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Draft Genome Sequence of NDM-5-Producing *Escherichia coli* Sequence Type 648 and Genetic Context of bla_{NDM-5} in Australia

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We report here the draft genome sequence of uropathogenic *Escherichia coli* sequence type 648 (ST648) possessing bla_{NDM-5} from a 55-year-old female in Australia with a history of travel to India. The plasmid-mediated bla_{NDM-5} was in a genetic context nearly identical to that of the GenBank entry of an IncX3 bla_{NDM-5} plasmid previously reported from India (*Klebsiella pneumoniae* MGR-K194).

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The Indian subcontinent has been reported as a geographical reservoir for the acquisition of NDM-producing *Enterobacteriaceae* (1). A 55-year-old female with chronic diarrhea had carbapenem-resistant *Escherichia coli* isolated from a urine sample in January 2014. She traveled to India in late 2013 and developed diarrhea but was not admitted to a medical facility. Upon her return to Australia, ongoing diarrhea prompted multiple hospital admissions. She was diagnosed with Crohn's disease. During admission, a midstream urine sample was collected, from which the carbapenem-resistant *E. coli* CR694 was identified.

Whole-genomic DNA of *E. coli* CR694 was prepared using the Nextera XT DNA sample preparation kit (Illumina, USA) and sequenced using the Illumina HiSeq 2000 (Illumina) at the Australian Genome Research Facility. *De novo* assembly was performed using CLC Genomics Workbench version 7.5 (CLC bio, Denmark). The draft genome consists of 5,523,407 bp. The contigs were initially annotated using RAST (http://rast.nmpdr.org/). A BLAST analysis and manual annotation utilized previously reannotated reference sequences and IS Finder (https://www-is.biotoul.fr/). The MLST, ResFinder, and PlasmidFinder (http://www.genomicepidemiology.org/) databases were used to characterize sequence typing (ST), antibiotic resistance mechanisms, and the plasmid Inc types, respectively, of *E. coli* CR694. ST648, plasmid Inc types of IncFII, IncFIB, IncX3, IncI1, and IncX4, and the genes bla_{NDM-5}, bla_{CMY-42}, *aac-6-Ib-cr*, *aadA5*, *erm*(B), *mph*(A), *sul1*, *tet*(B), and *dfrA17* were identified.

Additionally, the annotation through RAST identified the type 1 fimbriae genes *fimABCDEFGHI*, virulence determinants relevant for urinary tract adhesion (2). Further, five other types of fimbriae were identified as a membrane transport type VII protein secretion system, namely the (i) *htrE* fimbriae cluster, (ii) *stf* fimbriae cluster, (iii) alpha-fimbriae, (iv) colonization factor antigen I fimbriae (CFA/I fimbriae), and (v) *sfm* fimbrial cluster. A cluster responsible for curli production or type VIII secretion was identified. Siderophore enterobactin, aerobactin, and other hemin transport systems for iron acquisition were identified. In addition, type IV pilus and an IncF conjugal transfer system were identified. A gene for serum survival (*iss*) was also identified. The identified virulence determinants may have contributed to the infection and or colonization of CR694 in the urinary tract (2).

The contig pCR694-EC-NDM-5 carried the bla_{NDM-5} genetic context. bla_{NDM} has been reported to reside within a 10,099-bp transposon known as Tn*125* (3). bla_{NDM-5} on pCR694-EC-NDM-5 was found to be located within a truncated 3,167 bp Tn*125* structure, flanked by an IS*5* upstream and an IS*26* downstream. pCR694-EC-NDM-5 was identical to an NDM-5 IncX3 plasmid, pNDM-MGR194 (as a direct submission, with GenBank accession no. KF220657) (4). Both bla_{NDM-5} genetic contexts did not possess the Tn*125*-associated genes *groES*, *groEL*, and IS*CR27*. Both pCR694-EC-NDM-5 and pNDM-MGR194 are also highly similar to NDM-1 IncX plasmid pKPN5047 (GenBank accession no. NC_020811), containing a longer Tn*125* structure in which *groES*, *groEL*, and IS*CR27* are present.

The bla_{NDM-5} genetic context of pCR694-EC-NDM-5 has not been reported within *E. coli* or within Australia. NDM-5-producing *Enterobacteriaceae* have been reported in Japan, Algeria, the United Kingdom, and India, of which an *E. coli* ST648 harbored bla_{NDM-5} in both the aforementioned United Kingdom and Japan reports (5–8). This case of an NDM-5-producing typical uropathogenic *E. coli* isolate highlights the further intercontinental acquisition of carbapenemase-producing *Enterobacteriaceae* through travel to geographical reservoirs.

This work was approved by the Royal Brisbane and Women's Human Research Ethics Committee (HREC/13/QRBW/391: Epidemiology, clinical significance, treatment and outcome of infections by carbapenem-resistant *Enterobacteriaceae* and *Acinetobacter* spp. in Queensland).

Nucleotide sequence accession numbers. This project is registered as BioProject PRJNA268254 and BioSample SAMN03217331. The bla_{NDM-5} genetic context pCR694-EC-NDM-5 was submitted to the GenBank database and assigned the accession no. KP178355. The draft genome sequence of NDM-5-producing *E. coli* ST648 has been deposited in GenBank under accession no. JTGI00000000.

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