Complete Genome Sequence of the Subsurface, Mesophilic Sulfate-Reducing Bacterium *Desulfovibrio aespoeensis* Aspo-2

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*Desulfovibrio aespoeensis* Aspo-2, DSM 10631T, is a mesophilic, hydrogenotrophic sulfate-reducing bacterium sampled from a 600-m-deep subsurface aquifer in hard rock under the island of Åspö in southeastern Sweden. We report the genome sequence of this bacterium, which is a 3,629,109-bp chromosome; plasmids were not found.

*Desulfovibrio aespoeensis* was isolated from a borehole (KAS03) that intersected a water-conducting aquifer at 600-m depth (1). Knowledge about subsurface sulfate-reducing bacteria (SRB) is essential for evaluating adverse effects of their sulfate production on future spent nuclear fuel (SNF) waste repositories planned to be built 500 to 1,000 m underground. This is because metal canisters will be in use to encapsulate the SNF and many metals are susceptible to corrosion by sulfide (2). The safety case may consequently be challenged by subsurface SRB. Because *D. aespoeensis* readily reduces sulfate to sulfide with a very low $K_m$ for hydrogen (3), this species and other hydrogenotrophic SRB may increase anoxic corrosion rates of iron in SNF repositories (4). It has previously been shown that *D. aespoeensis* forms biofilms of metallic copper (5), which indicates the presence of genes involved in copper homeostasis (6). Since the isolation, this species and closely related strains (>98% 16S rRNA gene identity) have been found repeatedly in deep groundwater, strongly suggesting the deep biosphere as the natural habitat for *D. aespoeensis* (7, 8).

The draft genome of *Desulfovibrio aespoeensis* Aspo-2 was generated at the U.S. Department of Energy (DOE) Joint Genome Institute (JGI) using a combination of Illumina and 454 technologies (project 4086336 [NCBI project 37869], principal investigator [PI] Terry C. Hazen). An Illumina GAii shotgun library was generated at the U.S. Department of Energy (DOE) Joint Genome Institute through the Office of Science, Office of Biological and Environmental Research (BER), of the U.S. Department of Energy under contract number DE-AC02-05CH11231. The Swedish Research Council supported the isolation and phenotypic and phylogenetic characterizations of *D. aespoeensis*.

**Nucleotide sequence accession number.** The complete annotated genome of *D. aespoeensis* is available in Genbank under the accession no. CP002431.1.

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