

# High antimicrobial resistance and plasmid-carrying resistance genes in swine-origin mcr-1-positive *Escherichia coli* in Guangxi, South China

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## Research article

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# Abstract

**Background** The discovery of *mcr-1*-positive *Escherichia coli* (MCRPEC), a notable superbug, attracted great attention worldwide. Swine-origin multi-drug resistance MCRPEC is a potential threat to public health and safety. To date, few detailed studies regarding swine-origin MCRPEC in Guangxi, South China, have been reported. **Results** In this study, thirty-three MCRPEC harbored *mcr-1* genes were identified from 142 *E. coli* strains isolated from swine droppings and entrails in Guangxi in 2018. All MCRPEC isolates were assigned to 8 unique STs, including ST10, ST224 and ST410, which overlapped with the human-origin MCRPEC. Additionally, a total of six plasmid replicon types (IncFI, IncHI1, IncY, IncN, IncI1 and IncX1) were found. Moreover, the drug susceptibility of the MCRPEC isolates was tested with 27 antimicrobial agents belonging to 17 antimicrobial categories that are usually used in hospitals. There were 19 extended spectrum beta lactamase (ESBL) *E. coli* and 12 carbapenem resistant *E. coli* among the 33 MCRPEC strains. Importantly, the MCRPEC showed a high rate of resistance against two broad-spectrum carbapenem antibiotics, imipenem and meropenem, which are forbidden in livestock production use. Three MCRPEC strains were further identified to be extensively drug-resistant (XDR), and other isolates were recognized as multi-drug-resistant (MDR). Meanwhile, to detect whether plasmid-carrying antimicrobial resistance genes coexisted with the *mcr-1* gene in the MCRPEC isolates, a total of 22 plasmid-carrying antimicrobial resistance genes were tested for. The results showed that four ESBL genes and one *pAmpC* gene were identified. Eight of the MCRPEC isolates also contained the carbapenem gene *bla*NDM-5, which could cause untreatable infections. Moreover, ten non-lactamase genes were also detected. **Conclusion** This study indicated that swine-origin MCRPEC isolated in Guangxi seemed to have a high rate of resistance to both regular and final line of defense drugs as well as drug resistance genes, which pose a great threat to human public safety and health.

## Background

Superbug infection is one of the most serious threats to public and animal health. The emergence and rapid spread of multi-drug-resistant (MDR), extensively drug-resistant (XDR) and pan-drug-resistant (PDR) bacteria is a substantial public health concern around the world [1]. The transmissibility of antimicrobial resistance mediated by mobile plasmids is an important cause of XDR and PDR bacteria. For example, plasmids carrying the *MCR-1* gene were found in *E. coli*, thus suggesting that polymyxin, a last line of defense against carbapenem resistant *Enterobacteriaceae* [2], was ineffective.

Colistin (polymyxin E) has been used as a veterinary medicine and a feed additive for decades in animal production [3]. In 2015, the plasmid-mediated *mcr-1* gene was first discovered in food animals in South China [4]. At this time, a total of nine different *mcr* alleles, *mcr-1* to *mcr-9* [5–12], have been detected in different bacteria and spread to over 40 countries/regions.

CRE infection contributes to increased hospital mortality. The emergence of colistin resistant *E. coli* worsens the situation from a public health perspective. Moreover, swine-origin *E. coli* might present a potential zoonotic risk and could cause human infection. The previous epidemiological surveys of swine-

origin MCRPEC isolates focused on the global distribution and routine carriages of *mcr-1*. However, the understanding of swine-origin MCRPEC antimicrobial resistance phenotypes and plasmid-carrying resistance genes among MCRPEC in local areas are incomprehensive. To assess the hazards to public health and safety posed by MCRPEC isolates obtained from pig farms in Guangxi, South China in 2018, this study identified antimicrobial resistance phenotypes and genes in MCRPEC isolates and also ascertained the ST and plasmid replicon types.

## Results

### Identification of *mcr-1* positive *E. coli* (MCRPEC)isolates

One hundred and sixteen pig specimens with typical clinical symptoms of swine colibacillosis were collected from 44 middle to large pig farms in Guangxi in 2018. A total of 142 *E. coli* isolates were isolated from 116 samples. Seven-two (50.7%) *E. coli* isolates were tested with MICs of colistin  $\geq 4$  mg/L. To trace the prevalence of *mcr* genes, the 72 *E. coli* isolates were analyzed by screening for *mcr-1*, *mcr-2*, *mcr-3*, *mcr-4*, *mcr-5*, *mcr-6*, *mcr-7*, and *mcr-8*. Thirty-three MCRPEC isolates were observed, which accounted for 45.8% of the colistin resistant *E. coli* strains and 23.2% of the 142 total *E. coli* strains. Notably, none of the other *mcr* genes were detected.

The full-length 16S rRNA nucleotide sequences from the 33 MCRPEC strains were used to generate a phylogenetic tree by MEGA-X (Table 1). Thirty-three MCRPEC strains were aligned to 8 unique STs, including ST10, ST224, ST361, ST410, ST641, ST1408, and ST3345, and an unknown ST. ST10 and ST224 were recognized as the dominant STs, which accounted for 69.7% (23/33) (Table 1). All data about house-keeping genes were kept in one form (Supplementary material).

To identify the plasmid-carrying resistance genes in the MCRPEC isolates, the plasmid replicon types of MCRPEC were identified by multiple PCR. A total of 6 plasmid replicon types were detected in the 33 MCRPEC isolates. Additionally, IncFI (97.0%, 32/33), IncHI1 (12.1%, 4/33), IncY (48.5%, 16/33), IncN (15.2%, 5/33), IncI1 (3.0%, 1/33) and IncX1 (6.1%, 2/33) were the most common plasmid replicons among the 33 MCRPEC isolates (Table 1).

### Antimicrobial resistance in MCRPEC

To determine whether MCRPEC could threaten food safety and public health, rigorous drug resistance surveillance was vital and necessary. Twenty-seven antimicrobials that are widely used in human clinical treatment were tested (Table 2).

The resistance rates for each antimicrobial in the MCRPEC isolates were as follows: gentamicin (72.7%), amikacin (48.5%), ceftaroline (69.7%), piperacillin-tazobactam (24.2%), imipenem (36.4%), meropenem (24.2%), cefalexin (69.7%), cefuroxime (57.6%), cefotaxime (57.6%), ceftriaxone (57.6%), cefepime (39.4%), ceftazidime (0%), ciprofloxacin (75.8%), sulfadiazine (24.2%), trimethoprim-sulphamethoxazole

(0%), aztreonam (24.2%), ampicillin (97.0%), amoxicillin-clavulanic acid (0%), ampicillin-sulbactam (24.2%), chloramphenicol (84.8%), fosfomycin (78.8%), tetracycline (100%), doxycycline (72.7%), azithromycin (57.6%), polymyxin B (100%) and colistin (100%) (Figure 1a). According to the antimicrobial susceptibility testing of cephalosporin, nineteen (57.6%) ESBL-producing *E. coli* isolates and twelve (36.4%) carbapenem resistance *E. coli* isolates tested positive among the MCRPEC isolates (Fig. 1a). Importantly, the tested MCRPEC isolates showed a proportional resistance to imipenem and meropenem, which are both broad-spectrum carbapenem antimicrobials conventionally used for human clinical treatment that are forbidden in livestock production use.

On the basis of the definition standard for MDR, XDR, and PDR bacteria [13], all 33 MCRPEC isolates exhibited MDR (Fig. 1b). Moreover, three of the MDR MCRPEC isolates were identified as XDR (Fig. 1c). According to figure 1c, the swine original MCRPECs showed a great tendency to become XDR or PDR *E. coli*.

## **Coexistence of *mcr-1* with plasmids carrying ESBL, pAmpC, carbapenem resistance genes and non-lactamase antimicrobial resistance genes among the MCRPEC isolates**

To detect whether the *mcr-1* gene coexisted with ESBL, carbapenem and pAmpC genes and other  $\beta$ -lactamase genes in the MCRPEC strains, plasmids were isolated and purified without a chromosomal genome. Multiplex PCR was performed by using plasmids as a template. The results showed that  $\beta$ -lactamase genes existed in 23 (69.7%) of the MCRPEC isolates. The main  $\beta$ -lactamase gene types in this study were bla<sub>OXA-1</sub>, bla<sub>CTX-M</sub>, bla<sub>NDM</sub> and bla<sub>CMY</sub>. Two MCRPEC isolates harbored bla<sub>OXA-1</sub> genes. CTX-M group genes were found in 20 MCRPEC isolates, among which, bla<sub>CTX-M-123</sub>, bla<sub>CTX-M-14</sub> and bla<sub>CTX-M-24</sub> were found in 13, 19 and 1 of the MCRPEC isolate(s) respectively. Two MCRPEC isolates were found to carry bla<sub>CMY-2</sub>. Last, and most importantly, there were 8 MCRPEC isolates that contained the carbapenem gene bla<sub>NDM-5</sub> (24.2%) (Fig. 2a, Fig. 2b), which could cause untreatable infections.

Monitoring plasmid-carrying non-lactamase antimicrobial resistance genes could effectively assess and prevent the threat of MCRPEC to public health safety. Twelve plasmid carrying non-lactamase antimicrobial resistance genes were detected by PCR. The qnrA, qnrB, qnrS, and aac(6')-Ib-cr genes, which are closely associated with fluoroquinolone resistance, were detected and account for 36.4%, 36.4, 33.3% and 24.2%, respectively, of the isolates. The tetracycline resistance genes, tetA (100%), tetB (18.2%), and tetX (0%), were also present in the MCRPEC isolates. Moreover, sul1 (90.9%) and sul2 (78.8%) were prevalent in MCRPEC isolates, and the aadA (100%) genes were prevalent in the aminoglycoside-resistant MCRPEC isolates. The plasmid-encoded floR (100%) gene was the major resistance plasmid gene that encoded chloramphenicol resistance in the MCRPEC isolates (Fig. 2a).

## **Discussion**

China is the largest pork market in world. Colibacillosis caused by *E. coli* is the most common swine bacterial disease worldwide. Meanwhile, *E. coli* is the main route for antimicrobial resistance gene transfer. Animal husbandry has always been an important source of biological pollution. The large and irregular use of antimicrobial agents aggravate the rapid spread of plasmid-carrying antimicrobial resistance genes. Colistin had long been used as one feed additive in pig breeding programs until the discovery of the *mcr-1* gene. In 2015, Liu et al. first observed that the *mcr-1* gene in *E. coli* and subsequently colistin mobile resistance genes in different gram-negative bacteria had been widely reported worldwide [4]. MCRPEC prevalence among pigs not only impacts pig production but also poses threats against human health by influencing the farm surroundings and contaminating the food chain, which means a high prevalence of MCRPEC causes both clinical and epidemiological challenges.

MLST is increasingly used as a common tool for strain comparison in epidemiological determinations of antimicrobial resistance strains. The correlation among host populations, bacterial molecular biology and microbial resistance can be made understandable by the statistical analysis of accurate ST types and antimicrobial resistance data for the same bacterial species isolated from different host species. Three ST types (ST10, ST224, ST410) of swine-origin MCRPEC isolates were also found in human-origin *E. coli* isolates [14]. This finding suggests that the three ST types of swine-origin MCRPEC are likely to infect humans under appropriate conditions. Notably, in previous works of bacterial antimicrobial resistance monitoring, ST224 *E. coli* strains from human and swine carried antimicrobial resistance genes that posed threats to public health [15]. Meanwhile, all ST224 MCRPEC isolates in this study showed extremely high levels of multi-drug-resistance, and 3 strains of ST224 MCRPEC were identified as XDR. As the number of test samples was not large in this study, more meaningful work that separates zoonotic MCRPEC strains and analyzes ST types is needed in future studies.

Bacterial antimicrobial resistance is constantly evolving and horizontal gene transfer through plasmids plays a major role [16]. The identification of plasmid characteristics provides crucial knowledge that is essential to understand the contribution of plasmids to the transmission of antimicrobial resistance determinants. To date, the *mcr-1* gene has been found in eight different plasmid incompatibility groups (IncI2, IncFII, IncX4, IncHI1, IncHI2, IncP, IncF, and IncY) [17]. In this study, we found that IncFIA and IncFrep were highly carried in our 33 MCRPEC isolates. Moreover, bacteria contained more antimicrobial resistance genes when carrying IncFIA, IncFIB, IncFIC, IncFrep, and IncY. This result suggests that a combination of plasmid replicon types made it easier to obtain antimicrobial resistance genes following plasmid transmission.

Previous studies regarding swine-origin MCRPEC mostly focused on genes and transfer. However, the exploration of antimicrobial-resistance phenotypes has not often been pursued. In other words, antimicrobial selection was not comprehensively evaluated. Consequently, a total of 27 antimicrobials against *E. coli* were selected from 18 antimicrobial categories in this study. Antimicrobial-resistance phenotypes usually indicate two problems: damage from the bacteria themselves and a hazard below the surface. As noted above, three MCRPEC ST types that have been isolated from humans were observed in this study. According to the antimicrobial resistance test results, this is a warning sign, as nine isolates

were ESBL *E. coli* and eight isolates were CRE in ten of the ST224 MCRPEC isolates. Meanwhile, nine isolates were ESBL *E. coli* in thirteen of the ST10 MCRPEC isolates. In many past studies, ST10 and ST224 *E. coli* were usually observed to be MDR. This problem implies that ST10 and ST224 MCRPEC are typical zoonotic *E. coli* types and can pose a great threat to public health. Although it turns out that humans with superbug infections are increasingly limited, the development of new drugs could offer a glimmer of hope, such as tigecycline (0%). Of course, rational use of these antimicrobials is required to reduce the chances of developing antimicrobial resistance. Some studies showed that the production and transfer of plasmid-carrying tigacycline resistance genes were influenced by a high-pressure environment of the same antimicrobial type [18].

Plasmid-carrying resistance genes are a hidden threat, as they are the key to antimicrobial resistance transfer. The identification of plasmid-carrying resistance genes is essential for studying resistance genes transfer. In this study, we found seventeen ESBL *E. coli* that contained CTX-M group genes, which included bla<sub>CTX-M-123</sub>, bla<sub>CTX-M-14</sub>, and bla<sub>CTX-M-24</sub>, that were also found in ESBL *E. coli* from humans or other animals [19, 20]. Alarmingly, eight of the MCRPEC isolates carried bla<sub>NDM-5</sub> and bla<sub>CTX-M-14</sub> at the same time. Although some studies have found MCRPEC that carried bla<sub>NDM-5</sub>, most bacteria were isolated from hospitals, as carbapenems are strictly forbidden in animal use in China. A new study [21] showed that resistance gene transfer in *E. coli* occurs regardless of gender and age, but gene transfer has much to do with industrial and social attributes. The report also showed that women and children who farmed pigs and poultry were more likely to be vehicles for ESBL and carbapenem gene transfer. This finding implies that the earlier source of the bla<sub>NDM</sub> gene in MCRPEC was from humans, and bla<sub>NDM</sub> can be transferred between animal groups and humans with close contact.

## Conclusions

This study indicated that swine-origin MCRPEC isolated in Guangxi seemed to have a high rate of resistance to both regular and final line of defense drugs as well as drug resistance genes. The results of molecular detection showed coexistence of bla<sub>NDM-5</sub> and *mcr-1*, coexistence of ESBL genes (bla<sub>OXA-1</sub>, bla<sub>CTX-M14</sub>, bla<sub>CTX-M123</sub>, and bla<sub>CTX-M24</sub>) and *mcr-1* in *E. coli* isolates. The coexistence of bla<sub>NDM-5</sub>, ESBL genes and *mcr-1* in one *E. coli* isolate was worst. From a public health perspective, continued surveillance of MCRPEC is essential in swine, other food animals, and companion animals.

## Methods

### Sample collection and detection of MCRPEC isolates

A total of 142 nonrepetitive *E. coli* strains were collected retrospectively from 44 pig farms in Guangxi, China in 2018. The swine isolates were from anal swabs or lung, intestinal tract, heart, or lymph gland tissue collected from dead or unhealthy pigs. Samples from the collected tissues were inoculated onto MacConkey agar for 24 h at 37°C, followed by inoculation with eosin-methylene blue agar and Luria-Bertani (LB) agar. Then, 16S rRNA gene sequencing was used to confirm the *E. coli* isolates, and the full-

length nucleotide sequence of the 16S rRNA genes among the *E. coli* strains were determined by direct sequencing from PCR products and BLAST analysis (<http://www.ncbi.nlm.nih.gov/>). Then, a phylogenetic tree was generated with MEGA-X software. The plasmid genome of MCRPEC was extracted with a TIAPure Midi Plasmid Kit. These strains were stocked at  $-80^{\circ}\text{C}$  in glycerol medium.

The MCRPEC isolates were preliminarily screened by PCR amplification using special primer pairs for the *mcr-1*, *mcr-2*, *mcr-3*, *mcr-4*, *mcr-5*, *mcr-6*, *mcr-7*, and *mcr-8* genes [22]. To identify variants of *mcr-1*, the full-length nucleotide sequence of the *mcr-1* gene among the MCRPEC strains was determined by direct sequencing from the PCR products and BLAST analysis (<http://www.ncbi.nlm.nih.gov/>).

## Detection of multilocus sequence typing (MLST) and plasmid replicon types

The seven housekeeping genes, namely, *adk*, *fumC*, *gyrB*, *icd*, *mdh*, *purA*, and *recA*, were used to perform MLST analysis. PCR amplicons were purified, and DNA was sequenced. The gene sequences for seven housekeeping genes were uploaded to the EnteroBase database ([http://enterobase.warwick.ac.uk/species/ecoli/allele\\_st\\_search](http://enterobase.warwick.ac.uk/species/ecoli/allele_st_search)), and the sequence type (ST) of the *E. coli* was matched.

Incompatibility groups (HI1, HI2, I1, L/M, N, FIA, FIB, FIC, Frep, W Y, P, A/C, T, FIIS, K/B, B/O) were assigned by PCR-based replicon typing. For the IncX (X1, X2, X3, X4) replicon types, additional PCRs were conducted, as described previously [23, 24].

## Antimicrobial susceptibility testing

According to the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) consensus, a total of 27 commonly used human antimicrobials were selected from 18 antimicrobial categories (Table 2) in this study [13]. The *E. coli* isolates were inoculated on MH agar plates that contained different concentrations of different drug types. The MICs of each drug were measured and recorded. *E. coli* ATCC25922 was used as a quality control.

Minimum inhibitory concentrations (MICs) were determined by using the agar microdilution method according to the Clinical and Laboratory Standards Institute [25]. The breakpoints of colistin and cefalexin for Enterobacteriaceae were interpreted according to the US Food and Drug Administration (FDA) standard and the European Committee on Antimicrobial Susceptibility Testing (EUCAST, [http://www.eucast.org/clinical\\_breakpoints/](http://www.eucast.org/clinical_breakpoints/)) guidelines, respectively. MICs of  $\leq 2$  mg/L and  $\leq 16$  mg/L are considered as susceptible (S) for colistin and cephalixin, respectively, according to the EUCAST guidelines. Additionally, the CLSI-M100 document (2018, <http://www.clsi.org/m100/>) defined *E. coli* isolates with colistin MICs  $\geq 4$  mg/L as nonwild type (non-WT) and colistin MICs  $\leq 2$  mg/L as wild type (WT). In this study, we adopted the EUCAST Resistant/Susceptible breakpoints.

# Molecular identification of ESBL, pAmpC, and carbapenem resistance genes

The presence of ESBL, pAmpC, and carbapenem genes in the MCRPEC isolates were detected by multiplex PCR [2, 26]. The ESBL genes (*bla*<sub>CTX-M</sub>, *bla*<sub>TEM</sub>, *bla*<sub>OXA-1</sub>, and *bla*<sub>SHV</sub>), pAmpC (*bla*<sub>CMY</sub>, *bla*<sub>FOX</sub>, *bla*<sub>DHA</sub>), and carbapenem resistance genes (*bla*<sub>NDM</sub>, *bla*<sub>KPC</sub>, *bla*<sub>OXA-48</sub>, and *bla*<sub>IMP</sub>) were amplified using specific primers, as previously reported. The full-length DNA sequences for the ESBL, pAmpC, and carbapenem genes were determined using BLAST analysis (<http://www.ncbi.nlm.nih.gov/>).

## Detection of non-lactamase antimicrobial resistance genes

The detection of non-lactamase antimicrobial resistance genes in the *E. coli* isolates was performed by PCR amplification. The special primers included plasmid-encoded fluoroquinolone resistance genes (*qnrA*, *qnrB*, *qnrS*, *aac(6')-Ib-cr*) [27], tetracycline resistance genes (*tetA*, *tetB*, *tetX*) [18], sulfonamide resistance genes (*sul1*, *sul2*), aminoglycoside resistance genes (*aadA*), and chloramphenicol resistance genes.

## Abbreviations

MCRPEC: *mcr-1*-positive *Escherichia coli*; MDR: multi-drug-resistance; XDR: extensively-drug-resistant; PDR: pan-drug-resistant; CRE: carbapenem resistant *Enterobacteriaceae*

## Declarations

## Ethics approval and consent to participate

This study passed the inspection by Attitude of the Animal Care & Welfare Committee of Guangxi University. The Animal Experimental Ethical Inspection Form of Guangxi University number was GXU2018–53. Collection the specimens in this study approved by College of Animal Science and Technology, Guangxi University and all relevant pig-breeding companies, meanwhile conformed to the legal requirements of Guangxi Zhuang Autonomous Region.

## Consent for publication

Not applicable

## Availability of data and materials

The data were presented in the main manuscript and available to readers.

## Competing Interests

The authors declare that they have no conflict of interest.

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## Authors' contributions

JY carried out the experiment, analyzed samples and statistical data and wrote the manuscript. DS, QG and XS participated in experiment. WH, DW and CG isolated samples. XL and CH contributed to revise the manuscript. XW was corresponding authors, who mainly designed the study and supervised the whole program. All authors have read and approved the final manuscript.

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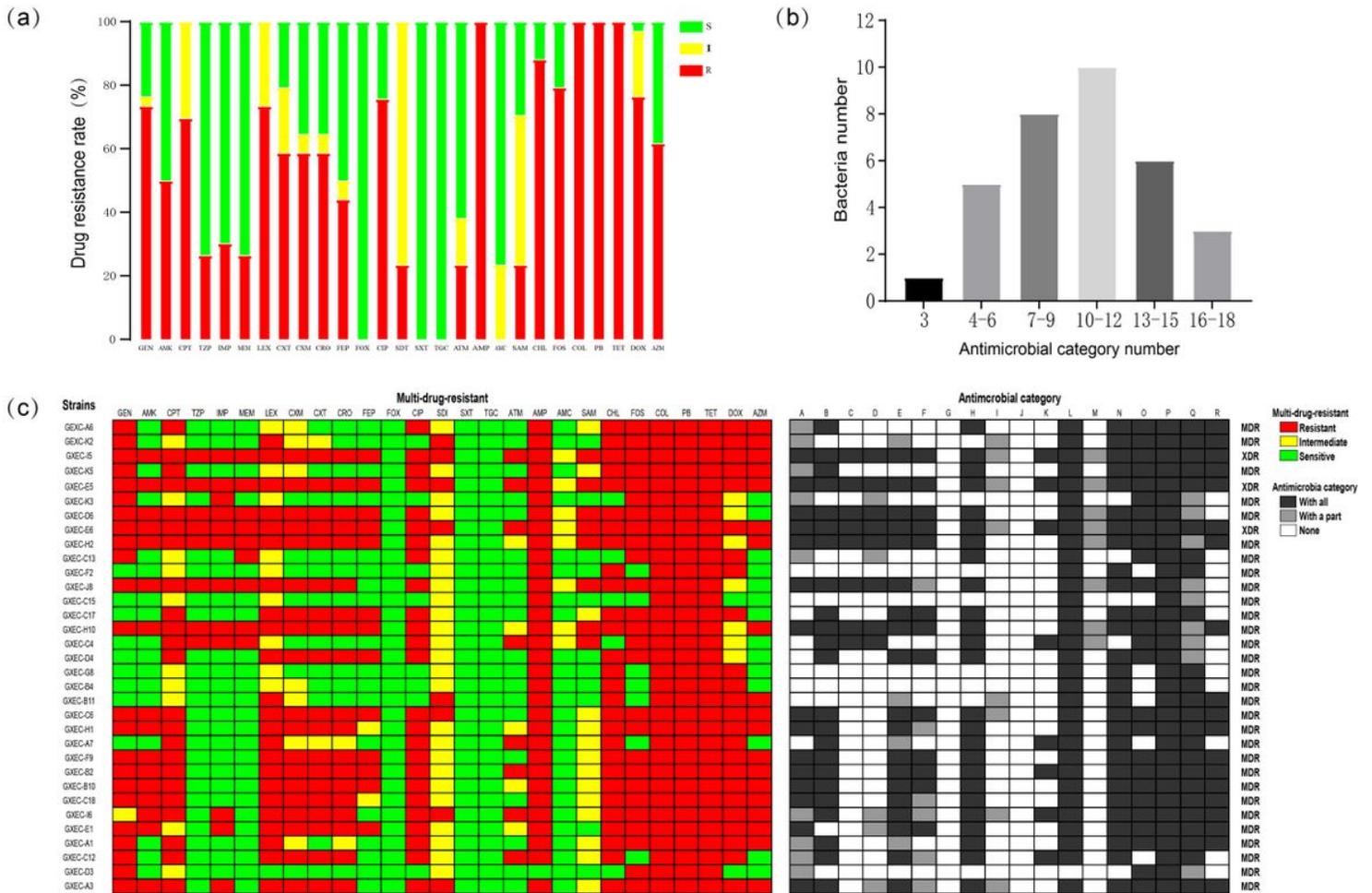
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**TABLE 2** The antimicrobial agents for 17 antimicrobial categories used to define the *E. coli* antimicrobial resistance

Antimicrobial category	Antimicrobial agent
Aminoglycosides	Gentamicin(GEN)
	Amikacin(AMK)
Anti-MRSA cephalosporin	Ceftaroline(CPT)
Antipseudomonal penicillins- $\beta$ -lactamase inhibitor	Piperacillin/tazobactam(TZP)
Carbapenem	Imipenem(IMP)
	Meropenem(MEM)
Non-extended spectrum cephalosporins	Cefalexin(LEX)
	Cefuroxime(CXM)
3rd and 4th generation cephalosporins	Cefotaxime(CTX)
	Ceftriaxone(CRO)
	Cefepime(FEP)
Cepharmycin	Cefoxitin(FOX)
Fluoroquinolone	Ciprofloxacin(CIP)
Folate pathway inhibitor	Sulfadiazine(SDI)
	Trimethoprim/sulfamethoxazole(SXT)
Glycylcycline	Tigecycline(TGC)
Monobactam	Aztreonam(ATM)
Penicilline	Ampicillin(AMP)
Penicilline- $\beta$ -lactamase inhibitors	Amoxicillin/clavulanic acid(AMC)
	Ampicillin-sulbactam(SAM)
Phenicol	Chloramphenicol(CHL)
Phosphoric acid	Fosfomycin(FOS)
Polymyxins	Polymyxin B(PB)
	Colistin(COL)
Tetracycline	Tetracycline(TET)
	Doxycycline(DOX)
Macrolides	Azithromycin(AZM)

## Figures



**Figure 1**

Fig. 1 Antimicrobial resistance traits of the 33 swine-origin MCRPEC isolates recovered from swine colibacillosis. (a) Antimicrobial resistance rate, the columns indicated the percentages of the 33 MCRPEC isolates that were sensitive (green), intermediate (yellow), or resistant (red) to 27 common antimicrobials. (b) Statistics of the multi-antimicrobial category. (c) The first panel includes 27 columns that represents the 27 antimicrobial agents that were sensitive (green), intermediate (yellow), or resistant (red). The next panel that includes 18 columns indicates the antimicrobial category of the 33 MCRPEC isolates, which include A: aminoglycosides, B: anti-MRSA cephalosporins, C: antipseudomonal penicillins +  $\beta$ -lactamase inhibitors, D: carbapenems, E: 1st and 2nd generation cephalosporins, F: 3rd and 4th generation cephalosporins, G: cephamycins, H: fluoroquinolones, I: folate pathway inhibitors, J: glycylicyclines, K: monobactams, L: penicillins, M: penicillins +  $\beta$ -lactamase inhibitors, N: phenicols, O: phosphonic acids, P: polymyxins, Q: tetracyclines, and R: Macrolides. The colors represent the following: resistant to all kinds agents of one antimicrobial category (black), resistant to some of the agents of one antimicrobial category (gray), no agent resistance (white). The rightmost section are judgments for MDR, XDR, or PDR.

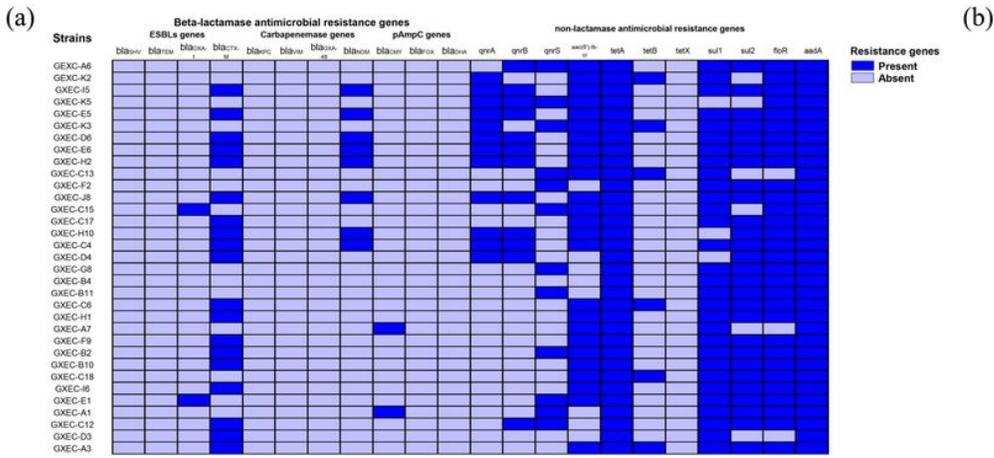


Figure 2

Fig. 2 Plasmid-carrying resistant genes of the 33 swine-origin MCRPEC isolates recovered from swine colibacillosis. (a) The panel includes 22 columns that show the presence or absence of plasmid-mediated resistance genes. Navy coloring represents a presence, and Light Blue coloring represents an absence. (b) The distribution of the total ESBL/Carbapenemase/pAmpC types among the 33 MCRPEC isolates.