Ammonium concentrations from CTD bottle samples collected during R/V Hugh R. Sharp cruises HRS1316 and HRS1317 in Chesapeake Bay from August to September of 2013

Website: https://www.bco-dmo.org/dataset/738619
Data Type: Cruise Results
Version: 1
Version Date: 2018-06-15

Project
» Collaborative Research: New Approaches to New Production (N-SPOT)
» Gene content, gene expression, and physiology in mesopelagic ammonia-oxidizing archaea (AmoA Archaea)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: **N**:38.48147 **E**:-76.35973 **S**:38.469 **W**:-76.53867
Temporal Extent: 2013-08-25 - 2013-09-16

Dataset Description

Related Datasets (also generated from samples during cruises HRS1316 and HRS1317): * Chesapeake Bay: Nitrous oxide https://www.bco-dmo.org/dataset/738594 * Chesapeake Bay: Ammonia oxidation rates https://www.bco-dmo.org/dataset/738599 * Chesapeake Bay: N2 to Ar ratio https://www.bco-dmo.org/dataset/738604 * Chesapeake Bay: Nitrate https://www.bco-dmo.org/dataset/738609 * Chesapeake Bay: Nitrite https://www.bco-dmo.org/dataset/738614 The results paper for these data has been submitted to the journal Estuaries and Coasts (Laperriere et al., submitted).

Methods & Sampling

Water samples were collected using a 12 x 10 L Niskin bottle rosette sampler equipped with a conductivity, temperature, and pressure instrument package (SBE9, Sea-Bird Electronics, Bellevue, Washington, U.S.A.) and a sensor for dissolved oxygen (SBE43, Sea-Bird).

Ammonium was measured at sea using the o-phthaldialdehyde-based fluorometric method (Holmes et al. 1999).

Data Processing Description

BCO-DMO Data Manager Processing Notes:
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions
* blank values in this dataset are displayed as "nd" for "no data." nd is the default missing data identifier in the BCO-DMO system.
* removed spaces between minutes and seconds
* removed trailing and leading spaces of values
* removed occasional space after decimal place in original longitude decimal degree format
* added timestamp in UTC (ISO format)

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Data Files

File
NH4.csv (Comma Separated Values (.csv), 2.96 KB) MD5:77339019aa95d30b77f321d671b67865 Primary data file for dataset ID 738619

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Related Publications

Holmes, R. M., Aminot, A., Kerouel, R., Hooker, B. A., & Peterson, B. J. (1999). A simple and precise method for measuring ammonium in marine and freshwater ecosystems. Canadian Journal of Fisheries and Aquatic Sciences, 56(10), 1801-1808. doi:10.1139/f99-128 https://doi.org/10.1139/cjfas-56-10-1801
Methods

Laperriere, S. M., Nidzieko, N. J., Fox, R. J., Fisher, A. W., & Santoro, A. E. (2018). Observations of Variable Ammonia Oxidation and Nitrous Oxide Flux in a Eutrophic Estuary. Estuaries and Coasts, 42(1), 33–44. https://doi.org/10.1007/s12237-018-0441-4
Results

,
Methods

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Parameters

Parameter	Description	Units
station	Station number	unitless
date	Date of sample collection (local EDT)	unitless
time	Time of sample collection (local EDT)	untiless
lat	Latitude (N)	degrees decimal minutes
lon	Longitude (W)	degrees decimal minutes
depth	Depth	meters
nh4	Ammonium concentration	micromoles per liter (umol/L)
replicate	Replicate number	unitless
ISO_DateTime_UTC	ISO timestamp based on the ISO 8601:2004(E) standard in format YYYY-mm-ddTHH:MMZ (UTC)	unitless
lat_dd	Latitude	decimal degrees
lon_dd	Longitude	decimal degrees

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Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	CTD Sea-Bird 9
Generic Instrument Description	The Sea-Bird SBE 9 is a type of CTD instrument package. The SBE 9 is the Underwater Unit and is most often combined with the SBE 11 Deck Unit (for real-time readout using conductive wire) when deployed from a research vessel. The combination of the SBE 9 and SBE 11 is called a SBE 911. The SBE 9 uses Sea-Bird's standard modular temperature and conductivity sensors (SBE 3 and SBE 4). The SBE 9 CTD can be configured with auxiliary sensors to measure other parameters including dissolved oxygen, pH, turbidity, fluorometer, altimeter, etc.). Note that in most cases, it is more accurate to specify SBE 911 than SBE 9 since it is likely a SBE 11 deck unit was used. more information from Sea-Bird Electronics

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

HRS1316

Website	https://www.bco-dmo.org/deployment/707119
Platform	R/V Hugh R. Sharp
Report	http://ezid.cdlib.org/id/doi:10.7284/902881
Start Date	2013-08-25
End Date	2013-09-01
Description	R/V Hugh R Sharp 1316. Mid-bay of Chesapeake Bay, 38°N 76°W.

HRS1317

Website	https://www.bco-dmo.org/deployment/707274
Platform	R/V Hugh R. Sharp
Report	http://ezid.cdlib.org/id/doi:10.7284/902882
Start Date	2013-09-12
End Date	2013-09-17
Description	R/V Hugh R Sharp 1317. Mid-bay of Chesapeake Bay, 38°N 76°W.

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Project Information

Collaborative Research: New Approaches to New Production (N-SPOT)

Website: https://dornsife.usc.edu/labs/capone

Coverage: Coastal Waters of Southern California, San Pedro Ocean Time-series (SPOT), located 17 km offshore between Los Angeles Harbor and Catalina Island

NSF Award Abstract:
Coastal marine ecosystems are seasonally dynamic and highly productive. Phytoplankton populations shift from nutrient replete conditions in the spring to nutrient poor conditions in other seasons. The San Pedro

Ocean Time-series (SPOT), located 17 km offshore between Los Angeles Harbor and Catalina Island, is a representative and accessible model coastal system with regular sampling and a substantial archive of relevant observations. The SPOT program has cataloged the dynamics, diversity, and productivity of microbial populations since 2000. With rising carbon dioxide (CO2) concentrations and resulting decreases in surface pH, it is critically important to understand the nutrient controls on primary production in coastal waters and the capacity of coastal ecosystems to sequester CO2. This project will examine rates of primary production, nitrogen uptake associated with primary production, and the oxidation of ammonium to nitrate (nitrification), at SPOT over two seasonal cycles. It will also contribute to the development of human resources in the marine sciences through the training of undergraduate and graduate students at the University of Southern California and the University of Maryland. The researchers participate in education outreach activities (e.g. through the Centers for Ocean Sciences Education Excellence programs), and will incorporate findings from this study in those presentations.

This project will investigate primary production and nitrogen (N) dynamics at SPOT and specifically implement an analysis of new production. The new production conceptual model has been a powerful organizing principle in biological oceanography and provides a means to constrain the amount of primary production that may be exported or "sequestered" from the system. Despite qualifications to the definitions of new and regenerated forms of N as originally articulated, the concept has, for the most part, been narrowly applied, specifying nitrate as the primary form of new N, and ammonium as the predominant recycled form. Evidence continues to accumulate that these definitions may warrant expansion. N fixation can be at times a substantial source of new N; similarly, forms of dissolved organic N (e.g., urea) may contribute significantly to recycled production, but the specific organisms taking part in these transformations are still uncertain. Nitrification in the upper water column may also compromise the strict definitions of new and recycled N. Scientists can now probe more deeply into new and regenerated production, and directly identify major agents of these processes using new molecular techniques. This project will quantify new and regenerated production in a coastal ecosystem, illuminating the predominant compounds involved. Rates of primary production, nitrate, ammonium and urea assimilation, N2 fixation, and nitrification will be determined in the upper water column in concert with monthly SPOT cruises. In tandem, two stable isotope probing (SIP) approaches (conventional SIP for nitrate, ammonium and urea uptake coupled to high throughput sequencing and microarray based Chip-SIP for N2 fixation) will be used to directly identify the major agents involved in these processes, along with the uptake of 13C-urea into nitrifier biomass. The following two hypotheses will be tested:

1. N2 fixation is a substantial source of new N in coastal waters of Southern California supporting export production.

2. Forms of dissolved organic N, and specifically urea, can be substrates for nitrification and contribute substantially to regenerated production.

See the related project "Direct Identification and Characterization of Marine Heterotrophic Nitrogen Fixers by Stable Isotope Probing", funded by OCE-1341178, that involved novel stable isotope probing (SIP) methods.

Gene content, gene expression, and physiology in mesopelagic ammonia-oxidizing archaea (AmoA Archaea)

Coverage: Epipelagic and mesopelagic, Equatorial Pacific

NSF award abstract:

Intellectual Merit. How organisms respond to their physical and chemical and environment is a central question in marine ecology. For microbes living in the mesopelagic - the ocean's "twilight zone" - an efficient response is particularly important to capitalize on the intermittent delivery of organic and inorganic compounds sinking from the surface ocean. These organisms must have a suite of metabolic and regulatory strategies used to cope with environmental variability, but these strategies are largely unknown. Understanding when and why metabolic genes are expressed is critical to our understanding of nutrient remineralization in the ocean. Marine group 1 (MG1) archaea are ubiquitous, abundant microbes in the meso- and bathypelagic and promising model organisms for investigating these questions. MG1 archaea are chemolithoautotrophs that oxidize ammonia for energy and fix carbon for biomass, and as such, play a central role in the ocean's coupled carbon and nitrogen cycles. Though MG1 have historically eluded cultivation, recent efforts have been successful at bringing representative MG1 archaea from the open ocean into culture and demonstrating their importance in the production of the greenhouse gas nitrous oxide. This project takes advantage of unique MG1 cultures and the

recently sequenced draft genome of one of the organisms - strain CN25 - to investigate the physiological and transcriptional responses of MG1 archaea to variations in their chemical environment, specifically:

1. Comparative transcriptomics of CN25 cells grown under a range of energy availability and nitrosative stress will identify select genes that can be used to diagnose the physiological state of natural populations

2. Improvements in the genomic and transcriptomic knowledge of MG1 archaea will facilitate a thorough reinterpretation of existing metagenomic and metatranscriptomic datasets, as well as provide a better contextual understanding in future studies

The investigators will conduct comparative transcriptomics of CN25 cells harvested in mid-exponential growth and stationary phase versus starved cells. Transcriptomes of cells grown at high nitrate concentrations and low pO2 with those grown in standard conditions will be characterized. A strand-specific, high-density RNAseq approach will be used to examine the expression of putative ORFs, polycistronic operons, and small RNAs, which, in addition to gene expression profiling, has the ancillary benefit of improving genome annotation. Finally, the investigators will sequence the genomes of two additional MG1 strains isolated from the open ocean, as well as single cells from environmental surveys, and leverage the combination with the CN25 genome to reanalyze available metagenomic and metatranscriptomic datasets. The results will define the transcriptional response of a model mesopelagic microbe to a range of chemical environments, and show how the physicochemical environment induces changes in gene expression and gene content that result in greenhouse gas production. This work will rapidly generate new knowledge of how some of the most ubiquitous, yet heretofore elusive, microorganisms respond to geochemical variability and shape our evolving understanding of the marine nitrogen cycle.

Broader Impacts. The scientific and societal impact of the project will be to elucidate the mechanisms of greenhouse gas production in a model marine organism that is of broad interest to biological and chemical oceanographers. Transcriptome sequencing will improve the assembly of the CN25 genome, the first genome of an MG1 archaeon from the open ocean. Both the genome and transcriptomes will be important references for researchers using metagenomics, metatranscriptomics, and metaproteomics in the ocean, as these techniques are reliant on a knowledgebase composed of both DNA sequence and physiology. Thus, the results add value to both existing and future studies. The proposed research will advance education, teaching, and training for the next generation of marine scientists by providing support for two early-career investigators, one postdoctoral researcher, and a secondary school teacher.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1260006
NSF Division of Ocean Sciences (NSF OCE)	OCE-1437310
NSF Division of Ocean Sciences (NSF OCE)	OCE-1740538

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