The complete genome sequence of Candidatus Thioglobus singularis strain PS1, the first cultured mixotrophic representative from the SUP05 clade.

Website: https://www.bco-dmo.org/dataset/628767
Version: final
Version Date: 2015-12-08

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
Morris, Robert	University of Washington (UW)	Principal Investigator, Contact
Allison, Dicky	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Table of Contents

Coverage

Spatial Extent: **N**:47.687 **E**:-122.402 **S**:47.687 **W**:-122.404
Temporal Extent: 2009-11-10

Dataset Description

The complete genome sequence of *Candidatus* Thioglobus singularis strain PS1, the first cultured mixotrophic representative from the SUP05 clade.

See Announcement.

N.B.: In bacterial nomenclature, ***Candidatus*** is a component of the taxonomic name for a bacterium that cannot be maintained in a bacteriology culture collection. Candidatus status may be used when a species or genus is well characterized but yet-uncultured. (Murray and Schleifer, 1994) With today's technology much information is obtained by 16S ribosomal RNA or even near-complete genomes with modern metagenomics techniques. [paraphrased from Wikipedia]

Methods & Sampling

Cultures of *T. singularis* were grown in one-liter polycarbonate bottles of filter sterilized seawater media as described in Marshall and Morris, 2012. . Cells were then filtered onto sterile 0.2 µm polyethersulfone filters (Pall, Port Washington, NY), placed in 15 mL Teflon tubes containing 2 ml of sucrose lysis buffer (SLB), and flash frozen in liquid nitrogen. Cells were later lysed by adding 100 µL of 1mg/mL lysozyme and incubating at 4 °C for 60 minutes, then by adding 465 µL of 10% SDS and 250 µL of proteinase K and incubating at 55 °C for 2 hours. DNA was extracted and purified from cell lysates using DNeasy Blood and Tissue and Minelute kits according the manufacturers instructions, respectively (QIAGEN, Germantown, MD). A total of 20.35 µg of

DNA was used to construct a mate pair library according to the SOLiD™ v3.0 mate-pair protocol (Life Technologies, Foster City, CA).

Data Processing Description

The *T. singularis* genome was assembled using SEAStAR v. 0.4.17 as described in Iverson et al (2012). The initial assembly was 97% complete and contained 177 gaps with a mean gap length of 198 bp. Gaps were closed by PCR with custom primers designed using Geneious 7.0.4 (Biomatters, Auckland, NZ). Amplification products were visualized, gel purified, and sequenced by Genewiz (Foster City, CA). The complete genome sequence (1,714,148bp) was confirmed by performing additional PCR reactions to resolve any irregularities in the assembly and by comparing read coverage, physical coverage and insert sizes of mate pairs covering the genome. Annotations were performed using the NCBI Prokaryotic Genome Automatic Annotation Pipeline and were checked against RAST annotations, IMG annotations , and in some cases by phylogenetic analyses. Discrepancies were corrected and final annotations were submitted to NCBI.

[table of contents | back to top]

Data Files

File
T_singularis_PS1.csv (Comma Separated Values (.csv), 366 bytes) MD5:3c0b78135bfe8117c4ea0a0158f7c888 Primary data file for dataset ID 628767

[table of contents | back to top]

Parameters

Parameter	Description	Units
entry	name of bacteria	text
GenBank_accession	link to NCBI GenBank	link
lat	Latitude	decimal degrees
lon	Longitude; West is negative	decimal degrees
depth	Sampling depth	meters
month	month sampling took place	text
year	year sampling took place	number
description	name of GenBank file with complete genome	text

[table of contents | back to top]

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.

[table of contents | back to top]

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.

[table of contents | back to top]

Funding

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

[table of contents | back to top]