Nitrite reductase genes sequence accessions from the 2004 R/V Endeavor RMP Sediment Cruise in San Francisco Bay (N-Cycling Microbial Communities project)

Website: https://www.bco-dmo.org/dataset/683969
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
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Dataset Description

09 Mar 2017 NOTE: The data were submitted to BCO-DMO and are in the process of being served

This dataset contains accession numbers and associated metdata for nitrite reductase genes sequences collected during the R/V *Endeavor,* 2004 Regional Monitoring Program (RMP) Sediment Cruise in San Francisco Bay (July 27-August 3, 2004). Sediment DNA extracts were PCR amplified with primers targeting *nirK (*copper-containing nitrite reductase) and *nirS (*cytochrome-cd1 nitrite reductase).

Related Manuscript:

Mosier, A. C., and C. A. Francis. 2010. Denitrifier abundance and activity across the San Francisco Bay estuary. *Environmental Microbiology Reports* 2:667-676. doi: 10.1111/j.1758-2229.2010.00156.x

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

Methods & Sampling

Sediment samples (upper 5-cm) were collected in conjunction with the Regional Monitoring Program (RMP) managed by the San Francisco Estuary Institute (http://www.sfei.org/). Surface sediment was retrieved using a modified Van Veen grab, and cores were taken from each grab sample using sterile, cut-off 5 mL syringes and immediately placed on dry ice prior to storage at –80C. DNA was extracted from approximately 250–300 mg of sediment from the upper 5 mm of the cores using the FastDNA SPIN kit for soil (MP Biomedicals) with a 30 s bead beating time at speed 5.5. Duplicate DNA extractions were performed for each sediment core. Sediment DNA extracts were PCR amplified with primers targeting *nirK* and *nirS*: nirK583FdegCF(5′-

TCATGGTGCTGCCGCGYGANGG; Santoro *et al.*, 2006) and nirK5R (Braker *et al.*, 1998); nirS1F and nirS6R (Braker *et al.*, 1998). Clone libraries of *nirK* and *nirS* gene fragments were constructed using the TOPO TA cloning(R) kit (Invitrogen) and 28–45 clones from each library were sequenced (ABI 3100 Capillary Sequencer). Sequences reported in this study have been deposited in GenBank under Accession No. GQ454031 to GQ454413 for *nirK* and GQ453671 to GQ454030 for *nirS*.

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'
* replaced unsupported characters in parameter names +-/()
* converted degrees decimal minutes to decimal degrees
* collection dates added from cruise report

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Data Files

File
nitrite_reductase.csv (Comma Separated Values (.csv), 150.81 KB) MD5:6c360c110a6a868edfa11b94c2c9f9e4 Primary data file for dataset ID 683969

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Parameters

Parameter	Description	Units
station	station where sample was taken	unitless
lat	latitude	decimal degrees
lon	longitude	decimal degrees
organism	organism analyzed	unitless
gene	gene analyzed	unitless
accession_range	Range of Genbank accession numbers	unitless
accession_id	Genbank accession number	
accession_link	Link to the accession at NCBI Genbank; HTML formatted link	
date	Date of sample collection in format yyyy-mm-dd.	unitless

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Instruments

Dataset-specific Instrument Name	Van Veen grab
Generic Instrument Name	Bottom Sediment Grab Samplers
Generic Instrument Description	These samplers are designed to collect an accurate representative sample of the sediment bottom. The bite of the sampler should be deep enough so all depths are sampled equally. The closing mechanism is required to completely close and hold the sample as well as prevent wash-out during retrieval. Likewise, during descent the sampler should be designed to minimize disturbance of the topmost sediment by the pressure wave as it is lowered to the bottom.

Dataset-specific Instrument Name	StepOnePlus Real-Time PCR System
Generic Instrument Name	Thermal Cycler
Dataset-specific Description	Genes quantified using gene-specific SYBR qPCR assays
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

RMP_2004_Sediment

Website	https://www.bco-dmo.org/deployment/707115
Platform	R/V Endeavor
Report	http://dmoserv3.bco-dmo.org/data_docs/N_Cycling_Microbial_Communities/cruise_reports/2004-07-27-Sediment.pdf
Start Date	2004-07-22
End Date	2004-08-03
Description	2004 Regional Monitoring Program (RMP) Sediment Cruise

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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.

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Funding

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

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