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Draft Genome Sequence of an NDM-5-Producing *Klebsiella pneumoniae* Sequence Type 14 Strain of Serotype K2

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We report here the draft genome sequence of uropathogenic *Klebsiella pneumoniae* sequence type 14 strain of serotype K2 possessing bla_{NDM-5}, isolated from a 65-year-old male in China without a history of travel abroad.

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Klebsiella pneumoniae is a major human pathogen causing hospital- and community-acquired infections (1, 2). The spread of NDM producers is now considered an endemic threat in *K. pneumoniae* and represents an important source of multidrug resistance around the world. *K. pneumoniae* sequence type 14 (ST14) has previously been described as a host lineage for the NDM-1 enzyme (3). Further, Serotype K2 has been described in one previous publication as frequently linked to ST14 (4).

Here, we report the unscaffolded whole-genome shotgun sequence of *K. pneumoniae* strain NUHL24835 recovered from a urine sample from a 65-year-old female patient hospitalized in the teaching hospital of Nanchang University, China, in 2015. The strain belongs to ST14 with a K2 capsular serotype and shows multiple resistances to clinically used antibiotics, including all β-lactams (ertapenem, meropenem, and imipenem showed MICs of >32 μg/ml), fluoroquinolones, aminoglycosides (except for amikacin), sulfonamides, and macrolides. It was susceptible to colistin and tigecycline.

The genomic DNA from *K. pneumoniae* NUHL24835 was sequenced by next-generation sequencing using an Illumina HiSeq 2000 instrument with a 2×151-bp paired-end approach. The draft genome of *K. pneumoniae* NUHL24835 comprises 5,387,996 bp, with a G+C content of approximately 58.53%. The protein-coding regions were predicted by Glimmer version 3.02 (http://www.cbcb.umd.edu/software/glimmer). In total, 5,191coding genes were identified, for a total length of 4,804,392 bp and 86.56% coverage of the genome. Eighty-four tRNA genes and 24 rRNA genes have putative functions assigned on the basis of the annotation.

The contigs were initially annotated using RAST (http://rast.nmpdr.org). A BLAST analysis and manual annotation utilized previously reannotated reference sequences and IS Finder (https://www-is.biotoul.fr). The MLST, ResFinder, and PlasmidFinder (http://www.genomicepidemiology.org) databases were used to characterize sequence typing, antibiotic resistance mechanisms, and the plasmid Inc types, respectively, of *K. pneumoniae* NUHL24835. ST14, plasmid Inc types of IncFII and IncX3, and the genes bla_{NDM-5}, $bla_{CTX-M-15}$, bla_{TEM-1}, *qnrS1*, *aadA5*, *sul1*, and *dfrA17* were identified. This finding is consistent with previously reported experimental results (5). A comparative analysis of the genome from our isolate with published *K. pneumoniae* genomes will be reported in the future.

A screening for (putative) virulence genes present in the BIGSdb-Kp database (http://bigsdb.web.pasteur.fr/klebsiella/klebsiella.html), performed using the BLASTn tool, revealed (i) the *kfuABC* system (6), which is responsible for ferric iron uptake, and (ii) the mannose-resistant *Klebsiella*-like (type III) fimbriae cluster *mrkABCDFHIJ* (7). Interestingly, the allantoin operon was not present in the genome of the *K. quasipneumoniae* subsp. *quasipneumoniae* type strain, suggesting recent horizontal acquisition by *K. pneumoniae* NUHL24835. The strain possessed a capsular *wzi*-2/K2 allele. Notably, the *rmpA* gene, previously associated with the hypermucoviscous phenotype in *K. pneumoniae* strains (8), was found in the genome of *K. pneumoniae* NUHL24835, suggesting the presence of a different capsular regulation mechanism. The identified virulence determinants may have contributed to the infection and/or colonization of *K. pneumoniae* NUHL24835 in the urinary tract.

Nucleotide sequence accession number. The whole-genome shotgun project of *K. pneumoniae* NUHL24835 has been deposited at GenBank under the accession number CP014004.

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