

Ammonia-Oxidizing Archaea (AOA) whole genome sequence accessions from samples collected during the 2006 R/V Endeavor RMP Sediment Cruise in San Francisco Bay August 2-9, 2006 (N-Cycling Microbial Communities project)

Website: <https://www.bco-dmo.org/dataset/684211>

Data Type: Cruise Results

Version:

Version Date: 2017-07-03

Project

» [Spatial and Temporal Dynamics of Nitrogen-Cycling Microbial Communities Across Physicochemical Gradients in the San Francisco Bay Estuary](#) (N-Cycling Microbial Communities)

Contributors	Affiliation	Role
Francis, Christopher	Stanford University	Principal Investigator, Contact
York, Amber D.	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Table of Contents

- [Coverage](#)
- [Dataset Description](#)
 - [Methods & Sampling](#)
 - [Data Processing Description](#)
- [Data Files](#)
- [Related Publications](#)
- [Parameters](#)
- [Deployments](#)
- [Project Information](#)
- [Funding](#)

Coverage

Spatial Extent: N:38.099 E:-121.815 S:38.024 W:-122.363

Dataset Description

This dataset contains Ammonia-Oxidizing Archaea (AOA) sequence accession information National Center for Biotechnology Information ([NCBI](#)). Samples were collected during the R/V Endeavor RMP Sediment Cruise in San Francisco Bay August 2-9, 2006.

For related datasets, click on the project link at the top of the page.

Methods & Sampling

The draft genome sequence of “Ca. Nitrosopumilus salaria” BD31 was obtained as described in Mosier et al. (2012a) and is available in the NCBI GenBank database under accession number [AEXL00000000](#). The raw sequence reads are available in the NCBI SRA database under accession number [PRJNA50075](#).

The draft genome sequence of “Ca. Nitrosoarchaeum limnia” BG20 was obtained as described in Mosier et al. (2012b) and is available in the NCBI GenBank database under accession number [AHJG00000000](#). The raw sequence reads are available in the NCBI SRA database under accession number [PRJNA50027](#).

The draft genome sequence of “Ca. Nitrosoarchaeum limnia” SFB1 was obtained as described in Blainey et al. (2011) and is available in the NCBI GenBank database under accession number [AEGP00000000](#). The version described in the paper is the first version, AEGP01000000.

Data Processing Description

BCO-DMO Data Manager Processing Notes:

* added a conventional header with dataset name, PI name, version date

* blank values replaced with no data value 'nd'

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

Data Files

File
AOA.csv (Comma Separated Values (.csv), 742 bytes) MD5:5ba6d2c1b8ca4e5ab6776b0a00657b1c Primary data file for dataset ID 684211

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

Related Publications

Blainey, P. C., Mosier, A. C., Potanina, A., Francis, C. A., & Quake, S. R. (2011). Genome of a Low-Salinity Ammonia-Oxidizing Archaeon Determined by Single-Cell and Metagenomic Analysis. PLoS ONE, 6(2), e16626. doi:[10.1371/journal.pone.0016626](https://doi.org/10.1371/journal.pone.0016626)

Methods

Mosier, A. C., Allen, E. E., Kim, M., Ferriera, S., & Francis, C. A. (2012). Genome Sequence of “Candidatus Nitrosoarchaeum limnia” BG20, a Low-Salinity Ammonia-Oxidizing Archaeon from the San Francisco Bay Estuary. Journal of Bacteriology, 194(8), 2119–2120. doi:10.1128/jb.00007-12

<https://doi.org/10.1128/JB.00007-12>

Methods

Mosier, A. C., Allen, E. E., Kim, M., Ferriera, S., & Francis, C. A. (2012). Genome Sequence of “Candidatus Nitrosopumilus salaria” BD31, an Ammonia-Oxidizing Archaeon from the San Francisco Bay Estuary. Journal of Bacteriology, 194(8), 2121–2122. doi:10.1128/jb.00013-12 <https://doi.org/10.1128/JB.00013-12>

Methods

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

Parameters

Parameter	Description	Units
Station	Station sample was collected	unitless
Latitude	Latitude of sample	decimal degrees
Longitude	Longitude of sample; west is negative	decimal degrees
Salinity	Salinity of sample	Practical Salinity Units (PSU)
Depth	Depth of sample	meters
Organism	Organism name (enriched and isolated from sediments)	unitless
Draft_Genome_Accession	Link to accession at NCBI for the draft genome	unitless
SRA_Accession	Link to accession at NCBI for SRA	unitless

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

Deployments

RMP_2006_Sediment

Website	https://www.bco-dmo.org/deployment/707112
Platform	R/V Endeavor
Report	http://dmoserv3.bco-dmo.org/data_docs/N_Cycling_Microbial_Communities/cruise_reports/2006-08-02-Sediment.pdf
Start Date	2006-08-02
End Date	2006-08-09
Description	2006 Regional Monitoring Program (RMP) Sediment Cruise

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

Project Information

Spatial and Temporal Dynamics of Nitrogen-Cycling Microbial Communities Across Physicochemical Gradients in the San Francisco Bay Estuary (N-Cycling Microbial Communities)

Coverage: San Francisco Bay

Description from the NSF award abstract:

This award is funded under the American Recovery and Reinvestment Act of 2009 (Public Law 111-5).

Although nitrogen (N) acts as a limiting nutrient in many marine ecosystems, from estuaries to the open ocean, N in excess can be extremely detrimental. Eutrophication is of particular concern in estuaries, with over half of the estuaries in the United States experiencing its effects. Harmful levels of N in estuaries can be diminished through tightly coupled processes in the microbial nitrogen cycle, including nitrification (chemoautotrophic oxidation of ammonia to nitrite and nitrate) and denitrification (the dissimilatory reduction of nitrate to N₂ gas). In fact, coupled nitrification-denitrification can remove up to 50% of external dissolved inorganic nitrogen inputs to estuaries, thereby reducing the risk of eutrophication. Despite the biogeochemical importance of both nitrification and denitrification in estuarine systems, surprisingly little is known regarding the underlying microbial communities responsible for these processes, or how they are influenced by key physical/chemical factors.

The investigators will work in San Francisco Bay - the largest estuary on the west coast of the United States -

using molecular, biogeochemical and cultivation approaches to explore how the distribution, diversity, abundance, and activities of key N-cycling communities are influenced by environmental gradients over temporal and spatial scales. Denitrifying communities will be studied using functional genes (*nirK* and *nirS*) encoding the key denitrification enzyme nitrite reductase, while genes encoding ammonia monooxygenase subunit A (*amoA*) will be used to study both ammonia-oxidizing bacteria (AOB) and the recently-discovered ammonia-oxidizing archaea (AOA)- members of one of the most ubiquitous and abundant prokaryotic groups on the planet, the mesophilic Crenarchaeota. Analyzing sediments from sites spanning a range of physical and chemical conditions in the Bay, seasonally over the course of several years, will represent an unprecedented opportunity to examine spatial, physical/chemical, and temporal effects on both denitrifier and ammonia-oxidizer communities in this large, urban estuary. Concurrently, an intensive cultivation effort will also be undertaken, in order to compile a novel culture collection of estuarine denitrifiers and ammonia-oxidizers, for which virtually nothing is currently known. Taken together, these complimentary approaches will help reveal how complex physical/chemical gradients influence the diversity and functioning of key estuarine N-cycling communities over time and space.

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

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0847266

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