

# Genome Sequence of “*Candidatus Thioglobus autotrophica*” Strain EF1, a Chemoautotroph from the SUP05 Clade of Marine Gammaproteobacteria

Vega Shah, Robert M. Morris

School of Oceanography, University of Washington, Seattle, Washington, USA

**Chemoautotrophic marine bacteria from the SUP05 clade of marine gammaproteobacteria often dominate low-oxygen waters in upwelling regions, fjords, and hydrothermal systems. Here, we announce the complete genome sequence of “*Candidatus Thioglobus autotrophica*” strain EF1, the first cultured chemoautotrophic representative from the SUP05 clade.**

Received 20 August 2015 Accepted 23 September 2015 Published 22 October 2015

**Citation** Shah V, Morris RM. 2015. Genome sequence of “*Candidatus Thioglobus autotrophica*” strain EF1, a chemoautotroph from the SUP05 clade of marine gammaproteobacteria. *Genome Announc* 3(5):e01156-15. doi:10.1128/genomeA.01156-15.

**Copyright** © 2015 Shah and Morris. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Robert M. Morris, [morrisrm@uw.edu](mailto:morrisrm@uw.edu).

Chemoautotrophic members of the SUP05 clade of marine gammaproteobacteria are abundant in the suboxic ocean (1–4). They are of particular interest because of their potential to mediate biogeochemical cycles in anoxic fjords, upwelling zones, and sulfidic regions, like the Black Sea (5–7). Cultivation-independent studies suggest that SUP05 organisms have critical roles in carbon fixation, denitrification, and sulfur oxidation (5, 8, 9). Here, we announce the complete genome sequence of “*Candidatus Thioglobus autotrophica*” strain EF1, the first cultured chemoautotrophic representative from the SUP05 clade. “*Ca. Thioglobus autotrophica*” EF1 is a member of the *sup05* subclade (designated here by lowercase italics) and was isolated from a redox gradient (60 m) in Effingham Inlet, British Columbia, Canada. The complete genome of “*Ca. Thioglobus autotrophica*” EF1 is circular, 1,512,449 bp long, and codes for 1,637 genes.

Genomic DNA was extracted from a total of 62 pure cultures grown anaerobically in 100-ml bottles. Cells were grown to early stationary phase ( $\sim 2.0 \times 10^6$  cells/ml) and then collected on sterile Supor-200 0.2- $\mu$ M polyethersulfone filters (Pall Corporation, Port Washington, NY). DNA was extracted as previously described (10). 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. *De novo* assembly of the “*Ca. Thioglobus autotrophica*” EF1 genome was conducted using Hierarchical Genome Assembly Process (HGAP), as previously described (11). 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 and complete *de novo* assemblies for small prokaryotic genomes (12). HGAP assembly of the “*Ca. Thioglobus autotrophica*” EF1 genome resulted in a single contiguous sequence that was closed using a single PCR. The complete genome sequence of “*Ca. Thioglobus autotrophica*” EF1 used 100% of the cleaned reads, with an average coverage of  $106\times$ , indicating high confidence in a single circular chromosome of 1,512,449 bp in length. Protein-coding

sequences were identified and annotated via the NCBI Prokaryotic Genome Annotation Pipeline and were checked against RAST annotations (13, 14), IMG annotations (15), and, in some cases, by phylogenetic analyses. Discrepancies were corrected, and final annotations were submitted to NCBI.

**Nucleotide sequence accession number.** The complete genome sequence of “*Ca. Thioglobus autotrophica*” strain EF1 is available in GenBank under the accession no. CP010552.

## ACKNOWLEDGMENTS

We thank Richard Keil and the captain and crew of the *RV Thompson* for their assistance in collecting the samples used to isolate “*Ca. Thioglobus autotrophica*” EF1 during the University of Washington undergraduate senior thesis cruise of 2013.

Sequencing, assembly, and annotation were supported by the National Science Foundation (NSF) grants OCE-1232840, OCE-1205232, and DGE-1068839.

## REFERENCES

- Sunamura M, Higashi Y, Miyako C, Ishibashi J, Maruyama A. 2004. Two bacteria phylotypes are predominant in the Suiyo seamount hydrothermal plume. *Appl Environ Microbiol* 70:1190–1198. <http://dx.doi.org/10.1128/AEM.70.2.1190-1198.2004>.
- Lavik G, Stührmann T, Brüchert V, Van der Plas A, Mohrholz V, Lam P, Mussmann M, Fuchs BM, Amann R, Lass U, Kuypers MMM. 2009. Detoxification of sulphidic African shelf waters by blooming chemolithotrophs. *Nature* 457:581–584. <http://dx.doi.org/10.1038/nature07588>.
- Canfield DE, Stewart FJ, Thamdrup B, De Brabandere L, Dalsgaard T, Delong EF, Revsbech NP, Ulloa O. 2010. A cryptic sulfur cycle in oxygen-minimum-zone waters off the Chilean coast. *Science* 330:1375–1378. <http://dx.doi.org/10.1126/science.1196889>.
- Beman JM, Carolan MT. 2013. Deoxygenation alters bacterial diversity and community composition in the ocean’s largest oxygen minimum zone. *Nat Commun* 4:2705. <http://dx.doi.org/10.1038/ncomms3705>.
- Hawley AK, Brewer HM, Norbeck AD, Paša-Tolić L, Hallam SJ. 2014. Metaproteomics reveals differential modes of metabolic coupling among ubiquitous oxygen minimum zone microbes. *Proc Natl Acad Sci U S A* 111:11395–11400. <http://dx.doi.org/10.1073/pnas.1322132111>.
- Zaikova E, Walsh DA, Stilwell CP, Mohn WW, Tortell PD, Hallam SJ. 2010. Microbial community dynamics in a seasonally anoxic fjord: Saanich Inlet, British Columbia. *Environ Microbiol* 12:172–191. <http://dx.doi.org/10.1111/j.1462-2920.2009.02058.x>.

7. Glaubitz S, Kiesslich K, Meeske C, Labrenz M, Jurgens K. 2013. SUP05 dominates the gammaproteobacterial sulfur oxidizer assemblages in pelagic redoxclines of the central Baltic and Black Seas. *Appl Environ Microbiol* 79:2767–2776. <http://dx.doi.org/10.1128/AEM.03777-12>.
8. Walsh DA, Zaikova E, Howes CG, Song YC, Wright JJ, Tringe SG, Tortell PD, Hallam SJ. 2009. Metagenome of a versatile chemolithoautotroph from expanding oceanic dead zones. *Science* 326:578–582. <http://dx.doi.org/10.1126/science.1175309>.
9. Mattes TE, Nunn BL, Marshall KT, Proskurowski G, Kelley DS, Kawka OE, Goodlett DR, Hansell DA, Morris RM. 2013. Sulfur oxidizers dominate carbon fixation at a biogeochemical hot spot in the dark ocean. *ISME J* 7:2349–2360. <http://dx.doi.org/10.1038/ismej.2013.113>.
10. Marshall KT, Morris RM. 2013. Isolation of an aerobic sulfur oxidizer from the SUP05/Arctic96BD-19 clade. *ISME J* 7:452–455. <http://dx.doi.org/10.1038/ismej.2012.78>.
11. Koren S, Schatz MC, Walenz BP, Martin J, Howard JT, Ganapathy G, Wang Z, Rasko DA, McCombie WR, Jarvis ED, Phillippy AM. 2012. Hybrid error correction and *de novo* assembly of single-molecule sequencing reads. *Nat Biotechnol* 30:693–700. <http://dx.doi.org/10.1038/nbt.2280>.
12. Roberts RJ, Carneiro MO, Schatz MC. 2013. The advantages of SMRT sequencing. *Genome Biol* 14:405. <http://dx.doi.org/10.1186/gb-2013-14-7-405>.
13. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
14. Overbeek R, Olson R, Pusch GD, Olsen GJ, Davis JJ, Disz T, Edwards RA, Gerdes S, Parrello B, Shukla M, Vonstein V, Wattam AR, Xia F, Stevens R. 2014. The SEED and the rapid annotation of microbial genomes using subsystems technology (RAST). *Nucleic Acids Res* 42:D206–D214. <http://dx.doi.org/10.1093/nar/gkt1226>.
15. Markowitz VM, Chen IM, Palaniappan K, Chu K, Szeto E, Grechkin Y, Ratner A, Jacob B, Huang J, Williams P, Huntemann M, Anderson I, Mavromatis K, Ivanova NN, Kyrpides NC. 2012. IMG: the integrated microbial genomes database and comparative analysis system. *Nucleic Acids Res* 40:D115–D122. <http://dx.doi.org/10.1093/nar/gkr1044>.