We present the draft genome sequence of *Pseudomonas stutzeri* TS44, a moderately halotolerant, arsenite-oxidizing bacterium isolated from arsenic-contaminated soil. The genome encodes genes for arsenite oxidation, arsenic resistance, and ectoine/hydroxyectoine biosynthesis. The genome information will be useful for exploring adaptation of *P. stutzeri* TS44 to an arsenic-contaminated environment.

*P. stutzeri* is a Gram-negative, rod-shaped, motile, and nonfluorescent denitrifying bacterium that exhibits metabolic diversity and is widely distributed in the environment (8). Currently, five genome sequences for *P. stutzeri* members have been published, including two nitrogen-fixing bacteria (*P. stutzeri* A1501, CP000304 [19] and *P. stutzeri* DSM4166, CP002622 [20]), a typical lactate utilization bacterium (*P. stutzeri* SDM-LAC, AGSX00000000 [6]), a type strain (*P. stutzeri* CGMCC 1.1803, CP002881 [4]), and a model organism for denitrification (*P. stutzeri* CCUG 16156, AGSL00000000 [15]). *P. stutzeri* TS44 was isolated from a highly arsenic-contaminated soil of a metal (gold, copper, and iron) mine in Huangshi, China (2). This strain is responsible for resistance to other metals (copper, mercury, chromium, cadmium, and zinc) were also identified.

The whole-genome sequence of strain TS44, sequenced by using a Roche 454 GS-FLX apparatus (12) and assembled using the Roche Newbler assembler, includes 4,278,818 bp distributed in 78 contigs, with a depth of 27-fold coverage and an average GC content of 64.4%. In addition, the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html) was used for annotation. The automatic outputs were modified manually.

The genome contains at least 20 genes encoding functions related to arsenite oxidation and resistance, mainly located on contig 00030 (AJXE01000030; *ars* operon, *arsC1-arsR-arsC2-ACR3-arsH-DSP-GAPDH-MFS*), an adjacent *aroA* operon, and contig 00031 (AJXE01000031; *ars* operon, *ACR3-arsR-arsH-GAPDH-MFS*). Notably, *aiaAB* (encoding arsenic oxidase) was absent in the other five *P. stutzeri* genomes, suggesting recent acquisition of *aiaAB* by strain TS44 via horizontal gene transfer. However, a two-component system, *aioS/aioR*, involved in regulating the expression of *aiaAB*, was not identified in the genome, indicating a potentially novel regulatory mechanism (10, 14). In addition, numerous genes responsible for resistance to other metals (copper, mercury, chromium, cadmium, and zinc) were also identified.

Genomic comparison demonstrated that all six sequenced *P. stutzeri* strains possess a complete cluster of ectoine/hydroxyectoine biosynthetic genes (*ectABCD-ask*) (16, 17). However, this entire *ectABCD-ask* cluster was not identified in the genomes of other *Pseudomonas* species (7). Compared to other *Pseudomonas* species, ectoine/hydroxyectoine biosynthesis is presumably a common strategy for *P. stutzeri* to survive under high-osmolarity conditions.

**Nucleotide sequence accession numbers.** The results of this genome shotgun project have been deposited with DDBJ/EMBL/GenBank under the accession number AJXE00000000. The version described in this paper is the first version, AJXE01000000.

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