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Data in Brief

Draft genome sequence of *Acidithiobacillus ferrooxidans* YQH-1Lei Yan ^{a,*}, Shuang Zhang ^a, Weidong Wang ^a, Huixin Hu ^a, Yanjie Wang ^a, Gaobo Yu ^a, Peng Chen ^b^a College of Life Science and Technology, Heilongjiang Bayi Agricultural University, Xinfeng Road No. 5, Daqing 163319, PR China^b School of Pharmacy, Lanzhou University, Tianshui Road No. 222, Lanzhou 730000, PR China

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ABSTRACT

Acidithiobacillus ferrooxidans YQH-1 is a moderate acidophilic bacterium isolated from a river in a volcano of Northeast China. Here, we describe the draft genome of strain YQH-1, which was assembled into 123 contigs containing 3,111,222 bp with a G + C content of 58.63%. A large number of genes related to carbon dioxide fixation, dinitrogen fixation, pH tolerance, heavy metal detoxification, and oxidative stress defense were detected. The genome sequence can be accessed at DDBJ/EMBL/GenBank under the accession no. LJBT000000000.

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Specifications	
Organism/cell line/tissue	<i>Acidithiobacillus ferrooxidans</i>
Strain (s)	YQH-1
Sequencer or array type	Sequencer; Illumina MiSeq
Data format	Processed
Experimental factors	Microbial strains
Experimental features	Draft genome sequence of <i>Acidithiobacillus ferrooxidans</i> YQH-1 assembly and annotation
Consent	N/A
Sample source location	Volcanic river in the Wudalianchi volcano, China

1. Direct link to deposited data

<http://www.ncbi.nlm.nih.gov/bioproject/?term=LJBT000000000>.

2. Experimental design, materials and methods

Acidithiobacillus ferrooxidans is a Gram-negative, motile, moderately thermophilic (20 to 40 °C), acidophilic (pH 1.0 to 4.5) and strictly chemolithoautotrophic bacterium [1]. It utilizes ferrous iron or reduced inorganic sulfur compounds as energy source and fixes carbon dioxide

from the atmosphere as a carbon source [2,3]. Strains of *A. ferrooxidans* are abundant in iron and sulfur bearing acidic environments and considered as important participants in the iron, sulfur and carbon cycles of the acid mine drainage ecosystem [4].

Research on *A. ferrooxidans* has been a promising area of study as this bacterium is known to be an important member of microbial consortia that is used to recover metals via a process known as bioleaching or biomining [3]. In this study, *A. ferrooxidans* YQH-1 was isolated from a river in Wudalianchi volcano, Northeast China (48° 40' 14" N, 126° 10' 16" E). The 16S rRNA sequence of YQH-1 available in GenBank database (accession number: KT633236) showed 99.64% identity with that of *A. ferrooxidans* ATCC 19859^T (accession number: AJ457808). To better understand the important information regarding the bioleaching capabilities, we performed a genomic analysis of *A. ferrooxidans* YQH-1.

Genomic DNAs were extracted using a Bacterial Genomic DNA Extraction Kit (Biomed, Beijing, China) according to the manufacturer's instructions. The genome of YQH-1 was sequenced using the Illumina MiSeq platform at the Biomarker Technologies Co., Ltd. (Beijing, China). A library with a fragment length of 500 bp was constructed, and a total of 854,755,347 bp paired-end reads of 300 bp were generated. The high-quality reads, which provided an approximately 285-fold depth of coverage were assembled with Velvet Version 1.2.10 [5]. Protein-coding sequences were predicted by Glimmer software version 3.0 [6], while Ribosomal RNA (rRNA) and transfer RNA (tRNA) genes were predicted using an RNAmmer 1.2 server [7] and tRNAscan-SE Search Server version 1.21 [8], respectively. Tandem repeats were predicted using Tandem Repeats Finder Version 4.04. Genes annotated using BLAST searches of nonredundant protein sequences from the

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Table 1
Genome features of *A. ferrooxidans* YQH-1 draft genome.

Attributes	Values
Genome size (bp)	3,111,222
Number of scaffolds	96
Scaffold N50 (bp)	99,137
G + C content (%)	58.63
Number of contigs	123
Contig N50 (bp)	69,681
CDS	3089
rRNAs	10
tRNAs	42
Pseudo genes	64
Tandem repeat sequence	115

NCBI, Swiss-Prot, NCBI Refseq, COG [9], and Rapid Annotation using Subsystem Technology (RAST) Version 2.0.

A total of 123 contigs were generated with N_{50} size of 69,681 bp. The assembled genome size of *A. ferrooxidans* YQH-1 was estimated to be 3,111,222 bp from 96 scaffolds with a mean G + C content of 58.63% (Table 1). In the whole genome, 2281 genes (73.84%) that encode known function proteins and 635 (20.55%) genes were considered to encode hypothetical proteins. Of the total, 173 (5.61%) genes have no database match.

RAST functional annotation predicted 183 genes were linked to carbohydrate metabolism, out of which 58 genes were predicted to be involved in carbon dioxide fixation (Fig. 1). The presence of these genes may explain the ability of YQH-1 in the natural carbon cycle. *A. ferrooxidans* YQH-1 contains several genes involved in iron and sulfur metabolism, such as encapsulating protein for DyP-type peroxidase and ferritin-like protein oligomers, sulfate and thiosulfate import ATP-binding protein CysA, sulfate transport system permease protein CysW, Sulfate and thiosulfate binding protein CysP et al. (Fig. 1). They may be responsible for the oxidation of ferrous iron and reduced inorganic sulfur compounds.

Additionally, 23 Nif genes involved in nitrogen metabolism were found, which indicated that *A. ferrooxidans* YQH-1 has nitrogen-fixation potential (Fig. 1). The Nif genes were also detected in the genomic sequences of *A. ferrooxidans* ATCC 23270 [4] and *A. ferrooxidans* ATCC 53993 (CP001132). These indicated that *A. ferrooxidans* has the genes involved in dinitrogen fixation and they are able to grow in diazotrophic conditions.

Fifteen genes related to potassium metabolism were detected, of which 14 were related to potassium homeostasis (Fig. 1), which may be responsible for the strain YQH-1 inhabiting an extreme acid environment [4]. There are 41 genes involved in heavy metal resistance and 35 genes involved in oxidative stress response. The presence of these genes may explain why *A. ferrooxidans* can live in hostile condition with high concentrations of heavy metal ions.

3. Nucleotide sequence accession number

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession LJBT00000000. The version described in this paper is LJBT00000000.

Acknowledgments

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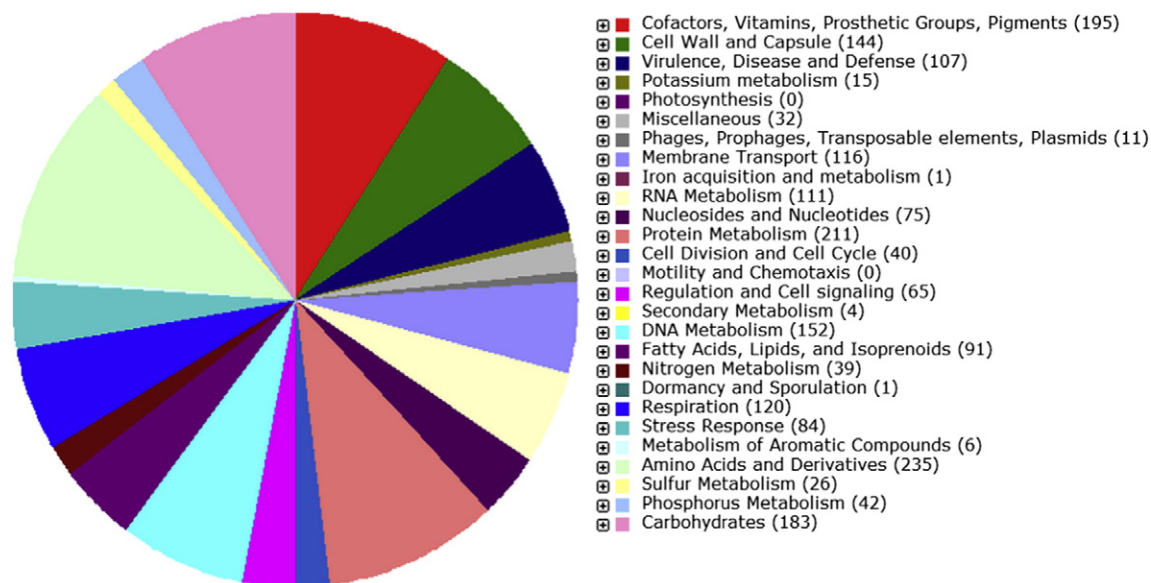


Fig. 1. Subsystem category distribution of *A. ferrooxidans* YQH-1 (based on RAST annotation server).