Deep-sea sulfate-reducing microorganisms must be considered as key actors in Earth’s sulfur cycles. Metagenomic studies have revealed that sulfate-reducing bacteria (SRB) are largely represented among the microorganisms that inhabit deep-sea environments (1–3). However, only a few SRB have been isolated from deep-sea environments (4–9). Among them, the Desulfovibrio genus is well-represented, with Desulfovibrio profundus, Desulfovibrio piezophilus, and Desulfovibrio hydrothermalis having been isolated previously (7–9). Here, we report the genome sequence of D. hydrothermalis, a piezo-mesophilic, hydrogenotrophic SRB isolated from a deep-sea hydrothermal chimney sample collected at a depth of 2,600 m (13°N on the East Pacific Rise) (7). It represents, with D. piezophilus (10), the second known genome of piezophilic bacteria in the genus Desulfovibrio, and thus gives the opportunity to specify the systems that are involved in the piezophilic lifestyles of Desulfovibrio species.

Genome sequencing was performed by the Genoscope (CEA, Évry, France), using 454-sequencing method (Roche) and Solexa technology. A mate-paired genomic library with 8-kb insert size was prepared according to the manufacturer’s protocols (454 Life Sciences Corporation, Branford, CT). Approximately 19-fold coverage of GS FLX Titanium (http://www.roche.com/) reads was assembled using Newbler. Gaps between contigs were closed with 1,038 PCR amplifications and the Consed editing software (http://www.phrap.org/). For the quality assessment, approximately 1,000-fold coverage of paired-end Illumina reads (36 bp) was mapped onto the whole-genome sequence.

The genome consists of two contigs of 284,269 bp and 3,418,665 bp, for a total of 3,702,934 bp, and of a circular plasmid of 5,328 bp. The average G+C contents for the chromosome and the plasmid DNA are 45.1% and 51.1%, respectively. A total of 3,543 coding DNA sequences (CDSs) were predicted, as well as 7 pseudogenes, 6 miscellaneous RNAs (misc-RNA), 5 disrupted rRNA operons, and 77 tRNA genes.

Phylogenetic analysis based on 16S rRNA shows that the closest sequenced genomes to D. hydrothermalis are those of Desulfovibrio salexigens and Desulfovibrio aesoepsis. Reciprocal best BLAST analysis indicated that D. hydrothermalis shares 2,824 and 2,069 orthologous proteins with D. salexigens and D. aesoepsis, respectively, and 1,974 proteins are common to the three species.

Like other Desulfovibrio species, D. hydrothermalis possesses all the genes necessary for the sulfate-reduction pathway. Fatty acid membrane composition has been shown to play an important role in hydrostatic pressure adaptation (11). In D. hydrothermalis, all fatty acid biosynthesis pathways are present. Interestingly, three copies of the fabG gene (DESAMv2_20244, DESAMv2_21138, and DESAMv2_21153), encoding a β-ketoacyl-acyl carrier protein (ACP) synthase II involved in monounsaturated fatty acid production and suggested to be involved in hydrostatic pressure adaptation (11), are found in the genome. Thus, the three copies of this gene might play a pivotal role in the adaptation strategy of D. hydrothermalis to hydrostatic pressure.

Comparative genomics, including the use of other Desulfovibrio species, will give insights into the adaptation of Desulfovibrio species to the piezophilic lifestyle that they encounter in the deep-sea biosphere.

**Nucleotide sequence accession numbers.** The final annotated genome of D. hydrothermalis is available in EMBL under the accession no. FO203522 (for the chromosome) and FO203523 (for the plasmid).

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