Draft Genome Sequence of a Novel Bacterial Strain, LSJC7, Belonging to the Family *Enterobacteriaceae* with Dual Resistance to Arsenic and Tetracycline

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Strain LSJC7, with dual resistance to arsenic and tetracycline, was isolated from an antimony tailing in China. Its 16S rRNA gene sequence has the highest similarity to that of *Enterobacter cloacae* subsp. *dissolvens* LMG 2683^T (97.02%). Here we present the approximately 4.6-Mbp draft genome sequence of strain LSJC7.

Metal contamination is considered a selective factor in the proliferation of antibiotic resistance through several coselection mechanisms (1). Strain LSJC7 is a novel Gram-negative member of the family *Enterobacteriaceae* in the order *Enterobacteriales* of the class *Gammaproteobacteria* that was isolated from an antimony tailing in Lengshuijiang, Hunan Province, China. Strain LSJC7 was isolated as part of a project aimed at screening metal-contaminated soils for arsenic-resistant bacteria. This strain was further shown to exhibit tetracycline resistance. The 16S rRNA gene sequence of strain LSJC7 (GenBank accession number [JX485634](#)) displays the highest similarity to that of *Enterobacter cloacae* subsp. *dissolvens* LMG 2683^T (97.02%) (5), followed by that of *Enterobacter hormaechei* ATCC 49162^T (96.93%) (10).

The genome sequence of strain LSJC7 was determined by using Illumina sequencing at BGI, Shenzhen, China. Raw pair-end reads were filtered before assembly, including low-quality reads, a high proportion of N, adapter contamination, and duplication. The filtered high-quality reads were assembled by using SOAPdenovo 1.05 (7), and gene prediction was performed by Glimmer 3.0 (3). Functional annotation of the predicted genes was performed by BLASTP searching of the KEGG, COG, Swiss-Prot, TrEMBL, NR, and GO protein databases. Transposons were determined by using RepeatMasker and RepeatProteinMasker (14), and tandem repeat sequences were analyzed by Tandem Repeats Finder (2). rRNAs were predicted by RNAmmer (6) or by alignment with an rRNA pool, and tRNAs and sRNAs were predicted by tRNAscan-SE (13) and Infernal (9) on the basis of the Rfam database (4), respectively. Genomic islands were predicted by using SIGI-HMM methods. Secreted proteins were predicted by using EffectiveT3 (<http://www.effectors.org>). The antibiotic resistance of strain LSJC7 was analyzed by using BLASTX with the ARDB database (8).

A total of 720 Mbp of data were obtained, representing about 155-fold coverage of the genome. The draft genome of strain LSJC7 contains 4,618,981 bp distributed over 18 scaffolds containing 34 contigs with a G+C content of 54.83%. The genome contains 69 tRNA genes, four rRNA operons, 24 sRNA genes, and 4,428 protein-coding genes with an average length of 906 bp, including 2,880 nonhypothetical protein-coding genes and 1,548 hypothetical protein-coding genes according to the results of a BLASTP searching of the COG database, and 429 proteins were identified as secreted proteins. In addition, one genomic island with a length of 3,420 bp was identified in the genome.

Analysis of the annotated genome revealed the presence of arsenic resistance genes, including two operons (*arsRDABC* and *arsRBC*) containing cytoplasmic arsenate reductase-encoding genes (12). Putative genes conferring resistance to tetracycline were detected in the genome, including putative ribosomal protection protein (*tetM*, *tetPb*, *otra*)-, tetracycline efflux pump (*otrB*, *tet39*, *tetB*)-, and tetracycline modification enzyme (*tet34*)-like genes (11). Further investigation of arsenic and tetracycline resistance-encoding genes will aid in the understanding of the mechanisms behind the coselection of metal resistance and antibiotic resistance.

Nucleotide sequence accession numbers. The draft genome sequence of strain LSJC7 has been deposited at DDBJ/EMBL/GenBank under accession no. [AMFN00000000](#). The version described in this paper is the first version, AMFN01000000.

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