



Draft Genome Sequence of a Colistin-Resistant *Klebsiella pneumoniae* Clinical Strain Carrying the *bla*_{NDM-1} Carbapenemase Gene

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ABSTRACT *Klebsiella pneumoniae* strain WCHKP1845, recovered from the sputum of a patient with pneumonia, was resistant to colistin and carried the carbapenemase gene *bla*_{NDM-1}. Here, we report its 5.4-Mb draft genome sequence, comprising 140 contigs with an average 57.33% G+C content. The genome contains 5,118 coding sequences and 88 tRNA genes.

Klebsiella pneumoniae is a major pathogen of human infections (1). *K. pneumoniae* strain WCHKP1845 was recovered from the sputum of a male patient with pneumonia in the Respiratory Intensive Care Unit at West China Hospital, Chengdu, Western China, in May 2016. Strain WCHKP1845 is resistant to meropenem (MIC, 64 μg/mL) and colistin (MIC, 16 μg/mL). Screening for the acquired carbapenem-hydrolyzing β-lactamase (carbapenemase) genes *bla*_{GES} (including noncarbapenemase variants), *bla*_{IMP}, *bla*_{IMI}, *bla*_{KPC}, *bla*_{NDM}, *bla*_{OXA-48}-like, and *bla*_{VIM} was performed using PCR as described previously (2–5). Strain WCHKP1845 was positive for *bla*_{NDM} and was therefore subjected to whole-genome sequencing.

The QIAamp DNA minikit (Qiagen, Hilden, Germany) was used to prepare genomic DNA from strain WCHKP1845, which was then sequenced using the HiSeq X10 Sequencer (Illumina, San Diego, CA, USA) with the 150-bp paired-end protocol and 200× coverage. A total of 1.5-Gb clean bases and 5,013,767 reads were generated, which were assembled into 140 contigs (76 contigs ≥1,000 bp in length; *N*₅₀, 334,879 bp) with a 57.33% G+C content using SPAdes version 3.9 (6). The genome size was about 5.4 Mb, which was annotated using Prokka version 1.11 (7). The genome of strain WCHKP1845 contained 5,118 coding sequences and 88 tRNA genes. The multilocus sequence typing (MLST) tool of the Center for Genomic Epidemiology (<http://genomic-epidemiology.org>) was used to assign strain WCHKP1845 to a sequence type (ST) based on the genome sequence. Strain WCHKP1845 belonged to ST1 (*gapA*, *infB*, *mdh*, *pgi*, *phoE*, *rpoB*, and *tonB*; 4-4-1-1-7-4-10). *K. pneumoniae* of ST1 has been found in China (8) and Europe (Spain) (9) (<http://bigsd.bpasteur.fr/klebsiella/klebsiella.html>).

Antimicrobial resistance genes were predicted using ResFinder from the Center for Genomic Epidemiology. Strain WCHKP1845 had the carbapenemase gene *bla*_{NDM-1} and a few other antimicrobial resistance genes, including *bla*_{TEM-1a} and *bla*_{SHV-1} (mediating resistance to penicillins), *fosA* (to fosfomycin), *oqxA* and *oqxB* (to quinolones), *strA* and *strB* (to aminoglycosides), *sul2* (to sulfonamides), and *tet*_(A) (to tetracycline). Of note, although strain WCHKP1845 was resistant to colistin, it did not carry the plasmid-borne colistin-resistant genes *mcr-1* and *mcr-2*. The interruption of *mgrB*, which encodes a negative-feedback regulator of the PhoQ-PhoP two-component system by insertion sequences, has been reported as the common mechanism of colistin resistance in

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carbapenem-resistant *K. pneumoniae* (10). However, the *mgrB* gene of strain WCHKP1845 is intact. Therefore, the mechanism of colistin resistance in strain WCHKP1845 remains unclear at present and warrants further investigation. Plasmid-Finder from the Center for Genomic Epidemiology predicted that strain WCHKP1845 carried five plasmid replicons, including IncQ1, IncR, IncX3, and two IncFII(K). *bla*_{NDM-1} is located on a 48,124 bp-contig that contains the IncX3 replicon, suggesting that *bla*_{NDM-1} is carried by an IncX3 plasmid.

Accession number(s). This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [MP0D0000000](https://www.ncbi.nlm.nih.gov/nuclink/MP0D0000000). The version described in this paper is the first version, MPOD01000000.

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