

# Draft Genome Sequence of the Multidrug-Resistant *Escherichia coli* Strain LR09, Isolated from a Wastewater Treatment Plant

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**We report the draft genome sequence of *Escherichia coli* O1:H6 strain LR09, which was isolated from a wastewater treatment plant and displays high resistance to five fluoroquinolone antimicrobials. The assembled data determine that the strain clusters with *E. coli* phylogroup F and harbors a plasmid conferring resistance to a broad spectrum of antibiotics.**

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Wastewater treatment plants provide an opportunity for the dissemination of mobile antimicrobial resistance determinants as bacteria previously exposed to antibiotics mix with naive strains (1). However, these multidrug-resistant bacteria have been otherwise poorly characterized. Here we report the draft genome sequence of *Escherichia coli* LR09, isolated in August 2006 from the Little Rock Wastewater Utility treatment plant in Little Rock, AR (2). This strain was isolated using media containing 200 ng  $\mu\text{l}^{-1}$  norfloxacin and was shown to be highly resistant to all fluoroquinolones tested (2), as well as to gentamicin, streptomycin, and ampicillin (all above 200 ng  $\mu\text{l}^{-1}$ ).

Genomic DNA was extracted from an overnight culture using the DNeasy blood and tissue kit (Qiagen). Sequencing libraries were prepared with both the TruSeq DNA sample prep kit (Illumina) and the Nextera mate pair sample prep kit (Illumina) and sequenced on the Illumina MiSeq platform, generating 12,384,122 paired-end 300-bp reads and 9,355,464 mate pair 250-bp reads, respectively. The draft genome sequence was assembled *de novo* with CLC Genomics Workbench version 6.5.1 (CLC bio), producing 124 contigs resulting in a total genome size of 5,338,463 bp and an  $N_{50}$  of 347,262 bp. Plasmid DNA was isolated using the Large-Construct kit (Qiagen) and sequenced to determine which contigs comprised plasmid DNA; however, closure of the plasmid sequences was not performed. The draft genome sequence was annotated using RAST (3) and predicted to contain 5,183 coding sequences and 88 tRNAs.

Phylogenetic analysis utilizing backbone single nucleotide polymorphisms (SNPs) from whole-genome sequences revealed that LR09 clusters with *E. coli* phylogroup F (4). Molecular serotyping using the *wzx*, *wzy*, and *fliC* loci indicated that LR09 is O1:H6. BLAST results were negative for molecular markers of known *E. coli* pathotypes, including toxins and toxin genes (*stx*<sub>1</sub>, *stx*<sub>2</sub>, *ehxA*, *hlyA*, LT, and ST) and genes for adhesins (*eae*, *bfpA*, *aggR*, and *pap*). The genome contains two small plasmids, a 1,460-bp plasmid with 99% sequence identity to *E. coli* strain 1/21 plasmid pKST21 (GenBank accession no. JF436966.1) and a 7-kb plasmid encoding a colicin and a DNA restriction and modifica-

tion system. In addition, LR09 possesses a 92-kb plasmid homologous to p12579\_1 from *E. coli* O55:H7 strain RM12579 (GenBank accession no. CP003110.1). This plasmid is a lysogenic bacteriophage that remains circularized and extrachromosomal (5). A fourth plasmid harbored in LR09 is a large (>163 kb) IncF virulence plasmid exhibiting homology to pRSB225 (GenBank accession no. JX127248.1) carried by an uncultured bacterium isolated from a wastewater treatment plant in Germany (6). Along with genes encoding putative virulence factors, this LR09 plasmid carries antibiotic resistance genes identified by ResFinder (7). These include genes for resistance to aminoglycosides [*strAB*, *aadA5*, and *aac(3)-IId*], beta-lactam (*bla*<sub>TEM-1B</sub>), macrolide [*mph(A)*], chloramphenicol (*catA1*), sulfonamide (*sul1*), tetracycline [*tet(B)*], and trimethoprim (*dhfrA17*). In addition, the genome contains an antibiotic resistance cassette conferring resistance to beta-lactam (*bla*<sub>OXA-1</sub>), chloramphenicol (*catB3*), and aminoglycosides and fluoroquinolones [*aac(6')-Ib-cr*], the latter gene of which was previously shown to be responsible for the acetylation of ciprofloxacin and norfloxacin in this isolate (2).

**Nucleotide sequence accession number.** The draft genome sequence of *E. coli* LR09 was deposited at DDBJ/EMBL/GenBank under accession no. [JDVF00000000](https://www.ncbi.nlm.nih.gov/nuccore/JDVF00000000).

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