Draft Genome Sequence of *Desulfovibrio sulfodismutans* ThAc01, a Heterotrophic Sulfur-Disproportionating Member of the *Desulfobacterota*

**Lewis M. Ward,a,b Emma Bertran,a,c David T. Johnston**

**Department of Earth and Planetary Sciences, Harvard University, Cambridge, Massachusetts, USA**
**Earth-Life Science Institute, Tokyo Institute of Technology, Tokyo, Japan**
**Department of Geosciences, Princeton University, Princeton, New Jersey, USA**

**ABSTRACT** Here, we describe the genome of *Desulfovibrio sulfodismutans* ThAc01, a *Desulfobacterota* member first isolated from freshwater mud and the first strain reported to be capable of growth via sulfur disproportionation. As such, this genome expands our understanding of the diversity of sulfur-disproportionating microorganisms.

*Desulfovibrio sulfodismutans* ThAc01 was first isolated from freshwater marine mud and was the first organism characterized as capable of growth via the disproportionation of either sulfite or thiosulfate to sulfide and sulfate (1, 2). Unlike many sulfur disproportionators that are incapable of growth via sulfate reduction (e.g., see reference 3), *D. sulfodismutans* is also able to grow via sulfate reduction coupled to the oxidation of small organic compounds, although this does result in slower growth than that during disproportionation (2). *D. sulfodismutans* was sequenced as part of a larger study to identify genetic markers to distinguish sulfate-reducing organisms from sulfur-disproportionating organisms (4–6).

Purified genomic DNA was ordered from the DSMZ. *D. sulfodismutans* was grown anaerobically at 35°C in medium 641 prior to DNA extraction at the DSMZ with a JetFlex genomic DNA purification kit from GenoMed. After submission to MicrobesNG, DNA libraries were prepared using a Nextera XT library preparation kit with a Hamilton Microlab STAR automated liquid-handling system. Libraries were sequenced by using an Illumina HiSeq 250-bp paired-end protocol. Adapters were trimmed from reads using Trimmomatic v0.30 (7), and *de novo* assembly was performed using SPAdes v3.7 (8). Annotation was performed using RAST v2.0 (9). Genome completeness was estimated with CheckM v1.0.12 (10), and the likelihood of the presence or absence of metabolic pathways was estimated with MetaPOAP v1.0 (11). The taxonomic assignment of the genome was determined with GTDB-Tk v0.3.2 (12). Hydrogenase proteins were classified with HydDB (13). All software was run using default parameters.

The *D. sulfodismutans* genome was recovered at 108× coverage as 1,080,467 reads, which were assembled into 295 contigs. The draft genome has an N\textsubscript{50} value of 37,406 bp and totals 4,376,887 bp, with 4,454 coding sequences and 54 RNAs. The genome has a GC content of 63.5%. The genome was determined to be 100% complete and 0.6% redundant and to have 0% strain heterogeneity by CheckM, based on the presence of conserved single-copy marker genes.

Metabolic pathways for sulfur disproportionation are expected to be indistinguishable from those for dissimilatory sulfate reduction (e.g., see reference 14); consistent with this expectation, the *D. sulfodismutans* genome encodes a full dissimilatory sulfate reduction pathway, including sulfate adenyltransferase, adenylylsulfate reductase, dissimilatory sulfite reductase, and the sulfite reduction-associated DsrMKJOP complex.

**Citation** Ward LM, Bertran E, Johnston DT. 2020. Draft genome sequence of *Desulfovibrio sulfodismutans* ThAc01, a heterotrophic sulfur-disproportionating member of the *Desulfobacterota*. Microbiol Resour Announc 9:e00202-20. https://doi.org/10.1128/MRA.00202-20.

**Editor** J. Cameron Thrash, University of Southern California

**Copyright** © 2020 Ward et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Lewis M. Ward, lewis_ward@fas.harvard.edu.

Received 26 February 2020
Accepted 6 March 2020
Published 26 March 2020
The *D. sulfodismutans* genome encodes a group A FeFe hydrogenase and a group 4e NiFe hydrogenase, as determined by HydDB. The *D. sulfodismutans* genome encodes a flagellum, consistent with the description of *D. sulfodismutans* as a motile organism (2). While truncation of the C-terminal domain of AprB was recently proposed as a marker for sulfur disproportionation in diverse bacteria (4), this marker is not present in *D. sulfodismutans* (i.e., the genome encodes a full-length AprB). This trait may be related to the ability of *D. sulfodismutans* to grow facultatively as a sulfur disproportionator or a sulfate reducer, in contrast to obligate sulfur-disproportionating organisms in the genus *Desulfofundus*, the genomes of which encode the truncated AprB.

Taxonomic assignment by GTDB-Tk places *D. sulfodismutans* in the Desulfovibrionaceae family of the Desulfobacterota phylum (formerly Deltaproteobacteria); however, GTDB-Tk does not place *D. sulfodismutans* within the genus *Desulfovibrio* but instead suggests that it may represent a separate novel genus-level lineage and therefore may require taxonomic reassignment.

Data availability. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under accession number JAAGRQ00000000. The FASTQ files of the raw reads were deposited in the NCBI SRA under accession number SRR11035950.

ACKNOWLEDGMENTS

Genomic DNA for strain DSM3696 was acquired from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ). Genome sequencing was provided by MicrobesNG, which is supported by the Biotechnology and Biological Sciences Research Council (grant BB/L024209/1). L.M.W. acknowledges support from an Agouron Institute postdoctoral fellowship and a Simons Foundation postdoctoral fellowship in marine microbial ecology. E.B. acknowledges the National Science Foundation (grant EAR-1149555) and D.T.J. acknowledges NASA Exobiology (grant NNX15AP58G) for funding this work.

REFERENCES

1. Bak F, Cypionka H. 1987. A novel type of energy metabolism involving fermentation of inorganic sulphur compounds. Nature 326:891–892. https://doi.org/10.1038/326891a0.

2. Bak F, Pfennig N. 1987. Chemolithotrophic growth of *Desulfovibrio sulfodismutans* sp. nov. by disproportionation of inorganic sulfur compounds. Arch Microbiol 147:184–189. https://doi.org/10.1007/BF00415282.

3. Firstner K, Liesack W, Thamdrup BO. 1998. Elemental sulfur and thiosulfate disproportionation by *Desulfocapsa sulfosolvens* sp. nov., a new anaerobic bacterium isolated from marine surface sediment. Appl Environ Microbiol 64:119–125. https://doi.org/10.1128/AEM.64.1.119-125.1998.

4. Bertran E. 2019. Cellular and intracellular insights into microbial sulfate reduction and sulfur disproportionation. PhD dissertation. Harvard University, Cambridge, MA.

5. Bertran E, Ward LM, Johnston DT. 2020. Draft genome sequence of *Acidianus ambivalens* DSM 3772, an aerobic thermophilic sulfur disproportionator. Microbiol Resour Announc 9:e01415-19. https://doi.org/10.1128/MRA.01415-19.

6. Bertran E, Ward LM, Johnston DT. 2020. Draft genome sequence of *Desulfobulbus* sp. nov., a new anaerobic bacterium isolated from marine surface sediment. Appl Environ Microbiol 64:119–125. https://doi.org/10.1128/AEM.64.1.119-125.1998.

7. Bolger AM, Lohse M, Usadel B. 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 30:2114–2120. https://doi.org/10.1093/bioinformatics/btu170.

8. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pjibelski AD, Pyshkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021.

9. Aziz RK, Bartels D, Best AA, DeLongh M, Disz T, Edwards RA, Formsmma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil KL, 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. https://doi.org/10.1186/1471-2164-9-75.

10. Parks DH, Imelfort M, Skennerton CT, Hugenholtz P, Tyson GW. 2015. CheckM: assessing the quality of microbial genomes recovered from isolates, single cells, and metagenomes. Genome Res 25:1043–1055. https://doi.org/10.1101/gr.186072.114.

11. Ward LM, Shih PM, Fischer WW. 2018. MetaPOAP: presence or absence of metabolic pathways in metagenome-assembled genomes. Bioinformatics 34:4284–4286. https://doi.org/10.1093/bioinformatics/bty510.

12. Parks DH, Chuvchina M, Waite DW, Rinke C, Skarshewski A, Chaumeil PA, Hugenholtz P. 2018. A standardized bacterial taxonomy based on genome phylogeny substantially revises the tree of life. Nat Biotechnol 36:996–1004. https://doi.org/10.1038/nbt.4229.

13. Sandgrenaard D, Pedersen CN, Greening C. 2016. HydDB: a Web tool for hydrogenase classification and analysis. Sci Rep 6:34212. https://doi.org/10.1038/srep34212.

14. Anthanatharama K, Hausmann B, Jungbluth SP, Kantor RS, Lavy A, Warren LA, Rappé MS, Pester M, Loy A, Thomas BC, Banfield JF. 2018. Expanded diversity of microbial groups that shape the dissimilatory sulfur cycle. ISME J 12:1715–1728. https://doi.org/10.1038/s41396-018-0078-0.