light. The instrument is designed to measure the amount of stimulated electromagnetic radiation produced by pulses of electromagnetic radiation emitted into a water sample or in situ. |

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

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## Deployments

**SO248**

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/741296 |
| **Platform** | R/V Sonne |
| **Start Date** | 2016-05-01 |
| **End Date** | 2016-06-03 |
| **Description** | Project: Latitudinal and depth-related contrasts in enzymatic capabilities of pelagic microbial communities: Predictable patterns in the ocean? For related research from this cruise, see https://www.pangaea.de/?q=SO248 |

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## Project Information

**Latitudinal and depth-related contrasts in enzymatic capabilities of pelagic microbial communities: Predictable patterns in the ocean? (Patterns of activities)**

**Coverage**: Atlantic Ocean, Arctic Ocean, Pacific Ocean, Greenland

*NSF Award Abstract:*
Heterotrophic microbial communities are key players in the marine carbon cycle, transforming and respiring organic carbon, regenerating nutrients, and acting as the final filter in sediments through which organic matter passes before long-term burial. Microbially-driven carbon cycling in the ocean profoundly affects the global carbon cycle, but key factors determining rates and locations of organic matter remineralization are unclear. In this study, researchers from the University of North Carolina at Chapel Hill will investigate the ability of pelagic microbial communities to initiate the remineralization of polysaccharides and proteins, which together constitute a major pool of organic matter in the ocean. Results from this study will be predictive on a large scale regarding the nature of the microbial response to organic matter input, and will provide a mechanistic framework for interpreting organic matter reactivity in the ocean.

Broader Impacts: This study will provide scientific training for undergraduate and graduate students from underrepresented groups. The project will also involve German colleagues, thus strengthening international scientific collaboration.

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## Funding

| Funding Source | Award |
|---|---|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1332881 |

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