

# Nitrifier Abundances from R/V Atlantis AT50-10 in the Eastern Tropical and Subtropical Pacific Ocean from May 2023 (CliOMZ project)

**Website:** <https://www.bco-dmo.org/dataset/970545>

**Data Type:** Cruise Results

**Version:** 1

**Version Date:** 2025-08-01

## Project

» [Collaborative Research: Underexplored Connections between Nitrogen and Trace Metal Cycling in Oxygen Minimum Zones Mediated by Metalloenzyme Inventories](#) (CliOMZ)

Contributors	Affiliation	Role
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## Abstract

These data include nitrifier abundances measured on R/V Atlantis (CliOMZ AT50-10 expedition) from Golfito, Costa Rica to San Diego, USA in May-June 2023. Instruments used were a CTD profiler and a quantitative PCR machine.

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## Coverage

**Location:** Eastern Tropical and Subtropical Pacific Ocean

**Spatial Extent:** N:8.9009 E:-90 S:-10 W:-101.816

**Temporal Extent:** 2023-05-13 - 2023-05-29

## Methods & Sampling

Discrete water samples were collected using a rosette sampler equipped with 24×10 L Niskin bottles. Different depths were sampled, ranging from 45 meters to 600 meters. Seawater was collected into acid-washed 4 L polycarbonate bottles, biomass was filtered onto 0.22 µm (25mm, Supor PES, Pall) membrane filters, which were subsequently frozen at -80°C until DNA extraction. DNA was extracted using the Qiagen DNeasy Blood & Tissue kit with modifications as previously described (Santoro et al. 2010). Quantitative PCR assays were conducted using group-specific assays for the 16S ribosomal RNA (rRNA) gene of marine ammonia-oxidizing archaea of the Nitrosopumilaceae family and nitrite-oxidizing bacteria of the Nitrospinae family following established protocols and thermocycling conditions (Mincer et al. 2007; Santoro et al. 2010). We modified the previously published primer for marine ammonia-oxidizing archaea (Mincer et al. 2007) to increase the coverage of members of the Nitrosopumilus genus (MGI\_F: 5'-GTC TAC CAG AAC ACG TYC-3', MGI\_R: 5'-WGG

CGT TGA CTC CAA TTG-3'). Gene copies were quantified on a CFX96 qPCR machine (Bio-Rad) with SYBR Green chemistry. All samples were run in triplicate against a standard curve spanning approximately  $10^1 - 10^6$  template copies. Linearized plasmids containing cloned inserts of the target genes (TOPO pCR4 vector, Invitrogen) were used as standards as described in (Santoro et al. 2017).

## Data Processing Description

16S rRNA gene copy numbers per liter were calculated by correcting for the amount of filtered seawater.

## BCO-DMO Processing Description

- Date values in primary data file converted from %d.%m.%y to %Y-%m-%d format.
- Latitude and longitude values have been corrected and rounded to 6 degrees of precision.

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## Data Files

File
<b>970545_v1_cliomz_nitrifier_abundances.csv</b> (Comma Separated Values (.csv), 2.75 KB) MD5:11ddb27ddb20f283c53500af087d4a2b
Primary data file for dataset ID 970545, version 1

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## Related Publications

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](https://doi.org/10.1111/j.1462-2920.2007.01239.x)  
*Methods*

Santoro, A. E., Casciotti, K. L., & Francis, C. A. (2010). Activity, abundance and diversity of nitrifying archaea and bacteria in the central California Current. *Environmental Microbiology*, 12(7), 1989–2006. doi:[10.1111/j.1462-2920.2010.02205.x](https://doi.org/10.1111/j.1462-2920.2010.02205.x)  
*Methods*

Santoro, A. E., Saito, M. A., Goepfert, T. J., Lamborg, C. H., Dupont, C. L., & DiTullio, G. R. (2017). Thaumarchaeal ecotype distributions across the equatorial Pacific Ocean and their potential roles in nitrification and sinking flux attenuation. *Limnology and Oceanography*, 62(5), 1984–2003. doi:[10.1002/lno.10547](https://doi.org/10.1002/lno.10547)  
*Results*

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## Parameters

Parameter	Description	Units
Cruise	Cruise name	unitless
Date	Date of sampling.	unitless
Latitude	Sampling latitude in decimal degrees; a positive value indicates a northern coordinate.	decimal degrees
Longitude	Sampling longitude in decimal degrees; a positive value indicates an eastern coordinate.	decimal degrees
Station	Station number of cruise AT50-10.	unitless
Cast	Cast number of cruise AT50-10.	unitless
Depth	Sampling depth in meters.	meters (m)
Mean_Nitrosopumilaceae	Nitrosopumilaceae abundances, mean of measurements from triplicate reactions.	16S rRNA gene copies per L
SD_Nitrosopumilaceae	Nitrosopumilaceae abundances, standard deviation of measurements from triplicate reactions	16S rRNA gene copies per L
Mean_Nitrospinaceae	Nitrospinaceae abundances, mean of measurements from triplicate reactions.	16S rRNA gene copies per L
SD_Nitrospinaceae	Nitrospinaceae abundances, standard deviation of measurements from triplicate reactions	16S rRNA gene copies per L

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## Instruments

<b>Dataset-specific Instrument Name</b>	Rosette Sampler equipped with 24x10 L Niskin Bottles
<b>Generic Instrument Name</b>	Niskin bottle
<b>Dataset-specific Description</b>	Discrete water samples were collected using a rosette sampler equipped with 24x10 L Niskin bottles.
<b>Generic Instrument Description</b>	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.

<b>Dataset-specific Instrument Name</b>	CFX96 Quantitative PCR Machine (Bio-Rad)
<b>Generic Instrument Name</b>	qPCR Thermal Cycler
<b>Dataset-specific Description</b>	16S rRNA gene abundances were quantified using a CFX96 quantitative PCR machine (Bio-Rad).
<b>Generic Instrument Description</b>	An instrument for quantitative polymerase chain reaction (qPCR), also known as real-time polymerase chain reaction (Real-Time PCR).

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## Deployments

### AT50-10

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/916122">https://www.bco-dmo.org/deployment/916122</a>
<b>Platform</b>	R/V Atlantis
<b>Report</b>	<a href="https://www.rvdata.us/search/cruise/AT50-10">https://www.rvdata.us/search/cruise/AT50-10</a>
<b>Start Date</b>	2023-05-02
<b>End Date</b>	2023-06-09

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## Project Information

### Collaborative Research: Underexplored Connections between Nitrogen and Trace Metal Cycling in Oxygen Minimum Zones Mediated by Metalloenzyme Inventories (CliOMZ)

**Coverage:** Eastern Tropical Pacific

#### NSF abstract:

Though scarce and largely insoluble, trace metals are key components of sophisticated enzymes (protein molecules that speed up biochemical reactions) involved in biogeochemical cycles in the dark ocean (below 1000m). For example, metalloenzymes are involved in nearly every reaction in the nitrogen cycle. Yet, despite direct connections between trace metal and nitrogen cycles, the relationship between trace metal distributions and biological nitrogen cycling processes in the dark ocean have rarely been explored, likely due to the

technical challenges associated with their study. Availability of the autonomous underwater vehicle (AUV) Clio, a sampling platform capable of collecting high-resolution vertical profile samples for biochemical and microbial measurements by large volume filtration of microbial particulate material, has overcome this challenge. Thus, this research project plans an interdisciplinary chemistry, biology, and engineering effort to test the hypothesis that certain chemical reactions, such as nitrite oxidation, could become limited by metal availability within the upper mesopelagic and that trace metal demands for nitrite-oxidizing bacteria may be increased under low oxygen conditions. Broader impacts of this study include the continued development and application of the Clio Biogeochemical AUV as a community resource by developing and testing its high-resolution and adaptive sampling capabilities. In addition, metaproteomic data will be deposited into the recently launched Ocean Protein Portal to allow oceanographers and the metals in biology community to examine the distribution of proteins and metalloenzymes in the ocean. Undergraduate students will be supported by this project at all three institutions, with an effort to recruit minority students. The proposed research will also be synergistic with the goals of early community-building efforts for a potential global scale microbial biogeochemistry program modeled after the success of the GEOTRACES program, provisionally called "Biogeoscapes: Ocean metabolism and nutrient cycles on a changing planet".

The proposed research project will test the following three hypotheses: (1) the microbial metalloenzyme distribution of the mesopelagic is spatially dynamic in response to environmental gradients in oxygen and trace metals, (2) nitrite oxidation in the Eastern Tropical Pacific Ocean can be limited by iron availability in the upper mesopelagic through an inability to complete biosynthesis of the microbial protein nitrite oxidoreductase, and (3) nitrite-oxidizing bacteria increase their metalloenzyme requirements at low oxygen, impacting the distribution of both dissolved and particulate metals within oxygen minimum zones. One of the challenges to characterizing the biogeochemistry of the mesopelagic ocean is an inability to effectively sample it. As a sampling platform, we will use the novel biogeochemical AUV Clio that enables high-resolution vertical profile samples for biochemical and microbial measurements by large volume filtration of microbial particulate material on a research expedition in the Eastern Tropical Pacific Ocean. Specific research activities will be orchestrated to test the hypotheses. Hypothesis 1 will be explored by comparison of hydrographic, microbial distributions, dissolved and particulate metal data, and metaproteomic results with profile samples collected by Clio. Hypothesis 2 will be tested by incubation experiments using  $^{15}\text{NO}_2^-$  oxidation rates on Clio-collected incubation samples. Hypothesis 3 will be tested by dividing targeted nitrite oxidoreductase protein copies by qPCR (quantitative polymerase chain reaction)-based nitrite oxidizing bacteria abundance (NOB) to determine if cellular copy number varies with oxygen distributions, and by metalloproteomic analyses of NOB cultures. The demonstration of trace metal limitation of remineralization processes, not just primary production, would transform our understanding of the role of metals in biogeochemical cycling and provide new ways with which to interpret sectional data of dissolved and particulate trace metal distributions in the ocean. The idea that oxygen may play a previously underappreciated role in controlling trace metals due not just to metals' physical chemistry, but also from changing biological demand, will improve our ability to predict trace metal distributions in the face of decreasing ocean oxygen content.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1924512</a>

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