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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Klebsiella pneumoniae* subsp. *pneumoniae* DSM 30104^T

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***Klebsiella pneumoniae* is a Gram-negative, rod-shaped, nonmotile, and opportunistic pathogenic species with clinical importance. It is a part of natural flora of humans and animals. Here we report the draft genome sequence of the type strain of *Klebsiella pneumoniae* subsp. *pneumoniae* (DSM 30104^T) to provide taxonomic and functional insights into the species.**

Klebsiella pneumoniae is a Gram-negative, nonmotile, facultative bacterium belonging to the family *Enterobacteriaceae* and shows close genetic relatedness to species of the genera *Escherichia*, *Salmonella*, *Shigella*, and *Yersinia* (10, 14, 15). At present, *K. pneumoniae* consists of three subspecies, namely, *K. pneumoniae* subsp. *pneumoniae*, *K. pneumoniae* subsp. *rhinoscleromatis*, and *K. pneumoniae* subsp. *ozaenae*. *K. pneumoniae* subsp. *pneumoniae* is an opportunistic pathogen that is present at mucosal surfaces in humans and can cause severe diseases, such as septicemia, pneumonia, and urinary tract infections, by nosocomial infection (10). Here we present the draft genome sequence of the type strain of *K. pneumoniae* subsp. *pneumoniae* (DSM 30104^T) to provide a taxonomic framework for and biological insights into the species.

The genomic DNA of strain DSM 30104^T was sequenced using a combination of a 100-bp single-ended Illumina Genome Analyzer IIx system (63,272,416 reads; 1,215-fold coverage) and a Roche 454 GS FLX Titanium system (335,528 reads) with an 8-kb paired-end library. The hybrid genome assembly was achieved by using Newbler assembler 2.6 (Roche), CLC genomics wb 4.8 (CLCbio), and CodonCode Aligner (CodonCode Co.). Gene prediction was carried out using Glimmer 3 (3), and gene annotation was performed using clusters of orthologous groups (COG) and SEED databases (4, 12). Comparative genomics was achieved according to the method of Chun et al. (2).

The final assembly contains 28 contigs (5,425 coding DNA sequences [CDS], 5,512,347 bp, 57.02% G+C ratio) and 77 tRNA genes. Among the protein-coding genes, 699 (12.8%) open reading frames (ORFs) matched hypothetical protein sequences in GenBank database and 467 (8.6%) ORFs were present only in strain DSM 30104^T by comparison of all ORFS with other *K. pneumoniae* genomes (5, 7, 9, 11, 13, 14). A clustering analysis based on average nucleotide identity (ANI) (6) revealed that strain DSM 30104^T was most closely related to *K. pneumoniae* KCTC 2242 (99.03% ANI). Lower ANI values (approximately 98.75% to 98.99%) were found in comparisons to other *K. pneumoniae* strains sequenced so far (5, 7, 9, 11, 13, 14). The KCTC 2242 strain was previously reported to produce 2,3-butanediol and to be used in industrial applications as a potential valuable fuel additive (11).

For investigating antibiotic resistance-related genes, all protein sequences were compared to sequences in the Antibiotic Resistance Genes Database (ARDB; version 1.1) (8). Fifteen antibiotic resistance genes were identified in the DSM 30104^T genome, including homologous genes coding for class A beta-lactamase, a multidrug resistance efflux pump, and a potassium antiporter (1). In addition, 10 genes were found to be related to lactamase function, including *gloB* and *ampC*, which have the functions of encoding a metallo-beta-lactamase superfamily hydrolase and beta-lactamase class C, respectively. The genome sequence of *K. pneumoniae* subsp. *pneumoniae* DSM 30104^T will serve as a valuable reference for understanding the pathogenic and epidemiologic traits of *K. pneumoniae* strains.

Nucleotide sequence accession numbers. The sequence determined in this whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under accession number AJJI00000000. The version described in this paper is the first version, AJJI01000000.

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