Data in Brief

Draft genome sequence of extremely acidophilic bacterium

Acidithiobacillus ferrooxidans DLC-5 isolated from acid mine drainage in Northeast China

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Abstract

Acidithiobacillus ferrooxidans type strain DLC-5, isolated from Wudalianchi in Heihe of Heilongjiang Province, China. Here, we present the draft genome of strain DLC-5 which contains 4,232,149 bp in 2745 contigs with 57.628% GC content and includes 32,719 protein-coding genes and 64 tRNA-encoding genes. The genome sequence can be accessed at DDBJ/EMBL/GenBank under the accession no. JNNH00000000.1.

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1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/bioproject/?term=JNNH00000000.

2. Experimental design, materials and methods

Acidithiobacillus ferrooxidans (A. ferrooxidans) is a Gram-negative, extremely acidophilic, mesophilic, chemolithotrophic bacterium and the most well-studied acidophilic organism which is usually found in acid environments such as acid mine drainage [1,2]. Due to its bioleaching capabilities, it is an important member of microbial consortia involved in the industrial recovery of metal under mesophilic conditions (bioleaching or biomining). Recently, A. ferrooxidans has played important roles in bioleaching and harnesses environmental contamination [3,4]. Like in other acidophilic iron-oxidizing bacterium, it grows optimally at about 35 °C in 9K inorganic medium at extremely low pH (pH 1.0–2.0) and fixes both carbon and nitrogen from the atmosphere [5]. A. ferrooxidans derives energy from oxidizing reduced sulfur compounds and Fe²⁺ ions to form sulfate and Fe³⁺, respectively [3].

A. ferrooxidans strain, DLC-5 was grown in 9K medium at 35 °C. DNA was isolated from 1.0–1.5 g of cell paste using Qiagen Genomic 500 DNA Kit (Qiagen, Hilden, Germany) with a modified protocol, st/FT, for cell lysis, as described in Valdes et al. [6]. Draft genome sequence of A. ferrooxidans type strain DLC-5 was obtained in Illumina Hiseq2000 sequencing technology by Shanghai Majorbio Bio-pharm Technology Co., Ltd. (Shanghai, China), using the Short Oligonucleotides Alignment Program (SOAP) denovo alignment tool (http://soap.genomics.org.cn/) processes reads assemble. A library containing 300-bp inserts was constructed. Altogether, 6,372,268 paired reads; 398,580 single reads; total 1,079,535,272 bp bases with average coverage of 221.1×. Reads were filtered to remove adapter sequences, low-quality bases (Phred score, <20), removing the 5' end that contains the bases of it is not A, G, C, T before shearing, remove reads with the containing 10% of N, giving up adapter and small fragments of length less than 25 bp after qualitative pruning. The reads were assembled into 881 contigs (>1000 bp; Contig...
Until now, two genome sequences of *A. ferrooxidans* strains ATCC 23270 and ATCC 53993 are available in the public databases [7,8]. These genomic data are useful for the experimental identification of unique proteins or estimation of the phylogenetic relationship among the related strains. Strain DLC-5 (CCTCC-M 2014362) is the type strain of *A. ferrooxidans*, isolated from Wudalianchi in Heihe of Heilongjiang Province, and the type species of the genus Acidithiobacillus, which currently contains five species. The draft genome sequences of strain DLC-5 have great importance to provide more explicit information for the physiology and metabolic potential of *A. ferrooxidans*. Further analysis of the genome sequence via gene engineering might improve the oxidation of Fe(II) efficiency by strain DLC-5. The genome includes two plasmids, for a total size of 3,142,890 bp, with one circular chromosome of 1,832,305 bp (58.3% GC content). For the main chromosome, 4,299 bp genes were predicted, 4,131 bp of which are protein-coding genes. 3,250 bp of protein coding genes were assigned to a putative function with the remaining annotated as hypothetical proteins. The properties and the statistics of the genome are summarized in Table 1. The distribution of genes into COGs functional categories is presented in Table 2.

Extremely acidophilic bacteria and archaea with special emphasis on bioleaching microorganisms are widely distributed in the extreme acidic environment. In this study, we analyzed the genome sequence of *A. ferrooxidans* DLC-5, which was isolated from acid mine drainage in Northeast China. Genome analysis of this strain revealed the presence of key functional characteristics. It may contribute to further studies on important process for bioleaching and acid mine drainage production, such as biofilm formation, energy resources utilization and quorum sensing that could play a role in a possible interrelationship of bioleaching heaps and other acidic environments. In addition, combining with genomes of other members in *Acidithiobacillus*, will make an important advance in understanding of the ecological roles that *Acidithiobacillus* species play in those acidic environments and their relationships with other extremely acidophilic microorganisms.

### 3. Nucleotide sequence accession number

The sequence of *A. ferrooxidans* DLC-5 under this Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession JNNH00000000.1. The version described in this paper is version JNNH00000000.1.

### Competing interests

The authors declare that there are no competing interests.

#### Table 1

| Attribute                        | Value  | % of total |
|----------------------------------|--------|------------|
| Genome size (bp)                 | 3,142,890 | 100.0     |
| DNA coding (bp)                  | 2,816,029  | 89.6      |
| DNA G + C (bp)                   | 1,832,305  | 57.63     |
| DNA scaffolds                     | 1333    | 3.10       |
| Total genes                      | 4299    | 100.0      |
| Protein coding genes             | 4131    | 96.1       |
| RNA genes                        | 168     | 3.9        |
| Pseudo genes                     | 0       | 0          |
| Genes in internal clusters       | 0       | 0          |
| Genes with function prediction   | 3312    | 77.0       |
| Genes assigned to COGs           | 3250    | 75.6       |
| Genes with Pfam domains          | 3486    | 81.1       |
| Genes with signal peptides       | 315     | 7.3        |
| Genes with transmembrane helices | 826     | 19.2       |
| CRISPR repeats                   | 0       | 0          |

#### Table 2

| Code | Value | % age | Description                                    |
|------|-------|-------|-----------------------------------------------|
| J    | 118   | 5.6   | Translation, ribosomal structure and biogenesis |
| A    | 1     | 0.0   | RNA processing and modification                |
| K    | 112   | 5.4   | Transcription                                  |
| L    | 157   | 7.5   | Replication, recombination and repair           |
| B    | 1     | 0.0   | Chromatin structure and dynamics                |
| D    | 29    | 1.4   | Cell cycle control, cell division, chromosome partitioning |
| V    | 51    | 2.4   | Defense mechanisms                             |
| T    | 59    | 2.8   | Signal transduction mechanisms                  |
| M    | 141   | 6.7   | Cell wall/membrane biogenesis                   |
| N    | 30    | 1.4   | Cell motility                                  |
| U    | 76    | 3.6   | Intracellular trafficking and secretion         |
| Q    | 96    | 4.6   | Posttranslational modification, protein turnover, chaperones |
| C    | 159   | 7.6   | Energy production and conversion                |
| G    | 93    | 4.4   | Carbohydrate transport and metabolism           |
| E    | 146   | 7.0   | Amino acid transport and metabolism             |
| F    | 41    | 2.0   | Nucleotide transport and metabolism             |
| H    | 89    | 4.3   | Coenzyme transport and metabolism               |
| I    | 59    | 2.8   | Lipid transport and metabolism                  |
| P    | 125   | 6.0   | Inorganic ion transport and metabolism          |
| Q    | 43    | 2.1   | Secondary metabolites biosynthesis, transport and catabolism |
| R    | 212   | 10.1  | General function prediction only                |
| S    | 134   | 6.4   | Function unknown                               |
| --   | 119   | 5.7   | Not in COGs                                    |

The total is based on the total number of protein coding genes in the genome.

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