Draft Genome Sequence of the Sulfur-Oxidizing Bacterium “*Candidatus Sulfurovum sediminum*” AR, Which Belongs to the *Epsilonproteobacteria*

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Sulfur-oxidizing bacteria are common microorganisms in a variety of sulfide-rich environments. They play important roles in the global sulfur cycle on earth. Here, we present a high-quality draft genome sequence of a sulfur-oxidizing bacterium, “*Candidatus Sulfurovum sediminum*” strain AR, which belongs to the class *Epsilonproteobacteria* and dominated an enrichment culture from a marine sediment collected off Svalbard, within the Arctic Circle. Its genome contains genes for sulfur oxidation and carbon fixation. The size of the draft genome is 2.12 Mb, and the G+C content is 39.4%.

Epsilonproteobacteria from various environments, including marine, freshwater, and deep-sea hydrothermal vents, have recently been identified as sulfur oxidizers by cultivation-independent methods (e.g., 16S rRNA gene sequencing) (1, 2, 12). They are capable of using sulfur compounds as an energy source and of performing carbon fixation through the reductive citric acid pathway (4, 7, 10). Despite the knowledge of these important contributions to the biogeochemical sulfur cycle, there are still many unanswered questions about the physiology and ecology of these microbes. Recently, the genome sequence of *Sulfurovum* sp. strain NCB37-1, a sulfur-oxidizing epsilonproteobacterium from deep-sea hydrothermal vents, was published (7). “*Candidatus Sulfurovum sediminum*” strain AR dominated an enrichment culture from a 78-m-deep marine sediment collected off Svalbard, within the Arctic Circle, when thiosulfate was used as the sole electron donor. Intriguingly, the enrichment contained ammonia-oxidizing archaea as well (9).

The genome of strain AR was sequenced by shotgun and mate-paired (library insert size of about 8 kb) end sequencing methods using the 454 GS-FLX Titanium platform (Roche Applied Science). Preparation and sequencing of the sample and analytical processing were performed according to the manufacturer's instructions at the National Instrumentation Center for Environmental Management, Seoul National University, Seoul South Korea. To increase the quality of the metagenomic sequences, we removed sequencing artifacts and short sequences. Assembly was performed using the Roche GS De Novo Assembler (Newbler assembler v. 2.3). The draft genome (ca. 2.12 Mb) contained 11 contigs and had a G+C content of 39.4%. Putative coding sequences (CDSs) were predicted using MetaGeneAnnotator, COG, Pfam, and RAST (3, 6, 8, 11). Of the 2,248 predicted CDSs in the genome, 613 (27.3%) matched hypothetical CDSs with unknown functions in the public genome databases. The average nucleotide sequence identity of strain AR contigs to *Sulfurovum* sp. strain NCB37-1 was about 73%, and thus, strain AR could be considered a novel species of the genus *Sulfurovum* (5).

Several proteins involved in sulfur oxidation (sulfide-quinone reductase, sulfite:cytochrome *c* oxidoreductase, dissimilatory sulfite reductase, and sulfur compound oxidation system) are en-

coded within “*Candidatus S. sediminum*” strain AR. In addition, strain AR contains a complete set of genes encoding essential enzymes of the reverse tricarboxylic acid cycle (ATP citrate lyase, succinate dehydrogenase, 2-oxoglutarate synthase, isocitrate dehydrogenase, malate dehydrogenase, succinyl coenzyme A synthase, and fumarate hydratase) for carbon fixation (4). However, the genes for aconitase, succinic dehydrogenase, and alpha-ketoglutarate dehydrogenase have not yet been identified. This is only the second genome of the genus *Sulfurovum* and paves the way for more detailed comparative genome analysis within this important, widespread genus that could provide important insights into the role of *Epsilonproteobacteria* in the sulfur cycle in marine sediments.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession no. [AJLE000000000](https://www.ncbi.nlm.nih.gov/nuclseq/AJLE000000000). The version described in this paper is the first version, [AJLE010000000](https://www.ncbi.nlm.nih.gov/nuclseq/AJLE010000000).

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