Draft Genome Sequence of the *Sulfobacillus thermosulfidooxidans* Cutipay Strain, an Indigenous Bacterium Isolated from a Naturally Extreme Mining Environment in Northern Chile

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***Sulfobacillus thermosulfidooxidans* strain Cutipay is a mixotrophic, acidophilic, moderately thermophilic bacterium isolated from mining environments of the north of Chile, making it an interesting subject for studying the bioleaching of copper. We introduce the draft genome sequence and annotation of this strain, which provide insights into its mechanisms for heavy metal resistance.**

Sulfobacillus thermosulfidooxidans strain Cutipay has been identified as a sulfur- and iron-oxidizing, Gram-positive, sporulating, acidophilic, and moderately thermophilic bacterium. It was microbiologically characterized as having an optimum growth temperature of 45°C and an optimum pH range of 2.0 to 2.5 when growing in the presence of Fe²⁺ and/or sulfur supplemented with yeast extract. It was originally named Cutipay from the indigenous Mapudungun word meaning “coming from the water,” because it was isolated from naturally occurring effluents in the extreme mining environment of the north of Chile. Using phylogenetic analyses, it was identified as a *Sulfobacillus thermosulfidooxidans* species first described by Golovacheva and Karavaiko in 1978 (2).

The draft genome sequence of *S. thermosulfidooxidans* strain Cutipay was determined by whole-genome shotgun sequencing using a mixed technology strategy consisting of a run of the Ion Torrent PGM 316 Chip (8) on an unpaired library and two runs of the Roche 454-GS Junior pyrosequencing platform (6) on one 3-kb mate pair library and 1 unpaired library generating a 116× coverage. Assembly was performed using wgs-assembler (Celera Assembler) version 7 (7). Identification of coding regions and annotation were performed using protocols described in references 3 and 5.

The *Sulfobacillus thermosulfidooxidans* Cutipay strain draft genome was assembled in 47 contigs. Using mate information, the final assembly has 3,862,012 total bp in 35 scaffolds. The maximum scaffold length is 1,134,202 bp, and the minimum length is 1,007 bp. The scaffold length has a mean of 110,343 bp, a median of 30,355 bp, and an *N*₅₀ length of 509,367 bp, while the genome has a GC content of 49.3%, which is similar to that of *Sulfobacillus thermosulfidooxidans* subspecies *thermotolerans* (4).

According to our analysis, 3,600 putative genes and 54 tRNAs were predicted. Three 5S, 16S, and 23S partial operons were found. Carbon and sulfur metabolism enzymes described previously have also been identified (1). Differences between arsenic resistances in the *arsRB* operon were found. The *arsRB* operon includes *arsR* regulator, *arsB* arsenite efflux pump, kumamolisin-As precursor, and glycosyl transferase codifying genes previously described in *S. thermosulfidooxidans* strain VKM B-1269 (9, 10). We have found another open reading frame (ORF) with no homology between the genes for glycosyl transferase and kumamolisin-As precursor present in *S. thermosulfidooxidans* strain

Cutipay and a putative *arsC* in another region of the genome. The *arsC* gene codes for an arsenate reductase not previously described in *S. thermosulfidooxidans* (9, 10), indicating new arsenic resistance capacities for this species. Genome analysis shows putative copper-sensing genes *copR* and *copS* and the gene for a DNA-binding transcriptional activator of copper-responsive regulon genes *cueR*, indicating the presence of a *copAZ* resistance operon.

In summary, using a novel mixed-sequencing strategy for an acidophilic organism, we obtained a high-quality draft. This new draft reveals a heavy metal resistance for *Sulfobacillus thermosulfidooxidans* that has not been previously described, and it provides evidence for future experimental research and understanding of survival in acidic environments.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [ALWJ000000000](https://www.ncbi.nlm.nih.gov/nuccore/ALWJ000000000). The version described in this paper is the first version, ALWJ01000000.

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