

Various Sequence Types of *Enterobacteriaceae* Isolated from Commercial Chicken Farms in China and Carrying the *bla*_{NDM-5} Gene

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Antimicrobial Agents

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ABSTRACT A total of 108 meropenem-resistant *Enterobacteriaceae* isolates were obtained from 1,658 rectal swabs collected from 15 unrelated commercial chicken farms in China between 2014 and 2016. These samples yielded 16 *Escherichia coli* and 2 *Klebsiella pneumoniae* isolates of diverse sequence types carrying a *bla*_{NDM-5}-bearing IncX3 plasmid. *K. pneumoniae* strain sequence type 709 (ST709) has two *bla*_{NDM-5}-carrying plasmids that were transferred together to *E.coli*.

KEYWORDS Escherichia coli, Klebsiella pneumoniae, bla_{NDM-5}, IncX3 plasmid

ultidrug-resistant organisms, including those that are carbapenemase-producing Enterobacteriaceae, are becoming a challenging threat to public health worldwide (1). Gene *bla*_{NDM-5}, a variant of *bla*_{NDM}, was first identified in 2011 in an *Escherichia coli* sequence type 648 (ST648) isolate from a patient in the United Kingdom (2). Since then, it has been reported in various parts of the world, including South Korea (3), Denmark (4), Algeria (5), and China (6–8). The cooccurrence of NDM-5 and other carbapenemase enzyme isolates from the same patient is extremely worrisome because it might lead to therapeutic failure and death. The first cooccurrence of NDM-4- and NDM-5producing Klebsiella pneumoniae in the same patient was reported in 2016 (9). In 2017, a carbapenem-resistant K. pneumoniae ST147 isolate harboring bla_{NDM-5} and bla_{OXA-181} from a hospitalized patient was found in the United States (10). In 2018, a bla_{NDM-5}- and bla_{OXA-48-like}-coproducing E. coli strain was first isolated in South Korea (11). Meanwhile, the first case of a clinical Klebsiella michiganensis isolate producing KPC-2, NDM-1, and NDM-5 was reported in China (12). A fusion plasmid (IncX3 and IncFIB) recoverable from an NDM-5-producing clinical E. coli isolate was recently characterized, and these types of recombination events presumably play a potential role in the development of new plasmids with extended resistance profiles (13). In this study, we identified the presence of various sequence types of Enterobacteriaceae carrying bla_{NDM-5} in chickens from multiple farms across seven Chinese provinces.

A total of 108 nonrepeated meropenem-resistant *Enterobacteriaceae* (97 *E. coli* and 11 *K. pneumoniae*) isolates (6.5%) were obtained from 1,658 rectal swabs collected from 15 unrelated commercial chicken farms in China between 2014 and 2016 (see Fig. S1 in the supplemental material). All of the *Enterobacteriaceae* isolates were selected on MacConkey agar plates supplemented with 2 μ g/ml meropenem. Species identification was performed with the BD Phoenix-100 system (Becton Dickinson) and confirmed by 16S rRNA gene sequencing. Antimicrobial susceptibility testing was performed on Mueller-Hinton agar plates testing for 16 antimicrobials according to CLSI guidelines (14), except polymyxin B, for which European Committee on Antimicrobial Susceptibility Testing breakpoints were used (15).

These Enterobacteriaceae isolates were then subjected to screening for the presence

Received 21 April 2018 Returned for modification 7 May 2018 Accepted 18 June 2018

Accepted manuscript posted online 23 July 2018

Citation Xiang R, Zhang A-Y, Ye X-L, Kang Z-Z, Lei C-W, Wang H-N. 2018. Various sequence types of *Enterobacteriaceae* isolated from commercial chicken farms in China and carrying the *bla*_{NDM-5} gene. Antimicrob Agents Chemother 62:e00779-18. https://doi.org/10 .1128/AAC.00779-18.

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(a)	Escherichia coli	Strain	ST Type	Year	PB	IPM	СТХ	CAZ	FOX	АМС	AK	CIP	DO	FOS	CHL	SXT (CRO	CN A	TM M	IEM		
	78 —	MY332	NONE ¹	2014	S	R	R	R	R	R	s	R	R	R	R	R	R	R	s	R		
	81	SH256	ST466	2014	S	R	R	R	R	R	R	R	R	S	R	R	R	R	S	R		
	73	ZT614	ST132	2016	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	mcr-1	, <u> </u>
		SC225	ST2	2014	S	R	R	R	R	R	1	R	S	S	R	R	R	R	S	R		<u>่ว</u> เ
		SC472	ST160	2015	R	R	R	R	R	R	S	R	Т	R	R	R	R	S	R	R	mcr-3	
		SC552	ST365	2015	S	R	R	R	R	R	s	R	R	R	R	R	R	S	R	R		ela
	100	ZT336	ST356	2016	S	R	R	R	R	R	s	R	S	S	S	R	R	S	S	R		l
	100	SC112	ST7	2014	S	R	R	R	R	R	s	R	R	S	R	R	R	S	S	R		d c
		SH428	ST471	2015	R	R	R	R	R	R	s	R	R	Т	R	R	R	S	Т	R	mcr-1	N 8
		SC64	ST666	2016	S	R	R	R	R	R	R	R	Т	S	R	R	R	R	s	R		∕ Iĭ
		MY146	ST479	2014	S	R	R	R	R	R	1	R	R	S	S	R	R	R	s	R		erc
	<u>الم</u>	MY213	ST529	2016	S	R	R	R	R	R	s	R	R	S	R	R	R	S	S	R		
		SC135	ST31	2016	S	R	R	R	R	R	S	R	R	R	R	R	R	S	S	R		
		SC119	ST305	2014	R	R	R	R	R	R	S	R	S	S	R	R	R	S	S	R		nic
		SC189	ST697	2015	R	R	R	R	R	R	S	R	R	S	R	R	R	S	R	R	mcr-1	ke
	100	SH326	ST39	2015	S	R	R	R	R	R	S	R	R	S	R	R	R	S	R	R		nt
																						5 unrelated commercial chicken farms
(b)	Klebsiella pneumoniae	Strain	ST Type	Year	PB	IPM	СТХ	CAZ	FOX	AMC	AK	CIP	DO	FOS	CHL	SXT	CRO	CN A	ТМ М	EM		ns
		SCKL B003	ST3354	2015	s	R	R	R	R	R	s	R	R	I	R	R	R	R	s	R		
		SCKL B138	ST709	2016	R	R	R	R	R	R	R	R	R	s	R	R	R	R	s	R		

FIG 1 Phylogenetic relationship, antimicrobial resistance phenotypes, source of isolate, and sequence types of the 18 different *Enterobacteriaceae*: (a) *Escherichia coli* and (b) *Klebsiella pneumoniae*. A phylogenetic tree based on a maximum-likelihood method was built by MEGA6 with nucleotide sequences of 8 MLST genes to reveal a more detailed relationship among the analyzed strains. Bootstrap values (percentages of 1,000 replications) of >50% are shown at each node. 1, Failure to find any corresponding ST type with MLST database blasting. S, susceptible; I, intermediate; R, resistant; PB, polymyxin B; IPM, imipenem; CTX, cefotaxime; CAZ, ceftazidime; FOX, cefoxitin; AMC, amoxicillin-clavulanate; AK, amikacin; CIP, ciprofloxacin; DO, doxycycline; FOS, fosfomycin; CHL, chloramphenicol; SXT, trimethoprim- sulfamethoxazole; CRO, ceftriaxone; CN, gentamicin; ATM, aztreonam; MEM, meropenem.

of bla_{NDM} and *mcr* genes by PCR assay (see Table S1 in the supplemental material) as previously described (16). Of 108 meropenem-resistant *Enterobacteriaceae* strains, 52 (48 *E. coli* and 4 *K. pneumonia*; 3.14%) were found to harbor the bla_{NDM-5} gene. Multilocus sequence typing (MLST) was performed as previously described (http:// bigsdb.pasteur.fr/); 16 different sequence types of *E. coli* isolates and 2 sequence types of *K. pneumoniae* isolates were found. Three of the 16 strains of *E. coli* were found to coharbor the *mcr-1* gene. Multidrug-resistant *E. coli* strain ZT614 ST132 was resistant to all 16 antimicrobials. Phylogenetic relationship, antimicrobial resistance phenotypes, and sequence types of the strains are shown in Fig. 1.

Conjugation experiments were performed between 18 different isolates (Fig. 1) and *E. coli* J53 Az^r as the recipient. Transconjugants were selected on Mueller-Hinton agar (MHA; Oxoid) plates that contained 200 μ g/ml sodium azide with 2 μ g/ml imipenem. All of them could successfully transfer their carbapenem resistance genes to the recipient strain *E. coli* J53 Az^r. There was no cotransfer of carbapenem and colistin resistance phenotype transconjugant. The total plasmid DNA from 18 transconjugants was extracted using a Qiagen plasmid minikit following manufacturer's recommendations (Qiagen, Hilden, Germany). Whole-genome sequencing was performed on the Illumina MiSeq platform (Majorbio, Shanghai) using a 350-bp paired-end TruSeq library with a 2 \times 300 run. A draft assembly of the plasmids was made with plasmidSPAdes (17). Predicted gaps were closed by PCR and Sanger sequencing the using specifically designed primers listed in Table S1. Identification of antibiotic resistance genes was done by ResFinder 3.0 (http://www.genomicepidemiology.org/), and plasmid replicon types were determined by using the PlasmidFinder tool (http://genomicepidemiology.org/).

Sequence analysis revealed that all of the transconjugants harbored a 46-kb $bla_{\rm NDM-5}$ -bearing IncX3 plasmid. BLASTN results showed that all 18 IncX3 plasmids had almost

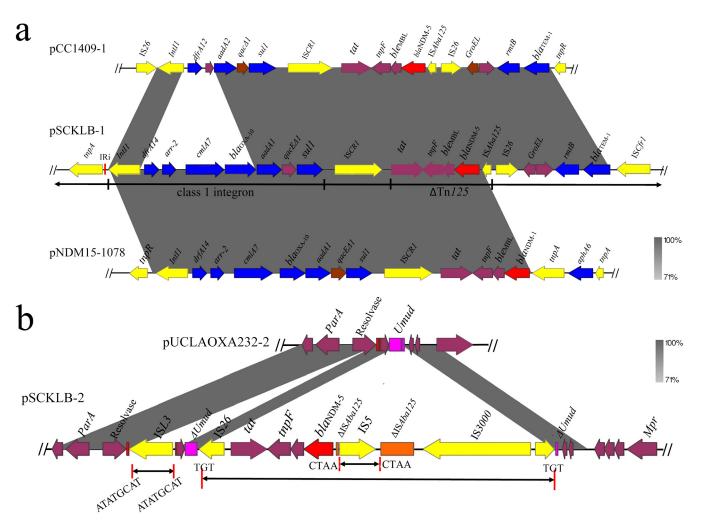


FIG 2 The genetic context of *bla*_{NDM-5} on pSCKLB138-1 and pSCKLB138-2 compared with other plasmids. (a) Genetic structure of *bla*_{NDM-5} gene on pSCKLB138-1 compared with pCC1409-1 and pNDM15-1078. (b) Genetic structure of *bla*_{NDM-5} gene on pSCKLB138-2 compared with pUCLAOXA232-2.

100% identity to the 46,161-bp plasmid pBJ114-46 (GenBank accession no. MF679143) with only 1 to 4 single-base changes (data not shown), indicating that the bla_{NDM-5} -bearing IncX3 plasmid was an important vector responsible for the dissemination of NDM-5 among *Enterobacteriaceae* isolates originating from chicken farms in China. Recently, a study identified the occurrence of similar IncX3 plasmids carrying bla_{NDM-5} in pigs originating from multiple farms across China (18), confirming that this mobile NDM vector is widespread in animal production.

Interestingly, a transconjugant of the ST709 *K. pneumoniae* strain named SCKLB138 harbored two bla_{NDM-5} -bearing plasmids, pSCKLB-1 and pSCKLB-2 (see Fig. S2 in the supplemental material). Plasmid pSCKLB-1 was found to comprise the IncFIB and IncFII replicons; the bla_{NDM-5} , bla_{OXA-10} , *rmtB*, aadA1, and bla_{TEM-1} genes; and some other resistance gene cassettes bounded by various insertion sequences. bla_{NDM-5} together with the bleomycin resistance gene ble_{MBL} , tat, and tnpF form part of the transposon Tn125 (Δ Tn125). Upstream of the ISAba125, IS26 and ISCfr1 were identified bracketing bla_{TEM-1} and the 16S rRNA methylase gene *rmtB*, conferring resistance to aminoglycosides. The same arrangement of Δ Tn125 and *rmtB* was found in ST147 *K. pneumoniae* plasmid pCC1409-1 (GenBank accession no. KT725789), except that the upstream of the bla_{TEM-1} gene of pCC1409-1 was truncated by Tn2 resolvase rather than ISCfr1 (Fig. 2a). The bla_{OXA-10} gene was localized downstream of bla_{NDM-5} in a class 1 integron with the dfrA14-arr-2-cmIA7- bla_{OXA-10} -aadA1 cassette array and the ISCR1 element behind the 3'-conserved segments. The region bracketed by bla_{NDM-1} and tnpR in plasmid pHN-

NDM0711 exhibited 99% identity to the corresponding region of pSCKLB-2 (Fig. 2a). Plasmid pSCKLB-2 was a 46-kb lncX3 bla_{NDM-5} -bearing plasmid. An IS5 was inserted with ISAba125 upstream of bla_{NDM-5} and the *ble*, *trpF*, and *tat* genes downstream from bla_{NDM-5} . Comparison of the genetic characteristics of pSCKLB-2 and pUCLAOXA232-2 (GenBank accession no. NZ_CP012563) showed that an ISL3 was inserted downstream of the resolvase gene, leading to the flanking 8-bp direct repeats (ATATGCAT). The bla_{NDM-5} -carrying region bracketed by IS26 and *tnpA* was inserted into the *umuD* gene, resulting in a pair of 3-bp direct repeats (TGT). The ISAba125 gene was interrupted by IS5 and split into two fragments, resulting in a pair of 4-bp direct repeats (CTAA) (Fig. 2b).

In conclusion, this study identified a self-transmissible IncX3 plasmid carrying bla_{NDM-5} that was an important vector responsible for the dissemination of NDM-5 among *Enterobacteriaceae* isolates originating from chicken farms in China. The cooccurrence of bla_{NDM-5} and other resistance *rmtB* and *mcr-1* genes in *Enterobacteriaceae* isolated in chicken farms strongly suggests a potential food chain dissemination pathway, which warrants further attention. To the best of our knowledge, this is the first report of two bla_{NDM-5} -carrying plasmids coexisting in a *K. pneumoniae* strain isolated from commercial chicken farms in China. The results highlight that the chicken farms are an important reservoir of *Enterobacteriaceae* carrying bla_{NDM-5} gene.

Accession number(s). The complete nucleotide sequences of plasmids pSCKLB-1 and pSCKLB-2 characterized in this study were submitted to the GenBank database and assigned accession numbers MH161191 and MH161192.

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at https://doi.org/10.1128/AAC .00779-18.

SUPPLEMENTAL FILE 1, PDF file, 0.7 MB.

ACKNOWLEDGMENTS

We thank the team of the curators of the Institut Pasteur MLST system (Paris, France) for importing novel MLST profiles at http://bigsdb.web.pasteur.fr.

This work was supported by China Agriculture Research System (CARS-40) National System for Layer Production Technology (CARS-40-K14), National Natural Science Fund of China (31772769), the general program of National Natural Science Foundation of China (31572547), and Special Fund for Agro-Scientific Research in the Public Interest of China (201403054).

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