Depth profiles of quantitative PCR of ammonia-oxidizing archaea and bacteria from R/V Kilo Moana KM1314 in the North Pacific Ocean

Website: https://www.bco-dmo.org/dataset/997806
Data Type: Other Field Results
Version: 1
Version Date: 2026-07-23

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
Qin, Wei	University of Illinois Urbana-Champaign (UIUC)	Principal Investigator
Shen, Hui	University of Illinois Urbana-Champaign (UIUC)	Scientist, Contact
Soenen, Karen	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This dataset reports depth-resolved abundances of archaeal and β-proteobacterial ammonia monooxygenase (amoA) genes collected at Stations 5, 8, and 13 in the northeastern Pacific Ocean during the R/V Kilo Moana cruise KM1314 in August 2013. One liter of seawater from each depth was filtered onto 0.22 µm Sterivex filters and stored at −80 °C prior to DNA extraction using a modified manual extraction protocol. Archaeal and bacterial amoA gene abundances were quantified by quantitative PCR using primer sets CrenAmoAQ-F/CrenAmoAModR and AmoA1-F/AmoA2-R on a LightCycler platform. Standard curves, amplification procedures, melting curve analyses, and gel electrophoresis verification followed established protocols. These measurements characterize vertical distributions of ammonia-oxidizing microorganisms in the upper 300 m of the water column and support analyses of nitrification activity and microbial community structure in the oligotrophic North Pacific.

Table of Contents

- Coverage
- Dataset Description
  - Methods & Sampling
  - Data Processing Description
  - BCO-DMO Curation Notes
- Data Files
- Related Publications
- Parameters
- Instruments
- Deployments
- Project Information
- Program Information
- Funding

Coverage

Location: Three stations in the North Pacific Ocean (49°17′31.89″N, 134°40′49.24″W; 50°00′00.00″N, 145°00′00.00″W; 30°00′00.00″N, 150°00′00.00″W) were sampled. Sampling depths ranged from the surface (0 m) to 300 m
Spatial Extent: **N**:50 **E**:-134.6803444 **S**:30 **W**:-150
Temporal Extent: 2013-08-14 - 2013-08-29

Methods & Sampling

At Stations 5, 8, and 13, one liter of seawater from each depth was collected by Niskin bottles attached at CTD, then filtered onto 0.22 µm Sterivex filters (GP-type, Millipore) and stored at −80 °C.

Data Processing Description

DNA was extracted using a modified manual extraction protocol as previously described (Urakawa et al. 2010). Archaeal and β-proteobacterial amoA genes were quantified by qPCR using primer sets CrenAmoAQ-F/CrenAmoAModR (Mincer et al. 2007) and AmoA1-F/AmoA2-R (Rotthauwe et al. 1997), respectively, on a LightCycler system (Roche), following previously described methods (Horak et al. 2013). Standard curve construction, amplification procedures, melting curves, and gel electrophoresis tests were carried out as previously described (Horak et al. 2013)

BCO-DMO Curation Notes

* Converted latitude and longitude values from degrees, minute, seconds to decimal degrees
* Rounded those fields to 7 decimals
* Renamed the column headers to comply with the database requirements (no spaces or special characters)

[table of contents | back to top]

Data Files

File
997806_v1_qpcr.csv (Comma Separated Values (.csv), 2.30 KB) MD5:b892fe942e26c0d27347754d83f04aaf Primary data file for dataset ID 997806, version 1

[table of contents | back to top]

Related Publications

Horak, R. E. A., Qin, W., Schauer, A. J., Armbrust, E. V., Ingalls, A. E., Moffett, J. W., Stahl, D. A., & Devol, A. H. (2013). Ammonia oxidation kinetics and temperature sensitivity of a natural marine community dominated by Archaea. The ISME Journal, 7(10), 2023–2033. https://doi.org/10.1038/ismej.2013.75
Methods

Mincer, T. J., Church, M. J., Taylor, L. T., Preston, C., Karl, D. M., & DeLong, E. F. (2007). Quantitative distribution of presumptive archaeal and bacterial nitrifiers in Monterey Bay and the North Pacific Subtropical Gyre. Environmental Microbiology, 9(5), 1162–1175. doi:10.1111/j.1462-2920.2007.01239.x
Methods

Rotthauwe, J. H., Witzel, K. P., & Liesack, W. (1997). The ammonia monooxygenase structural gene amoA as a functional marker: molecular fine-scale analysis of natural ammonia-oxidizing populations. Applied and Environmental Microbiology, 63(12), 4704–4712. https://doi.org/10.1128/aem.63.12.4704-4712.1997
Methods

Urakawa, H., Martens-Habbena, W., & Stahl, D. A. (2010). High Abundance of Ammonia-Oxidizing Archaea in Coastal Waters, Determined Using a Modified DNA Extraction Method. Applied and Environmental Microbiology, 76(7), 2129–2135. doi:10.1128/aem.02692-09 https://doi.org/10.1128/AEM.02692-09
Methods

[table of contents | back to top]

Parameters

Parameter	Description	Units
Datetime_of_sampling	Date and time of sampling in UTC time zone	unitless
Latitude	Latitude of sampling location	decimal degrees
Longitude	Longitude of sampling location	decimal degrees
Station_ID	Station identification	unitless
Depth_m	Depth of sampling	meters (m)
AOA_amoA_Calculated_Abundance	abundance of amoA genes of Ammonia Oxidizing Archaea (AOA)	copies per milliliter (copies/mL)
stdev_AOA	Standard deviation of abundance of amoA genes of AOA	copies per milliliter (copies/mL)
AOB_amoA_Calculated_Abundance	abundance of amoA genes of Ammonia Oxidizing Bacteria (AOB)	copies per milliliter (copies/mL)
stdev_AOB	Standard deviation of abundance of amoA genes of AOB	copies per milliliter (copies/mL)

[table of contents | back to top]

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	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.

Dataset-specific Instrument Name	LightCycler system (Roche)
Generic Instrument Name	qPCR Thermal Cycler
Generic Instrument Description	An instrument for quantitative polymerase chain reaction (qPCR), also known as real-time polymerase chain reaction (Real-Time PCR).

[table of contents | back to top]

Deployments

KM1314

Website	https://www.bco-dmo.org/deployment/536050
Platform	R/V Kilo Moana
Start Date	2013-08-07
End Date	2013-09-05

[table of contents | back to top]

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.

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1046017

[table of contents | back to top]