Two *Thiomicrospira* strains, WB1 and XS5, were isolated from the Kebrit Deep brine-seawater interface in the Red Sea, Saudi Arabia. Here, we present the draft genome sequences of these gammaproteobacteria, which both produce sulfuric acid from thiosulfate in culture.

Strains WB1 and XS5 were enriched and purified at 28°C using a sulfur-oxidizing-bacteria (SOB) medium, which includes the following ingredients: (NH₄)₂SO₄ (1.0 g/liter), MgSO₄·7H₂O (15% [wt/vol]). After autoclaving, the medium was supplemented to contain 10 mM Na₂S₂O₃, 0.5 g/liter K₂HPO₄, 5 mM H₄Cl, 5 mM EDTA, and 10 mM NaHCO₃. Bromothymol purple was added as pH indicator at a concentration of 4 mg/liter, and the mixture was folded based on read mapping. The genome completeness (100%) was assessed using CheckM (version 1.0.3) (9). Protein-coding open reading frames were predicted by Glimmer (version 3.02) (10). rRNAs were predicted by RNAmer (version 1.2) (11), and tRNAs were predicted by tRNAscan-SE (version 1.21) (12).

The genome of WB1, as presented here, is composed of 6 contigs, with a total length of 2,279,450 bp (N₅₀, 568,675 kbp) and a G+C content of 53.73%. It contains 2,072 protein-coding genes, 43 tRNAs, and 3 rRNAs. For strain XS5, the genome is composed of 23 contigs, with a total length of 2,633,068 bp (N₅₀, 2,522,699 bp) and a G+C content of 50.12%. It contains 2,432 protein-coding genes, 45 tRNAs, and 6 rRNAs. Functional annotation by RAST (13) showed the presence of the gene for the osmolarity sensor protein EnvZ and genes related to thiosulfate and sulfur metabolism, supporting the high-salinity adaptation and observed sulfuric acid production during culturing.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers LQBN00000000 for WB1 and LQBO00000000 for XS5.

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