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GENOME ANNOUNCEMENT

Genome Sequence of *Klebsiella oxytoca* 11492-1, a Nosocomial Isolate Possessing a FOX-5 AmpC β-Lactamase

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***Klebsiella oxytoca* strain 11492-1 was isolated from a perianal swab culture from a patient at the University of Maryland Medical Center in 2005. The *K. oxytoca* 11492-1 draft genome contains multiple antibiotic resistance genes, including a FOX-5 AmpC β-lactamase encoded on a large IncA/C plasmid.**

The genus *Klebsiella* is comprised of diverse organisms that range from nitrogen-fixing plant endosymbionts (6, 11) to nosocomial pathogens capable of causing pneumonia, septicemia, meningitis, and urinary tract infections in humans (12, 14). In addition, *K. pneumoniae* has been linked to the occurrence of pyogenic liver abscesses, which were originally described in Taiwan but have been reported globally in recent years (5, 9, 13). *K. pneumoniae* is a significant nosocomial pathogen often encoding multiple antibiotic resistance markers. *K. oxytoca* is less frequently associated with human disease (7, 12); however, *K. oxytoca* has recently been linked to antibiotic-associated hemorrhagic colitis (8).

K. oxytoca 11492-1 was isolated from a perianal swab culture from a patient in the intensive care unit (ICU) at the University of Maryland Medical Center (UMMC) in April 2005. There were no *K. oxytoca* isolates cultured from this patient on either surveillance cultures or clinical cultures upon admission of the patient to the UMMC ICU, suggesting that the patient most likely acquired the isolate while residing in the ICU. *K. oxytoca* was also isolated from a blood culture during the same admission, suggesting that this patient had a systemic *K. oxytoca* infection.

K. oxytoca was identified by API 20E and Vitek 2 biochemical assays (bioMérieux). In addition, *K. oxytoca* 11492-1 was indole positive, as are other *K. oxytoca* isolates, and encodes a bla_{OXY-2} β-lactamase (10). BLAST analysis of a partial 16S rRNA gene sequence (991 nucleotides) from the draft genome of *K. oxytoca* 11492-1 exhibited 99% nucleotide identity over the entire sequence length to the 16S rRNA gene of *K. oxytoca* ATCC 13182T (KOU78183). Genomic DNA was isolated from an overnight culture using the Sigma GenElute kit (Sigma-Aldrich). The genome sequence of *K. oxytoca* 11492-1 was generated using paired-end libraries with 300-bp inserts on the Illumina HiSeq2000. The draft genome is 6.18 Mb with approximately 95× sequence coverage and was assembled using the Velvet assembly program (15). The final assembly includes 213 contigs after filtering for contigs of >200 bp.

Antibiotic susceptibility was determined by disk diffusion assays (4), which demonstrated that *K. oxytoca* 11492-1 is resistant to broad-spectrum cephalosporins and sulfamethoxazole-trimethoprim. *K. oxytoca* 11492-1 also contains a large IncA/C plasmid encoding a FOX-5 AmpC β-lactamase.

Bioinformatic detection of previously identified *K. pneumoniae* virulence-associated genes demonstrated that *K. oxytoca* 11492-1 does not carry genes associated with the mucoid phenotype (1). Interestingly, the *K. oxytoca* 11492-1 genome does contain genes for allantoin metabolism, which is an anaerobic process associated primarily with *K. pneumoniae* isolates from liver abscesses (3). Additionally, the *K. oxytoca* 11492-1 genome has citrate fermentation genes, which were previously identified in some clinical *K. pneumoniae* isolates such as the MGH 78578 sputum isolate (2) and the nitrogen-fixing plant endosymbiont *K. pneumoniae* 342 (6).

K. oxytoca 11492-1 possesses a unique combination of virulence, antibiotic resistance, and metabolic genes that highlight the need for additional studies into the genomic diversity of *K. oxytoca*. To our knowledge, this is the first-described *K. oxytoca* genome in the public domain.

Nucleotide sequence accession number. The 11492-1 draft genome sequence has been deposited at DDBJ/EMBL/GenBank under the accession number AIEM01000000.

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