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Complete Genome Analysis of *Sulfobacillus acidophilus* Strain TPY, Isolated from a Hydrothermal Vent in the Pacific Ocean

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Sulfobacillus acidophilus **strain TPY is a moderately thermoacidophilic bacterium originally isolated from a hydrothermal vent in the Pacific Ocean. Ferrous iron and sulfur oxidation in acidic environments in strain TPY have been confirmed. Here we report the genome sequence and annotation of the strain TPY, which is the first complete genome of *Sulfobacillus acidophilus*.**

Sulfobacillus acidophilus strain TPY, isolated from a hydrothermal vent in the Pacific Ocean (12°42′29″N, 104°02′01″W; water depth, 3,083 m) has been identified as a moderately thermophilic acidophilic bacterium (12). Phylogenetic analyses showed that strain TPY belongs to the species *Sulfobacillus acidophilus*. The previous experiments proved that TPY could tolerate high temperatures and low pH and that its optimal growth temperature is approximately 50°C and the optimal pH is 1.8 (12). This spore-forming, Gram-positive strain with high GC content has the ability to oxidize elemental sulfur and ferrous ion as electron donors (11).

The complete genome of *Sulfobacillus* sp. strain TPY was sequenced with the Roche 454 GS FLX pyrosequencing platform, and approximately 26× coverage of the entire genome was obtained. All the reads were assembled by Newbler software (version 2.5.1) and generated 133 contigs. Gaps were closed by primer walking using PCR amplification. The finished genome was then predicted using Glimmer 3.0 (2) for the protein-coding region and annotated using the BLAST tool (NCBI). Identification of tRNA and rRNA genes was carried out with the tRNAscan-SE and RNAmmer programs, respectively (9, 10). The function and metabolism analysis was done by comparing the coding genes with the databases of COG and KEGG (6–8, 13).

Strain TPY contains a circular chromosome with 3,551,206 bp and a GC content of 56.7%. The genome includes 52 tRNAs, 5 copies of 16S-23S-5S rRNA, and 3,770 open reading frames with an average length of 826 bp. Among all the coding regions, we found 48 ABC transporter-related-protein genes, 2 CRISPRs (clustered regularly interspaced short palindromic repeats), and 1 possible CRISPR (3–5).According to the annotation results, 30 proteins were found to be involved in the process of sulfur transfer, oxidation of element sulfur, and reduction of sulfate. We found four ferredoxins, which play a role as electron-transfer agents in some processes, such as oxidative metabolism, photosynthesis, and nitrogen fixation (15). In strain TPY, energy comes from the electron transfer in the process of sulfur and iron oxidation. There is a similarity in the method of obtaining between strain TPY and *Acidithiobacillus ferrooxidans*. The electron transfer model of sulfur oxidation in *À. ferrooxidans* is complicated (14) and may involve QH2, cytochrome complex *bc*$_1$ (1), a ubiquinone pool, and cytochrome *c* oxidase (Cyt *aa*$_3$). The model for electron transfer during iron oxidation is related to two transcriptional units, the *petI* and *rus* operons. At the beginning of iron oxidation, the electron flowed through Cyc2 to rusticyanin. Then some electrons passed through Cyc1 to Cyt *aa*$_3$ along the electron flow, and others moved through CycA1 to NADH dehydrogenase, reversing the electron flow (14). Here we found only that Cyt *aa*$_3$, a subunit of the cytochrome complex *bc*$_1$, and cytochrome *c* are present in strain TPY. It was therefore inferred that there may be some differences in electron transfer during sulfur or iron oxidation between strain TPY and *A. ferrooxidans*. The strain TPY is the first completely sequenced genome of a *Sulfobacillus acidophilus* strain, and it will be helpful for understanding its unique physiology and metabolic potential.

Nucleotide sequence accession number. The annotated genome sequence of *Sulfobacillus acidophilus* strain TPY has been deposited in GenBank under accession number CP002901.

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