Water column amoA and Nitrospina-like 16S rRNA gene abundances from qPCR in the Eastern Tropical South Pacific using seawater collected on R/V Atlantis (AT15-61) cruise in Jan-Feb 2010 and R/V Melville (MV1104) cruise in Mar-Apr 2011.

Website: https://www.bco-dmo.org/dataset/826781
Data Type: experimental, Cruise Results
Version: 1
Version Date: 2020-10-14

Project
» Expression of Microbial Nitrification in the Stable Isotopic Systematics of Oceanic Nitrite and Nitrate (Microbial Nitrification)

Contributors	Affiliation	Role
Casciotti, Karen L.	Stanford University	Principal Investigator
Santoro, Alyson E.	University of California-Santa Barbara (UCSB)	Contact
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Abstract
Water column amoA and Nitrospina-like 16S rRNA gene abundances from qPCR in the Eastern Tropical South Pacific using seawater collected on R/V Atlantis (AT15-61) cruise in Jan-Feb 2010 and R/V Melville (MV1104) cruise in Mar-Apr 2011.

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Coverage

Spatial Extent: **N**:-9.943 **E**:-80 **S**:-20.01 **W**:-100
Temporal Extent: 2010-02-02 - 2011-04-20

Dataset Description

These data appear in the following:

- Figure S7 of Santoro, et al. (2020)
- Table S5 of Santoro, et al. (2020)
- Figure S6 in pre-print on ESSOAr (doi.org/10.1002/essoar.10503499.1)

Methods & Sampling

Seawater samples were obtained during the R/V Atlantis (AT15-61) and R/V Melville (MV1104) cruises in Jan-Feb

2010 and Mar-Apr 2011. Water samples were collected at discrete depths using a standard 24-bottle Niskin rosette sampler equipped with an SBE9plus conductivity-temperature-depth (CTD) sensor package (SeaBird Electronics, Bellevue, WA). Samples for nucleic acid extraction and qPCR were collected from the rosette in 2-4 L polycarbonate bottles. Cells were harvested by pressure filtration onto 25 mm diameter, 0.2 µm pore-size polyethersulfone membrane filters (Supor-200, Pall Corporation, Port Washington, NY) housed in polypropylene filter holders (Whatman SwinLok, GE Healthcare, Pittsburgh, PA) using a peristaltic pump and silicone tubing. DNA was extracted according to Santoro,et al. (2010). For DNA extraction and analysis methods followed Santoro, et al. (2010). Sample volumes of 1-4 liters were filtered depending on the biomass present at each station and depth, and the filters were flash frozen in liquid nitrogen in 2 mL gasketed bead beating tubes (Fisher Scientific).

Data Processing Description

- Water samples were collected, filtered with peristaltic pressure onto 25 mm 0.2 µm pore size Supor filters.
- DNA was extracted according to Santoro et al. 2010.
- Abundance of bacterial amoA genes by quantitative PCR (qPCR) using SYBR Green chemistry followed that of Santoro et al. (2010).
- Abundance of archaeal amoA genes belonging to one of two ecotypes (WCA and WCB) were quantified using TaqMan assays following protocols described in Mosier and Francis (2011).
- Nitrospina-like 16S rRNA genes were quantified using the SYBR Green assay described in Mincer et al. (2007).

Data processing: Reported abundances are the mean of triplicate qPCR reactions. Gene abundances per qPCR reaction were converted to abundance per liter of seawater using the volume of seawater filtered, the DNA extraction elution volume, and the volume of extract added to each reaction. Conversion assumes 100% DNA extraction efficiency.

BCO-DMO processing:

- Added a conventional header with dataset name, PI name, version date
- Adjusted parameter names to comply with database requirements.
- Combined year, month, day fields into one date field.
- Units in parentheses removed and added to Parameter Description metadata section.
- Default missing identifier of 'NaN' replaced with 'nd' ('nd' is BCO-DMO system default missing data identifier).
- BDL (below detection limit) identifier maintained

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Data Files

File	
ETSP_qPCR_TableS5.csv	(Comma Separated Values (.csv), 6.48 KB) MD5:4924026426755a0dfb0ab239582f8db4
Primary data file for dataset ID 826781	

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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
Methods

Mosier, A. C., & Francis, C. A. (2011). Determining the Distribution of Marine and Coastal Ammonia-Oxidizing Archaea and Bacteria Using a Quantitative Approach. Methods in Enzymology, 205–221. doi:10.1016/b978-0-

12-381294-0.00009-2 https://doi.org/10.1016/B978-0-12-381294-0.00009-2
Methods

Santoro, A. E., Buchwald, C., Knapp, A. N., Berelson, W. M., Capone, D. G., & Casciotti, K. L. (2020). Nitrification and nitrous oxide production in the offshore waters of the Eastern Tropical South Pacific. doi:10.1002/essoar.10503499.1
Results

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
Methods

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Parameters

Parameter	Description	Units
ISO_Date_Local	Date of sampling in ISO format (yyyy-mm-dd), Time zone in 2010 was GMT-5, Time zone in 2011 was GMT-4	yyyy-mm-dd
Latitude	Latitude of sample collection	decimal degrees
Longitude	Longitude of sample collection	decimal degrees
Station	Station number	unitless
Cast	Cast number	unitless
Depth	Depth of sample collection	meters (m)
Vol_filtered	Volume of seawater filtered (in liters)	liters (L)
AOB_amoA	Abundance of ammonia-oxidizing betaproteobacterial ammonia monooxygenase subunit A (amoA) genes	copies per milliliter (copies/mL)
AOB_amoA_SD	Standard deviation of abundance of ammonia-oxidizing betaproteobacterial monooxygenase subunit A (amoA) genes	copies per milliliter (copies/mL)
AOA_amoA	Abundance of ammonia-oxidizing archaeal monooxygenase subunit A (amoA) genes	copies per milliliter (copies/mL)
AOA_amoA_SD	Standard deviation of abundance of ammonia-oxidizing archaeal monooxygenase subunit A (amoA) genes	copies per milliliter (copies/mL)
WCA_amoA	Abundance of Water Column A clade archaeal monooxygenase subunit A (amoA) genes	copies per milliliter (copies/mL)
WCA_amoA_SD	Standard deviation of abundance of Water Column A clade archaeal monooxygenase subunit A (amoA) genes	copies per milliliter (copies/mL)
WCB_amoA	Abundance of Water Column B clade archaeal monooxygenase subunit A (amoA) genes	copies per milliliter (copies/mL)
WCB_amoA_SD	Standard deviation of abundance of Water Column Bclade archaeal monooxygenase subunit A (amoA) genes	copies per milliliter (copies/mL)
NIT_16S	Abundance of Nitrospina-like 16S rRNA genes	copies per milliliter (copies/mL)
NIT_16S_SD	Standard deviation of abundance of Nitrospina-like 16S rRNA genes	copies per milliliter (copies/mL)
Year	Deployment year	unitless
Month	Deployment month	unitless
Day	Deployment day	unitless

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Instruments

Dataset-specific Instrument Name	CTD Sea-Bird 9 plus
Generic Instrument Name	CTD Sea-Bird 9
Dataset-specific Description	SBE9plus conductivity-temperature-depth (CTD) sensor package (SeaBird Electronics, Bellevue, WA)
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	24-bottle Niskin rosette sampler
Generic Instrument Name	Niskin bottle
Dataset-specific Description	24-bottle Niskin rosette sampler
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	BioRad CFX96 quantitative PCR machine
Generic Instrument Name	qPCR Thermal Cycler
Dataset-specific Description	BioRad CFX96 quantitative PCR machine (Bio-Rad, Inc. in Hercules, CA)
Generic Instrument Description	An instrument for quantitative polymerase chain reaction (qPCR), also known as real-time polymerase chain reaction (Real-Time PCR).

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Deployments

AT15-61

Website	https://www.bco-dmo.org/deployment/58785
Platform	R/V Atlantis
Start Date	2010-01-29
End Date	2010-03-03
Description	See more information at R2R: https://www.rvdata.us/search/cruise/AT15-61

MV1104

Website	https://www.bco-dmo.org/deployment/555585
Platform	R/V Melville
Start Date	2011-03-23
End Date	2011-04-23
Description	See more information at R2R: https://www.rvdata.us/search/cruise/MV1104

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Project Information

Expression of Microbial Nitrification in the Stable Isotopic Systematics of Oceanic Nitrite and Nitrate (Microbial Nitrification)

Coverage: Eastern Tropical South Pacific

Description from NSF award abstract:
Closing the marine budgets of nitrate and nitrous oxide are central goals for researchers interested in nutrient-driven changes in primary productivity and climate change. With the implementation of new methods for oxygen isotopic analysis of seawater nitrate, it will be possible to construct a budget for nitrate based on its oxygen isotopic distribution that is complementary to nitrogen isotope budgets. Before we can effectively use oxygen isotopes in nitrate to inform the current understanding of the marine nitrogen cycle, we must first understand how different processes that produce (nitrification) and consume (assimilation, denitrification) nitrate affect its oxygen isotopic signature.

In this study, researchers at the Woods Hole Oceanographic Institution will provide a quantitative assessment of the oxygen isotopic systematics of nitrification in the field and thus fill a key gap in our understanding of 18O variations in nitrate, nitrite, and nitrous oxide. The primary goal is to develop a quantitative prediction of the oxygen isotopic signatures of nitrite and nitrate produced during nitrification in the sea. The researchers hypothesize that oxygen isotopic fractionation during nitrification is the primary factor setting the 18O values of newly produced nitrate and nitrite. Secondly, they hypothesize that oxygen atom exchange is low where ammonia oxidation and nitrite oxidation are tightly coupled, but may increase in regions with nitrite accumulation, such as in the primary and secondary nitrite maxima. They will test these hypotheses with a series of targeted laboratory and field experiments, as well as with measurements of nitrite and nitrate isotopic distributions extending through the euphotic zone, primary nitrite maximum, and secondary nitrite maximum of the Eastern Tropical South Pacific. The results of these experiments are expected to provide fundamental information required for the interpretation of 18O isotopic signatures in nitrite, nitrate, and N2O in the context of underlying microbial processes. A better understanding of these features and the processes involved is important for quantifying new production, controls on the N budget, and N2O production in the ocean -- which should lead to a better understanding of the direct and indirect interactions among the nitrogen cycle, marine chemistry, and climate.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0961098

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