**Genome Sequences of Five Clinical Isolates of Klebsiella pneumoniae**

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*Klebsiella pneumoniae* is a nosocomial pathogen of emerging importance and displays resistance to broad-spectrum antibiotics, such as carbapenems. Here, we report the genome sequences of five clinical *K. pneumoniae* isolates, four of which are carbapenem resistant. Carbapenem resistance is conferred by hydrolyzing class A β-lactamas found adjacent to transposases.

Whole-genome sequence analysis enables the identification of the molecular basis of antibiotic resistance and facilitates a survey for virulence determinants that can be targeted to reduce the pathogenic effects of the clinical isolates in different models of infection (9–11). To this end, we sequenced the genomes of five clinical isolates of *K. pneumoniae* isolated from patients in a Chicago area hospital.

Total genomic DNA was extracted with the QiAamp DNA minikit, according to the manufacturer’s protocol, and the genomic library was prepared with the TruSeq PCR-free kit with single indexing (12–14). The genomes were sequenced on the Illumina MiSeq platform using a paired-end library with 250-bp read length and assembled into draft genomes with SPAdes 3.5.0 (15). The average G+C content was 57.3%, and the total genome length varied between 5.3 and 5.9 Mbp, which is in accordance with reports for other *K. pneumoniae* genomes and is indicative of the varied moblome of this species (9).

Contigs were annotated using Prokka genome annotation version 1.0.0 (16), predicting on average 5,451 coding sequences, 77 tRNAs, and 7 rRNAs. Annotation revealed the presence of genes associated with a type VI secretion in all genomes (17, 18), while none of the isolates featured virulence factors related to the mucoid phenotype, *rmpA* (19) or *magA* (20), when queried against the UniProt database (>99% identity) to various plasmids previously described in *K. pneumoniae* (24). Understanding the evolutionary origin of the acquisition of the *K. pneumoniae* resistance gene complement will help track the spread of antibiotic resistance among clinical isolates. Future genome-wide association studies utilizing the cataloged genomic plasticity and antibiotic resistance phenotypes will assist in better defining the pathogenic potential of individual isolates in different models of infection (25, 26).

**Nucleotide sequence accession numbers.** The annotated draft genome sequences for *K. pneumoniae* strains K1, OC217, OC511, OC648, and Z3209 have been deposited in GenBank under accession numbers LOEJ0000000, LOEF0000000, LOEJ0000000, LOEH0000000, and LOEG0000000, respectively.

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