

# Draft Genome Sequence of the Obligately Alkaliphilic Sulfate-Reducing Bacterium *Desulfonatronum thiodismutans* Strain MLF1

Denis Trubitsyn,<sup>a</sup> Corey Geurink,<sup>a</sup> Elena Pikuta,<sup>b</sup> Christopher T. Lefèvre,<sup>c</sup> W. Michael McShan,<sup>d</sup> Allison F. Gillaspay,<sup>e</sup> Dennis A. Bazylinski<sup>a</sup>

School of Life Sciences, University of Nevada at Las Vegas, Las Vegas, Nevada, USA<sup>a</sup>; Department of Mathematical, Computer and Natural Sciences, Athens State University, Athens, Alabama, USA<sup>b</sup>; CEA/CNRS/Aix-Marseille Université, Biologie Végétale et Microbiologie Environnementales, Laboratoire de Bioénergétique Cellulaire, Saint Paul, France lez Durance, France<sup>c</sup>; Department of Pharmaceutical Sciences, University of Oklahoma Health Sciences Center, Oklahoma City, Oklahoma, USA<sup>d</sup>; The Laboratory for Molecular Biology and Cytometry Research/Genomics Division, University of Oklahoma Health Sciences Center, Oklahoma City, Oklahoma, USA<sup>e</sup>

***Desulfonatronum thiodismutans* strain MLF1, an alkaliphilic bacterium capable of sulfate reduction, was isolated from Mono Lake, California. Here we report the 3.92-Mb draft genome sequence comprising 34 contigs and some results of its automated annotation. These data will improve our knowledge of mechanisms by which bacteria withstand extreme environments.**

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Address correspondence to Dennis A. Bazylinski, dennis.bazylinski@unlv.edu.

Highly alkaline aquatic environments (pH >9.0) are relatively uncommon on Earth and include soda lakes (some of which are hypersaline) and some hydrothermal springs. Despite the hostile conditions in soda lakes, they are among the most productive aquatic environments on the planet (1, 2). Prokaryotes whose growth and survival depends on high pH are termed alkaliphiles (2). Alkaliphilic bacteria face the major problem of maintaining an internal pH at a level not higher than approximately pH 8.5 and use a number of strategies to mitigate this problem (2). The enzymes of alkaliphiles have been used in a variety of industrial applications (e.g., alkaline proteases are widely used in the detergent industry) (3). A good example of an obligate alkaliphile is *Desulfonatronum thiodismutans*, an anaerobic sulfate-reducing bacterium isolated from Mono Lake, California (4). This species grows chemolithoautotrophically or chemolithoheterotrophically on hydrogen gas. It appears to possess a high affinity to molecular hydrogen and in natural ecosystems it is found in tight symbiotic relations with primary anaerobes (e.g., saccharolytic spirochetes) that produce hydrogen as a product of fermentation (4).

The genome of *D. thiodismutans* strain MLF1 was sequenced with an Illumina MiSeq instrument using paired-end 150-bp chemistry. Sequencing resulted in 5,840,423 mapped reads with a mean length of 190. 5,320,956 reads were in aligned pairs, with a mean distance of 241. Paired reads were assembled *de novo* using CLC Genomics Workbench, and contigs with a length of >2 kb were considered for further analysis. The genome size for *D. thiodismutans* was previously estimated to be  $\sim 1.6 \times 10^9$  Da ( $\sim 2.88$  Mb) (4). Based on this genome size, our sequencing coverage was  $\sim 280$ -fold. The *de novo* assembly resulted in a draft genome comprising 34 contigs with a total of 3,923,724 bp. The mean G+C content determined by genome sequencing is 58.74% (compared to  $59.0 \pm 0.1$  mol% as determined by high-pressure liquid chromatography [HPLC]) (4, 5). Automated annotation by RAST (6) generated 3,737 predicted coding sequences, including 1,329 hypothetical proteins and 51 total RNAs. Our results are

similar to those of *Desulfonatronum lacustre* DSM 10312, whose genome size was determined to be 3,761,451 bp (GenBank accession number JAFE01000000). Although both species share many phenotypic similarities, including the dissimilatory sulfate reduction and the requirement for high pH for growth, the genome of *D. thiodismutans* contains 78 unique genes, based on a function-based comparison in RAST, while that of *D. lacustre* DSM 10312 contains 74 unique genes. For example, *D. thiodismutans* possesses genes involved in capsule formation and for encoding a beta-lactamase.

Our genomic study of *D. thiodismutans* should provide valuable information on the evolution and mechanisms of alkalitolerance, lithotrophy, and the inorganic fermentation of thiosulfates and sulfites. In addition, some magnetotactic bacteria appear to be strains of *D. thiodismutans* (7, 8). Genome comparisons between these and the type strain might provide evidence on how magnetosome genes are acquired (e.g., by horizontal gene transfer) or lost.

**Nucleotide sequence accession number.** This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession number [JPIK00000000](http://www.ncbi.nlm.nih.gov/nuccore/JPIK00000000).

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