Members of the genus *Desulfotomaculum* are sulfate-reducing, spore-forming Gram-positive bacteria that are widely distributed within mesothermic and thermal ecosystems (1). Evidence of their presence in terrestrial geothermal hot springs has been obtained several times using molecular approaches (2), but only three species of this genus have been isolated so far, the most recent being *Desulfotomaculum hydrothermale* (3). Here, we report the first draft genome sequence of a *Desulfotomaculum* species isolated from a terrestrial hot spring in Tunisia: *D. hydrothermale*. The strain was shown to reductively detoxify arsenate ([As(V)]), in the presence of pyruvate as an electron donor, without the strain is able to reduce Fe(III) to Fe(II) (3). Metal reduction in this strain would use a different pathway, which needs to be specified. The *D. hydrothermale* genome encodes an arsenite resistance protein (DESHYv2_110039) that exhibits homology to the intrinsic membrane protein ArsB (8). A gene (DESHYv2_110038) encoding a transcriptional regulator belonging to the AsrR family (9) was found immediately upstream of *asrB*. Even if no homolog to the arsenate reductase gene *asrC* (10) has been identified so far, this gene cluster could be of great importance for arsenite reduction and for the tolerance capacity of this strain.

Insights into the arsenite resistance process of *Desulfotomaculum* species could be gained through comparative genomics and biochemical analyses of the arsenite resistance mechanisms, which are in progress in our laboratories.

**Nucleotide sequence accession numbers.** The whole-genome shotgun project has been deposited at DDBJ/EMBL/Genbank under the accession no. CAOS0100001 to CAOS01000016.

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