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Complete Genome Sequence and Updated Annotation of *Desulfovibrio alaskensis* G20▽

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***Desulfovibrio alaskensis* G20 (formerly *Desulfovibrio desulfuricans* G20) is a Gram-negative mesophilic sulfate-reducing bacterium (SRB), known to corrode ferrous metals and to reduce toxic radionuclides and metals such as uranium and chromium to sparingly soluble and less toxic forms. We present the 3.7-Mb genome sequence to provide insights into its physiology.**

Desulfovibrio desulfuricans G100A is a deltaproteobacterium that was isolated from a producing oil well in Ventura County, California (8). Strain G20 is a spontaneously nalidixic acid-resistant derivative of G100A that is also lacking the endogenous cryptic 2.3-kb plasmid, pBG1 (6).

Strictly anaerobic sulfate-reducing bacteria (SRB) of the *Desulfovibrio* genus have provided a rich experimental system for understanding energy conversion because of their ability to respire sulfate, ferment organic acids, and live in syntrophic associations. Hydrogen metabolism appears to be fundamental for these growth modes. In 1981, Odom and Peck (4) proposed the hydrogen-cycling model as an explanation for the hydrogen transients seen during growth on organic acids with sulfate. This model requires both cytoplasmic and periplasmic hydrogenases. As the second SRB to have a complete genome sequence available, G20 revealed the lack of conservation of annotated cytoplasmic hydrogenases necessary for this cycle. Therefore, either "hydrogen cycling" does not make an essential contribution to the SRB energy budget or different members of the genus have derived different solutions to the electron flow to sulfate. Importantly, these electron pathways are critical to understanding ferrous metal corrosion (5) and the capacity for reduction of toxic radionuclides and metals such as uranium and chromium to sparingly soluble and less toxic forms (3).

It was observed that the 16S rRNA gene sequence of *D. desulfuricans* G20 was >97% identical to those of *Desulfovibrio alaskensis*. DNA-DNA hybridization results (performed by Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH) between the G20 strain, *D. alaskensis* (ID 04-514), and the *D. desulfuricans* subsp. *desulfuricans* type strain DSM 642^T showed that G20 and *D. alaskensis* were 84.3% similar. With a 70% threshold value for definition of bacterial species (7), these strains are related at the species level. Neither belongs to the *D. desulfuricans* species. We propose reclassification of *D. desulfuricans* G20 as *Desulfovibrio alaskensis* G20.

The original genome annotation was performed as described in reference 1. To update the gene predictions, the gene-calling algorithm Prodigal (2) was used, and the two sets of gene calls were compared. All original genes not predicted by Prodigal were eliminated unless there were shotgun proteomic or gene expression array data to support their inclusion (A. Arkin, personal communication). All other differences were resolved manually. The updated annotation is available at http://genome.ornl.gov/microbial/ddes.

The *D. alaskensis* G20 genome is 57.8% GC and contains 3.7 Mbps, 66 tRNA genes, and 4 rRNA cistrons. The original annotation predicted 3,775 protein coding genes and 9 pseudogenes, whereas the updated annotation predicts 3,258 protein coding genes and 25 pseudogenes. The updated annotation confirmed 2,834 genes, lengthened 74, shortened 280, added 54, deleted 554 genes, changed 19 to pseudogenes, changed 2 pseudogenes to real genes, added 4 new pseudogenes, deleted 5 pseudogenes, and modified 14 other genes. Approximately 25% of the original protein coding genes were changed in some way.

Nucleotide sequence accession number. This genome has been deposited at DDBJ/EMBL/GenBank under the accession number CP000112. The version described in this paper is the second version.

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