

Depth profiles of lipid biomarkers KM1314

Website: <https://www.bco-dmo.org/dataset/997800>

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Project

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

Program

» [Dimensions of Biodiversity](#) (Dimensions of Biodiversity)

Table of Contents

- [Coverage](#)
 - [Dataset Description](#)
 - [Parameters](#)
 - [Project Information](#)
 - [Program Information](#)
 - [Funding](#)
-

Coverage

Spatial Extent: Lat:0 Lon:0

[[table of contents](#) | [back to top](#)]

Parameters

Parameters for this dataset have not yet been identified

[[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 N₂O 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](#)]