

Genome Sequence of *Desulfovibrio* sp. A2, a Highly Copper Resistant, Sulfate-Reducing Bacterium Isolated from Effluents of a Zinc Smelter at the Urals

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***Desulfovibrio* sp. A2 is an anaerobic Gram-negative sulfate-reducing bacterium with remarkable tolerance to copper. It was isolated from wastewater effluents of a zinc smelter at the Urals. Here, we report the 4.2-Mb draft genome sequence of *Desulfovibrio* sp. A2 and identify potential copper resistance mechanisms.**

Sulfate-reducing bacteria (SRB) are anaerobic prokaryotes which are widely distributed in nature and can also be present in animals (4, 8, 10). SRB gain energy by dissimilatory reduction of sulfate. In ecosystems with elevated metal concentrations, the resulting sulfide leads to the formation of insoluble metal sulfides (2, 11). Here we present the draft genome sequence of *Desulfovibrio* sp. A2, a deltaproteobacterial, Gram-negative SRB isolated from a settling pond of the Chelyabinsk Electrolytic Zinc Smelter in the Urals, Russia (5). Genomic DNA was isolated from pure cultures by alkaline lysis (1). Pyrosequencing was carried out with the FLX genome sequencer (Roche, Switzerland). A total of 688,685 reads of an average length of 359 bp were assembled with the GS De Novo Assembler version 2.3 (Roche, Switzerland). This resulted in 90 contigs of an average size of 51,866 nucleotides, with the largest contig encompassing 282,791 nucleotides. The draft genome sequence thus consists of 4,154,665 bases with a GC content of 67.2% and a 60-fold sequencing coverage. Automatic gene annotation was carried out by the Institute for Genome Sciences (IGS; University of Maryland). The genome contains 3,885 candidate protein-encoding genes of an average size of 906 bp, in addition to 58 tRNA and 3 rRNA genes. Phylogenetic analysis of 16S rRNA genes placed *Desulfovibrio* sp. A2 (AY770382) in a cluster with *Desulfovibrio* sp. A1 (AY928661) and A4 (AY928662), which exhibit overall sequence similarity of 99.1 to 99.5% (5). *Desulfovibrio vulgaris* Miyazaki F (CP001197) was the most closely related strain with an annotated genome (overall sequence similarity, 99.1%).

Investigation of the role of sulfidogenesis by SRB in the formation of nonferrous metal sulfides and their use to precipitate metals is receiving increasing attention (3, 6, 7). Nevertheless, the response of SRB to toxic heavy metals is still poorly understood. *Desulfovibrio* sp. A2 was previously shown

to be able to tolerate up to 40 mM copper in liquid media under anoxic conditions, using lactate as electron donor and carbon source (5). Inspection of the draft genome suggests the presence of at least 7 genes involved in copper homeostasis: a putative CPx-type copper ATPase (DA2_3734) located close to a gene coding for a predicted cytoplasmic copper chaperone (DA2_3733), a three-component efflux transporter of the resistance nodulation cell division family (DA2_2500-2), a second cytoplasmic copper binding chaperone (DA2_1523), and a Cu-Fe protein (DA2_2478) related to a metal tolerance protein of *Desulfovibrio aminophilus* DSM12254 (9). Two additional CPx-type heavy metal ATPases (DA2_2201 and DA2_2368) could also be involved in copper tolerance. Finally, two multicopper oxidases of types 2 (DA2_547) and 3 (DA2_1349) could be involved in the oxidation of periplasmic Cu(I) to less toxic Cu(II). The presence of these latter oxygen-requiring enzymes is in line with the recent realization that *Desulfovibrio* and other SRB are not strict anaerobes but can tolerate oxygen and use it as an electron acceptor. Insight into the copper resistance mechanism of *Desulfovibrio* sp. A2 can now be gained through biochemical analysis of the putative copper-homeostatic genes, which is in progress in our laboratory.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. AGFG00000000. The version described in this paper is the first version, AGFG01000000.

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