16S rRNA gene clones and accessions from bacterioplankton in the NE Pacific Ocean from R/V Thomas G. Thompson TN268 in the Northeast Pacific from August to September 2011 (Sulfur Oxidizers project)

Website: https://www.bco-dmo.org/dataset/626613
Data Type: Cruise Results, experimental
Version: final
Version Date: 2015-11-17

Project
» Mixotrophic bacteria and the cryptic marine sulfur cycle: Mechanisms of carbon assimilation and sulfur oxidation in the Arctic96BD-19 GSO clade (Sulfur Oxidizers)

Contributors	Affiliation	Role
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Coverage

Spatial Extent: **N**:45.934 **E**:-127.9353 **S**:45.8602 **W**:-130.0138

Dataset Description

16S rRNA gene clones from bacterioplankton in the northeastern Pacific Ocean.

These data are reported and discussed in Mattes et al., 2013. doi:10.1038/ismej.2013.113

Methods & Sampling

Bacterial 16S rRNA gene clone libraries were constructed by amplifying community 16S rRNA genes with bacterial primers 27F_B and 1492R (5′-GGYTACCTTGTTACGACTT -3′) as described previously (Morris et al 2012). Briefly, amplifications were performed using community genomic DNA extracted from (CTD17, 1 450 m) and (CTD7, 2 850m), Apex Taq polymerase (Genesee Scientific, San Diego, CA), and the following conditions: 35 cycles, annealing at 55ºC for 1 min, elongation at 72ºC for 2 min, and denaturation at 94ºC for 30 s. Amplicons were purified and cloned using the pGEM-T-Easy vector (Promega, Madison, WI) following the manufacturer's instructions. The resulting transformations were sent to High Throughput Sequencing (HTSeq.org, Seattle, WA), where clones were isolated and sequenced by Sanger sequencing using the M13F (5'-TGTAAAACGACGGCCAGT-3') and M13R (5'-CAGGAAACAGCTATGAC-3') primers. (See Data).

Data Processing Description

Nearly full-length 16S rRNA gene sequences were obtained for frequently occuring lineages by selecting and purifying a subset of clones using the Qiagen plasmid mini-prep kit (QIAGEN, Germantown, MD). Sequencing was performed using the following primer pairs (M13R-, 519F (5′-CAGC(A/G)GCCGCGGTAATAC-3′), 338F (5′-ACTCCTACGGGAGGCAGC-3′), and 926R (5′-CCGTCAATTC(A/C)TTT (A/G)AGTTT-3′)) by GeneWiz, Inc. (LaJolla, CA). Sequences were assembled with the CAP3 Sequence Assembly Program (Huang and Madan 1999) and annotated by using the Bayesian method of (Wang et al 2007), which contained a custom training set augmented with marine environmental clades (Iverson et al 2012), and by using the SILVA least common ancestor classification tool (Pruesse et al 2007). In silico restriction analysis and other DNA sequence manipulation operations were performed with the Sequence Manipulation Suite (Stothard 2000). Restriction fragments were verified for a subset of clones to confirm predicted fragment sizes. Bacterial 16S rRNA sequences generated during this study were submitted to Genbank (accession numbers KC522839-KC522949 -- See Data).

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Data Files

File
16S_rRNA_NP.csv (Comma Separated Values (.csv), 30.73 KB) MD5:78e737275952468fc17afca488e2406a Primary data file for dataset ID 626613

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Parameters

Parameter	Description	Units
clone_ID_predicted	sample identification; includes the CTD and station number(if available) and the depth	text
lat	Latitude	decimal degrees
lon	Longitude; West is negative	decimal degrees
HaeIII_TRF_bp_predicted	predicted length of the terminal restriction fragment after digestion by the HaeIII enzyme	number of base pairs
NCBI_accession	link to NCBI GenBank	link
SILVA_class	Classification of rRNA sequences using SILVA database (Pruesse et al. (2007))	text
Bayesian_class	Bayesian Classification; classification of rRNA sequences using a naive Bayesian classification (Wang et al.(2007); p-values at each taxonomic level shown are greater than 0.7	text

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Deployments

TN268

Website	https://www.bco-dmo.org/deployment/626431
Platform	R/V Thomas G. Thompson
Start Date	2011-08-11
End Date	2011-09-01
Description	This was a two leg cruise. The National Science Foundation's Ocean Observatory Initiative-Regional Scale Nodes cruise (August 19 – September 1, 2011) from Seattle, WA to Hydrate Ridge and Axial Seamount. The cruise began August 11 when it left the port of Seattle.

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Project Information

Mixotrophic bacteria and the cryptic marine sulfur cycle: Mechanisms of carbon assimilation and sulfur oxidation in the Arctic96BD-19 GSO clade (Sulfur Oxidizers)

Website: http://morrislab.ocean.washington.edu/

Coverage: North Pacific Ocean

Description from NSF award abstract:
The ocean serves an immense reservoir of carbon, nitrogen, phosphorus, sulfur, and other elements required for all life. The active and diverse microbial populations that inhabit the oceans are responsible for mediating nutrient transformations that maintain the chemistry of seawater. A recent study identified a ubiquitous group of marine bacteria from the Arctic96BD-19 gamma-proteobacterial sulfur oxidizer (GSO) lineage that is closely related to known sulfur oxidizing species that fix inorganic carbon and oxidize sulfide in low-oxygen waters. The potential for GSOs to use reduced forms of sulfur in oxygenated waters suggests that they are a keystone species that link the marine carbon and sulfur cycles. The only known isolates from the Arctic96BD-19 lineage of GSOs are now in culture, allowing fundamental questions about their roles in carbon and sulfur cycling to be investigated. Preliminary data suggest that they use energy from the oxidation of sulfur to assimilate carbon. This project seek to address the overarching hypothesis that sulfur transformations provide the Arctic96BD- 19 lineage of GSOs with energy for organic and inorganic carbon cycling throughout the water column.

Three specific hypotheses will be tested.
1. Arctic96BD-19 cells assimilate either organic carbon or fixes inorganic carbon, depending on environmental conditions.
2. Arctic96BD-19 cells oxidize thiosulfate via formation of a tetrathionate intermediate, or using the branched thiosulfate oxidation pathway.
3. Arctic96BD-19 cells are ubiquitous sulfur oxidizers that assimilate organic and inorganic carbon through the Pacific Northwest.

A combination of laboratory growth studies of the investigator's pure cultures and comparative genomic analyses will be used. The genomic data will be used to determine whether the Arctic96BD-19 cultures possess the genetic potential to oxidize reduced sulfur to sulfate (based on possession of known core and ancillary sulfur oxidation genes), which potential oxidation pathways are used, and whether they can fix inorganic carbon. These data will help guide the physiology studies by determining the most likely forms of inorganic and organic compounds that can be utilized.

Marine bacteria are critical players in global nutrient cycles, but many of their individual and community functions in the ecosystem are not well understood. Future oceanographers will need to use cultivation-dependent and cultivation-independent methods to identify metabolic process that shape microbial communities and impact biogeochemical cycles. Student education, scientific advancement, and public awareness are all important components of this project.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1232840

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