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Full-Genome Sequence of *Escherichia coli* K-15KW01, a Uropathogenic *E. coli* B2 Sequence Type 127 Isolate Harboring a Chromosomally Carried $bla_{CTX\text{-}M\text{-}15}$ Gene

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We present here the full-genome sequence of *Escherichia coli* K-15KW01, an extended-spectrum-β-lactamase-producing uropathogenic strain. Assembly and annotation of the draft genome resulted in a 5,154,641-bp chromosome and revealed a chromosomally contained $bla_{CTX\text{-}M\text{-}15}$ gene embedded at the right-hand extremity of an IS*Ecp1* element in a plasmid-like structure (36,907 bp).

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The production of extended-spectrum β-lactamases (ESBLs) is one of the most important mechanisms of antibacterial resistance in *Enterobacteriaceae*. Most ESBLs can be divided into 4 groups: TEM, SHV, OXA, and CTX-M types (1). Currently, CTX-Ms are the most prevalent type of ESBLs described (2, 3). The last decade has seen a high degree of diversification of these enzymes and an explosive global spread driven primarily by their carriage on resistance plasmids and by the spread of extraintestinal pathogenic *Escherichia coli* clones (4). Meanwhile, it has become widely recognized that the dissemination of ESBL-producing bacteria is an issue that is no longer restricted to the medical health care system. In the last few years, there has been an increase in the detection of ESBL-producing strains in the general community (5, 6).

In a recent study, we isolated an ESBL-producing *E. coli* isolate (B2 sequence type 127 [ST127]) harboring a $bla_{CTX\text{-}M\text{-}15}$ gene from a healthy asymptomatic carrier shedding the same strain for 5 months in fecal samples (7). Despite repeated attempts, the $bla_{CTX\text{-}M\text{-}15}$ gene from this isolate could not be transferred by conjugation. Southern blot hybridization provided evidence for a chromosomal location of $bla_{CTX\text{-}M\text{-}15}$ (data not shown). Therefore, genomic DNA was isolated from K-15KW01 and subjected to sequencing using Pacific Biosciences single-molecule real-time (SMRT) technology at the ChunLab at Seoul National University, South Korea. The K-15KW01 genome was assembled *de novo* using the SMRT Analysis 2.3.0 software to a single chromosome of 5,154,641 bp in size, with a G+C content of 50.4%. Genome annotation was conducted through the NCBI Prokaryotic Genome Annotation Pipeline (PGAP) (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/) (8).

By full-genome sequencing, the chromosomal location of the $bla_{CTX\text{-}M\text{-}15}$ gene could be proven. The $bla_{CTX\text{-}M\text{-}15}$ gene was embedded at the right-hand extremity of an IS*Ecp1* element in a plasmid-like structure (36,907 bp) located between a putative gene encoding for an oxalyl-coenzyme A (CoA) decarboxylase domain (positions 978270 to 978743) and a formyl-CoA-oxalate CoA-transferase (gene *frc*) (positions 1015704 to 1016954). Moreover, on this plasmid-like structure, a tunicamycin resistance determinant (*tmrB*), an aminoglycoside N(3′)-acetyl transferase III (*aacC2*), the cr variant of *aac(6′)-Ib* encoding an aminoglycoside acetyltransferase conferring resistance to fluoroquinolones, the β-lactamase gene $bla_{OXA\text{-}1}$, and the chloramphenicol acetyltransferase *catB3* were carried.

E. coli B2:ST127 has recently been described as an emerging clone with extremely high uropathogenic potential (9) and has been associated with community-acquired urinary tract infections (CAUTI) in Britain (10). The detection of uropathogenic *E. coli* (UPEC) B2:ST127 isolates harboring chromosomally carried $bla_{CTX\text{-}M\text{-}15}$ in a healthy person is a matter of concern, since UPEC isolates spread easily via person-to-person contact or fecal-oral transmission (11).

Accession number(s). Sequence and annotation data of the genome of *E. coli* strain K-15KW01 were deposited in the GenBank database with the accession no. CP016358.

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