A multidrug-resistant *Escherichia coli* isolate from an abdominal lesion displayed resistance to all β-lactams tested, including carbapenems, in addition to macrolides, fluoroquinolones, and tetracycline. Sequence analyses demonstrated the presence of \( \text{bla}_{\text{NDM-5}} \) in addition to at least 13 genes and 6 efflux pumps associated with antibiotic resistance.

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Numerous multidrug-resistant *Escherichia coli* isolates were obtained during the course of an investigation into health care-associated transmission in a tertiary care facility (5). All 39 outbreak-related isolates were very closely related (>92% similar) by pulsed-field gel electrophoresis (PFGE) and by WGS analysis (range, 1 to 28 single nucleotide polymorphisms in the core genome). One isolate, *E. coli* 1400026, obtained from an abdominal lesion, was selected for the annotation described here. DNA was extracted using the Maxwell 16 (Promega, Madison, WI) instrument. The availability of this genomic sequence enables further comparative genomic analyses within *E. coli* strains and also provides information on the genetic background of antibiotic resistance.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. JTKA00000000. The version described in this paper is version JTKA01000000.

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