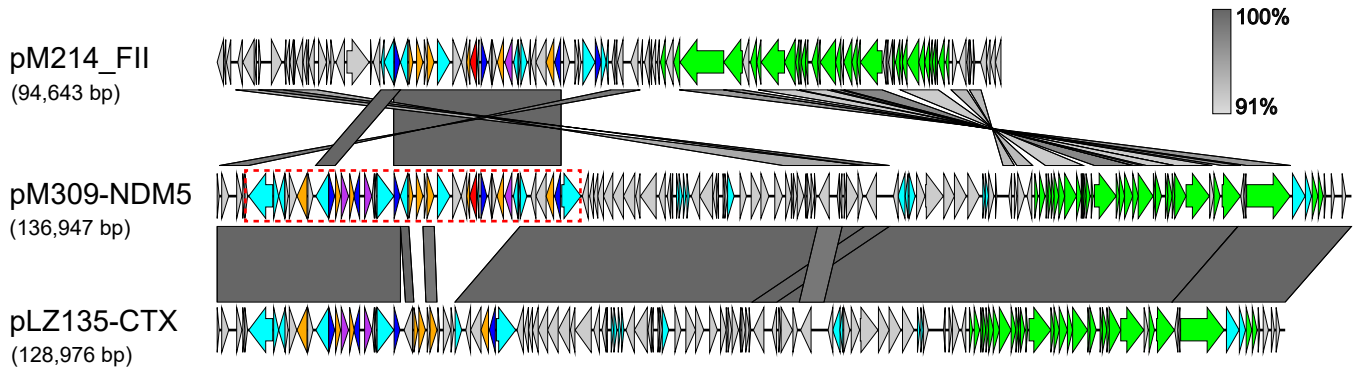


FIG S1

(A)



(B)

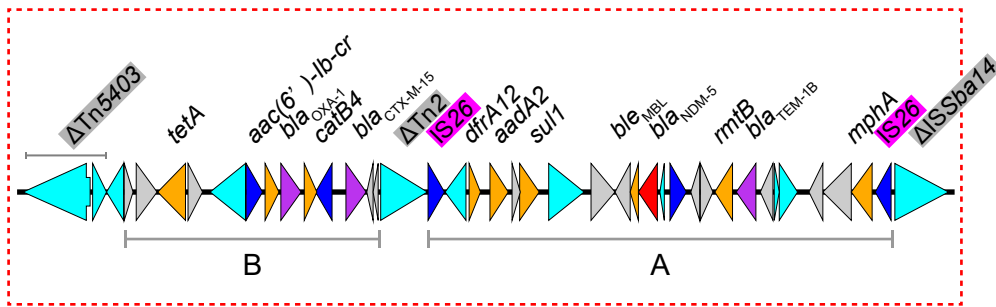


FIG S1. Genomic structure of the *bla*_{NDM-5}-harboring plasmid pM309-NDM5 identified in *E. coli* isolate M309. (A) Related plasmids (pM214_FII and pLZ135-CTX) are included for comparison, and homologous regions are shaded in dark gray. The red dotted rectangle indicates the antimicrobial resistance gene cluster. *bla*_{NDM-5}, red; other β -lactamase genes, purple; other antimicrobial-resistance genes, orange; IS26 transposase genes, blue; other mobile genetic elements, cyan; conjugal transfer genes, green; other accessory genes, light gray. (B) A magnified image of the multidrug-resistance region shown by red dotted rectangle in (A).

FIG S2

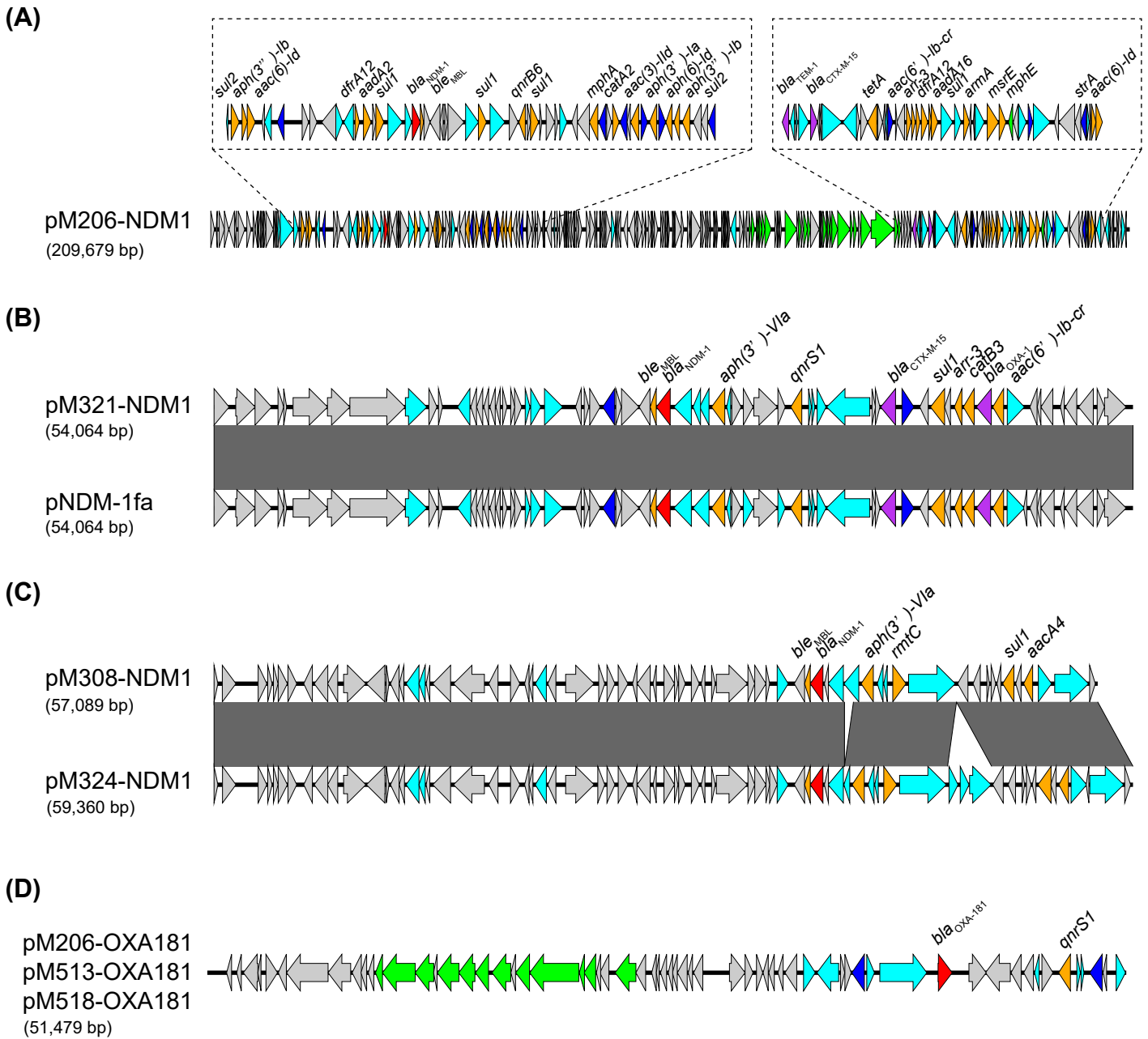


FIG S2. Genomic structure of the *bla*_{NDM}- or *bla*_{OXA-181}-harboring plasmids identified in this study. (A) Genomic structure of the *bla*_{NDM-1}-harboring plasmids pM206-NDM1 identified in the *E. xiangfangensis* isolates M206. *bla*_{NDM-1}, red; other β -lactamase genes, purple; other antimicrobial-resistance genes, orange; IS26 transposase genes, blue; other mobile genetic elements, cyan; conjugal transfer genes, green; other accessory genes, light gray. (B) Genomic structure of the *bla*_{NDM-1}-harboring plasmid pM321-NDM1 identified in *K. pneumoniae* isolate M321. A similar plasmid pNDM-1fa (GenBank accession number CP014757.1) is included for comparison, and homologous regions are shaded in dark gray. Gene colors are the same as indicated for (A). (C) Genomic structures of the *bla*_{NDM-1}-harboring plasmids pM308-NDM1 and pM324-NDM1 identified in *E. xiangfangensis* isolate M308 and M324, respectively. Gene colors are the same as indicated for (A). (D) Genomic structures of the *bla*_{OXA-181}-harboring plasmids pM206-OXA181, pM513-OXA181, and pM518-OXA181 identified in *E. xiangfangensis* isolate M206, *E. coli* M513, and *E. coli* M518, respectively. Gene colors are the same as described for (A), except that red denotes the *bla*_{OXA-181} gene.

Table S1. Summary of *bla*_{NDM}-harboring plasmids in the clinical and environmental isolates analyzed in this study

Species	Clinical isolates (n = 78)				Environmental isolates (n = 14)			
	Type of <i>bla</i> _{NDM} -harboring plasmid			Total	Type of <i>bla</i> _{NDM} -harboring plasmid			Total
	IncFII	IncX3	Others		IncFII	IncX3	Others	
<i>Escherichia coli</i> (n = 48)	31	8	5	44	4	1	0	5
<i>Klebsiella pneumoniae</i> (n = 19)	7	2	8	17	1	0	1	2
<i>Klebsiella quasipneumoniae</i> (n = 2)	0	1	0	1	0	1	0	1
<i>Enterobacter xiangfangensis</i> (n = 11)	0	0	11	11	0	0	0	0
<i>Enterobacter asburiae</i> (n = 1)	0	0	0	0	0	1	0	1
<i>Lelliottia nimipressuralis</i> (n = 1)	0	1	0	1	0	0	0	0
<i>Citrobacter freundii</i> (n = 7)	0	3	0	3	0	3	1	4
<i>Citrobacter amalonaticus</i> (n = 1)	0	1	0	1	0	0	0	0
<i>Leclercia adecarbosylata</i> (n = 1)	0	0	0	0	0	1	0	1
Total	38	16	24	78	5	7	2	14

Table S3. Antibiogram of the clinical and environmental isolates of CPE

Antibiotic	% of clinical isolates (n = 77)			% of environmental isolates (n = 14)			<i>P</i> value [†]
	S	I	R	S	I	R	
Meropenem	1.3	0.0	100.0	0.0	0.0	100.0	0.67
Imipenem	0.0	3.9	96.1	0.0	0.0	100.0	-
Ceftazidime	0.0	0.0	100.0	0.0	0.0	100.0	-
Cefmetazole	0.0	7.8	92.2	7.1	28.6	64.3	0.02*
Ampicillin/sulbactam	0.0	0.0	100.0	0.0	0.0	100.0	-
Piperacillin/tazobactam	0.0	0.0	100.0	0.0	0.0	100.0	-
Aztreonam	3.9	2.6	93.5	42.9	0.0	57.1	<0.001*
Gentamicin	9.1	0.0	90.9	42.9	0.0	57.1	0.001*
Amikacin	23.4	6.5	70.1	64.3	0.0	35.7	0.002*
Ciprofloxacin	1.3	1.3	97.4	35.7	0.0	64.3	<0.001*
Levofloxacin	3.9	1.3	94.8	42.9	7.1	50.0	<0.001*
Chloramphenicol	22.1	20.8	57.1	64.3	0.0	35.7	<0.001*
Minocyclin	20.8	28.6	50.6	28.6	21.4	50.0	0.52
Sulfamethoxazole/trimethoprim	5.2	0.0	94.8	0.0	0.0	100.0	0.38
Colistin	97.4	1.3	1.3	100.0	0.0	0.0	0.54
Fosfomycin	63.6	23.4	13.0	71.4	14.3	14.3	0.57

S, susceptible; I, intermediate; R, resistant. [†]Percentages of susceptible isolates were compared by chi-square test. **P* < 0.05.