Copper data with 10 uM SA lingand from Hood Canal, Puget Sound, Washington, USA from R/V Clifford A. Barnes CB960, CB974, CB980, CB985, 2011-2012 (Nitrification and Marine Planktonic Biodiversity project)

Website: https://www.bco-dmo.org/dataset/540987
Version: 2014-11-17

Project
» Significance of nitrification in shaping planktonic biodiversity in the ocean (Nitrification and Marine Planktonic Biodiversity)

Program
» Dimensions of Biodiversity (Dimensions of Biodiversity)

Contributors	Affiliation	Role
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Abstract
Copper data with 10 uM SA lingand from Hood Canal, Puget Sound, Washington, USA from R/V Clifford A. Barnes CB960, CB974, CB980, CB985, 2011-2012 (Nitrification and Marine Planktonic Biodiversity project)

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Dataset Description

Water samples were collected at various depths from the Hood Canal and the Cu2 + concentrations, organic ligand (L) concentrations and their corresponding conditional stability constants (K) were characterized using a competitive ligand exchange adsorptive cathodic stripping voltammetry (CLE-ACSV) adapted from Jacquot et al. (2013) and Moffett and Dupont (2007) with salicylaldoxime (SA) as the competing ligand.

Methods & Sampling

All samples for total dissolved copper on this cruise were well above our detection limit of 100pM determined from the standard deviation of procedural blanks using our ICP-MS methods.

Cu speciation was determined using cathodic stripping voltammetry on samples titrated with added copper.

Data Processing Description

Data points below the detection limit of the cathodic stripping voltammetry technique (~ 0.15 nM) were not

used in the titration. However, all titrations had a significant number of points to fit a non-linear regression curve. In instances where the fit did not converged, or converged at a non-realistic value (e.g. negative numbers) the data were flagged.

The standard error for [Cu2+] is asymmetric because it is not determined the same way - hence the different values.

The Cu2+ error propagation was derived from the standard deviations of K and [L] when used in equation 11 from Moffett and Dupont 2007 to calculate [Cu2+].

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Related Publications

Jacquot, J. E., Horak, R. E. A., Amin, S. A., Devol, A. H., Ingalls, A. E., Armbrust, E. V., … Moffett, J. W. (2014). Assessment of the potential for copper limitation of ammonia oxidation by Archaea in a dynamic estuary. Marine Chemistry, 162, 37–49. doi:10.1016/j.marchem.2014.02.002
Methods

Moffett, J. W., & Dupont, C. (2007). Cu complexation by organic ligands in the sub-arctic NW Pacific and Bering Sea. Deep Sea Research Part I: Oceanographic Research Papers, 54(4), 586–595. doi:10.1016/j.dsr.2006.12.013
Methods

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Parameters

Parameters for this dataset have not yet been identified

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Instruments

Dataset-specific Instrument Name	BASI CGME
Generic Instrument Name	BASi Controlled Growth Mercury Electrode
Dataset-specific Description	BioAnalytical Systems (BASi) Controlled Growth Mercury Electrode set to the Static Mercury Drop setting (drop size: 14) and interfaced with a BASi Epsilon ε2 voltammetric analyzer.
Generic Instrument Description	Bioanalytical Systems (BASi) Mercury drop electrodes are generated by the BASi Controlled Growth Mercury Electrode (CGME) in three modes: DME (Dropping Mercury Electrode) - mercury is allowed to flow freely from the reservoir down the capillary and so the growth of the mercury drop and its lifetime is controlled by gravity. (The optional 100 um capillary is recommended for this mode.) SMDE (Static Mercury Drop Electrode) - the drop size is determined by the length of time for which the fast-response capillary valve is opened, and the drop is dislodged by a drop knocker. The dispense/knock timing is microprocessor-controlled and is typically coordinated with the potential pulse or square-wave waveform. This mode can also used to generate the Hanging Mercury Drop Electrode required for stripping experiments. CGME (Controlled Growth Mercury Electrode) - the mercury drop is grown by a series of pulses that open the capillary valve. The number of pulses, their duration, and their frequency can be varied by PC control, providing great flexibility in both the drop size and its rate of growth. This CGME mode can be used for both polarographic and stripping experiments. http://www.basinc.com/products/ec/cgme.php

Dataset-specific Instrument Name	CTD SBE 911plus
Generic Instrument Name	CTD Sea-Bird SBE 911plus
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	GO-FLO
Generic Instrument Name	GO-FLO Bottle
Dataset-specific Description	10 L Teflon-coated Go-Flo bottles (General Oceanics) attached to Kevlar wire
Generic Instrument Description	GO-FLO bottle cast used to collect water samples for pigment, nutrient, plankton, etc. The GO-FLO sampling bottle is specially designed to avoid sample contamination at the surface, internal spring contamination, loss of sample on deck (internal seals), and exchange of water from different depths.

Dataset-specific Instrument Name	ICP Mass Spec
Generic Instrument Name	Inductively Coupled Plasma Mass Spectrometer
Dataset-specific Description	Finnegan Element 2 (Thermo Scientific)
Generic Instrument Description	An ICP Mass Spec is an instrument that passes nebulized samples into an inductively-coupled gas plasma (8-10000 K) where they are atomized and ionized. Ions of specific mass-to-charge ratios are quantified in a quadrupole mass spectrometer.

Dataset-specific Instrument Name	Voltammetry Analyzers
Generic Instrument Name	Voltammetry Analyzers
Dataset-specific Description	BASi Epsilon ε2 voltammetric analyzer
Generic Instrument Description	Instruments that obtain information about an analyte by applying a potential and measuring the current produced in the analyte.

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Deployments

CB960

Website	https://www.bco-dmo.org/deployment/540518
Platform	R/V Clifford A. Barnes
Start Date	2011-07-18
End Date	2011-07-22

CB974

Website	https://www.bco-dmo.org/deployment/540519
Platform	R/V Clifford A. Barnes
Start Date	2012-05-07
End Date	2012-05-13

CB980

Website	https://www.bco-dmo.org/deployment/540522
Platform	R/V Clifford A. Barnes
Start Date	2012-07-16
End Date	2012-07-22

CB985

Website	https://www.bco-dmo.org/deployment/540524
Platform	R/V Clifford A. Barnes
Start Date	2012-08-25
End Date	2012-08-30

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Project Information

Significance of nitrification in shaping planktonic biodiversity in the ocean (Nitrification and Marine Planktonic Biodiversity)

Microorganisms sustain the biogeochemical cycling of nitrogen, one of the most important nutrient cycles on earth. A key step in this cycle, the oxidation of ammonia to nitrite by autotrophic microorganisms, was for a century thought mediated by a few restricted bacterial genera. Significant ammonia oxidation, perhaps most, is now attributed to a previously enigmatic group of Archaea - the ammonia-oxidizing archaea (AOA) - of high abundance in both marine and terrestrial environments. The investigators prior physiological and environmental analyses, the foundation for this proposal, have shown that AOA are active within the marine photic zone and that their competitive fitness in the marine environment is at least in part attributable to an extremely high affinity for ammonia, growing at near maximum growth rates at concentrations of ammonia that would not sustain known bacterial ammonia oxidizers, and an unusual copper-based respiratory system that may render them more competitive in iron limited environments. The compelling inference from these prior analyses is that AOA alter and possibly control the forms of fixed nitrogen available to other microbial assemblages within the photic zone by converting ammonia, a nearly universally available form of nitrogen, into nitrite, a form only available to nitrite oxidizing bacteria and some phytoplankton. If correct, this has a significant impact on biodiversity.

The PIs will use the most recent technological advances in protein and high throughput sequencing to evaluate the significance of nitrification in shaping biodiversity (genomic and metagenomics), activity (transcriptome, proteome and stable isotope probing), and in controlling availability of an important trace element (copper). In turn, by resolving the environmental and biotic variables that influence the diversity, distribution and activity of AOA, they will advance general understanding of their taxonomy. More directly, functional knowledge of the contribution of AOA to regenerated nitrate will improve estimates of new ocean production ("biological pump") based on nitrate assimilation, which in the past has mostly neglected the importance of nitrification as a major source of nitrate. Together these studies will transform understanding of the marine nitrogen cycle, estimates of new production, and will ultimately provide a better understanding of the impact of human activity on this critical nutrient cycle.

The nitrogen cycle has been profoundly affected by anthropogenic inputs of reactive nitrogen into terrestrial, marine, and atmospheric systems having, or predicted to have, major impacts on marine biological production, increased N20 emissions, nitrogen pollution, and eutrophication. Likewise, there is a poor understanding of the relationship between nitrogen cycling and productivity in marine ecosystems. Marine systems are increasingly affected by ocean acidification and by atmospheric inputs of reactive nitrogen. Since both changes greatly alter nitrogen available to microorganisms, the characterization of the response of these environmentally relevant AOA is of tremendous relevance to understanding the affect of acidification and anthropogenic nitrogen inputs on major ocean processes.

The proposed project encompasses and integrates the three dimensions (functional genetic, and taxonomic) of biodiversity. First, the project is framed by function: microbial control of one of the most important nutrient cycles on earth, the nitrogen-cycle. Second, it is motivated by recent genetic analyses that associate activities of a novel clade of Archaea (provisionally assigned to a new kingdom within the Archaea, the Thaumarchaeota) with control of ammonia oxidation in the ocean. Third, it is built upon a compelling synthesis of physiological and environmental data that lead to its central hypothesis that by altering and possibly controlling the form of nitrogen, the AOA also alter biodiversity and ecological function in one of the most productive environments on earth. It identifies a specific taxonomic imperative. The tremendous genetic diversity among the globally abundant AOA catalogued almost exclusively by gene sequencing surveys and therefore lacking formal description makes it essential to resolve membership into ecologically relevant groups or clades as a prelude to

developing a formal taxonomy. The investigators have assembled a group of researchers with specific expertise in each of dimension and uniquely qualified to address the research objectives outlined in an integrative way.

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Program Information

Dimensions of Biodiversity (Dimensions of Biodiversity)

Website: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446

Coverage: global

(adapted from the NSF Synopsis of Program)
Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [MORE from NSF]

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1046098

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