Genome announcement

Complete genome sequence of the bioleaching bacterium

*Leptospirillum* sp. group II strain CF-1

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\textbf{A R T I C L E   I N F O}

\textbf{Article history:}
Received 13 January 2016
Accepted 2 February 2016
Available online 4 February 2016

\textbf{Keywords:}
*Leptospirillum* group II
Bioleaching
Oxidative stress
Genome sequencing

\textbf{A B S T R A C T}

We describe the complete genome sequence of *Leptospirillum* sp. group II strain CF-1, an acidophilic bioleaching bacterium isolated from an acid mine drainage (AMD). This work provides data to gain insights about adaptive response of *Leptospirillum* spp. to the extreme conditions of bioleaching environments.

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Bacteria of *Leptospirillum* genus are Gram-negative, spiral-shaped, aerobic, acidophilic and chemolithoautotrophic bacteria (Coram and Rawlings, 2016). Based on 16S rRNA phylogeny there are four recognized groups (I–IV) (Goltsman et al., 2013). They oxidize ferrous (Fe\textsuperscript{2+}) to ferric ions (Fe\textsuperscript{3+}) to obtain energy, a relevant process to the metal solubilization and recovery (Rawlings, 2002).

High levels of metal and metalloids present in acidic environments might induce oxidative damage to biomolecules through reactive oxygen species (ROS) production (Jones et al., 2013; Norambuena et al., 2012). Thus, the ROS maintenance in safe limits may be critical in determining the abundance of these microorganisms. In order to gain insights about genetic elements involved in oxidative stress tolerance in this work we addressed the sequencing of the genome of *Leptospirillum* sp. group II strain CF-1 (Lo et al., 2007).

The genome sequencing was carried out on the PacBio RSII technology (PacificBiosciences, Menlo Park, CA, USA), (Eid et al., 2009) applying chemistry P4-C2. The SMRTbell™ template library was prepared according to the instructions from the provider following the greater than 10 kb Template Preparation protocol.

The genome assembly was performed using the RS_HGAP_Assembly2 protocol included in SMRT Portal version 2.1.1 applying standard parameters. Thus, two chromosomal contigs of 2.2 and 0.5 Mbp could be assembled, which afterwards could be merged comparing different RS_HGAP_Assembly 1 resulting in MAUVE (PMID 15231754). The final consensus sequence was trimmed, circularized and adjusted to dnaA as the first gene. Thus, sequencing rendered one chromosome with 140 fold coverage and finishing quality of QV 60 was estimated.

The genome of *Leptospirillum* sp. group II CF-1 consisted of 2,709,324 bp in size and a 54.6% G + C content (Table 1). The genome was annotated by NCBI Prokaryotic Genome Annotation Pipeline, resulting in 2736 genes assigned as follow: 2460 protein coding sequences (CDSs), 48 tRNA, 6 rRNA, 1 ncRNA and 221 pseudogenes.

The annotation predicted six genes encoding thioredoxins (AKS22784.1, AKS23742.1, AKS23718.1, AKS24757.1, AKS24442.1, and AKS24660.1) and 1 encoding thioredoxin reductase (AKS24474.1) which are involved in protein repair. Also a gene encoding a methionine sulfoxide reductase (AKS24661.1) was detected. Sequences predicted to encode H$_2$O$_2$ scavenging proteins including one rubredoxin (AKS22816.1, one cytochrome c peroxidase (AKS24198.1) and two peroxiredoxins (AKS24659.1; AKS23913.1) were found. DNA repair protein MutS (AKS23749.1) and two ATP-dependent DNA helicases UvrD/PcrA (AKS24182.1; AKS23445.1) were also predicted.
Table 1

Features of *Leptospirillum* group II strain CF-1 genome.

<table>
<thead>
<tr>
<th>Features</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genome size (bp)</td>
<td>2,709,324</td>
</tr>
<tr>
<td>GC content (%)</td>
<td>546</td>
</tr>
<tr>
<td>Chromosome</td>
<td>1</td>
</tr>
<tr>
<td>Total number of genes</td>
<td>2736</td>
</tr>
<tr>
<td>Protein coding genes (CDSs)</td>
<td>2460</td>
</tr>
<tr>
<td>tRNAs (5S, 16S, 23S)</td>
<td>6</td>
</tr>
<tr>
<td>ncRNA</td>
<td>1</td>
</tr>
</tbody>
</table>

Chaperones are important for protein folding maintenance and repair (Rajaram et al., 2014); the presence of genes for DnaK (AKS23626.1), DnaJ (AKS23625.1; AKS24497.1), GroEL (AKS23719.1), GroES (AKS23720.1), and two Hsp20 (AKS24337.1; AKS23988.1) was predicted. Interestingly, no genes encoding superoxide dismutase, superoxide reductase, and catalase were detected. Furthermore, no genes related to the metabolism and function of the glutathione-based system could be found. This data suggest that alternative ROS scavenger systems might be present in this and other strains of *Leptospirillum* sp. group II.

Nucleotide accession numbers

The Genome sequence was deposited at Genbank under accession number CP012147. The CF-1 strain was deposited in German Collection of Microorganisms and Cell Culture (DMSZ) under number DSM 101788.

Acknowledgements

We acknowledge support from Fondecyt grants no 1120746 (G.L.) and 1150834 (O.O.), and Conicyt doctoral fellowship (AF) from government of Chile. We gratefully acknowledge Jill Banfield (University of California Berkeley, Berkeley, CA 94720, USA) for providing *Leptospirillum* group II CF-1 strain.

References


