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GENOME ANNOUNCEMENT

Complete Genome Sequence of *Klebsiella oxytoca* E718, a New Delhi Metallo-β-Lactamase-1-Producing Nosocomial Strain

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We report the complete genome sequence of *Klebsiella oxytoca* E718, a New Delhi metallo-β-lactamase-1 (NDM-1)-producing strain isolated from a renal transplant patient. The genome contains a 6,097,032-bp chromosome and two multidrug resistance plasmids with sizes of 324,906 bp and 110,781 bp.

Klebsiella oxytoca is a member of the *Enterobacteriaceae* and the second-most-common *Klebsiella* species recovered in clinical medicine. It is an important opportunistic pathogen that can cause various nosocomial and community infections, including septicemia, pneumonia, urinary tract infection, and antibiotic-associated hemorrhagic colitis (4, 8). Carbapenems such as imipenem and meropenem are the drugs of last resort for treating infections caused by extended-spectrum-β-lactam-resistant Gram-negative bacteria. As a consequence, the emergence of carbapenem-resistant strains, particularly *Escherichia coli* and *Klebsiella pneumoniae*, has become a worldwide problem (6, 7). Although present to a lesser extent, several important carbapenemases, including *K. pneumoniae* carbapenemase (KPC) and New Delhi metallo-β-lactamase-1 (NDM-1), have also been identified in *K. oxytoca* clinical isolates (3, 5).

Complete genome sequencing was performed on *K. oxytoca* E718, which was isolated from a 56-year-old man in Taiwan in 2010 (5). The patient underwent renal transplantation in Jangxi, China, and was presented to a hospital in Taiwan 1 week later with abdominal pain and dysuria. Four ertapenem-resistant *K. oxytoca* isolates were recovered and confirmed to be of the same strain, and all were positive for $bla_{\text{NDM-1}}$. This is the first case of hospital-acquired infection caused by an NDM-1-producing *K. oxytoca* strain in Taiwan.

Genomic sequencing was performed first with a shotgun library prepared using Nextera (Illumina) on one lane of an Illumina GAII system (Illumina). In addition, two paired-end libraries across a distance of 3 kb or 8 kb on the genomic DNA were prepared and sequenced using 454 GS Junior (Roche). The shotgun reads were assembled using CLC Genomic Workbench (CLCBio) and Newbler (Roche). Gap filling between the assembled contigs was performed by adding Sanger reads with the aid of Consed software (2). Ambiguities of homopolymers and repetitive sequences were manually inspected and corrected, with data input from the MiSeq (Illumina) sequencer. Sequence annotation was performed using RAST Server software (1) followed by manual inspection.

The completed *K. oxytoca* E718 genome composed of a circular chromosome of 6,097,032 bp (56.4% G+C content) and two circular plasmids of 324,906 bp (pKOX_R1) and 110,781 bp (pKOX_NDM1) (unpublished data). Annotation of the chromosome revealed 5,668 protein-coding genes, 84 tRNA genes, and 25 rRNA genes. Among the protein-coding genes, 59% were assigned to putative functional categories.

Comparative genomics analysis will provide further understanding of the *K. oxytoca* genome and contribute to the knowledge of genomic evolution of the *Klebsiella* genus.

Nucleotide sequence accession number. The genome sequence of *K. oxytoca* E718 has been deposited in NCBI GenBank under accession number CP003683.

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