

Antimony (Sb) is an industrially significant metalloid that has been exploited by humans for the last 3,000 years. Although Sb is more toxic than its well-known group 15 neighbor, arsenic, relatively little is known about the fate and transport of Sb in the environment, especially with respect to the involvement of microorganisms in mediating redox transformations. The isolation and description of the first microorganism capable of using antimonate [Sb(V)] as a terminal electron acceptor to support growth was accomplished. The microorganism, designated *Desulfuribacillus stibiiarsenatis* MLFW-2, was an obligately anaerobic member of the order *Bacillales* of the phylum *Firmicutes*. It was isolated from anoxic sediments collected from the drainage area of a geothermal spring near the southern shore of alkaline, hypersaline Mono Lake, CA. *D. stibiiarsenatis* was capable of using formate, lactate, pyruvate, or H<sub>2</sub> as electron donors with nitrate, nitrite, dimethylsulfoxide (DMSO), selenate [Se(VI)] selenite [Se(IV)], arsenate [As(V)], or Sb(V) as electron acceptors. Consistent with the environment from which it was isolated, *D. stibiiarsenatis* was found to be mesophilic, slightly alkaliphilic, and halotolerant. Dissimilatory Sb(V) reduction by *D. stibiiarsenatis* was accompanied by the precipitation of antimonite [Sb(III)] as microcrystals of antimony trioxide.

The genome of *D. stibiiarsenatis* was sequenced and 14 genes encoding the catalytic subunits of anaerobic respiratory reductases of the DMSO reductase (DMSOR) family of complex iron-sulfur molybdoenzymes were identified. The putative involvement of each of the genes in the anaerobic respiratory chain of *D. stibiiarsenatis* was evaluated by monitoring their relative expression during growth on nitrate, Se(VI), As(V), and Sb(V) using reverse transcription-quantitative polymerase chain reaction (RT-qPCR). The analyses identified the most probable terminal reductase for each of the oxyanions tested. Homologs of the potential operon encoding the terminal Sb(V) reductase were found to occur in microorganisms belonging to six different described phyla and two candidate phyla across both prokaryotic domains of life. Lastly, the physiological response of *D. stibiiarsenatis* to Sb(V) and As(V) was examined using RNA sequencing. Sb was found to elicit a stronger oxidative stress response than As, with the cell envelope, DNA, proteins, and cofactors being the primary targets of damage.