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2 Short-form paper

3 An IncX3 epidemic plasmid carrying *bla*<sub>NDM-5</sub> in *Escherichia coli* from swine in multiple  
4 geographic areas in China

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20 Six imported pigs originating from Guangdong, Henan, and Hunan provinces in China during October  
21 2015-February 2017 were culture positive for meropenem-resistant *Escherichia coli*. The samples  
22 yielded 9 *E. coli* isolates of diverse sequence types carrying *bla*<sub>NDM-5</sub> on IncX3 (8 isolates from 5  
23 farms) or IncFII (1 isolate from 1 farm) plasmids. The *mcr-1* gene was co-harboured by four isolates.  
24 The IncX3 plasmids (~46 kb) carrying *bla*<sub>NDM-5</sub> were identical or nearly identical to each other.

25 (74 words)

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27 The presence of carbapenemase-producing *Enterobacteriaceae* (CPE) in livestock animals is  
28 concerning as this may facilitate expansion of the gene pool from which pathogenic bacteria  
29 can pick up the resistance genes and consumers may be subsequently exposed through the  
30 food chain (1,2). For this reason, there is a need to enhance the monitoring of carbapenem  
31 resistance in the food supply (1). In Hong Kong, 80% of the food animals are imported from  
32 mainland China and involved farm suppliers from multiple provinces in the country (3).

33 From September 2008 to February 2017, rectal swabs were obtained from randomly  
34 selected fresh pig carcasses at a centralized slaughterhouse in Hong Kong by trained  
35 veterinary staff, as part of an ongoing surveillance (3). Each swab was collected from a single  
36 animal and was inoculated into nutrient broth with 10 mg/L vancomycin and 0.5 mg/L  
37 meropenem (4), followed by subculture on MacConkey agar plate supplemented with 2 mg/L  
38 meropenem. Five to ten colonies from each selective plate were picked. MALDI-TOF MS  
39 was used for bacterial identification. The agar dilution (for colistin) and disc diffusion (for  
40 other antibiotics) methods were used to determine antimicrobial susceptibility (5,6). Isolates  
41 from the same animal were considered to be unique if the resistance profiles for meropenem  
42 and colistin were different.

43 In total, 856 pigs were cultured over 263 sampling dates (Table S1). Six pigs  
44 originating from six different farms were culture positive for meropenem-resistant *E. coli*  
45 (Table 1). According to the susceptibility patterns, a total of nine isolates were considered to  
46 be unique and investigated further. All isolates exhibited positive CarbaNP test result and  
47 were resistant to ertapenem, imipenem and meropenem. The presence of carbapenemase  
48 genes and *mcr-1* were investigated by PCR and sequencing (7-9). The *bla*<sub>NDM-5</sub> gene was  
49 identified in all nine isolates, of which four were colistin-resistant and co-harbored *mcr-1*.  
50 The isolates were further investigated by MLST and replicon typing (7,9,10). Plasmids  
51 carrying *bla*<sub>NDM-5</sub> were of X3 (n=8, size ~45 kb) or F36 (n=1, size ~100 kb). Of the four *mcr-*

52 *I* gene identified, three were harbored on plasmids of different replicon types (X4, FIB and  
53 Y). In conjugation experiments (9,10), there was no co-transfer of carbapenem and colistin  
54 co-resistance but the plasmids carrying *bla*<sub>NDM</sub> or *mcr-1* could be separately transferred at  
55 frequencies of  $10^{-4}$  to  $10^{-5}$  and  $10^{-1}$  to  $10^{-6}$  transconjugants per donor cell, respectively.

56 Six isolates (one from each animal, Table 1) were sequenced by an Illumina MiSeq  
57 platform at >150-fold coverage. The plasmids were assembled de novo using a CLC  
58 Genomics Workbench (Qiagen, Redwood City, United States) and gaps were closed by  
59 additional PCRs and Sanger sequencing (7,9,10). ISfinder ([https://www-](https://www-is.biotoul.fr/about.php)  
60 [is.biotoul.fr/about.php](https://www-is.biotoul.fr/about.php)) was used to identify and annotate insertion sequences. In strain P748,  
61 *bla*<sub>NDM-5</sub> was found in a contig (size ~32 kb) with 100% coverage and 98% identity to  
62 p28078-NDM (accession no. MF156713).

63 Complete sequences of the five IncX3 plasmids with sizes of ~46 kb were obtained  
64 (Table S2). They have a plasmid scaffold typical of IncX3 plasmids (Figure 1a). The genetic  
65 load regions in the five plasmids were compared with two reference IncX3 plasmids (pNDM-  
66 HN380 and pIncX-SHV) (Figure 1b). In the *bla*<sub>NDM</sub>-carrying plasmids, an ISL3 with 8-bp  
67 flanking direct repeats (ATATGCAT) was found downstream of the resolvase gene. The  
68 *umuD* gene was split into two fragments (*umuDA1* and *umuDA2*) at the same position as in  
69 pIncX-SHV, resulting in a pair of 3-bp direct repeats (TGT). In pNDM-HN380, *bla*<sub>NDM</sub> was  
70 inserted as an IS26-IS*Aba125* transposon-like structure (Figure 1b). Subsequently, the  
71 upstream IS*Aba125* was disrupted by IS5 (10). In four plasmids with link to Guangdong and  
72 Henan provinces, the sequences inserted between the two *umuD* fragments were 100%  
73 identical (10117 bp in length). This inserted sequence differs from that in pNDM-HN380 by  
74 a deletion of 7874 bp (Figure 1b). The remaining plasmid with link to Henan has an  
75 additional deletion (616 bp) at the junction between the IS5 and IS*Aba125* $\Delta$ 1 remnant. In the  
76 five NDM-5 plasmids, IS5 was inserted at the same position leading to the flanking 4-bp

77 direct repeats (CTAA). In pNDM-HN380, IS5 was inserted at a different position in the  
78 opposite orientation.

79 To explore the geographical distribution of potentially related *bla*<sub>NDM</sub>-carrying IncX3  
80 plasmids, the complete sequence of pP768-NDM5 (chosen as a representative) was used to  
81 query the GenBank. Twenty-two plasmids related to pP768-NDM-5 were identified by a  
82 query of the GenBank (Figure 1c). These include 14 plasmids from China, four from  
83 Myanmar and one each from Canada, India, Kuwait and Oman (Table S3). The plasmids do  
84 not carry resistance genes other than *bla*<sub>NDM</sub>. Multiple NDM variants were carried by the  
85 plasmids. These include NDM-1 and variants that differed by one to three amino acids,  
86 including NDM-4 (M154L), NDM-5 (V88L, M154L), NDM-7 (D130N, M154L) and NDM-  
87 17 (V88L, M154L, E170K).

88 We identified the occurrence of similar IncX3 plasmids carrying *bla*<sub>NDM-5</sub> in pigs  
89 originating from multiple farms across three different Chinese provinces. The involvement of  
90 IncX3 plasmids (represented by pNDM-HN380) in the dissemination of NDM in multiple  
91 geographic areas in China was initially reported by our group in 2012 (7). Subsequently,  
92 sporadic reports of pNDM-HN380-like plasmids carrying different NDM variants have also  
93 been reported in India, Arabian Peninsula, Europe and Australia (11-14). Recently, a Chinese  
94 national survey and several provincial studies revealed that IncX3 plasmids harbouring  
95 different *bla*<sub>NDM</sub> variants were frequently found among clinical isolates of different  
96 multilocus sequence types and species, suggesting that it is an important vector responsible  
97 for the wide dissemination of NDM in China (15-17). IncX3 plasmids have a narrow host  
98 range and have mainly been found in *Enterobacteriaceae* (18). Our finding from analysis of  
99 complete plasmid sequences indicated that the five IncX3 plasmids originating from pigs are  
100 related to pNDM-HN380 as well as plasmids originating from many other geographic areas,  
101 thus confirming that this mobile NDM vector is widespread in the ecosystem.

102 As carbapenems have never been licensed for use in food animals in China, the  
103 NDM-producing pig isolates detected in the present study may have been introduced to the  
104 farms via human activity or contaminated feeds. It is worrisome that some of the NDM-  
105 producing isolates in the present study were found to co-harbour *mcr-1* in another plasmid or  
106 the chromosome. Nonetheless, our isolates co-harbours *mcr-1* were recovered before the  
107 ban of colistin in animal feeds was implemented in November 2016 in China.

108 In conclusion, this study identified an epidemic IncX3 plasmid carrying *bla*<sub>NDM-5</sub>  
109 disseminated among *E. coli* originating from pigs with epidemiological links to  
110 geographically segregated areas in China.

111 **Accession number(s).** The complete sequence of the five IncX3 plasmids have been  
112 deposited into the GenBank database under accession numbers MF547511 (pP744-NDM5),  
113 MF547510 (pP768-NDM5), MF547509 (pP785-NDM5), MF547507 (pP788A-NDM5), and  
114 MF547508 (pP855-NDM5).

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193 **Table 1.** Sources and characteristics for nine NDM-positive *E. coli* isolates

Strain	Specimen	Source <sup>b</sup>	Date collected	MLST	<i>bla</i> <sub>NDM-5</sub>	<i>mcr-1</i>	Replicon type of plasmid harboring		Resistance patterns <sup>d</sup>
							<i>bla</i> <sub>NDM</sub>	<i>mcr-1</i>	
P744A	Pig 1	Henan (A1)	Oct 2015	ST 10	+	–	X3	none	Chl, Nit
P744T <sup>a</sup>	Pig 1	Henan (A1)	Oct 2015	ST 1602	+	+	X3	X4	Chl, Cip, Nit
P748 <sup>a</sup>	Pig 2	Hunan (B)	Jan 2016	ST 167	+	–	F36	none	Gen, Chl, Cip, Nit
P768	Pig 3	Henan (A2)	May 2016	ST 117	+	–	X3	none	Gen, Chl, Cip
P768-11 <sup>a</sup>	Pig 3	Henan (A2)	May 2016	ST 871	+	+	X3	FIB	Cip
P785 <sup>a</sup>	Pig 4	Guangdong (C1)	Jun 2016	ST 7512	+	+	X3	Chromosomal <sup>c</sup>	Gen, Chl, Cip, Nit
P788A	Pig 5	Guangdong (C2)	Jun 2016	ST1286	+	–	X3	none	Nit
P788A-32 <sup>a</sup>	Pig 5	Guangdong (C2)	Jun 2016	ST 7510	+	+	X3	Y	Gen, Chl, Nit
P855 <sup>a</sup>	Pig 6	Guangdong (C3)	Feb 2017	ST 7511	+	–	X3	none	Gen, Chl, Cip, Nit

194 <sup>a</sup>The six isolates were investigated further by genome sequencing.195 <sup>b</sup>Province (farm) origin of the pig196 <sup>c</sup>Chromosomal location of *mcr-1* in the isolate was confirmed by genome sequencing.197 <sup>d</sup>Resistance patterns for amikacin (Ak), chloramphenicol (Chl), ciprofloxacin (Cip), fosfomycin (Fos), gentamicin (Gen) and nitrofurantoin  
198 (Nit)

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201 **Figure 1.** Comparisons of IncX plasmids in this study. (a) Circular map of the plasmid  
202 pP768-NDM5. This plasmid was used to illustrate the backbone shared by all the analyzed  
203 plasmids and the location of the genetic load region. (b) Comparison of the genetic load  
204 region in 5 plasmids harbouring *bla*<sub>NDM-5</sub> with two reference plasmids (pIncX-SHV and  
205 pNDM-HN380). (c) Alignment of pP768-NDM5 with 22 plasmids identified in the GenBank  
206 (last accessed 27 Oct 2017). The circular maps were generated with the BLAST Ring  
207 IMAGE Generator and each plasmid was colored by the geographical origin (China, blue;  
208 Myanmar, yellow; Oman, orange; India, red; Canada, pink and Kuwait, purple) in the following  
209 order (outer to inner circles): pP768-NDM5, pCREC-A6-NDM, pSCE516-2, pNDM5\_IncX3,  
210 pEc1929, pECNDM101, pAD-19R, pNDM5\_WCHEC0215, pK518\_NDM5, pK516\_NDM5,  
211 NUHL24835, pNDM-QD28, pNDM-QD29, pEC50-NDM7, pZHDC40, pJEG027,  
212 pM216\_X3, pM213\_X3 and pM110\_X3, pOM26-1, pNDM-MGR194 and pKpN01-NDM7,  
213 pKW53T-NDM (full details of plasmids in Table S3).

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