

Emergence of tigecycline resistance in *Escherichia coli* co-producing MCR-1 and NDM-5 during tigecycline salvage treatment

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Objective: Here, we report a case of severe infection caused by *Escherichia coli* that harbored *mcr-1*, *bla*_{NDM-5} and acquired resistance to tigecycline during tigecycline salvage therapy.

Methods: Antimicrobial susceptibility testing, Southern blot hybridization, and complete genome sequence of the strains were carried out. The genetic characteristics of the *mcr-1* and *bla*_{NDM-5} plasmids were analyzed. The whole genome sequencing of *mcr-1*-containing plasmid was completed. Finally, putative single nucleotide polymorphisms and deletion mutations in the tigecycline-resistant strain were predicted.

Results: Three *E. coli* isolates were obtained from ascites, pleural effusion, and stool of a patient; they were resistant to almost all the tested antibiotics. The first two strains separated from ascites (E-FQ) and hydrothorax (E-XS) were susceptible to amikacin and tigecycline; however, the third strain from stool (E-DB) was resistant to tigecycline after nearly 3 weeks' treatment with tigecycline. All three isolates possessed both *mcr-1* and *bla*_{NDM-5}. The *bla*_{NDM-5} gene was found on the IncX3 plasmid, whereas the *mcr-1*, *fosA3* and *bla*_{CTX-M-14} were located on the IncHI2 plasmid. Mutations in *acrB* and *lon* were the reason for the resistance to tigecycline.

Conclusion: This is the first report of a colistin-, carbapenem-, and tigecycline-resistant *E. coli* in China. Tigecycline resistance acquired during tigecycline therapy is of great concern for us because tigecycline is a drug of last resort to treat carbapenem-resistant Gram-negative bacterial infections. Furthermore, the transmission of such extensively drug-resistant isolates may pose a great threat to public health.

Keywords: *mcr-1*, *bla*_{NDM-5}, tigecycline-resistance, *acrB*, *lon*

Introduction

The emergence of multidrug-resistant Gram-negative bacteria, especially those producing carbapenemases, continues to threaten public health because of the limited availability of antimicrobials for treatment. Colistin and tigecycline are drugs of last resorts to treat these severe infections. The rapid transmission of the colistin-resistance gene *mcr-1* located on mobile elements has caused great concern since its initial discovery. Co-carriage of *mcr-1* and *bla*_{NDM-5} has been reported in isolates from animals, food, and even humans since 2016.¹⁻⁵ Tigecycline is effective against most carbapenemase-producing bacteria and was recently approved for clinical use in China; nevertheless, acquisition of resistance to tigecycline during therapy has been frequently reported.⁶⁻¹⁰ The mechanism of tigecycline resistance has not yet been clearly elucidated. It has been reported that resistance-nodulation-division (RND)-type transporters, primarily the AcrAB efflux pump, play an important role.¹¹ Here, we report a case of intra-abdominal

infection and pyothorax. Three extensively drug-resistant (XDR) *Escherichia coli* isolates with resistance to colistin and carbapenems were isolated from the patient. The first two strains, from ascites (E-FQ) and hydrothorax (E-XS), were susceptible to amikacin and tigecycline; however, the third strain from stool (E-DB) acquired resistance to tigecycline during tigecycline therapy. Fortunately, following combined antibiotic susceptibility tests in vitro, the infection was finally controlled.

To the best of our knowledge, this is the first report of a colistin-, carbapenem-, and tigecycline-resistant *E. coli* in China. The aim of our study was to clarify the resistance mechanisms of these XDR pathogens.

Materials and methods

Patient and isolate data

Three carbapenem-resistant strains of *E. coli* were isolated from a 46-year-old male patient. The patient had a history of hepatocellular carcinoma and was admitted to our hospital for intra-abdominal infection and pyothorax after liver resection in March 2017. To identify the bacteria and guide the antibiotic treatment, ascites and hydrothorax were cultured, and the patient underwent a stool screening. The first two strains cultured from ascites and hydrothorax were separated on March 8, 2017. The third, from stool, was isolated on March 28, 2017. All three isolates were identified by the VITEK 2 system (Sysmex-bioMérieux, Marcy l'Etoile, France).

PCR and Sanger sequencing

PCR and sequencing were used to identify the *mcr-1* and *bla*_{NDM-5} genes in all three isolates. Mutations in *acrB* and *lon* were confirmed by PCR and Sanger sequencing (primers in Table S1).

Antimicrobial susceptibility test

Antibiotic susceptibilities, including imipenem, meropenem, amikacin, levofloxacin, cefotaxime, aztreonam, amoxicillin–clavulanic acid, and fosfomycin, were determined by the broth microdilution method according to the guidelines provided by the Clinical and Laboratory Standards Institute.¹² Minimum inhibitory concentrations (MICs) of tigecycline and colistin were interpreted by EUCAST guidelines (<http://www.eucast.org/>). MIC by Etest followed the manufacturer's instructions for some drugs, including cefoperazone/sulbactam, ciprofloxacin, aztreonam, and trimethoprim–sulfamethoxazole. *E. coli* ATCC 25922 was used as a quality control strain for the antibiotic susceptibility test. The interactions of

amoxicillin–clavulanic acid and aztreonam were assessed using the checkerboard method¹³ with slight modifications. The combinations in the 96-well plates were performed as follows: aztreonam was diluted by twofold dilutions along the x-axis of the plates (from 1/64 MIC to 2 MIC), while amoxicillin–clavulanic acid was diluted by twofold dilutions along the y-axis (from 1/32 MIC to 2 MIC). Subsequently, each well was inoculated with the tested bacterial suspension (5×10^5 CFU/mL). The plates were then incubated at 37°C overnight. The interaction between aztreonam and amoxicillin–clavulanic acid was determined by quantifying the fractional inhibitory concentration index (FICI) using the following formula: FIC of aztreonam = MIC of aztreonam in combination/MIC of aztreonam alone; FIC of amoxicillin–clavulanic acid = MIC of amoxicillin–clavulanic acid in combination/MIC of amoxicillin–clavulanic acid alone. $FICI = FIC_A + FIC_{CB}$. “Synergy” was defined when $FICI \leq 0.5$; $0.5 < FICI \leq 0.75$ means “partial synergy”; $0.76 < FICI \leq 1$ denotes “additive”; $1 < FICI \leq 4$ denotes “indifferent”; while “antagonistic” in cases in which the $FICI > 4$.

Pulsed-field gel electrophoresis (PFGE) and Southern blotting analysis

Genetic relationships among the isolates were evaluated by PFGE. Genomic DNA was digested with restriction enzyme XbaI (TaKaRa, Dalian, China) and was electrophoresed on a CHEF-mapper XA PFGE system (Bio-Rad, Berkeley, CA, USA) at 14°C and 6 V/cm and with alternating pulses at a 120° angle in a 5–35 seconds pulse time gradient for 22 hours. To ascertain the plasmid locations, genomic DNA was digested with S1-nuclease (TaKaRa, Kusatsu, Japan) and was electrophoresed for 18 hours at 14°C with run conditions of 6 V/cm and pulse times from 2.16 to 63.8 seconds. The DNA fragments were transferred to a positively charged nylon membrane (Millipore, Billerica, MA, USA) and then were hybridized with a digoxigenin-labeled *bla*_{NDM-5} and *mcr-1*-specific probe. An NBT/BCIP color detection kit (Roche, Mannheim, Germany) was then used to detect the target gene. The *Salmonella enterica* serotype Braenderup H9812 was used as the size marker.

Genomic DNA extraction and analysis

Genomic DNA from strain E-FQ, E-XS, E-DB was sequenced with an Illumina HiSeq 2000 (Illumina Inc., San Diego, CA, USA) following a paired-end 2×100-bp protocol. The total genomic DNA of E-DB was also extracted and sequenced via the single molecule real-time technique using a PacBio RS II platform and was assembled de novo using

Canu v1.5. Gene prediction and annotation were performed with in silico online tools (<http://rast.nmpdr.org/rast.cgi>). Sequence comparison was performed using BLAST (<http://blast.ncbi.nlm.nih.gov>). Determination of plasmid replicons, resistance genes, and multi-locus sequence typing (MLST) was performed using online CGE tools (<http://www.genomicepidemiology.org/>). A comparison of genetic environment of *mcr-1*- and *bla*_{NDM-5}-containing plasmids and their related plasmids was performed with EasyFig 2.2.2.¹⁴ The reads of E-DB were mapped against the reference genome of E-FQ and E-XS with the CLC Genomics Workbench 9 software (Qiagen, Valencia, CA, USA). The putative single nucleotide polymorphisms and deletion mutations were predicted.

Nucleotide sequence accession numbers

The next-generation sequencings of E-FQ, E-XS, and E-DB were subjected to National Center for Biotechnology Information under accession numbers PVQI00000000, PVQH00000000, and PVQG00000000. The complete sequences of pE-DB-*mcr* were submitted to GenBank under accession number MH128771.

Results

Patient information

A 46-year-old male patient presented to our hospital (a tertiary-care hospital in Hangzhou) with recurrent fever, pyothorax, and intra-abdominal infection in March 2017. The patient had a history of chronic hepatitis B and liver cancer. He had undergone a liver resection for the hepatocellular cancer 9 months prior. The patient had recurrent fever and abdominal pain after the surgery. A colonic fistula was found on imaging studies and during enteroscopy. The patient was treated with imipenem (0.5 g q8h for 8 days) and tigecycline (50 mg q12h for 7 days) prior to this admission.

The results of laboratory examinations were as follows: white blood cell count, 15,200/mm³; neutrophil percentage,

91%; platelet count, 79,000/mm³; alpha-fetoprotein, 1,238.3 ng/mL; C-reactive protein, 62.6 mg/L, and procalcitonin, 0.5 µg/L. A series of pathogen cultures from ascites, plural effusion, and stool grew XDR *E. coli* that were resistant to almost all tested antibiotics. The first two strains separated from ascites (E-FQ) and hydrothorax (E-XS) after admission were susceptible to amikacin and tigecycline; however, the third strain from stool (E-DB) was susceptible to amikacin but was resistant to tigecycline after nearly 3 weeks' treatment with tigecycline (50 mg q12 h for 17 days and 100 mg q12 h for 3 days) in our hospital.

The patient underwent ileum colostomy and abdominal cavity drainage, while amoxicillin-clavulanic acid combined with aztreonam was used for 1 week according to the in vitro combined antibiotic susceptibility test (FICI 0.125). The bacterium was finally eliminated. However, the patient died in the fourth month of hospitalization in our hospital because of cancer recurrence.

Isolate characteristics

The antimicrobial susceptibility testing results showed that three *E. coli* strains were resistant to almost all tested antibiotics (Table 1). The first two strains E-FQ and E-XS were susceptible to amikacin (MIC =8 mg/L) and tigecycline (MIC =1 mg/L); however, the third strain E-DB was resistant to tigecycline (MIC =8 mg/L). PCR and sequencing identified that all three isolates contained genes *mcr-1* and *bla*_{NDM-5}. These isolates expressed indistinguishable band patterns by XbaI PFGE analysis (Figure S1). In addition to *mcr-1* and *bla*_{NDM-5}, the three strains were found to harbor resistance genes for aminoglycosides (*aph(4)-Ia*, *aadA1*, *strB*, *strA*, *aacA4*, *aac(3)-IId* and *aac(3)-IVa*), beta-lactam (*bla*_{CTX-M-14}), fluoroquinolone (*aac(6')Ib-cr*), fosfomycin (*fosA*), phenicol (*flor*), sulfonamide (*sul1* and *sul2*), trimethoprim (*dfpA1*), and tetracycline (*tet(A)*), that were consistent with an extremely drug-resistant profile. Plasmid incompatibility

Table 1 Sources and MICs for the three *Escherichia coli* isolates and *E. coli* ATCC 25922

Isolates	Date of isolation	Source	MLST	MIC (mg/L)												
				IMP	MEM	CST	TGC	AK	LVX	CTX	FEP	FOS	AT ^a	CI ^a	CPS ^a	TS ^a
E-FQ	March 8, 2017	Human ascites	2736	16	32	8	1	8	64	>256	256	1,024	12	>32	>256	>32
E-XS	March 8, 2017	Human hydrothorax	2736	16	32	8	1	8	64	>256	256	1,024	12	>32	>256	>32
E-DB	March 28, 2017	Human feces	2736	32	32	4	8	8	128	>256	>256	1,024	16	>32	>256	>32
ATCC 25922		Laboratory		0.125	<0.125	0.25	0.125	2	<0.125	0.125	<0.125	1				

Notes: ^aMICs were interpreted by Etest by following the manufacturer's instructions for CPS, CI, TS, and AT.

Abbreviations: MLST, multi-locus sequence typing; MIC/s, minimum inhibitory concentration/s; IMP, imipenem, MEM, meropenem, CST, colistin, TGC, tigecycline, AK, amikacin, LVX, levofloxacin, CTX, cefotaxime, FEP, cefepime, FOS, fosfomycin, AT, aztreonam, CI, ciprofloxacin, CPS, cefoperazone/sulbactam, TS, trimethoprim-sulfamethoxazole.

typing detected the presence of the plasmid replicons IncA/C2, IncFIA, IncHI2A, IncHI2, IncX3, and IncFIB. MLST demonstrated that the isolates belonged to sequence type 2736. The reads of strain E-DB were mapped against the reference genome of E-FQ and E-XS. The difference between E-DB and E-FQ was less than five single nucleotide variants (Table 2), meanwhile, the difference between E-DB and S-XS was also less than five.

Genetic context of plasmids

S1 nuclease PFGE and Southern blot showed the presence of *mcr-1* in an ~244–330 kb plasmid and *bla*_{NDM-5} in an ~33–55 kb plasmid (Figure S1), belonging to IncHI2 and IncX3 by analysis of whole genome sequencing. *mcr-1*-containing plasmid pE-DB-*mcr* was 230,365 bp in size with an average G+C content of 51%. In the multidrug resistance (MDR) region, it harbored resistance genes for aminoglycosides (*aph(4)-Ia*, *aacA4*, and *aac(3)-IVa*), fosfomycin (*fosA3*), phenicol (*floR*), sulfonamide (*sul2*) and beta-lactam (*bla*_{CTX-M-14}). Around the colistin resistance gene *mcr-1*, it had a structure of IS*Apl1*-*mcr-1*-*hp*-#IS*Apl1*(237 bp)-IS*Kpn26*-#IS*Apl1*(237 bp)-IS*Kpn26*-#IS*Apl1* (837 bp) (Figure 1A). The *mcr-1* element was flanked by two IS*Apl1* elements in the same orientation, and the IS*Apl1* upstream was inserted by an IS*Kpn26* into two parts (837 bp and 237 bp), with a duplication of IS*Kpn26* and one part of IS*Apl1* (237 bp) that was highly similar to plasmid pls1 (GenBank accession no. KX458104) (Figure 1B). BLASTn comparisons demonstrated that the genetic surrounding of *bla*_{NDM-5} was relatively similar to the sequences of the *bla*_{NDM-5}-carrying plasmid pCREC-532_3 (GenBank accession no. NZ_CP024833.1), pNDM_MGR194 (GenBank accession no. NC_022740.1), and pNDM-QD28 (GenBank accession no. KU167608.1), with a structure of Tn3-IS3000-IS*Aba125*-IS5-*bla*_{NDM-5}-*trpF*-*dsbC*-ISL3 (Figure 1C).

Tigecycline resistance

Antimicrobial susceptibility showed that E-FQ and E-XS were sensitive to tigecycline (MIC 1 mg/L), while strain E-DB was resistant to tigecycline (MIC 8 mg/L). The putative single nucleotide and deletion mutations in E-DB were predicted. *acrB* and *lon* were the only two genes found in both mappings (Table 2). Mutations in *acrB* and *lon* were confirmed by PCR and Sanger sequencing. As to *acrB*, it is a single nucleotide mutation that causes a change of arg to cys (R620C). As to *lon*, it is a single nucleotide polymorphism mutation that resulted in the change of pro to leu (P403L) (Table 2).

Discussion

To our knowledge, this is the first report of an isolate harboring *mcr-1* and *bla*_{NDM-5} acquiring resistance to tigecycline during therapy. Since its discovery in Southern China, *mcr-1* has already been discovered in >40 countries/regions covering five of seven continents and where it plays an important role in polymyxin resistance.¹⁵ Searches for *mcr-1*-bearing plasmids deposited in GenBank suggest that IncHI2 is one of the most dominant replicon types of plasmid carrying *mcr-1* plasmids (45/219, 20.5%); IncHI2 plasmids had the largest size, with sequence lengths up to 267,486 bp that were always integrated alongside a large MDR gene cassette.¹⁶ In our study, we found that the *mcr-1*-containing plasmid also harbored the fosfomycin resistance gene *fosA3* and beta-lactam *bla*_{CTX-M-14}. The horizontal diffusion of these resistance genes is particularly worrisome because the regimen of colistin plus fosfomycin remains a therapeutic alternative in cases of multidrug-resistant bacteria. There is increasing evidence that IS*Apl1* plays a pivotal role in the mobilization of *mcr-1*. Tn6330, with the structure IS*Apl1*-*mcr-1*-*orf*-IS*Apl1*, was proposed as a key element mediating translocation of *mcr-1*

Table 2 The putative single nucleotide variants and deletion mutations in *Escherichia coli* E-DB compared with E-FQ and E-XS

Reference position	Gene and product	Nucleotide sequence	Amino acid sequence
<i>E. coli</i> E-FQ			
contig_44_3,490	<i>acrB</i> , multidrug efflux RND transporter permease subunit	C1858T	R620C
contig_44_25,952	<i>lon</i> , ATP-dependent protease La	G1148A	P403L
contig_128_9,752	ISL3, transposase	G191T	A64S
contig_12_1,269	<i>radC</i> , DNA repair protein	G174A	V247I
contig_147_2,477	Not an ORF	T2477C	None
<i>E. coli</i> E-XS			
contig_77_52,399	<i>acrB</i> , multidrug efflux RND transporter permease subunit	C1858T	R620C
contig_77_29,937	<i>lon</i> , ATP-dependent protease La	G1148A	P403L
contig_43_206	<i>orfA</i> , IS1 transposase	T204C	R68R
contig_43_209	<i>orfA</i> , IS1 transposase	C207T	H69H
contig_53_80	Not an ORF	A80G	None

Abbreviation: ORF, open reading frame.

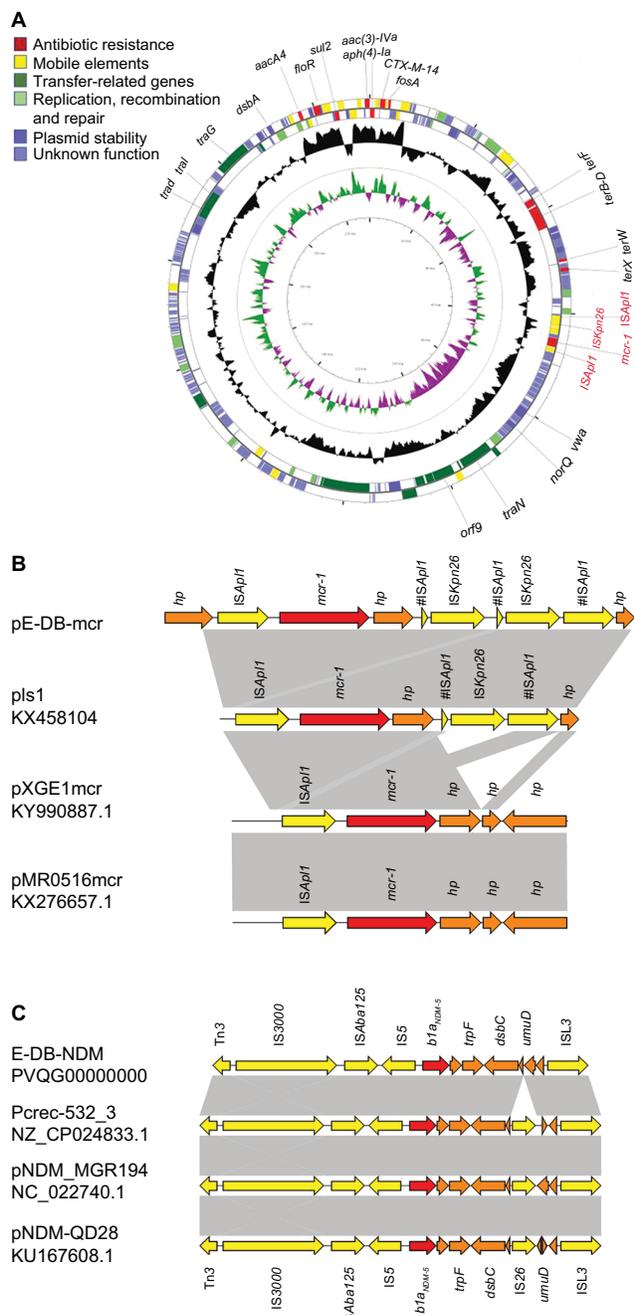


Figure 1 Characteristics of *mcr-1* bearing IncHI2 plasmid and the genetic environment of *mcr-1* and *bla*NDM-5.

Notes: (A) Structure of plasmid pE-DB-mcr. The two outer circles represent ORFs in the plus (outside) and minus (inside) orientations, respectively. Functions are color coded as explained in the key. The two inner circles represent the G+C content plotted against the average G+C content of 51% (black circle) and GC skew information (green and purple circles). (B) The genetic environment of *mcr-1*. The *mcr-1* element was flanked by two *ISApI1* elements in the same orientation, and the *ISApI1* upstream was divided by an *ISKpn26* into two parts, with a copy of *ISKpn26* and one part of *ISApI1* that was highly similar to plasmid *pls1*. (C) The genetic environment of *bla*_{NDM-5} with a structure of Tn3-*IS3000*-*ISAbal25*-*IS5*-*bla*_{NDM-5}-*trpF*-*dsbC*-*ISL3*. Light gray shades indicate shared regions with a high degree of homology. Red and yellow arrows indicate antimicrobial resistance genes and mobile elements genes, respectively. Brown arrows indicate genes for hypothetical proteins as well as proteins of unknown function.

Abbreviation: ORF, open reading frame.

into various plasmid backbones through formation of a circular intermediate.^{17,18} In our study, the *ISApI1* in upstream of Tn6330 was inserted by an *ISKpn26* in two parts, and we infer that this insertion may increase the stability of Tn6330 in the backbone of IncHI2.

Tigecycline belongs to the group called glycylcyclines that binds to 16S rRNA and prevents mRNA decoding. Compared with earlier class tetracyclines, the bulky side chain attached to the C-9 position of ring D is the key to escape common tetracycline resistance mechanisms, for example, tetracycline efflux pumps and ribosomal protection.¹⁹ Tigecycline is also not affected by most of the common mechanisms that affect other classes of antimicrobial agents, including target site modifications, enzymatic degradation of the drug molecule, and DNA gyrase mutations.²⁰ However, the reports of clinical tigecycline resistance were published soon after its use in medical practice. Tigecycline resistance occurring in carbapenem-resistant Enterobacteriaceae (CRE) during therapy has been reported in many cases.⁷⁻¹⁰ It had been reported that Tet proteins can mutate to acquire high-level tigecycline resistance,²¹ but in most cases, tigecycline resistance is due to the constitutive expression of RND efflux pumps; for example, AcrAB in *E. coli*.²² In *E. coli*, the tripartite efflux system AcrAB-TolC is the pump in charge of the efflux of dyes, bile salts, detergents, and a large group of antibiotics, including the tetracyclines. AcrB is an RND pump situated in the inner membrane that functions in a complex with two other proteins, an outer membrane channel TolC and a periplasmic adaptor protein AcrA. AcrB is the major site for substrate recognition and energy transduction of the entire tripartite system.^{23,24} In one study, the author found a trend toward higher *acrB* expression as tigecycline MIC increases.²⁵ Several global transcriptional regulators of the *araC* family, *ramA*, *marA*, *soxS*, and *rarA*, may participate in tigecycline resistance via AcrAB efflux pump activation,²⁵⁻²⁷ of which *ramA*, *marA*, and *soxS* are regulated by the *lon*.^{28,29} Nicoloff et al found that about half of the selected spontaneous tetracycline- or chloramphenicol-resistant *E. coli* mutants carried additional *lon* mutations.³⁰ *lon* mutation causes low MDR by stabilizing MarA and SoxS, two transcriptional activators, whose induction increases resistance to many antimicrobial drugs. The first-step *lon* mutation greatly increases the rate of development of higher resistance via acquisition of new sets of mutations.²⁹ In this case, with tigecycline treatment, mutations in *acrB* (R620C) and *lon* (P403L) in strain E-DB caused activation of the AcrAB-TolC efflux pump, leading to the high MIC of 8 mg/L for tigecycline.

CRE are often associated with severe health care-associated infections with high mortality ranging from 32.1% to 71%.³¹ NDM-type beta-lactamase are the second most common carbapenemases found among CRE in China.³² These carbapenemases cannot be inhibited by β -lactamase inhibitors but remain susceptible to aztreonam, although most metallo-beta-lactamase-producing CRE isolates also harbor extended-spectrum β -lactamases that confer resistance to aztreonam. Therefore, many NDM producers remain susceptible only to tigecycline, colistin, and to a lesser extent to fosfomycin.³³ In our disseminated infection case, the colistin- and tigecycline-resistant CRE made the treatment more complex and challenging, and even more worrisome, because the *E. coli* harbored *fosA3* and *bla*_{CTX-M-14}. In addition to the surgical intervention, amoxicillin-clavulanic acid combined with aztreonam was used on the basis of the combined antibiotic susceptibility test, and the bacterium was finally eliminated. This regimen may promisingly combat *E. coli* harboring *mcr-1* and *bla*_{NDM-5}. Combined antibiotic susceptibility test in vitro is important in the so-called “post-antibiotic” era.

Conclusion

This is the first report of a colistin-, carbapenem- and tigecycline-resistant *E. coli* in China. Tigecycline resistance acquired during tigecycline therapy is a great concern because tigecycline is a drug of the last resort for carbapenem-resistant Gram-negative bacteria infections. Furthermore, the transmission of such extensively drug-resistant isolates may pose a great threat to public health. Appropriate treatment schemes that effectively kill the XDR pathogen are imperative.

Ethics statement

The clinical isolates of *E. coli* E-FQ, E-XS, E-DB were part of routine hospital laboratory procedure. The patient's next of kin had provided written informed consent for details to be used in the manuscript.

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Author contributions

Conceived and designed the experiments: YY and PZ; performed the experiments: QW, PZ, YW, and DZ; analyzed the data: DZ, FZ, and YJ; wrote the manuscript: QW, PZ, XL,

and XD. All authors contributed to data analysis, drafting or revising the article, gave final approval of the version to be published, and agree to be accountable for all aspects of the work.

Disclosure

The authors report no conflicts of interest in this work.

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Supplementary materials

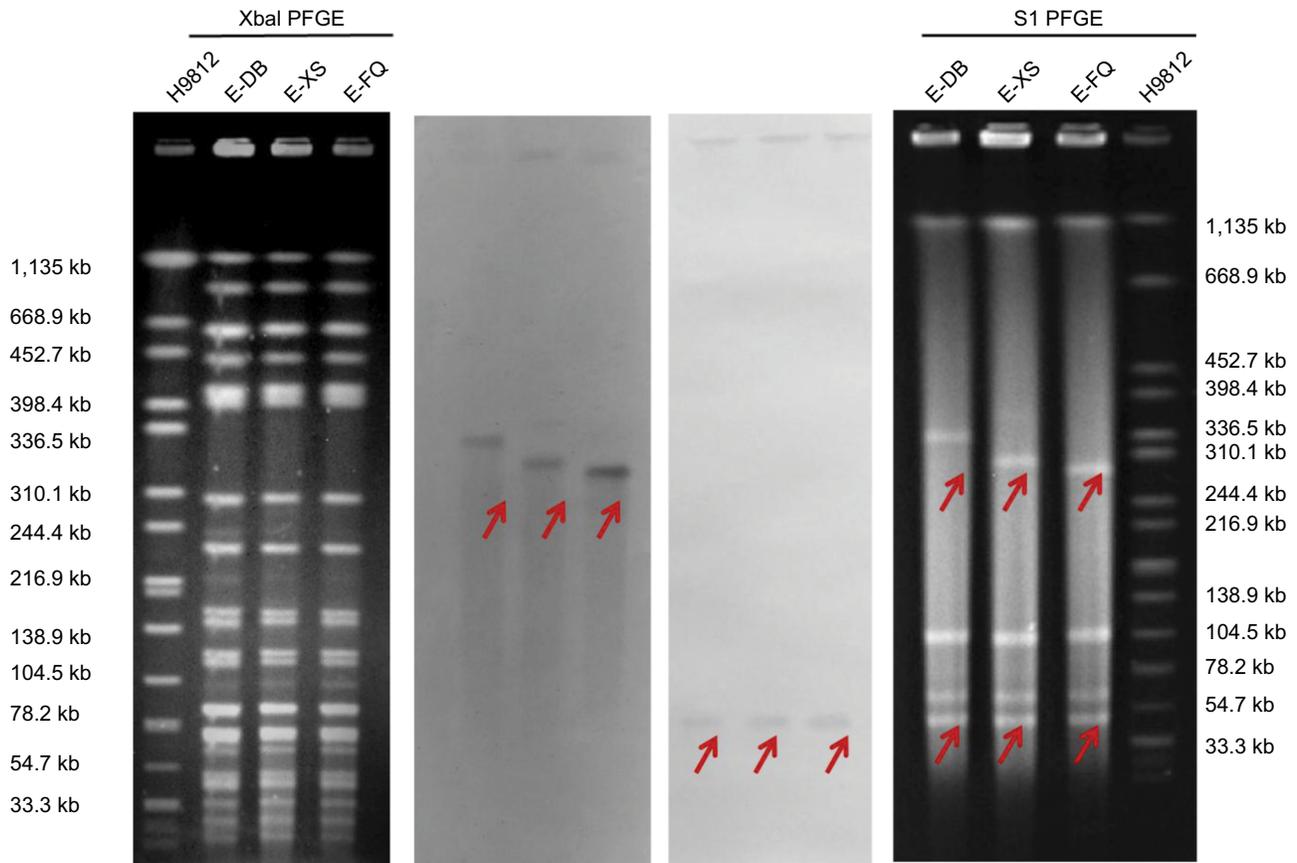


Figure S1 *Escherichia coli* isolates E-FQ, E-XS, and E-DB expressed indistinguishable band patterns by XbaI PFGE analysis. Analysis by S1 nuclease PFGE and Southern blot showed the presence of the *mcr-I* plasmid in a ~244–330 kb plasmid and *bla*_{NDM-5} in a ~33–55 kb plasmid.

Abbreviation: PFGE, pulsed-field gel electrophoresis.

Table S1 Primers used in mapping the *mcr-I* genetic environment and confirming mutations in *acrB* and *lon*

Name of primers	Sequence
140-27-F	AAGAAAACGGCAACACTCGC
140-27-R	TCGGGCATCTGGCAAAGAAT
5-140-F	TGGAAATGGGGAAGTGGTTCG
5-140-R	GCATGCCAGTAGCGGATTTG
AcrB-RND-F	GTCAGTACTGGTGGCGTTGA
AcrB-RND-R	ATCAGAGTGCTTCGCTGCTT
La-F	ATAGCAATACCGGCACTCGG
La-R	CCACCGGGGGTAGGTAATAAC

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