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Genome announcement

Complete genome sequence of *Klebsiella pneumoniae* J1, a protein-based microbial flocculant-producing bacterium

Changlong Pang[a], Ang Li[a], Di Cui[a,b,*], Jixian Yang[a], Fang Ma[a], Haijuan Guo[a,c,*]

[a] State Key Laboratory of Urban Water Resource and Environment, Harbin Institute of Technology, Harbin 150090, People's Republic of China
[b] Research Center on Life Sciences and Environmental Sciences, Harbin University of Commerce, Harbin 150076, People's Republic of China
[c] School of Civil Engineering and Architecture, Taizhou University,Taizhou 318000, People's Republic of China

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ABSTRACT

Klebsiella pneumoniae J1 is a Gram-negative strain, which belongs to a protein-based microbial flocculant-producing bacterium. However, little genetic information is known about this species. Here we carried out a whole-genome sequence analysis of this strain and report the complete genome sequence of this organism and its genetic basis for carbohydrate metabolism, capsule biosynthesis and transport system.

Microbial flocculants, the extracellular polymeric substrate (EPS) extracted from the bacteria, are widely used to treat domestic sewage and industrial wastewater because these substances are biodegradable, harmless, and highly efficient (Salehizadeh and Shojaosadati, 2001). The microbial flocculants extracted from *Klebsiella pneumoniae* J1 belongs to a protein-based microbial flocculant, which showed good adsorption abilities for sulfamethoxazole and heavy metals (Wei et al., 2014; Xing et al., 2013; Yang et al., 2015). This microbial flocculants has high molecular weight of about 8.510×10^6 Da. Meanwhile, it has numerous adsorption sites, strong bridging, and high flocculating activity (Xing et al., 2013). Until now, the biosynthetic pathway and related genes for producing microbial flocculants in strain J1 have not been determined. In order to improve the microbial flocculant yield using metabolic engineering methods, we sequenced the complete genome of *K. pneumoniae* J1.

Genomic DNA from *K. pneumoniae* J1 was extracted using the Wizard Genomic DNA Purification Kit. The quantity and quality of genomic DNA were evaluated on the Qubit. A 10 kb insert SMRTbell library was constructed and then was sequenced on the single molecule real-time (SMRT) DNA sequencing platform by Pacific Biosciences RS II sequencer (Eid et al., 2009). A total of 150,292 polymerase reads on one SMRT cell for 3 h movie times was led to a total of 1,660,840,952 nucleotide bases. After filtering to remove any reads having low accuracy values less than 0.8, 1,462,007,585 read bases were obtained with 0.85 read quality. All of the filtered sequences were *de novo* assembled using RS hierarchical genome assembly process assembly protocol 2.0 in SMRT analysis software version 2.3.0 (Chin et al., 2013), and it resulted in one circularized complete chromosome sequences and two circular plasmid sequences, with 270-fold coverage. The functional annotation was achieved on the Rapid Annotation using Subsystems Technology (RAST) server (Aziz et al., 2008). The CRISPRs were identified by CRISPRs Finder (Grissa et al., 2007). The features for the complete genome sequence of *K. pneumoniae* J1 are summarized in Table 1.

Table 1
Klebsiella pneumoniae J1 genome features.

Features	Chromosome	pJ1-1	pJ1-2
Size (bp)	5,278,493	74,973	53,400
GC content (%)	57.2	52.3	49.8
Protein coding genes (CDSs)	5032	86	59
rRNAs (5S, 16S, 23S)	25	0	0
tRNAs	88	0	0

Based on the annotation of RAST, we identified 881 (17%) and 546 (10%) genes related to carbohydrate metabolism and amino acids metabolism. Capsule plays an important role in the environmental adaptation of *K. pneumoniae*. We found the genes involved in capsular polysaccharide synthesis, such as the capsule synthesis-related tyrosine kinase *wzc*, but not capsule polysaccha-

* Corresponding authors at: State Key Laboratory of Urban Water Resource and Environment, Harbin Institute of Technology, Harbin 150090, People's Republic of China.
E-mail addresses: jscz_dd@hotmail.com (D. Cui), guohaijuan@163.com (H. Guo).

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ride synthesis. This imply that the J1 may own different strategy for capsule polysaccharide biosynthesis. What is more, two CRISPRs clusters (with 7 and 15 spacers) and eight CRISPRs-related genes were detected by CRISPRs finder, which provides acquired resistance against the foreign genetic material (Barrangou et al., 2007).

Nucleotide sequence accession numbers

K. pneumoniae J1 has been deposited in DSMZ with the accession number DSM 101559. Genome information for the chromosome and plasmids of *K. pneumoniae* J1 were deposited in GenBank under the accession numbers CP013711, CP013712 and CP013713, respectively.

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