

Coexistence of a *bla*_{NDM-5}-Harboring IncHI2 Plasmid and an IncF Multidrug-Resistance Plasmid in a Clinical *Escherichia coli* Strain from Urine Sample of a Patient with Lower Limb Fracture

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Objective: This study aimed to report the genome of carbapenem-resistant ST58 *Escherichia coli* strain EC6622, isolated from the urine sample of a patient with lower limb fracture, and to explore the genomic characteristics of the *bla*_{NDM-5}-harboring IncHI2/IncHI2A plasmid and the multi-resistance IncF plasmid carried by strain EC6622.

Methods: The genome of *E. coli* strain EC6622 was fully sequenced using the Illumina and PacBio platforms, followed by hybrid assembly of the genome sequences. The identification of antibiotic resistance genes (ARGs) and the genetic context of ARGs were accomplished using bioinformatics tools. Comparative genomic analyses of the resistance plasmids carried by *E. coli* strain EC6622 were performed.

Results: *E. coli* strain EC6622, belonging to ST58 (Achman scheme) or ST87 (Pasteur scheme), harbored *bla*_{NDM-5} on IncHI2/IncHI2A plasmid pEC6622-1. *bla*_{NDM-5} was embedded in Δ ISKox3-IS3000- Δ ISAbal25-IS5-*bla*_{NDM-5}-*ble*_{MBL}-*trpF*-*dsbC*- Δ *cutA*-IS26- Δ ISVsa5-IS3000-IS1A. In addition, two class 1 integrons were also found in the IncHI2/IncHI2A plasmid pEC6622-1. IncFIB_{AP001918}/IncFII plasmid pEC6622-2 carried one 23-kb multidrug-resistant (MDR) region, including *tet(A)*-*tetR(A)*, class 1 integron, and a Tn3-like region containing *mer* operon and *bla*_{TEM-1B} gene, which were nearly identical to those of seven IncF plasmids distributed in *E. coli* strains.

Conclusion: In the carbapenem-resistant *E. coli* strain EC6622 isolated from the urine sample of a 70-year-old patient with a lower limb fracture, the carbapenemase gene *bla*_{NDM-5} was carried by the IncHI2/IncHI2A plasmid (pEC6622-1), while a coexisting IncFIB_{AP001918}/IncFII hybrid multidrug-resistance plasmid (pEC6622-2) was also identified. These findings provide detailed genetic information that enhances our understanding of the resistance mechanisms and potential dissemination routes of *bla*_{NDM}-harboring *E. coli*.

Keywords: *E. coli*, IncHI2/IncHI2A plasmid, *bla*_{NDM-5}, Tn3000, IncFIB_{AP001918}/IncFII plasmid

Introduction

New Delhi metallo- β -lactamase (NDM), a member of the Ambler Class B metallo- β -lactamase, can hydrolyze almost all β -lactam antibiotics, including carbapenems.¹ NDM-producing bacterial pathogens pose significant therapeutic challenges for clinicians and have attracted considerable attention.^{2,3} Since the first report of NDM-1 in *Klebsiella pneumoniae* in 2008,⁴ over 80 variants of NDM have been reported based on data from the beta-lactamase database (BLDB)⁵ on May 30, 2025, with NDM-1 and NDM-5 commonly detected in Enterobacterales.⁶ NDM carbapenemases have been detected in Enterobacterales, *Pseudomonas* and *Acinetobacter*.⁷ Among Enterobacterales, *K. pneumoniae* and *Escherichia coli* were the predominant carriers of *bla*_{NDM}.⁷



NDM-5 was first identified in a multidrug-resistant (MDR) *E. coli* ST648 strain isolated from a 41-year-old patient in the UK who had a travel history to India in 2011.⁸ Since then, NDM-5 carbapenemases have been reported globally,⁷ and NDM-5 has predominantly been found in *E. coli* strains.⁹ NDM-5 is distinct from NDM-1 because of just two amino acid changes (Val88Leu and Met154Leu), which result in greater resistance to broad-spectrum cephalosporins and carbapenems.⁸ The *bla*_{NDM-5} gene has been reported to be carried by various plasmids with different incompatibility types, such as IncX3, IncF, and IncC, which can promote the dissemination of *bla*_{NDM-5} among Enterobacteriaceae via horizontal gene transfer. The *bla*_{NDM} genes have appeared in various genetic contexts, implying that multiple mechanisms have facilitated the mobilization of *bla*_{NDM}.⁷ Numerous mobile elements, including IS*Aba125*, IS26, IS3000, ISCR1, IS5, Tn125, Tn3000, and Tn3 are thought to be crucial for the spread of *bla*_{NDM}.^{7,10}

In this study, we report a carbapenem-resistant and MDR *E. coli* strain, EC6622, isolated from the urine sample of a 70-year-old patient with a lower limb fracture, which harbored the metallo-beta-lactamase gene *bla*_{NDM-5} on an IncHI2/IncHI2A plasmid.

Materials and Methods

Isolation and Characterization of the Strain EC6622

Strain EC6622 was isolated from the urine sample of a 70-year-old female patient with a lower limb fracture in 2021. The present study complies with the Declaration of Helsinki. Strain identification and antimicrobial susceptibility testing were performed using the VITEK 2 COMPACT system (BioMérieux, France), strain identification and antimicrobial susceptibility testing (AST) according to the manufacturer's instructions. AST results were interpreted according to the Clinical and Laboratory Standards Institute guidelines (M100-S24). In addition, identification of the strain EC6622 was also further confirmed using 16S rRNA gene sequencing.

Whole-Genome Sequencing, Assembly and Annotation

Strain EC6622 was sequenced by Genewiz Biotechnology Co. Ltd. (Suzhou, China), utilizing both the PacBio long-read and Illumina short-read platforms. PacBio reads were assembled using the HGAP version 4.0/Falcon version 0.3.¹¹ Subsequently, Illumina reads were used to correct sequencing errors using Pilon version 1.22.¹² Finally, the complete genome of strain EC6622, including both chromosomes and plasmids, was uploaded to the NCBI GenBank database¹³ and simultaneously annotated using the NCBI Prokaryotic Annotation Pipeline.¹⁴

Bioinformatic Analysis to the Genome of the *E. coli* Strain EC6622

Antibiotic resistance genes (ARGs) in the genome of the *E. coli* strain EC6622 were detected using ResFinder 4.1¹⁵ and CARD-RGI,¹⁶ and chromosomal point mutations mediating antimicrobial resistance were detected by the software PointFinder 4.1.1.¹⁷ Virulence genes of the genome of *E. coli* strain EC6622 were identified using ABRicate program (<https://github.com/tseemann/abricate>) in the VFDB database. Multilocus sequence typing (MLST) analysis of *E. coli* strain EC6622 was performed using the software MLST 2.0,¹⁸ selecting databases as “*Escherichia coli*#1” and “*Escherichia coli*#2”, respectively. The O and H serotypes were determined using SerotypeFinder 2.0.¹⁹ Using PlasmidFinder 2.1,²⁰ the replicon types of the plasmids carried by the *E. coli* strain EC6622 were identified. The insertion sequences (ISs) adjacent to the ARGs carried by the *E. coli* strain EC6622 genome were determined using the ISfinder.²¹ Sequence similarity searches were performed against the GenBank non-redundant (nr) database using MegaBLAST.²² Plasmid comparison and visualization were performed using the BLAST Ring Image Generator (BRIG) 0.95²³ and Easyfig 2.2.5.²⁴

Nucleotide Sequence Accession Numbers

The complete genome of *E. coli* strain EC6622 was submitted to the GenBank nucleotide database with accession numbers CP096587–CP096589.

Results

Identification and AST of the *E. coli* Strain EC6622

Strain EC6622 was isolated from the urine sample of a 70-year-old female patient with a lower limb fracture and identified as *E. coli* using the VITEK 2 COMPACT system, which was also confirmed by 16S rRNA gene sequencing. Antimicrobial susceptibility testing results indicated that the *E. coli* strain EC6622 exhibited resistance to cephalosporins (cefoxitin, cefuroxime, cefuroxime axetil, ceftriaxone, ceftazidime, and cefepime), carbapenems (imipenem and ertapenem), quinolones (levofloxacin), sulfamethoxazole/trimethoprim, and β -lactam/ β -lactamase inhibitor combinations (amoxicillin-clavulanic acid and piperacillin/tazobactam) (Table 1).

Genomic Characteristics of the Multidrug Resistant (MDR) *E. coli* Strain EC6622

The genome of the *E. coli* strain EC6622 comprised a 4.76-Mb chromosome as well as two plasmids with sizes of 262.41 kb (pEC6622-1) and 140.10 kb (pEC6622-2), respectively. MLST analysis revealed that *E. coli* strain EC6622 could be classified as sequence type (ST) 58 (Achman scheme) or ST87 (Pasteur scheme). Strain EC6622 was identified as *E. coli* serotype O155:H21 according to SerotypeFinder analysis. According to the PlasmidFinder results, plasmid pEC6622-1 was an IncHI2/IncHI2A hybrid plasmid and plasmid pEC6622-2 was an IncFIB_{AP001918}/IncFII hybrid plasmid.

ResFinder results showed that *E. coli* strain EC6622 carried multiple acquired ARGs present on both plasmids pEC6622-1 and pEC6622-2. The 262.41-kb IncHI2/IncHI2A plasmid pEC6622-1 contained ARGs encoding resistance to beta-lactams (one metallo-beta-lactamase gene *bla*_{NDM-5}, a beta-lactamase gene *bla*_{OXA-10}, and a beta-lactamase gene similar to *bla*_{TEM-176}), aminoglycosides (*aph(3'')-Ib*, *aph(6)-Id*, *aph(3')-Ia*, *aph(4)-Ia*, *aac(3)-IV*, *aadA1*, and *aadA2b*), sulfonamides (*sul3*), chloramphenicol (*floR* and *cmlA1*), tetracycline (*tet(A)-tetR(A)*), trimethoprim (*dfrA14*), rifampicin (*ARR-2*), and quinolones (*qnrS1*). The 140.10-kb IncF plasmid pEC6622-2 harbored disinfectant resistance genes (*qacE* and *sitABCD*), tetracycline resistance genes (*tet(A)-tetR(A)*), beta-lactam resistance gene (*bla*_{TEM-1B}), sulfonamide resistance gene (*sul1*), aminoglycoside resistance gene (*aadA1*), and trimethoprim resistance gene (*dfrA1*). While the chromosome of strain EC6622 lacked acquired resistance genes, a chromosomally encoded *gyrA* mutation (S83L) was identified via PointFinder analysis, which was associated with resistance to nalidixic acid and ciprofloxacin.

Notably, a series of efflux pump genes were identified on the chromosome of strain EC6622 (Table 2) using the CARD-RGI, including key components of major transporter systems such as the resistance-nodulation-cell division (RND) antibiotic efflux pump AcrAB-TolC, the major facilitator superfamily (MFS) antibiotic efflux pump EmrAB-TolC, the ATP-binding cassette (ABC) antibiotic efflux pump genes *yojI* and *msbA*, and the small multidrug resistance (SMR) antibiotic efflux pump *kpnE* and *kpnF*. The chromosome also encoded other important efflux pumps like MdfA

Table 1 Minimum Inhibitory Concentration of the *E. coli* Strain EC6622

Antibiotics		MIC (μ g/mL)	R or S
Categories	Name		
Cephalosporins	Cefoxitin	≥ 64	R
	Cefuroxime	≥ 64	R
	Cefuroxime axetil	≥ 64	R
	Ceftriaxone	≥ 64	R
	Ceftazidime	≥ 64	R
	Cefepime	16	R
Carbapenems	Imipenem	≥ 16	R
	Ertapenem	≥ 8	R
Quinolones	Levofloxacin	4	R
Tetracyclines	Tigecycline	≤ 0.5	S
Sulfonamides	Sulfamethoxazole/Trimethoprim	≥ 320	R
β -lactam/ β -lactamase inhibitor combinations	Piperacillin/tazobactam	≥ 128	R
	Amoxicillin-clavulanic acid	≥ 32	R

Abbreviations: S, Susceptible; R, Resistant.

Table 2 Efflux Pump Genes Carried by the Chromosome of the *E. coli* Strain EC6622

Families of Efflux Pumps	Efflux Pump Genes
RND antibiotic efflux pump	<i>gadX, mdtF, mdtE, CRP, AcrF, AcrE, AcrS, rsmA, acrD, mdtC, mdtB, mdtA, marA, acrA, acrB, cpxA, baeR, AcrAB-TolC with MarR mutation, AcrAB-TolC with AcrR mutation</i>
MFS antibiotic efflux pump	<i>emrB, emrA, emrR, emrK, emrY, mdtH, mdtG, mdfA, leuO, mdtM, mdtN, mdtO, mdtP</i>
ABC antibiotic efflux pump	<i>yojI, msbA</i>
SMR antibiotic efflux pump	<i>kpnE, kpnF</i>
RND antibiotic efflux pump and MFS antibiotic efflux pump	<i>evgS, evgA, H-NS</i>
RND antibiotic efflux pump and MFS antibiotic efflux pump and ABC antibiotic efflux pump	<i>soxR with mutation soxS with mutation</i>

(MFS antibiotic efflux pump), MdtH (MFS antibiotic efflux pump), and MdtG (SMR antibiotic efflux pump). These chromosomally encoded efflux systems collectively contribute to resistance against a remarkably broad spectrum of drug classes through antibiotic efflux mechanisms, encompassing fluoroquinolones, macrolides, beta-lactams, tetracyclines, aminoglycosides, and disinfecting agents (Table S1).

The virulence factors of *E. coli* strain EC6622 were located on both the chromosome and the plasmid pEC6622-2 (Table 3). Chromosomal virulence factors included those associated with T2SS, T3SS effectors, curli fibers, enterobactin, type 1 fimbriae, among others (Tables 3 and S2). The plasmid pEC6622-2, meanwhile, carried virulence factors related to the salmochelin siderophore (Tables 3 and S2).

Comparative Analysis of the MDR Region in IncHI2/IncHI2A Plasmid Carried by the *E. coli* Strain EC6622

The acquired ARGs carried by the IncHI2/IncHI2A plasmid (pEC6622-1) of *E. coli* strain EC6622 were mainly situated on two fragments of the IncHI2/IncHI2A plasmid, forming two large MDR regions (Figure 1A).

For the approximately 41-kb “MDR region 1” of the IncHI2/IncHI2A plasmid pEC6622-1, which was bracketed by $\Delta IS1X2$ and IS26, it contained the *bla*_{NDM-5} gene. The metallo-beta-lactamase gene *bla*_{NDM-5} in the IncHI2/IncHI2A plasmid (pEC6622-1) of *E. coli* strain EC6622 was located on the composite transposon Tn3000, bracketed by two copies of IS3000 in opposite orientations. The *bla*_{NDM-5} was flanked by $\Delta ISAbal25$ -IS5 and the bleomycin resistance gene *ble*_{MBL} was located adjacent to *trpF-dsbC- Δ cutA*. One IS26 was located downstream of *trpF-dsbC- Δ cutA*. Notably, one $\Delta ISKox3$ and one IS1A were inserted upstream and downstream of Tn3000, forming $\Delta ISKox3$ -IS3000- $\Delta ISAbal25$ -IS

Table 3 Virulence Genes Carried by the Chromosome and Plasmid pEC6622-2 of the *E. coli* Strain EC6622

Sequence	Category	VF Genes
Chromosome	T2SS	<i>gspC, gspD, gspE, gspF, gspG, gspH, gspI, gspJ, gspK, gspL, gspM</i>
	T3SS effectors	<i>espLI, espRI, espXI, espX5</i>
	Curli fibers	<i>csgB, csgD, csgF, csgG</i>
	OmpA	<i>ompA</i>
	Enterobactin	<i>entA, entB, entE, entC, fepB, entS, fepD, fepG, fepC, entF, fes, fepA, entD</i>
	Adherence	<i>fdeC</i>
	<i>E. coli</i> common pilus	<i>ecpR, ecpB, ecpC, ecpD, ecpE</i>
Type I fimbriae	<i>fimH, fimG, fimF, fimD, fimC, fimI, fimA, fimE, fimB</i>	
pEC6622-2	Salmochelin siderophore	<i>iroB, iroC, iroD, iroE, iroN</i>

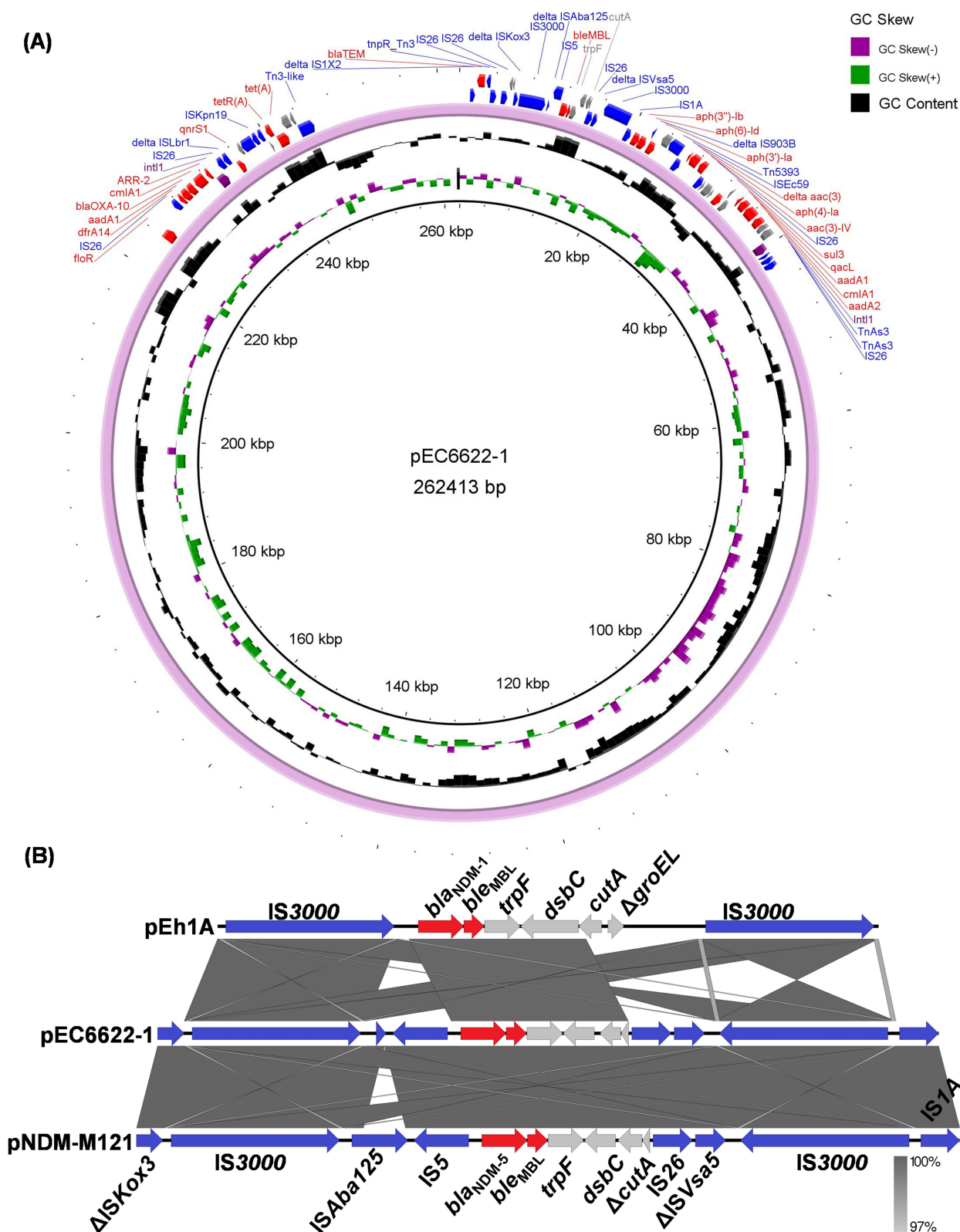


Figure 1 The genetic context of the ARGs carried by the IncHI2/IncHI2A plasmid pEC6622-1 of the *E. coli* strain EC6622. **(A)** Two large MDR regions mainly situated on the IncHI2/IncHI2A plasmid pEC6622-1. **(B)** Comparison of the genetic context of *bla*_{NDM-1} carried by the IncHI2/IncHI2A plasmid pEC6622-1 with those of the plasmid pEh1A, in which the transposon Tn3000 was first described, and the plasmid pNDM-M121 in *E. coli* strain ECNB21-M121. Resistance, transposase, and integrase genes are shown by red, blue, and purple arrows, respectively.

5-*bla*_{NDM-5}-*ble*_{MBL}-*trpF*-*dsbC*- Δ *cutA*-IS26- Δ IS*Vsa5*-IS3000-IS1A (Figure 1A and B). A series of aminoglycoside resistance genes was embedded between IS1A and IS26, located adjacent to Tn3000. Notably, one complex class 1 integron was found on the 41-kb “MDR region 1” of the IncHI2/IncHI2A plasmid pEC6622-1, which was composed of the integrase gene *intI1* and gene cassettes, including *aadA2*, *cmlA1*, *aadA1*, Δ *qacL*, and *sul3* (Figure 1A and B).

For the approximately 18-kb “MDR region 2” of the IncHI2/IncHI2A plasmid pEC6622-1, bracketed by IS26 and Tn3-like elements, one more class 1 integron flanked by two direct repeats of IS26 was found. It contained the integrase gene (*intI1*) and gene cassettes, including *ARR-2*, *cmlA1*, *bla*_{OXA-10}, *aadA1*, and *dfrA14*. The gene *qnrS1* encoding quinolone resistance, carried by the plasmid pEC6622-1, was located on a truncated Tn6396 with an incomplete Δ IS*Lbr1* inserted upstream of the gene *qnrS1* (Figure 1A).

Comparative Analysis of the MDR Region in IncF Plasmid of the *E. coli* Strain EC6622

The acquired ARGs carried by the IncF plasmid pEC6622-2 were found to be present on one ~23-kb fragment within the IncF plasmid, resulting in a large MDR region (Figure 2). In the MDR region, the tetracycline resistance genes *tet(A)*–

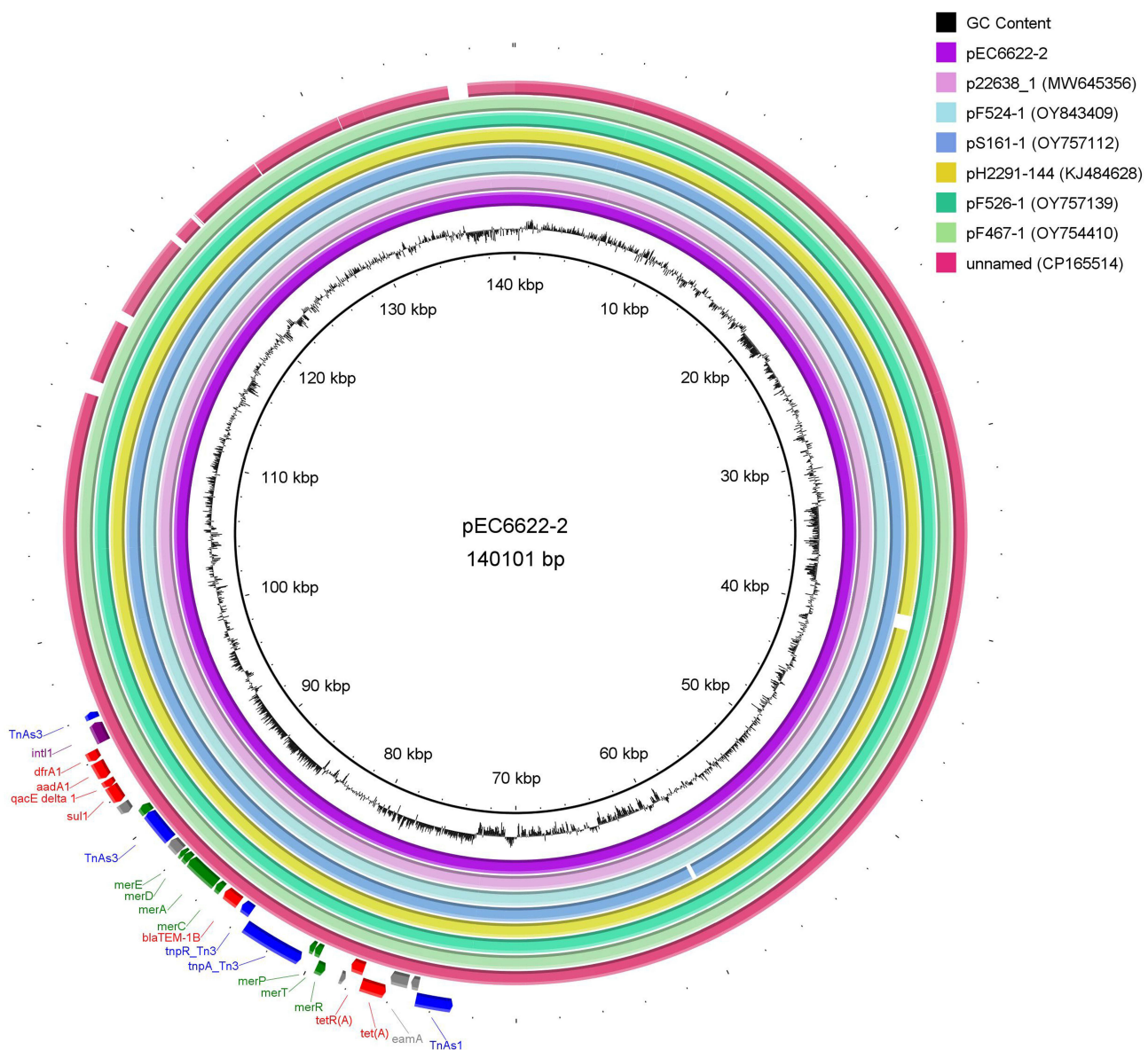


Figure 2 Comparative analysis of the 23-kb MDR region carried by the IncFIB_{AP001918}/IncFII plasmid pEC6622-2 in *E. coli* strain EC6622 with another seven related IncF plasmids generated by BRIG. Resistance, transposase, *mer*, and integrase genes are shown by red, blue, yellow, and purple arrows, respectively.

tetR(A) were adjacent to a Tn3-like region containing *mer* operon (*merRTPCADE* genes) and β -lactamase *bla*_{TEM-1B}. In addition, a class 1 integron was found in the MDR region of the IncF plasmid pEC6622-2, composed of one integrase gene *intI1* and gene cassettes, including *dfrA1*, *aadA1*, *qacEΔ1*, and *sul3*.

A BLAST search of the GenBank nr database revealed that the 23-kb MDR region in the IncF plasmid pEC6622-2 was nearly identical to that of seven plasmids (coverage = 100% and identity \geq 99%). Eight plasmids harboring the ~23-kb MDR region were all found in the *E. coli* strains (Figure 2). Notably, seven of these eight plasmids were identified as the IncFIB_{AP001918}/IncFII hybrid plasmids, similar to the plasmid pEC6622-2 in *E. coli* strain EC6622, and one plasmid was identified as the IncFIB_{AP001918}/IncFII_{pHN7A8} hybrid plasmid (Table 4).

Discussion

In this study, we isolated an NDM-5-producing carbapenem-resistant *E. coli* strain EC6622 belonging to ST58 (Achman scheme) or ST87 (Pasteur scheme), which was isolated from a urine sample of a 70-year-old female patient with a lower limb fracture. *E. coli* is the most frequent cause of Gram-negative bacterial agents.^{25,26} Urinary tract infections (UTIs) are among the most frequent bacterial infections globally and are found in both community and healthcare environments.²⁷ Uropathogenic *E. coli* strains have been identified as a common cause of UTIs.^{28,29} *E. coli* ST58 has gained recognition as an emerging global uropathogen frequently progressing to sepsis.³⁰ Notably, *E. coli* ST58 has been identified globally in diverse sources, including food,³⁰ poultry,³¹ as well as hospital- and community-acquired infections.^{31,32} This widespread occurrence underscores the significant One Health concern posed by this bacterial lineage, which circulates among humans, animals, and the environment.

In our study, the metallo-beta-lactamase gene *bla*_{NDM-5} in NDM-5-producing *E. coli* strain EC6622 was located in a 262.41-kb IncHI2/IncHI2A hybrid plasmid (pEC6622-1). NDM-5 was initially discovered on an IncF plasmid in *E. coli* strain belonging to ST648, which was collected from a 41-year-old patient in the UK with a history of travel to India.⁸ Notably, *bla*_{NDM-5} was identified as the most common variant in *bla*_{NDM}-harboring plasmids of *E. coli*⁹ and it was the second most prevalent variant in *bla*_{NDM}-harboring plasmids of *K. pneumoniae*.³³ The global dissemination of NDM is partially linked to the spread of diverse *bla*_{NDM}-harboring plasmids,^{34,35} which mostly belong to the IncX3, IncFII, and IncC replicon types.⁹ Herein, we characterized one strain of *E. coli* harboring *bla*_{NDM-5} located on a 262.41-kb IncHI2/IncHI2A hybrid plasmid. The IncHI2 plasmid is a subgroup of IncHI, which is the most active in acquiring exogenous ARGs, including the colistin resistance gene *mcr-1*.³⁶ The *bla*_{NDM-5}-carrying IncHI2/IncHI2A-type plasmids have been identified not only in *E. coli* ST58, but also in *E. coli* ST1431,³⁷ as well as in clinical *Salmonella* isolates³⁸ and *Klebsiella* isolates.³⁹

The *bla*_{NDM-5} gene harbored by the 262.41-kb IncHI2/IncHI2A hybrid plasmid pEC6622-1 of *E. coli* strain EC6622 was embedded in the transposon Tn3000, bracketed by two copies of IS3000 in opposite orientations. IS3000 was

Table 4 The Plasmids Harboring the 23-Kb MDR Region Nearly Identical to That of IncFIB_{AP001918}/IncFII Plasmid pEC6622-2 in *E. coli* Strain EC6622

Plasmid Name	GenBank Accession No.	Plasmid Replicons
p22638_1	MW645356	IncFIB _{AP001918} :IncFII
pF524-1	OY843409	IncFIB _{AP001918} :IncFII
pS161-1	OY757112	IncFIB _{AP001918} :IncFII
pH2291-144	KJ484628	IncFIB _{AP001918} :IncFII
pF526-1	OY757139	IncFIB _{AP001918} :IncFII
pF467-1	OY754410	IncFIB _{AP001918} :IncFII
Plasmid unnamed	CPI65514	IncFIB _{AP001918} :IncFII _{pHN7A8}

originally described in the *In60* integron but oriented in the opposite direction of gene cassettes.⁴⁰ The transposon *Tn3000* was first described in the *IncFII_K* plasmid pEh1A from *Enterobacter hormaechei*, which was conserved among plasmids from different continents.⁴¹ Acman et al¹⁰ found that *Tn3000* was predominantly found in the Indian subcontinent, mainly in the *Klebsiella* genus. In *Acinetobacter spp.*, the *bla_{NDM}* is usually embedded in the composite transposon *Tn125* bracketed by two *ISAbal25*.^{7,42} However, in Enterobacteriaceae, *Tn125* is interrupted or truncated, and the various remnants of *Tn125* are always flanked by two copies of the same insertion sequences,⁷ such as *Tn3000*. Generally, the initial spread of *bla_{NDM}* is facilitated by *Tn125* mobilization, followed by transposition by *Tn3000*, *IS26*, and other elements.¹⁰

E. coli strain EC6622 also contained one *IncFIB_{AP001918}/IncFII* multi-resistance plasmid (pEC6622-2) harboring a *Tn3*-like region containing *mer* operon and *bla_{TEM-1B}* gene. *IncF* plasmids, a prevalent incompatibility type, have been found worldwide in strains of Enterobacteriales from diverse origins and sources, with sizes ranging from 50 to 200 kb, and contain a wide variety of ARGs for all major antibiotic classes, such as β -lactams, aminoglycosides, chloramphenicol, tetracyclines, and quinolones.^{43–45} Among the TEM variants, TEM-1B is the most prevalent.⁴⁶ *bla_{TEM-1B}* is frequently discovered within *Tn3*-like transposons, which are widely present in both Gram-negative and Gram-positive bacteria.⁴⁷

In this study, two class 1 integrons carried by the *IncHI2/IncHI2A* plasmid pEC6622-1 and one class 1 integron harbored by the *IncFIB_{AP001918}/IncFII* plasmid pEC6622-2 were found in the genome of *E. coli* strain EC6622. Class 1 integrons are common genetic elements that are crucial for the dissemination of antibiotic resistance,⁴⁸ enabling bacteria to acquire and exchange ARGs located on gene cassettes. Class 1 integrons usually contain an integrase gene (*intI1*), integron recombination site (*attI1*), variable region promoter (Pc), and gene cassettes.⁴⁹ Among all integrons, class 1 integrons have the highest detection rate in clinical isolates (50–70%), which is associated with the emergence and dissemination of antibiotic-resistant bacteria.^{50,51}

Conclusion

In this study, we report the whole-genome sequences of a carbapenem-resistant *E. coli* strain EC6622 harboring *bla_{NDM-5}* carbapenemase gene on an *IncHI2/IncHI2A* plasmid (pEC6622-1), belonging to ST58 (Achman scheme) or ST87 (Pasteur scheme), isolated from the urine sample of a female patient with a lower limb fracture. In addition to the *bla_{NDM-5}*-carrying *IncHI2/IncHI2A* plasmid pEC6622-1, one *IncFIB_{AP001918}/IncFII* hybrid multidrug-resistance plasmid (pEC6622-2) was also identified in the *E. coli* strain EC6622. The metallo-beta-lactamase gene *bla_{NDM-5}* in *IncHI2/IncHI2A* plasmid was located on the composite transposon *Tn3000*. Notably, the class 1 integrons were found on both *IncHI2* plasmid pEC6622-1 and the *IncF* plasmid pEC6622-2.

Ethical Approval Statement

This study was approved by the Ethics Committee of the Zhuhai People's Hospital (Permission Number: [2020] No. 28). This study focused on bacteria and did not include sensitive personal information. Therefore, informed consent was not required, according to the "Measures for the Ethical Review of Biomedical Research Involving Humans" (https://www.gov.cn/gongbao/content/2017/content_5227817.htm).

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Disclosure

The authors declare that this research was conducted in the absence of any commercial or financial relationships that could be construed as potential conflicts of interest.

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