The Complete Genome Sequence of Candidatus Thioglobus autotrophica strain EF1, the first cultured chemoautotrophic representative from the SUP05 clade.

Website: https://www.bco-dmo.org/dataset/628759
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
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Table of Contents

Coverage

Spatial Extent: **Lat**:49.037 **Lon**:-125.208
Temporal Extent: 2013-01-01

Dataset Description

The complete genome sequence of "*Candidatus* Thioglobus autotrophica" strain EF1, the first cultured chemoautotrophic 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

Genomic DNA was extracted from a total of 62 pure cultures grown anaerobically in 100 ml bottles. Cells were grown to early stationary phase (~2.0x106 cells/ml) and then collected on sterile Supor-200 0.2 uM polyethersulfone filters (Pall, Port Washington, NY). DNA was extracted as described in Marshall and Morris, 2012. Clone library preparation for genome sequencing was performed at the University of Washington's Genome Science Department using Pacific Bioscience's single molecule real-time (SMRT) sequencing technology.

Data Processing Description

De novo assembly of the *T. autotrophica* EF1 genome was conducted using the Hierarchical Genome Assembly Process (HGAP) (Koren et al, 2012). Briefly, single reads were mapped to seed reads, a Celera assembler created overlapping consensus sequences, and the remaining inDel and base substitution errors were removed. This method has been found to produce highly accurate, complete de novo assemblies for small prokaryotic genomes (Roberts et al, 2013). HGAP assembly of the *T. autotrophica* EF1 genome resulted in a single contiguous sequence that was closed using a single PCR reaction. The complete genome sequence of *T. autotrophica* EF1 used 100% of cleaned reads with an average coverage of 106x, indicating high confidence in a single circular chromosome 1,512,449 bp in length. Protein coding sequences were identified and annotated via NCBI's automatic Prokaryotic Genome 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_autotrophica_EF1.csv (Comma Separated Values (.csv), 367 bytes) MD5:ec1af06f67fe2920f431e1d8ead41600 Primary data file for dataset ID 628759

[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]