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GENOME SEQUENCES

Draft Genome Sequences of Two Carbapenemase-Producing *Klebsiella pneumoniae* Strains Isolated from Blood Cultures

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ABSTRACT Carbapenemase-producing *Klebsiella pneumoniae* represents an emerging public health issue. Here, we present the draft whole-genome sequences of *K. pneumoniae* clinical strains KPL0.1 (OXA-48 carbapenemase) and KPL0.2 (NDM-1 carbapenemase). These genome sequences should help in investigating pathophysiological mechanisms of digestive colonization or infection with these highly resistant bacteria.

Carbapenemase-producing *Enterobacteriaceae* (CPE) are resistant to most beta-lactams, including last-line options such as carbapenems, and are an emerging public health issue (1). *Klebsiella pneumoniae* colonizes the human gastrointestinal tract and can persist in the hospital environment, and outbreaks of carbapenemase-producing *K. pneumoniae* are frequently described (2). In France, the most frequently identified carbapenemases are OXA-48 (86% of the CPE) and NDM (9% of the CPE) (3). Two strains of carbapenemase-producing *K. pneumoniae* were isolated in the Lille University Teaching Hospital (CHU Lille, France), KPL0.1 (producing OXA-48 carbapenemase) and KPL0.2 (producing NDM-1 carbapenemase). Both strains were isolated from blood cultures using the Virtuo automated system (bioMérieux, Marcy-l'Étoile, France) and identified by matrix-assisted laser desorption ionization–time of flight (MALDI-TOF) mass spectrometry (Bruker Daltonics, Inc., Billerica, MA). KPL0.1 was isolated from a 77-year-old patient following digestive surgery, and KPL0.2 came from an 84-year-old patient with a urinary tract infection.

The DNA of each isolate was extracted using a QIAamp DNA minikit (Qiagen, Hilden, Germany), and quality control was performed using a Qubit v3.0 fluorometer (Thermo Fisher Scientific, Waltham, MA). Libraries were prepared using the Nextera XT DNA Library prep kit (Illumina, San Diego, CA), followed by paired-end (2 × 150-bp) sequencing on a HiSeq platform (Illumina). Genome coverage was about 650× for each isolate. Paired reads were filtered, and Nextera adapters were removed using Trimmomatic on a Galaxy server using default settings (4). Processed reads were *de novo* assembled with Unicycler. Genomes were annotated using the Prokaryotic Genome Annotation Pipeline (PGAP) v4.5 (5).

The draft genome of KPL0.1 consists of 5,825,863 bp and has a mean G+C content of 56.70%. A total of 5,628 protein-coding genes were annotated, including 92 RNA-coding genes and 75 tRNAs, and the remaining genes were annotated as hypothetical proteins. KPL0.1 belongs to sequence type 307 (ST-307) and possesses the KL102 capsule locus (6). The following resistance genes were predicted using ResFinder v3.0 (7): five beta-lactam resistance genes (bla_{OXA-48}, bla_{SHV-28}, bla_{TEM-1B}, $bla_{CTX-M-15}$, bla_{OXA-1}), four aminoglycoside resistance genes [*aac(3)-IIa*, *aph(3")-Ib*, *aph(6)-Id*, *aac(6')-Ib-cr*], five fluoroquinolone resistance genes [*qnrS1*, *qnrB1*, *aac(6')-Ib-cr*, *oqxA*, *oqxB*], and

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individual antimicrobial resistance genes (fosfomycin, *fosA*; phenicol, *catB4*; sulfonamide, *sul2*; trimethoprim, *dfrA14*; tetracycline, *tetA*).

The draft genome of KPL0.2 consists of 5,741,089 bp with a mean G+C content of 56.94%. A total of 5,570 protein-coding genes were annotated, including 93 RNA-coding genes and 79 tRNAs, and the remaining genes were annotated as hypothetical proteins. KPL0.2 belongs to ST-147 and possesses the KL64 capsule locus. The following resistance genes were predicted: five beta-lactam resistance genes (bla_{NDM-1}, bla_{SHV-11}, bla_{TEM-1B}, $bla_{CTX-M-15}$, bla_{OXA-1}), four aminoglycoside resistance genes [*aac(3)-IIa*, *strA*, *aph(6)-Id*, *aac(6′)-Ib-cr*), four fluoroquinolone resistance genes [*qnrB1*, *aac(6′)-Ib-cr*, *oqxA*, *oqxB*], and individual antimicrobial resistance genes (fosfomycin, *fosA*; phenicol, *catB4*, sulfonamide, *sul1*; trimethoprim, *dfrA1*; tetracycline, *tetA*).

ST-147 was identified as one of the three major STs of carbapenemase-producing *K. pneumoniae* in a worldwide study; ST-147 is usually recovered from India, Italy, and Greece (8). ST-307 is described as highly prevalent in Italy (9). Overall, these two strains are representative of the carbapenemase-producing *K. pneumoniae* isolates in Europe. Further studies are warranted to investigate the pathophysiological mechanisms of digestive colonization or infection with these highly resistant bacteria.

Data availability. These two draft whole-genome shotgun projects have been deposited at DDBJ/ENA/GenBank under the accession numbers QHMA00000000 (KPL0.1) and PYBH00000000 (KPL0.2). The versions described in this paper are QHMA01000000 (KPL0.1) and PYBH01000000 (KPL0.2). The SRA accession number is SRP155589.

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