Data in Brief

Draft genome of iron-oxidizing bacterium *Leptospirillum* sp. YQP-1 isolated from a volcanic lake in the Wudalianchi volcano, China

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A B S T R A C T

*Leptospirillum* sp. YQP-1, a member of iron-oxidizing bacteria was isolated from volcanic lake in northeast China. Here, we report the draft genome sequence of the strain YQP-1 with a total genome size of 3,103,789 bp from 85 scaffolds (104 contigs) with 58.64% G + C content. The genome sequence can be accessed at DDBJ/EMBL/GenBank under the accession no. LIEB00000000.

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Organism/cell line/tissue

| Specifications          | Leptospirillum sp. |
|------------------------|-------------------|
| Strain (s)             | YQP-1             |
| Sequencer or array type| Sequence: Illumina MiSeq |
| Data format            | Processed         |
| Experimental factors   | Microbial strains |
| Experimental features  | Draft genome sequence of *Leptospirillum* sp. YQP-1 assembly and annotation |
| Consent                | N/A               |
| Sample source location | Volcanic lake in the Wudalianchi volcano, China |

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/bioproject/?term=LIEB00000000.

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2. Experimental design, materials and methods

The *Leptospirillum* genus was validly described by Hippe [1], though the first bacterium of this genus was identified by Markosyan [2]. Phylogenetically, it belongs to the class Nitrospira. *Leptospirillum* spp. are found in volcano habitat and acid mine drainage environment [3,4]. Cells of the *Leptospirillum* genus are Gram-negative, motile vibroid to spirilla-shaped, but cocci or pseudococci also can be formed [3]. This genus comprises four species, viz., *Leptospirillum ferrooxidans*, *Leptospirillum ferriphilum*, *Leptospirillum feerrodiazotrophum*, and *Leptospirillum thermoferrooxidans* [3,5]. Until recently, only four genomes are available in the GenBank, including complete genomes of *L. ferriphilum* ML-04 [6], *L. ferriphilum* YSK (CP007243), and *L. ferrooxidans* C2-3 [4], as well as draft genome of *L. ferriphilum* DSM 14647 [7]. As an important iron-oxidizing genus, more investigations at genomic level are required to improve understanding of its physiology, ecology, genetics and potential in biotechnological applications.

*Leptospirillum* sp. YQP-1 was isolated from a volcanic lake of the Wudalianchi volcano, northeast China in July 2013. This strain has been deposited in the China Center for Type Culture Collection (accession number: CCTCC M 2014196) (http://www.cctcc.org/index.php). The 16S rRNA gene sequence of YQP-1 available in GenBank database (accession number: KJ573504) showed more than 99% identity with several *Leptospirillum* strains, such as *Leptospirillum* sp. 3.2 (accession number: EU372651), *L. ferrooxidans* P3a (accession number: AF356837). This indicated that this strain belongs to *Leptospirillum* genus.

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Genomic DNA was isolated from *Leptospirillum* sp. YQP-1 using a bacterial genomic DNA extraction kit (Biomed, Beijing, China) according to the manufacturer’s instructions. Quality check was performed using a NanoDrop spectrophotometer (Thermo Scientific, Waltham, USA). The draft genome sequence of the YQP-1 strain was obtained by paired-end sequencing on the Illumina MiSeq platform at the Biomarker Technologies Co., Ltd. (Beijing, China). De novo assembly was performed using Velvet Version 1.2.10 [8]. Protein-coding sequences were predicted by Glimmer software version 3.0 [9], while ribosomal RNA (rRNA) and transfer RNA (tRNA) genes were predicted using RNAmmer 1.2 server [10] and tRNAscan-SE Search Server version 1.21 [11], respectively. Genes annotated using BLAST searches of nonredundant protein sequences from the NCBI, Swiss-Prot, COG [12], and KEGG [11], respectively. Genes annotated using BLAST searches of nonredundant protein sequences from the NCBI, Swiss-Prot, COG [12], and KEGG [11], respectively.

Table 1

| Attributes          | Values                   |
|---------------------|--------------------------|
| Genome size (bp)    | 3,103,789                |
| Number of scaffolds | 85                       |
| Scaffold N50 (bp)   | 101,596                  |
| G + C content (%)   | 58.64                    |
| Number of contigs   | 104                      |
| Contig N50 (bp)     | 86,194                   |
| CDS                 | 3038                     |
| tRNAs               | 8                        |
| tRNAs               | 42                       |
| Pseudo genes        | 55                       |
| Tandem repeat sequence | 106                    |

The genome size of *Leptospirillum* sp. YQP-1 was estimated to be 3,103,789 bp from 85 scaffolds with a mean G + C content of 58.64%. It contains 104 contigs with N50 contig length of 86,194 bp. A total of 3038 coding sequences (CDS) were identified including 50 RNA genes (8 rRNA and 42 tRNA genes). The number of tandem repeat sequence was 106 with total length of 12,049 bp, which made up 0.3882% of genome (Table 1). Further studies of *Leptospirillum* sp. YQP-1 which might help many beneficial applications such as for bioremediation and bioleaching, are essential and required to be extended.

3. Nucleotide sequence accession number

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession LJEB00000000. The version described in this paper is LJEB00000000.

Conflict of interest

The authors declare that there is no conflict of interests with respect to the work published in this paper.

Acknowledgments

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