





# Genome Sequences of Two NDM-1 Metallo- $\beta$ -Lactamase-Producing Multidrug-Resistant Strains of *Klebsiella pneumoniae* with a High Degree of Similarity, One of Which Contains Prophage

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**ABSTRACT** We report genome sequences of two NDM-1 metallo- $\beta$ -lactamase-producing multidrug-resistant *Klebsiella pneumoniae* isolates of sequence type 147 (ST147) from one hospital. The genomes are highly similar and differ in prophage located in the chromosome of *K. pneumoniae* KPB-1470/16 and in the additional plasmid-carrying *bla*<sub>OXA-48</sub> gene in *K. pneumoniae* KPB-417/16.

*Klebsiella pneumoniae* carrying New Delhi metallo- $\beta$ -lactamase (NDM-1) emerging worldwide has raised public health concern. NDM-1 hydrolyzes a wide range of  $\beta$ -lactam antibiotics, including carbapenems, which are the last-resort antibiotics for the treatment of infections caused by resistant bacteria. Nosocomial infections caused by carbapenem-resistant *K. pneumoniae* are associated with high rates of morbidity and mortality (1, 2). This pathogen was included in the critical level of the “global priority list of antibiotic-resistant bacteria” designed by the World Health Organization (3). The dissemination of NDM-1 is associated with diverse sequence types (STs) of *K. pneumoniae*, including ST147 (2, 4, 5).

Here, we report the genome sequences of two ST147 *K. pneumoniae* strains (KPB-1470/16 and KPB-417/16) isolated from endotracheal aspirates of two adult patients in the Moscow neurosurgical intensive care unit (ICU) on 28 March 2016 and 5 September 2016, respectively. The strains were deposited in the State Collection of Pathogenic Microorganisms and Cell Cultures “SCPM-Obolensk” (accession numbers SCPM-O-B-8045 and SCPM-O-B-7954, respectively). Both strains are resistant to amoxicillin-clavulanic acid, ampicillin-sulbactam, cefuroxime, ceftazidime, cefoperazone-sulbactam, cefepime, imipenem, ciprofloxacin, gentamicin, amikacin, and nitrofurantoin.

Genome sequencing was performed using an Illumina MiSeq instrument according to the manufacturer’s instructions. For each genome, reads were assembled *de novo* using SPAdes v. 3.9.0 (6). The final assemblies had mean coverages of 36 $\times$  and 43 $\times$  and consisted of 5,625,359 bp (GC content of 57.0% and 115 contigs) and 5,637,851 bp (GC content of 57.0% and 110 contigs) for KPB-417/16 and KPB-1470/16, respectively.

Draft genomes were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (7). A total of 5,367 and 5,399 protein-coding sequences and 106 and 109 tRNAs were annotated for KPB-417/16 and KPB-1470/16, respectively. Sequences of four plasmid replicon types (IncHIIB, IncFIA, IncFIB, and IncFII) were identified in both genomes by using PlasmidFinder (8). In addition, sequences of IncL/M plasmid were

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determined in the KPB-417/16 genome. Six different *bla* genes (*bla*<sub>SHV-11</sub>, *bla*<sub>CTX-M-15</sub>, *bla*<sub>TEM-1</sub>, *bla*<sub>OXA-1</sub>, *bla*<sub>OXA-9</sub>, and *bla*<sub>NDM-1</sub>) that code for extended-spectrum  $\beta$ -lactamase were defined in both genomes using ResFinder (9). An additional *bla*<sub>OXA-48</sub> gene was identified in IncL/M plasmid sequences of *K. pneumoniae* KPB-417/16. Moreover, genes that determine resistance to aminoglycosides [*aadA1*, *aadA2*, *armA*, *aph(3')-via*, and *aac(6')Ib-cr*], fluoroquinolones (*oqxAB*), phosphomycins (*fosA*), macrolides [*msr(E)* and *mph(E)*], phenicols (*catB4*), sulfonamides (*sul1*), and trimethoprim (*dfrA12*) have been identified in chromosome and plasmid sequences of both genomes. Some resistance genes [*aac(3)-IIa*, *qnrS1*, and *catA2*] were determined in plasmid sequences of strain KPB-1470/16 only.

Both strains exhibit a high average nucleotide identity of 99.99% between each other but differ from one another in the plasmid composition mentioned above as well as by the presence of additional prophage sequences located in the chromosome of *K. pneumoniae* KPB-1470/16. Similar prophage sequences were detected in the genome of *K. pneumoniae* strain TGH13 (GenBank accession number CP012745) isolated in Greece that belongs to ST147 as well.

According to our knowledge, this is the first report of genome sequences of NDM-1 metallo- $\beta$ -lactamase-producing strains of *K. pneumoniae* isolated in Russia. The characteristics of the presented genomes are a step toward a better understanding of the population of clinical multidrug-resistant *K. pneumoniae* strains.

**Accession number(s).** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession numbers [NPJW00000000](#) and [NPII00000000](#) for strains KPB-417/16 and KPB-1470/16, respectively.

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