Thermovibrio ammonificans HB1 genome manual curation

Website: https://www.bco-dmo.org/dataset/809272
Data Type: Other Field Results
Version: 1
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Project
» Alternative carbon fixation strategies in the model organism Thermovibrio ammonificans: A model system to study energy limitation in the deep biosphere (Deep Biosphere Energy Limitation)

Program
» Center for Dark Energy Biosphere Investigations (C-DEBI)

Contributors	Affiliation	Role
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Abstract

Thermovibrio ammonificans HB1 genome manual curation. Methods are further described in Giovannelli et al. (2012).

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Dataset Description

Thermovibrio ammonificans HB1 genome manual curation. Methods are further described in Giovannelli et al. (2012).

Data Processing Description

Manual curation of the genome was performed using blastn and blastp against the non-redundant database, the conserved domain database, the Kyoto Encyclopedia of Genes and Genomes, and the PFAM database. Coding sequence similarities were compared using translated protein sequence. Metabolic pathways were reconstructed on the basis of available genomic, physiologic, and biochemical information and using Kyoto Encyclopedia of Genes and Genomes and SEED pathways as template.

Plots generated using this dataset can be found at:
http://genomevolution.org/r/9vb3
http://genomevolution.org/r/9vb4
http://genomevolution.org/r/9vb8

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Data Files

File
tam_genome.csv(Comma Separated Values (.csv), 833.15 KB) MD5:39f20860ff9745d30cd629cabb919bbe Primary data file for dataset ID 809272

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Related Publications

Giovannelli, D., Ricci, J., Pérez-Rodríguez, I., Hügler, M., O'Brien, C., Keddis, R., … Vetriani, C. (2012). Complete genome sequence of Thermovibrio ammonificans HB-1T, a thermophilic, chemolithoautotrophic bacterium isolated from a deep-sea hydrothermal vent. Standards in Genomic Sciences, 7(1), 82–90. doi:10.4056/sigs.2856770
Results

Giovannelli, D., Sievert, S. M., Hügler, M., Markert, S., Becher, D., Schweder, T., & Vetriani, C. (2020). Figure S4 [Data set]. figshare. https://doi.org/10.6084/M9.FIGSHARE.3178528
https://doi.org/10.6084/m9.figshare.3178528
Results

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Parameters

Parameter	Description	Units
Organism	taxid of the organism	unitless
Chromosome	chromosome where the gene is located	unitless
Contig	chromosome where the gene is located	unitless
Gene	locus name for the gene	unitless
Strand	DNA strand where the gene is	unitless
Start	start position in base pairs	unitless
Stop	stop position in base pairs	unitless
Called_By	gene prediction by	unitless
Product	gene function name	unitless
Product_From	product called by which database	unitless

Color	product called by which database	unitless
Accession	accession number of the match from blastp	unitless
Organism_Name	name of the organism	unitless
Positivities	% of positivities in the sequence alignment	unitless
Identities	% of identities in the sequence alignment	unitless
NR	function assigned by NCBI NR database	unitless
SPTR	function assigned by SPTR	unitless
PFAM	function assigned by PFAM	unitless
TIGRFAM	function assigned by TIGRFAM	unitless
KEGG	function assigned by KEGG	unitless
COGs	COG function assigned	unitless

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Project Information

Alternative carbon fixation strategies in the model organism Thermovibrio ammonificans: A model system to study energy limitation in the deep biosphere (Deep Biosphere Energy Limitation)

Coverage: Deep Biosphere

Project Abstract from C-DEBI:
Despite being the largest ecosystem on earth, the deep biosphere is considered to be energy limited. Chemoautotrophy is an important source of organic carbon in the deep biosphere, and significantly contributes to the deep carbon cycle. We investigated the carbon fixation strategies in the model organism Themovibrio ammonificans in relationship to the presence of different terminal electron acceptor. T. ammonicans uses the reverse Tricarboxylic Acid cycle (rTCA) as carbon fixation pathways, however our comparative genomic analysis reveals the presence of an incomplete Wood-Ljungdahl (WL) pathway. Carbon isotopic fractionation value support the rTCA cycle as carbon fixation pathway, however a difference in carbon fractionation is present when growing T. ammonificans with sulfur instead of nitrate as terminal electron acceptor. Transcriptomic analysis showed that the putative carbon monoxide dehydrogenase (type V) is expressed under both conditions. We also identified a putative oxidoreductase involved in the respiration of elemental sulfur, and propose a new pathway of sulfur reduction. The presence of incomplete yet functional alternative pathways of carbon fixation in subsurface organisms may be more widespread that previously thought, and may provide an evolutionary advantage in surviving under energy limiting conditions.

C-DEBI Project Page: https://www.darkenergybiosphere.org/award/alternative-carbon-fixation-strategies-in-the-model-organism-thermovibrio-ammonificans-a-model-system-to-study-energy-limitation-in-the-deep-biosphere/

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Program Information

Center for Dark Energy Biosphere Investigations (C-DEBI)

Website: http://www.darkenergybiosphere.org

Coverage: Global

The mission of the Center for Dark Energy Biosphere Investigations (C-DEBI) is to explore life beneath the seafloor and make transformative discoveries that advance science, benefit society, and inspire people of all ages and origins.

C-DEBI provides a framework for a large, multi-disciplinary group of scientists to pursue fundamental questions about life deep in the sub-surface environment of Earth. The fundamental science questions of C-DEBI involve exploration and discovery, uncovering the processes that constrain the sub-surface biosphere below the oceans, and implications to the Earth system. What type of life exists in this deep biosphere, how much, and how is it distributed and dispersed? What are the physical-chemical conditions that promote or limit life? What are the important oxidation-reduction processes and are they unique or important to humankind? How does this biosphere influence global energy and material cycles, particularly the carbon cycle? Finally, can we discern how such life evolved in geological settings beneath the ocean floor, and how this might relate to ideas about the origin of life on our planet?

C-DEBI's scientific goals are pursued with a combination of approaches:
(1) coordinate, integrate, support, and extend the research associated with four major programs—Juan de Fuca Ridge flank (JdF), South Pacific Gyre (SPG), North Pond (NP), and Dorado Outcrop (DO)—and other field sites;
(2) make substantial investments of resources to support field, laboratory, analytical, and modeling studies of the deep subseafloor ecosystems;
(3) facilitate and encourage synthesis and thematic understanding of submarine microbiological processes, through funding of scientific and technical activities, coordination and hosting of meetings and workshops, and support of (mostly junior) researchers and graduate students; and
(4) entrain, educate, inspire, and mentor an interdisciplinary community of researchers and educators, with an emphasis on undergraduate and graduate students and early-career scientists.

Note: Katrina Edwards was a former PI of C-DEBI; James Cowen is a former co-PI.

Data Management:
C-DEBI is committed to ensuring all the data generated are publically available and deposited in a data repository for long-term storage as stated in their Data Management Plan (PDF) and in compliance with the NSF Ocean Sciences Sample and Data Policy. The data types and products resulting from C-DEBI-supported research include a wide variety of geophysical, geological, geochemical, and biological information, in addition to education and outreach materials, technical documents, and samples. All data and information generated by C-DEBI-supported research projects are required to be made publically available either following publication of research results or within two (2) years of data generation.

To ensure preservation and dissemination of the diverse data-types generated, C-DEBI researchers are working with BCO-DMO Data Managers make data publicly available online. The partnership with BCO-DMO helps ensure that the C-DEBI data are discoverable and available for reuse. Some C-DEBI data is better served by specialized repositories (NCBI's GenBank for sequence data, for example) and, in those cases, BCO-DMO provides dataset documentation (metadata) that includes links to those external repositories.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0939564

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