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GENOME ANNOUNCEMENT

Genome Sequence of Multidrug-Resistant *Escherichia coli* EC302/04, Isolated from a Human Tracheal Aspirate

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***Escherichia coli* is an important etiologic agent of lower respiratory tract infections (LRTI). Multidrug-resistant *E. coli* EC302/04 was isolated from a tracheal aspirate, and its genome sequence is expected to provide insights into antimicrobial resistance as well as adaptive and virulence mechanisms of *E. coli* involved in LRTI.**

Lower respiratory tract infections (LRTI) caused by multidrug-resistant bacteria are a common problem worldwide (2, 6), and significant morbidity and mortality associated with LRTI have been reported (5). *Escherichia coli* is one of the common etiologic agents of LRTI among the Gram-negative bacteria (2, 6); it may exist initially as a colonizer but can progress to cause severe infections such as ventilator-associated pneumonia (VAP) in the respiratory tract (6). Patients admitted to intensive care units (ICU) are often at a higher risk of contracting severe LRTI than those in the general wards (15).

E. coli EC302/04 is a multidrug-resistant bacterium isolated from the tracheal aspirate of an ICU patient in 2004 and has been characterized previously (10, 13). Strain EC302/04 was nonsusceptible to ampicillin (10 μg), gentamicin (10 μg), streptomycin (10 μg), kanamycin (30 μg), chloramphenicol (30 μg), amoxicillin-clavulanic acid (30 μg), and cefoperazone (30 μg). Although the genetic makeup of *E. coli* is widely studied, there is limited genomic information for LRTI-associated *E. coli*. Therefore, the genome data harnessed from strain EC302/04 would enhance the understanding of its antimicrobial resistance and adaptive and virulence mechanisms.

The genome sequencing of strain EC302/04 was performed using the Illumina HiSeq 2000 (100-bp read length) with an insert size of 300 bp. The reads were trimmed and assembled *de novo* using CLC Genomics workbench 5.0 (CLC Bio, Denmark). A total of 82 contigs were generated, with an accumulated length of 4,846,195 bp (312-fold coverage) and an average GC content of 51%. The contig N_{50} is 201,460 bp, and the longest assembled contig is 350,759 bp. The genome annotation was performed by the RAST annotation server (3), which led to the identification of 4,738 open reading frames with an average length of 904 bp and a coding percentage of 88.4. Using RNAmmer (12) and tRNAscan-SE (14), 4 rRNAs and 70 tRNAs were found.

Based on *in silico* analysis, the multilocus sequence type and serotype of strain EC302/04 were ST349 and O166:H15, respectively. The genome sequence revealed two multiple antibiotic resistance (*mar*) regulons, *marRAB* and *marC* (1), which have been reported to be involved in resistance to various antibiotics such as chloramphenicol, cephalosporins, and tetracycline (7, 9). Genes encoding other enzymes involved in antimicrobial resistance which were identified in EC302/04 include β-lactamases ($bla_{\text{TEM-1}}$, bla_{AmpC}) and streptomycin 3′-*O*-adenylyltransferase. It has been demonstrated that biofilm formation on the endotracheal tube facilitates the bacterial entry into the lower respiratory tract, contributing to colonization and LRTI in intubated patients (2, 6, 8). The genome of EC302/04 also possesses genes encoding several biofilm formation-associated proteins such as LuxS, responsible for the production of autoinducer 2 (AI-2) (4), and the YjgK cluster (11). Type 1 pilus FimH adhesin, which has been reported to be critical in *E. coli* biofilm formation and has the ability to bind nonspecifically to abiotic surfaces (4), was also identified in EC302/04.

To the best of our knowledge, this is the first genome sequence of an *E. coli* isolate from human tracheal aspirate, and the availability of this genome data will aid in the understanding of the pathogenesis of the organism.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AMFM00000000. The version described in this paper is the first version, AMFM01000000. The BioProject designation for this project is PRJNA174602.

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