



High-Quality Draft Genome Sequence of *Desulfovibrio carbinoliphilus* FW-101-2B, an Organic Acid-Oxidizing Sulfate-Reducing Bacterium Isolated from Uranium(VI)-Contaminated Groundwater

Bradley D. Ramsay,^a Chiachi Hwang,^a  Hannah L. Woo,^b Sue L. Carroll,^c Susan Lucas,^d James Han,^d Alla L. Lapidus,^d Jan-Fang Cheng,^d Lynne A. Goodwin,^d Samuel Pitluck,^d Lin Peters,^d Olga Chertkov,^d Brittany Held,^d John C. Detter,^d Cliff S. Han,^d Roxanne Tapia,^d Miriam L. Land,^d Loren J. Hauser,^d Nikos C. Kyrpides,^d Natalia N. Ivanova,^d Natalia Mikhailova,^d Ioanna Pagani,^d Tanja Woyke,^d Adam P. Arkin,^{e,f} Paramvir Dehal,^{e,f} Dylan Chivian,^{e,f} Craig S. Criddle,^g Weimin Wu,^g Romy Chakraborty,^{f,h} Terry C. Hazen,^{b,f,i,j}  Matthew W. Fields^{a,f,k}

Center for Biofilm Engineering, Montana State University, Bozeman, Montana, USA^a; Department of Civil and Environmental Engineering, The University of Tennessee, Knoxville, Tennessee, USA^b; Environmental Sciences Division, Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA^c; Department of Energy Joint Genome Institute, Walnut Creek, California, USA^d; Physical Biosciences Division, Lawrence Berkeley National Laboratory, Berkeley, California, USA^e; ENIGMA, Lawrence Berkeley National Laboratory, Berkeley, California, USA^f; Department of Civil and Environmental Engineering, Stanford University, Stanford, California, USA^g; Earth Sciences Division, Lawrence Berkeley National Laboratory, Berkeley, California, USA^h; Department of Microbiology, The University of Tennessee, Knoxville, Tennessee, USAⁱ; Department of Earth & Planetary Sciences, The University of Tennessee, Knoxville, Tennessee, USA^j; Department of Microbiology & Immunology, Montana State University, Bozeman, Montana, USA^k

***Desulfovibrio carbinoliphilus* subsp. *oakridgensis* FW-101-2B is an anaerobic, organic acid/alcohol-oxidizing, sulfate-reducing δ -proteobacterium. FW-101-2B was isolated from contaminated groundwater at The Field Research Center at Oak Ridge National Lab after *in situ* stimulation for heavy metal-reducing conditions. The genome will help elucidate the metabolic potential of sulfate-reducing bacteria during uranium reduction.**

Received 23 January 2015 Accepted 2 February 2015 Published 12 March 2015

Citation Ramsay BD, Hwang C, Woo HL, Carroll SL, Lucas S, Han J, Lapidus AL, Cheng J-F, Goodwin LA, Pitluck S, Peters L, Chertkov O, Held B, Detter JC, Han CS, Tapia R, Land ML, Hauser LJ, Kyrpides NC, Ivanova NN, Mikhailova N, Pagani I, Woyke T, Arkin AP, Dehal P, Chivian D, Criddle CS, Wu W, Chakraborty R, Hazen TC, Fields MW. 2015. High-quality draft genome sequence of *Desulfovibrio carbinoliphilus* FW-101-2B, an organic acid-oxidizing sulfate-reducing bacterium isolated from uranium(VI)-contaminated groundwater. *Genome Announc* 3(2):e00092-15. doi:10.1128/genomeA.00092-15.

Copyright © 2015 Ramsay et al. 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 Terry C. Hazen, tchazen@utk.edu, or Matthew W. Fields, matthew.fields@biofilm.montana.edu.

Desulfovibrio carbinoliphilus subsp. *oakridgensis* FW-101-2B was isolated from groundwater of well FW-101 at The Field Research Center (FRC) at Oak Ridge National Lab (ORNL). The FRC is part of the Y-12 security complex, located in the Bear Creek drainage. ICP-MS analysis of FW-101 groundwater in late 2001 estimated uranium concentrations between 20 and 250 ppm, and chromium concentrations between 35 and 85 ppm. Previous studies have demonstrated reduction of nitrate and uranium levels in the subsurface upon bio-stimulation with ethanol at the FRC (1–3). During bio-stimulation, an increase was observed in DNA sequences corresponding to sulfate-reducing bacteria. Groundwater from well FW-101 at the FRC site was collected during the uranium-reduction phase of a previously described biostimulation experiment (3) and used as inoculum for an enrichment culture for sulfate-reducing bacteria. The enrichment was grown at room temperature anaerobically in ES4D medium (pH 6.7). The ES4D medium has the same ingredients as a previously described medium, LS4D, except ethanol replaced the lactate (4).

The genome was sequenced by 454 GS FLX Titanium and paired-end Illumina GAii (2×35 bp). The pyrosequencing and Illumina reads were assembled using the Newbler (Roche) and Velvet (5), respectively. Phred/Phrap/Consed (<http://www.phrap.com>) was used for genome finishing. Genes were identified using Prodigal (6) and used to search the National Center for Biotechnology Information (NCBI) nonredundant database, UniProt,

TIGRFam, Pfam, PRIAM, KEGG, COG, and InterPro databases. Additional annotation was performed within the (IMG-ER) platform (7).

Sequence determination revealed a 4.1-Mb genome with 66.5% G+C content, which is comparable to *D. carbinoliphilus* (63% G+C) and *Desulfovibrio vulgaris* (63.3% G+C). The COG predictions categorize 581 of the 3,737 protein-encoding genes as pertaining to information storage and processing, 1,183 as cellular processes, 1,576 as metabolism genes, and 596 as poorly characterized functions. Sequencing detected 2 plasmids of different sizes and G+C content, pFW10101 (97,864 bp, 67% G+C) and pFW10102 (21,111 bp, 57.5% G+C).

FW-101-2B was most closely related to *D. carbinoliphilus* D41^T. The ANIb values calculated by JSpecies (8) showed that FW-101-2B was more similar to *D. vulgaris* Miyazaki (69.11%), *D. vulgaris* Hildenborough (67.45%), and *D. vulgaris* DP4 (67.41%) than *Syntrophobacter fumaroxidans* (64.68) and *Desulfovibrio desulfuricans* ATCC 27774 (60.93%). The small-subunit (SSU) rRNA gene and sulfite reductase gene (*dsrAB*) of FW-101-2B was most similar to *D. carbinoliphilus* D41^T at 99% and 92% similarity, respectively.

Although FW-101-2B is phylogenetically very similar to *D. carbinoliphilus* D41^T, physiological evidence would support classification of a new strain. Thus, we propose the classification as *D.*

carbinoliphilus subsp. *oakridgensis*. This is the first genome sequence of a *D. carbinoliphilus* strain.

Nucleotide sequence accession numbers. The whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. [ADFE00000000](https://www.ncbi.nlm.nih.gov/nuccore/ADFE00000000). The version described in this paper is the version [ADFE00000000.2](https://www.ncbi.nlm.nih.gov/nuccore/ADFE00000000.2).

ACKNOWLEDGMENTS

Work conducted by ENIGMA (Ecosystems and Networks Integrated with Genes and Molecular Assemblies) is supported by the Office of Science, Office of Biological and Environmental Research, U.S. Department of Energy contract DE-AC02-05CH11231. The work at Lawrence Livermore National Laboratory was supported under contract DE-AC52-07NA27344, and work at Los Alamos National Laboratory was supported under contract DE-AC02-06NA25396.

REFERENCES

1. Wu W-M, Carley J, Luo J, Ginder-Vogel MA, Cardenas E, Leigh MB, Hwang C, Kelly SD, Ruan C, Wu L, Van Nostrand J, Gentry T, Lowe K, Mehlhorn T, Carroll S, Luo W, Fields MW, Gu B, Watson D, Kemner KM, Marsh T, Tiedje J, Zhou J, Fendorf S, Kitanidis PK, Jardine PM, Criddle CS. 2007. *In situ* bioreduction of uranium (VI) to submicromolar levels and reoxidation by dissolved oxygen. *Environ Sci Technol* 41: 5716–5723. <http://dx.doi.org/10.1021/es062657b>.
2. Wu W, Carley J, Watson D, Gu B, Brooks S, Kelly SD, Kemner K, van Nostrand JD, Wu L, Xu M, Zhou J, Luo J, Cardenas E, Hwang C, Fields MW, Marsh TL, Tiedje JM, Green SJ, Kostka JE, Kitanidis PK, Jardine PM, Criddle CS. 2011. Bioreduction and immobilization of uranium *in situ*: a case study at a USA Department of Energy radioactive waste site, Oak Ridge, Tennessee. *Huanjing Kexue Xuebao* 31:449–459.
3. Hwang C, Wu W, Gentry TJ, Carley J, Corbin GA, Carroll SL, Watson DB, Jardine PM, Zhou J, Criddle CS, Fields MW. 2009. Bacterial community succession during *in situ* uranium bioremediation: spatial similarities along controlled flow paths. *ISME J* 3:47–64. <http://dx.doi.org/10.1038/ismej.2008.77>.
4. Clark ME, He Q, He Z, Huang KH, Alm EJ, Wan X-F, Hazen TC, Arkin AP, Wall JD, Zhou J-Z, Fields MW. 2006. Temporal transcriptomic analysis as *Desulfovibrio vulgaris* Hildenborough transitions into stationary phase during electron donor depletion. *Appl Environ Microbiol* 72: 5578–5588. <http://dx.doi.org/10.1128/AEM.00284-06>.
5. Zerbino DR, Birney E. 2008. Velvet: algorithms for *de novo* short read assembly using de Bruijn graphs. *Genome Res* 18:821–829. <http://dx.doi.org/10.1101/gr.074492.107>.
6. Hyatt D, Chen G-L, LoCascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. *BMC Bioinformatics* 11:119. <http://dx.doi.org/10.1186/1471-2105-11-119>.
7. Markowitz VM, Mavromatis K, Ivanova NN, Chen IM, Chu K, Kyrpides NC. 2009. IMG ER: a system for microbial genome annotation expert review and curation. *Bioinformatics* 25:2271–2278. <http://dx.doi.org/10.1093/bioinformatics/btp393>.
8. Richter M, Rosselló-Móra R. 2009. Shifting the genomic gold standard for the prokaryotic species definition. *Proc Natl Acad Sci U S A* 106: 19126–19131. <http://dx.doi.org/10.1073/pnas.0906412106>.