Microbial enzyme activities: glucosidase and peptidase activities of bulk 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/743224
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 in bulk (not filter-fractionated) 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 in bulk (not filter-fractionated) 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.

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]. Incubations with the seven low molecular weight substrates were set up in a 96-well plate. For each substrate, triplicate wells were filled with a total volume of 200 L seawater for experimental incubations; triplicate wells were filled with 200 L autoclaved seawater for killed control incubations. Substrate was added at saturating concentrations. A saturation curve was determined with surface water from each station to determine saturating concentrations of substrate. The saturating concentration was identified as the lowest tested concentration of substrate at which additional substrate did not yield higher rates of hydrolysis. Fluorescence was measured over 24-48 hours incubation time with a plate reader (TECAN spectrafluor plus; 360 nm excitation, 460 emission), with timepoints taken every 4-6 hours. Hydrolysis rates were calculated from the rate of increase of fluorescence in the incubation over time relative to a set of standards of known concentration of fluorophore. Scripts to calculate hydrolysis rates and produce the figures shown here are available in the associated Github repository [Hoarfrost, 2017].

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_bulk_MCAMUF_joined.csv (Comma Separated Values (.csv), 190.91 KB) MD5:c167b9519194948fd6b8028ff343b72a Primary data file for dataset ID 743224

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Related Publications

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

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. ara:arabinogalactan: 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	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)
rep3_rate	replicate 3 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)

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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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