Dissolved organic carbon and amino acid data from the NBP1207 cruise in Chile during 2012

Website: https://www.bco-dmo.org/dataset/701885
Data Type: Cruise Results
Version: 1
Version Date: 2017-06-02

Project
» The Microbial Carbon Pump and Bacterial Carbon Sequestration in the Ocean (MCP)

Program
» US Antarctic Marine Living Resources Program (AMLR)

Contributors	Affiliation	Role
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Abstract
Dissolved organic carbon and amino acid data from the NBP1207 cruise in Chile during 2012.

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Coverage

Spatial Extent: **N**:-53.9594 **E**:-57.5446 **S**:-60.0544 **W**:-62.5061
Temporal Extent: 2012-08-06 - 2012-08-14

Dataset Description

Dissolved organic carbon and amino acid data from NBP1207.

Methods & Sampling

Methodology from **Shen, Y., et al. (2017), Bioavailable dissolved organic matter and biological hot spots during austral winter in Antarctic waters, J. Geophys. Res. Oceans, 121, doi:10.1002/2016JC012301.**

Study Area and Sample Collection

Sampling was conducted as part of the Antarctic Marine Living Resources (AMLR) Program aboard the RVIB Nathaniel B. Palmer off the Antarctic Peninsula and South Shetland Islands (SSI) during August 2012 (Figure 1). The sampling areas are characterized by the confluence of different water masses originating from the Antarctic Circumpolar Current, Bellingshausen Sea, and Weddell Sea. A total of 110 seawater samples were

collected from discrete depths (5, 10, 15, 50, 75, 100, 200, 750 m) at 25 stations within the historic AMLR research area, extending from the southern Drake Passage to the Bransfield Strait (Figure 1). A rosette sampler system with 24, 12 L bottles and a Seabird Conductivity-Temperature-Depth (CTD) instrument was used for water collections. Water samples for chlorophyll-a (chl-a) were filtered (GF/F; 0.7 mm pore size; Whatman) immediately following collection. Samples for POC measurements were collected mostly at 5 and 200 m, filtered (GF/F; Whatman; precombusted at 4508C for 5 h), and stored frozen until analysis. Water samples for analyses of DOC and amino acids were stored frozen (2808C) in 60 mL high density polyethylene screw-cap bottles immediately after collection. Hydrographic data were obtained from the CTD sensors and were used to determine the depth of upper mixed layer and to identify water masses (Table 1).

Chemical Analyses

The filters for chl-a determinations were extracted in 7 mL of methanol for 24 h, centrifuged, and measured for fluorescence using an acidification module in a Turner Trilogy fluorometer. Readings were calibrated with a 5-point calibration curve using a chl-a standard obtained from Sigma, the concentration of which was determined using a Lambda-18 spectrophotometer. Samples (GF/F filters) for POC analysis were treated with 10% v/v hydrochloric acid (HCl), dried at 608C, and analyzed using an Exeter Analytical CEC 440HA elemental analyzer.

Water samples for DOC and amino acid measurements were filtered through 0.2 mm pore size membranes (SuporVR -200, Life Sciences). The Supor membranes were cleaned with methanol and then rinsed thoroughly with Milli-Q UV-Plus water before use. The DOC samples were acidified to pH 2–3 with 2 mol L21 HCl. Concentrations of DOC were determined by high-temperature combustion using a Shimadzu total organic carbon TOC-V analyzer equipped with an autosampler. Milli-Q UV-Plus water and seawater reference standards were injected every sixth sample [Benner and Strom, 1993]. Blanks (Milli-Q water) were negligible and the measured concentrations of reference standards were within the reported range (41–44 mmol L21). The coefficient of variation among four injections of a given DOC sample was typically 61.1%.

The D-enantiomer and L-enantiomer of amino acids were analyzed using an Agilent 1260 ultrahigh-performance liquid chromatography (UPLC) system equipped with a fluorescence detector (excitation: 330 nm; emission: 450 nm) [Shen et al., 2015]. Amino acids were determined in all samples that were filtered through Supor membranes (0.2 mm pore size) and in a subset of unfiltered samples as total dissolved amino acids (TDAA) and total particulate amino acids (TPAA), respectively. Hydrolysis and derivatization followed the procedures described by Kaiser and Benner [2005]. Briefly, water samples (100 mL) were dried and hydrolyzed using a vapor-phase technique with 6 mol L21 HCl at 1508C for 32.5 min. Amino acid enantiomers were derivatized with o-phthaldialdehyde and N-isobutyryl-L-cysteine and were separated on a Poroshell 120 EC-C18 (4.6 3 100 mm, 2.7 mm particles) column. A linear binary gradient was used starting with 100% potassium di-hydrogen phosphate (KH2PO4; 48 mmol L21, pH56.25) to 61% KH2PO4 and 39% methanol:acetonitrile (13:1, v/v) at 13.3 min, 46% KH2PO4 at 19.2 min, 40% KH2PO4 at 21.3 min, and 20% KH2PO4 at 22 min. Eighteen amino acids were included in the analysis: asparagine1aspartic acid (Asx), glutamine1glutamic acid (Glx), serine (Ser), histidine (His), glycine (Gly), threonine (Thr), b-alanine (b-Ala), arginine (Arg), alanine (Ala), c-aminobutyric acid (c-Aba), tyrosine (Tyr), valine (Val), phenylalanine (Phe), isoleucine (Ile), leucine (Leu), and lysine (Lys). Acid-catalyzed racemization was corrected according to Kaiser and Benner [2005]. This method has a limit of quantification of 0.5 nmol L21 for individual amino acids. D-enantiomers of Asx, Glx, Ser, and Ala are reported in this study.

Concentrations of TDAA and TPAA were determined as the total concentrations of the eighteen dissolved and particulate amino acids, respectively. DOC-normalized yields of TDAA were calculated as the percentage contributions of amino acid carbon to the total DOC, using equation (1) and being reported in units of %DOC:

TDAA (%DOC) = ([TDAA-C] / [DOC]) x 100

where [DOC] and [TDAA-C] are the concentrations of bulk DOC and carbon measured in the total dissolved amino acids, respectively. This calculation excluded the two nonprotein amino acids (b-Ala and c-Aba) that are thought to be byproducts of decomposition [Cowie and Hedges, 1994].

Data Processing Description

Processing description from **Shen, Y., et al. (2017), Bioavailable dissolved organic matter and biological hot spots during austral winter in Antarctic waters, J. Geophys. Res. Oceans, 121, [doi:10.1002/2016JC012301](doi:10.1002/2016JC012301).**

The significance of least squares linear regression analyses between variables was determined using the enter approach in SPSS 20.0 (IBM Statistical Package for the Social Sciences Inc.). Normality of residuals was tested using a Kolmogorov-Smirnov test (two-tailed, a50.05). Statistical differences between variables were analyzed using the nonparametric Mann-Whitney U test (two-tailed, a50.05), which makes no assumptions of equal group size and normality of data distribution.

BCO-DMO Data Processing Description:

- reformatted column names to comply with BCO-DMO standards
- filled all empty cells with "nd"
- added ISO_DateTime_UTC column to meet community standards

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Data Files

File
DOC_aminoAcids.csv (Comma Separated Values (.csv), 21.82 KB) MD5:15793b87a27ff3687c14d64e9d6a309b Primary data file for dataset ID 701885

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Parameters

Parameter	Description	Units
sample_ID	Sample ID	unitless
date	Sampling date; YYYY/MM/DD	unitless
time	Sampling time; HH:MM:SS	unitless
lon	Longitude	decimal degrees
lat	Latitude	decimal degrees
potemp_C	CTD Potential Temp sensor 90	celsius
salinity	CTD Salinity	PSU
depth	Sampling depth	meters
DOC_uM	Dissolved organic carbon	umol/L
TDN_uM	Total dissolved nitrogen	umol/L
TDAA_nM_filtered	Total dissolved amino acids; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
TDAA_pcentDOC_filtered	Percentage of DOC that is measured as TDAA; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	percent
L_Asx_filtered	Dissolved L-asparagine + L-aspartic acid; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
D_Asx_filtered	Dissolved D-asparagine + D-aspartic acid; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Glx_filtered	Dissolved L-glutamine + L-glutamic acid; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
D_Glx_filtered	Dissolved D-glutamine + D-glutamic acid; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L

L_Ser_filtered	Dissolved L-serine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
D_Ser_filtered	Dissolved D-serine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_His_filtered	Dissolved L-histidine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Thr_filtered	Dissolved L-threonine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
Gly_filtered	Dissolved glycine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Arg_filtered	Dissolved L-arginine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
beta_Ala_filtered	Dissolved beta-alanine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Ala_filtered	Dissolved L-alanine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
gamma_Aba_filtered	Dissolved gamma-aminobutyric acid; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
D_Ala_filtered	Dissolved D-alanine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Tyr_filtered	Dissolved L-tyrosine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Val_filtered	Dissolved L-valine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Phe_filtered	Dissolved L-phenylalanine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Ileu_filtered	Dissloved L-isoleucine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Leu_filtered	Dissolved L-leucine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
L_Lys_filtered	Dissolved L-lysine; Samples were filtered through Supor membranes (0.2-um pore size) before amino acid analysis	nmol/L
TAA_nM_unfiltered	Total amino acids (i.e. Total dissolved + total particulate amino acids); Samples were NOT filtered before amino acid analysis	nmol/L
TAA_unfiltered	Percentage of total organic carbon that is measured as TAA; Samples were NOT filtered before amino acid analysis	nmol/L
L_Asx_unfiltered	Total L-asparagine + L-aspartic acid; Samples were NOT filtered before amino acid analysis	nmol/L
D_Asx_unfiltered	Total D-asparagine + D-aspartic acid; Samples were NOT filtered before amino acid analysis	nmol/L
L_Glx_unfiltered	Total L-glutamine + L-glutamic acid; Samples were NOT filtered before amino acid analysis	nmol/L
D_Glx_unfiltered	Total D-glutamine + D-glutamic acid; Samples were NOT filtered before amino acid analysis	nmol/L
L_Ser_unfiltered	Total L-serine; Samples were NOT filtered before amino acid analysis	nmol/L
D_Ser_unfiltered	Total D-serine; Samples were NOT filtered before amino acid analysis	nmol/L
L_His_unfiltered	Total L-histidine; Samples were NOT filtered before amino acid analysis	nmol/L
L_Thr_unfiltered	Total L-threonine; Samples were NOT filtered before amino acid analysis	nmol/L

Gly_unfiltered	Total glycine; Samples were NOT filtered before amino acid analysis	nmol/L
L_Arg_unfiltered	Total L-arginine; Samples were NOT filtered before amino acid analysis	nmol/L
beta_Ala_unfiltered	Total beta-alanine; Samples were NOT filtered before amino acid analysis	nmol/L
L_Ala_unfiltered	Total L-alanine; Samples were NOT filtered before amino acid analysis	nmol/L
gamma_Aba_unfiltered	Total gamma-aminobutyric acid; Samples were NOT filtered before amino acid analysis	nmol/L
D_Ala_unfiltered	Total D-alanine; Samples were NOT filtered before amino acid analysis	nmol/L
L_Tyr_unfiltered	Total L-tyrosine; Samples were NOT filtered before amino acid analysis	nmol/L
L_Val_unfiltered	Total L-valine; Samples were NOT filtered before amino acid analysis	nmol/L
L_Phe_unfiltered	Total L-phenylalanine; Samples were NOT filtered before amino acid analysis	nmol/L
L_Ileu_unfiltered	Dissloved L-isoleucine; Samples were NOT filtered before amino acid analysis	nmol/L
L_Leu_unfiltered	Total L-leucine; Samples were NOT filtered before amino acid analysis	nmol/L
L_Lys_unfiltered	Total L-lysine; Samples were NOT filtered before amino acid analysis	nmol/L
ISO_DateTime_UTC	Date/Time (UTC) ISO formatted	unitless

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Instruments

Dataset-specific Instrument Name	Seabird Conductivity-Temperature-Depth instrument
Generic Instrument Name	CTD Sea-Bird
Dataset-specific Description	Used for water collections
Generic Instrument Description	Conductivity, Temperature, Depth (CTD) sensor package from SeaBird Electronics, no specific unit identified. This instrument designation is used when specific make and model are not known. See also other SeaBird instruments listed under CTD. More information from Sea-Bird Electronics.

Dataset-specific Instrument Name	Turner Trilogy Fluorometer
Generic Instrument Name	Fluorometer
Dataset-specific Description	Used to measure fluorescence
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	Shimadzu total organic carbon TOC-V analyzer
Generic Instrument Name	Total Organic Carbon Analyzer
Dataset-specific Description	Used to measure DOC
Generic Instrument Description	A unit that accurately determines the carbon concentrations of organic compounds typically by detecting and measuring its combustion product (CO2). See description document at: http://bcodata.whoi.edu/LaurentianGreatLakes_Chemistry/bs116.pdf

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Deployments

NBP1207

Website	https://www.bco-dmo.org/deployment/701892
Platform	RVIB Nathaniel B. Palmer
Start Date	2012-08-01
End Date	2012-08-17
Description	U.S. Antarctic Marine Living Resources (AMLR) Program https://ezid.cdlib.org/id/doi:10.7284/902908

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Project Information

The Microbial Carbon Pump and Bacterial Carbon Sequestration in the Ocean (MCP)

Coverage: South Shetland Islands off the Antarctic Peninsula

NSF Award Abstract:

The Biological Pump has long been recognized as an important sink for atmospheric CO2 concentrations through the sequestration of carbon in ocean sediments. The contributions of bacteria to the sequestration of carbon in the ocean reservoir of refractory dissolved organic carbon (RDOC) have only recently been recognized. This process, conceptualized as the Microbial Carbon Pump (MCP), also appears to play a significant role in carbon sequestration and the regulation of atmospheric CO2.

In this project, researchers at the University of South Carolina at Columbia will build upon the framework of the MCP to address the following hypotheses: 1) The production and composition of bacterial DOC vary with biological (e.g. community structure) and physicochemical (e.g. nutrients) parameters in the ocean, 2) Bacteria sequester carbon in semi-labile DOC (SDOC) that persists for years to decades in mesopelagic waters, 3) Microbial communities in mesopelagic and bathypelagic waters have the metabolic potential to produce and degrade bacterial DOC. Naturally-occurring bacterial DOC in these waters is very resistant to microbial degradation, 4) Heterotrophic bacteria are the predominant source of bacterial SDOC and RDOC. These hypotheses will be addressed using a combination of field (NW Pacific Ocean and Sargasso Sea) and experimental approaches to investigate spatial variability in the production and decomposition of bacterial DOC and to relate these processes to community structure and environmental conditions. This study will provide

estimates of the reservoirs of bacterial SDOC and RDOC in the ocean and critical insights about the ocean carbon cycle and the regulation of atmospheric CO2 concentrations. It will also lay a foundation for addressing how the MCP and bacterial carbon sequestration will respond to climate change.

Broader Impacts: This project will strengthen collaborations between the PI's laboratory and Dr. Hiroshi Ogawa's laboratory at the Atmosphere and Ocean Research Institute in Japan. This collaboration includes participation on a Japanese-sponsored expedition to the North Pacific Ocean aboard the R/V Hakuro maru. Additionally, it will support a postdoctoral associate and a doctoral student who will participate on research expeditions to the NW Pacific Ocean and Sargasso Sea. Their research will focus on the MCP, and they will present their findings at national conferences in years 2 and 3.

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Program Information

US Antarctic Marine Living Resources Program (AMLR)

Since 1986, the NOAA Antarctic Ecosystems Research Division (AERD) has managed the U.S. AMLR Program's field studies in Antarctic waters to investigate the effects of commercial fisheries on the marine ecosystem, including effects on local seal and seabird populations. Studies conducted by U.S. AMLR/AERD researchers include: Annual research vessel survey to map prey distribution and abundance, and to measure environmental variables in a study area off the Antarctic Peninsula; Research at land stations to determine effects of fishing on pinniped and seabird populations during their reproductive cycles; and Accounting for the status and role of mesopelagic species such as myctophids, Pleurogramma, etc.

Additional research and activities conducted by the AERD in support of the AMLR Program's objectives include: Monitoring commercial fishing vessels to determine catch statistics, by-catch amount and composition, and occurrence of marine mammal and seabird interactions; Conducting research on the improvement of field methodologies, effects of instrumentation, degree of data biases, and occurrence of sampling errors; Collaborate with international partners, including participation in their field programs; and Providing leadership and advice to CCAMLR's Commission and Scientific Committee and its Working Groups.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1233373

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