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Antibiotic Resistance and Adhesive Antigen of *Escherichia coli* Isolated from Pigs in Farm and Slaughterhouse in Hau Giang Province, Vietnam

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Abstract | A total of 42 *Escherichia coli* (*E. coli*)-suspected fecal samples were collected from high density swine farms and slaughterhouse to ascertain positivity, examine antimicrobial susceptibility, prevalence of antibiotic-resistance genes, and adhesive antigens. The results of the antimicrobial susceptibility test using the disc diffusion method indicated that those *E. coli* strains isolated from pigs' feces were significantly resistant to ampicillin (61.30%, 81.81%), followed by streptomycin (54.84%, 63.64%). However, those *E. coli* strains were still sensitive to some of the antibiotics, especially ofloxacin (100%). A total of 71.43% of *E. coli* strains depicted resistance against multiple antibiotics, and the resistant pattern of ampicillin and streptomycin was the most predominant. Detection and confirmation by PCR assay revealed that *blaampC* antibiotic-resistance gene was the most abundant resistant marker in the analyzed *E. coli* strains with 83.87% and 81.81% detection rate in the farm and slaughterhouse, respectively. However, *mcr-1* gene was not detected in *E. coli* strains in the slaughterhouse. A total of 54.76% of *E. coli* strains isolated from fecal samples in the farm and the slaughterhouse harbored multiple antibiotic-resistance genes. Adhesive-antigen genes of *E. coli* strains were detected by PCR, and only F18 (23.81%) and F41 (21.43%) genes were found in those evaluated strains. These results indicated that *E. coli* strains isolated from fecal samples of pigs in the small-scale farm and slaughterhouse harbored diverse antibiotic-resistance and adhesive-antigen genes, causing threats to animal and human health.

Keywords | Adhesive antigen, Antibiotic resistance, *E. coli*, Pigs, Slaughterhouse, Small-scale farm

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INTRODUCTION

Escherichia coli (*E. coli*) is one of the severe foodborne pathogens that cause diseases in animals and humans (Smith and Fratamico, 2018; Lateif et al., 2024). It can survive in the intestines of animals and can transmit to other animals and humans via direct or indirect contact

with their feces (Ercumen et al., 2017). In the Mekong Delta Vietnam, especially in Hau Giang province, there is a high density of swine farming (Thanh Duong and Can, 2005). However, it is primarily small-scale farms with unguaranteed hygiene. Therefore, it possesses an infectious risk of *E. coli* transmission on farms and humans (Ferens and Hovde, 2011; Abdalla et al., 2022; Utama et

al., 2023). Moreover, unsanitary slaughtering processes at slaughterhouses have been identified as the source of bacterial contamination that causes food poisoning for consumers, especially *E. coli*. Research in the UK has confirmed that slaughtering is essential in determining the quality of meat and the product before processing or distributing it to sales units and consumers (Wei, 2013).

On the other hand, pathogenic *E. coli* strains are likely to possess one or more types of adhesion antigens. Adhesion antigens are essential factors of *E. coli* strains that cause gastrointestinal diseases. Based on the adhesion factors on the bacterial surface, such as F4, F5, F6, F17, F18, and F41, *E. coli* can attach and infect the host's small intestine to elicit diseases (Pabón-Rodríguez et al., 2023). When examining pigs with post-weaning diarrhea in Europe, Luppi et al. (2016) reported that the prevalence of fimbriae among *E. coli* isolates was F4 (45.1 %), F18 (33.9 %), F5 (0.6 %), F6 (0.6 %), F41 (0.3 %). *E. coli* strains carrying genes encoding these adhesion factors can be transmitted and cause human disease through contaminated food sources (Frömmel et al., 2013). In addition, antibiotic-resistant *E. coli* strains in farms and slaughterhouses are also a matter of concern. According to research on antibiotic resistance of *Enterobacteriaceae* in wastewater at livestock and poultry slaughterhouses in Germany, the rate of multidrug-resistant *E. coli* accounted for 57.00% in pig slaughterhouses (Homeier-Bachmann et al., 2021). The study by Santos et al. (2022) at a pig slaughterhouse in Brazil also showed that isolated *E. coli* strains were resistant to 12 out of 13 tested antibiotics, including ampicillin and chloramphenicol (95.20%), amoxicillin (85.80%), streptomycin and tetracycline (80.95%). Drug-resistant *E. coli* in slaughterhouses will become a source of drug resistance, spreading to the environment and consumers along the meat distribution chain, causing a significant impact on the treatment of veterinary and human diseases (Wolny-Koładka and Lenart-Boron, 2016). Additionally, Ketkhaio et al. (2021) have found that *E. coli* isolated from pig feces samples from piglets, fattening pigs, and finishing pigs in Thailand had the highest resistance rate to trimethoprim/sulfamethoxazole (53.90%) and colistin (48.50%). The study also showed high resistance rates to colistin in two intensive pig farms supplemented with colistin in feed at 84.60% and 58.10%, respectively. Therefore, the prevalence of *E. coli* strains harbors adhesive antigens, and antibiotic-resistance ability is required to prevent disease outbreaks in pigs and humans.

Therefore, this study aims to determine the prevalence of adhesive antigens and antibiotic resistance genes in those *E. coli* strains isolated from pigs' feces in the representative small-scale farm and slaughterhouse in Hau Giang province of the Mekong Delta, Vietnam. It provides epidemiological information on controlling and preventing diseases caused

by *E. coli* in pigs and humans.

MATERIALS AND METHODS

THE *E. COLI* STRAINS USED IN THIS STUDY

This study used 42 *E. coli* strains isolated from healthy pigs' feces, including three small-scale farms (n=31) and a slaughterhouse (n=11) in Hau Giang province of the Mekong Delta, Vietnam, in December 2023. The farms and a slaughterhouse were in Long My town of Hau Giang province, where the finishing pigs from those farms and others were slaughtered at the examined slaughterhouse. Those samples were collected from different pigs simultaneously in the farms and the slaughterhouse.

Those *E. coli* strains were isolated from healthy pigs' feces and identified by biochemical tests following the guidelines of Barrow and Feltham (2003). These strains were kept at -80 °C in the Veterinary Food Hygiene Laboratory, Faculty of Veterinary Medicine, College of Agriculture, Can Tho University, Vietnam.

THE ANTIMICROBIAL SUSCEPTIBILITY OF *E. COLI* STRAINS ISOLATED FROM PIGS' FECES

Forty-two *E. coli* strains were examined for the antimicrobial susceptibility of seven antibiotics using the Kirby-Bauer diffusion method (Bauer et al., 1966) and compared to CLSI Standards (2022). *Escherichia coli* ATCC 25922 served as the quality control. Those strains which showed intermediate susceptibility were classified as susceptible strains.

This study used antibiotic discs, including ampicillin (Am, 10 µg), amoxicillin/clavulanic acid (Ac, 20/10 µg), colistin (Co, 10 µg), streptomycin (Sm, 10 µg), tetracycline (Te, 30 µg), ofloxacin (Of, 5 µg), and trimethoprim/sulfamethoxazole (Bt, 1.25/23.75 µg) supplied by Nam Khoa Biotek Ltd. (Vietnam). Those antibiotics were selected depending on the current use of antibiotics in those farms and previous reports in the Mekong Delta, Vietnam.

PREVALENCE OF ANTIBIOTIC-RESISTANCE GENES IN *E. COLI* ISOLATED FROM PIGS' FECES

Forty-two *E. coli* strains were examined for antimicrobial susceptibility and used to detect antibiotic-resistance gene prevalence. The DNA of those *E. coli* strains was extracted using the heat-shock method (Ahmed and Dabool, 2017) and stored at -20°C for use in this experiment.

The PCR reaction used Mastermix 2X (Bioline, Canada) in a total of 25 µL: Mastermix 2X (12.5 µL), forward primer (0.5 µL), reverse primer (0.5 µL), distilled water (9.5 µL), and DNA template (2.0 µL).

The antibiotic-resistance genes were detected due to the antibiotic classes used in the antimicrobial susceptibility test, including β -lactam (*blaampC*), tetracycline (*tetA*), aminoglycoside (*aadA1*), polymyxin (*mcr-1*), sulfonamide (*sulIII*), and quinolone (*qnrA*). The primer sequences and PCR conditions were conducted following the guidelines for *blaampC* (Caroff et al., 1999), *tetA* (Randall et al., 2004), *aadA1* (Randall et al., 2004), *mcr-1* (Wu et al., 2021), *sulIII* (Saenz et al., 2010), and *qnrA* (Cattoir and Nordmann, 2009). In this study, the negative control was distilled water, while the positive controls were *E. coli* strains, which harbored these genes, isolated from domestic animals previously in the Mekong Delta.

PREVALENCE OF ADHESIVE ANTIGENS IN *E. COLI* ISOLATED FROM PIGS' FECES

Forty-two *E. coli* strains were continuously examined to detect five genes encoding for adhesive antigens, including F4, F5, F6, F18, and F41. The PCR assays were conducted following similar steps to detect antibiotic-resistance genes. The primer sequences and PCR conditions were performed following the guidelines for F4, F6, and F18 (Boerlin et al., 2005), F5 (Ojeniyi et al., 1994), and F41 (Franck et al., 1998). In this study, the negative control was distilled water, while the positive controls were *E. coli* strains, which harbored these genes, isolated from pigs previously in the Mekong Delta.

STATISTICAL ANALYSIS

Statistical analysis was used to clarify the difference in the rate of antibiotic resistance of *E. coli* strains isolated from pigs' feces and antibiotic resistance and adhesive antigens among those strains. The Chi-square method was used at the significance rate of 95% in the Minitab 17.0 software.

RESULTS AND DISCUSSION

The antimicrobial susceptibility results of *E. coli* strains isolated from pigs' feces indicated that those *E. coli* strains were mainly resistant to ampicillin and streptomycin at 66.67% and 57.14%, respectively (Table 1). Those *E. coli* strains in the farms were resistant to ampicillin and streptomycin at 61.30% and 54.84%, while the *E. coli* strains in the slaughterhouse were resistant to these antibiotics at 81.81% and 63.64%.

There was no significant difference in the rate of antibiotic resistance of those *E. coli* strains between the farms and the slaughterhouse ($P>0.05$); however, the rate of *E. coli* resistance to colistin in the slaughterhouse was higher than that in the farms ($P<0.05$). No *E. coli* strains showed resistance to ofloxacin in this study.

A total of 71.43% of *E. coli* strains showed multiple resistance

to two to six examined antibiotics. Among resistance patterns, the Am+Sm (ampicillin + streptomycin) pattern was the most popular in *E. coli* strains isolated from farms and a slaughterhouse, at 29.03% and 18.18%, respectively (Table 2, Figure 1).

Table 1: The antibiotic resistance of *E. coli* isolated from pigs' feces on the farms and the slaughterhouse

Antibiotics	Small-scale farms (n=31)		Slaughterhouse (n=11)		Total (n=42)	
	No. of strains	Per-cent-age (%)	No. of strains	Per-cent-age (%)	No. of strains	Per-cent-age (%)
Ampicillin	19	61.30	9	81.81	28	66.67
Amoxicillin/Clav. acid	6	19.35	4	36.36	10	23.81
Streptomycin	17	54.84	7	63.64	24	57.14
Tetracycline	7	22.58	3	27.27	10	23.81
Colistin	5	16.13	5	45.45	10	23.81
Ofloxacin	0	0.00	0	0.00	0	0.00
Bactrim	8	25.80	5	45.45	13	30.95

No: number; clav. Acid: clavulanic acid; Bactrim: sulfamethoxazole/ trimethoprim

Table 2: Multiple antibiotic-resistant patterns of *E. coli* isolated from pigs' feces.

No. of resistant antibiotics	Patterns	No. of strains	Per-centage
Small-scale farm (n=31)			
2	Am+Sm	9	29.03
	Am+Ac	2	6.45
	Sm+Bt	2	6.45
3	Am+Te+Sm	3	9.67
	Ac+Sm+Co	3	9.67
4	Am+Ac+Sm+Bt	2	6.45
	Subtotal	21	67.74
Slaughterhouse (n=11)			
2	Am+Sm	2	18.18
	Am+Co+Te	1	9.09
3	Am+Sm+Ac	1	9.09
	Am+Bt+Co	1	9.09
4	Am+Sm+Te+Ac	1	9.09
	Am+Co+Sm+Ac	1	9.09
5	Am+Co+Sm+Te+Ac	1	9.09
6	Am+Bt+Co+Sm+Te+Ac	1	9.09
	Subtotal	9	81.81
Total		30	71.43

No: number; ampicillin (Am), amoxicillin/clavulanic acid (Ac), colistin (Co), streptomycin (Sm), tetracycline (Te), ofloxacin (Of), trimethoprim/ sulfamethoxazole (Bt)

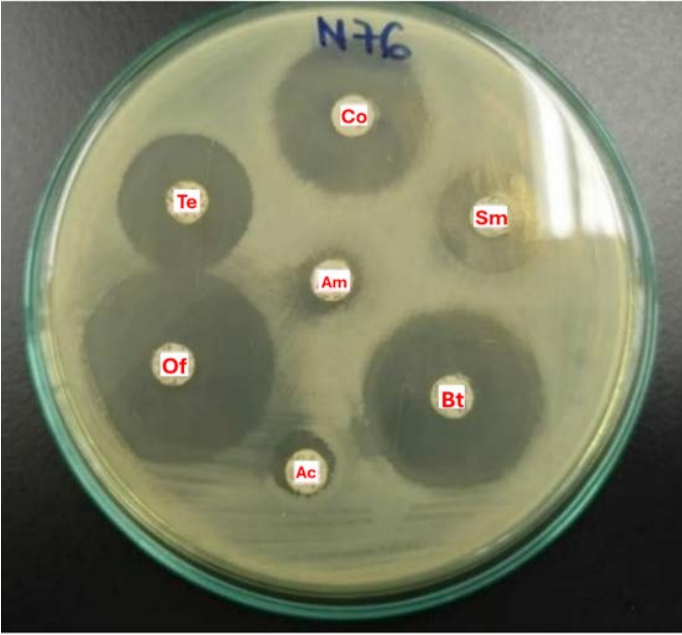


Figure 1: The antimicrobial susceptibility of *E. coli* isolated from pigs’ feces. Resistance to ampicillin (Am), amoxicillin/clavulanic acid (Ac) Susceptibility to colistin (Co), streptomycin (Sm), bactrim (Bt), ofloxacin (Of), and tetracycline (Te).

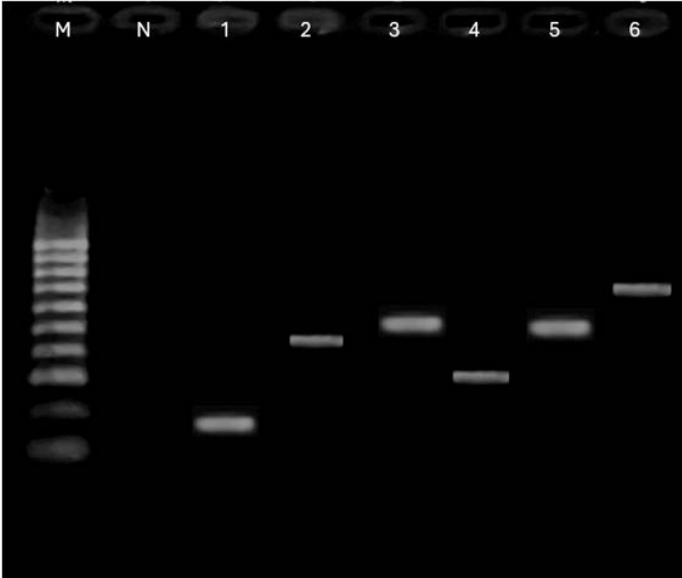


Figure 2: The PCR results for detecting antibiotic-resistance genes in *E. coli* isolated from pigs’ feces M: Ladder (100 bp), N: negative control, 1: *blaampC* (191 bp), 2: *aadA1* (447 bp), 3: *tetA* (577 bp), 4: *mcr-1* (309 bp), 5: *qnrA* (546 bp), 6: *sulIII* (722 bp).

The PCR results revealed that *E. coli* strains isolated from pigs’ feces on farms and in a slaughterhouse could harbor most of the examined antibiotic-resistance genes. Among genes, *blaampC* was the most frequently detected in *E. coli* strains on farms and a slaughterhouse at 83.87% and 81.81%, followed by *tetA* at 80.65% and 45.45%, respectively. However, gene *mcr-1* was not detected in *E. coli* strains in the slaughterhouse (Table 3, Figure 2). In this

study, most antibiotic-resistance genes (*tetA*, *aadA1*, *mcr-1*, *sulIII*) were found in *E. coli* strains isolated from the farms higher than that in the slaughterhouse ($P<0.05$), except *blaampC* and *qnrA* ($P>0.05$).

Table 3: The prevalence of antibiotic-resistance genes Cdetected in *E. coli* isolated from pigs’ feces.

Genes	Small-scale farms (n=31)		Slaughterhouse (n=11)		Total (n=42)	
	No. of positive strains	Per-centage (%)	No. of positive strains	Per-centage (%)	No. of positive strains	Per-centage (%)
<i>blaampC</i>	26	83.87	9	81.81	35	83.33
<i>aadA1</i>	17	54.84	2	18.18	19	45.24
<i>tetA</i>	25	80.65	5	45.45	30	71.43
<i>mcr-1</i>	5	16.13	0	0.00	5	11.90
<i>qnrA</i>	5	16.13	1	9.09	6	14.29
<i>sulIII</i>	18	58.06	2	18.18	20	47.62

No: number.

Table 4: Patterns of multiple antibiotic-resistance genes in *E. coli* isolated from pigs’ feces.

No. of antibi- otic resist- ance genes	Pattern	No. of strains	Per- centage
Small-scale farm (n=31)			
2	<i>blaampC+tetA</i>	4	12.09
	<i>blaampC+aadA1</i>	1	3.23
	<i>blaampC+sulIII</i>	1	3.23
	<i>tetA+sulIII + qnrA</i>	2	6.45
3	<i>blaampC+aadA1+tetA</i>	1	3.23
	<i>blaampC+tetA+sulIII</i>	1	3.23
	<i>blaampC+aadA1+sulIII</i>	1	3.23
	<i>tetA+aadA1+sulIII</i>	2	6.45
4	<i>blaampC+tetA+aadA1+sulIII</i>	1	3.23
	<i>blaampC+tetA+mcr-1+sulIII</i>	2	6.45
5	<i>blaampC+tetA+aadA1+mcr-1+sulIII + qnrA</i>	1	3.23
	Subtotal	17	54.84
Slaughterhouse (n=11)			
2	<i>blaampC + tetA</i>	1	9.09
	<i>blaampC + aadA1</i>	1	9.09
	<i>blaampC + sulIII</i>	1	9.09
	<i>tetA+sulIII + qnrA</i>	1	9.09
3	<i>blaampC+tetA+aadA1</i>	1	9.09
	<i>blaampC+tetA+sulIII</i>	1	9.09
	Subtotal	6	54.55
Total		23	54.76

No: number

54.76% of *E. coli* strains could harbor multiple antibiotic-resistance genes from two to five genes with diverse gene patterns, and *blaampC* was present in most of the patterns. One *E. coli* strain was isolated from pigs' feces in the farms harboring 5/6 examined genes (Table 4).

Among the adhesive antigens examined, F18 and F41 were found in those *E. coli* strains at 23.81% and 21.43%, respectively. The adhesive antigens of F4, F5, and F6 were not detected in those *E. coli* strains. F41 (29.03%) was found frequently in *E. coli* strains on farms, followed by F18 (3.23%). F18 (81.82%) was only found in isolated *E. coli* strains in the slaughterhouse (Table 5).

Table 5: Prevalence of adhesive-antigen genes in *E. coli* isolated from pigs' feces.

Ad-hesive antigens	Small-scale farm (n=31)		Slaughterhouse (n=11)		Total (n=42)	
	No. of positive strains	Per-centage	No. of positive strains	Per-centage	No. of positive strains	Per-centage
F4	0	0.00	0	0.00	0	0.00
F5	0	0.00	0	0.00	0	0.00
F6	0	0.00	0	0.00	0	0.00
F18	1	3.23	9	81.82	10	23.81
F41	9	29.03	0	0.00	9	21.43

No: number.

Escherichia coli is one of the severe pathogens causing diseases in animals and humans. Antibiotics, used to treat or prevent diseases, intend to increase antibiotic resistance in bacteria, including *E. coli* (MacGowan and Macnaughton, 2017). In this study, although those *E. coli* strains were still susceptible to most examined antibiotics, those strains exhibited high rates of resistance to ampicillin and streptomycin. These antibiotics have been frequently used to treat pigs' diseases on the farms for a long time in our survey. This might be a reason for the formation of the resistance of *E. coli* to these antibiotics. Strom et al. (2017) noted that multidrug resistance in *E. coli* strains isolated from pigs was more common on medium-sized farms than on small-sized farms. In addition, *E. coli* can be resistant to multiple antibiotics, mainly due to the overuse of antibiotics in animal husbandry. Fairbrother and Nadeau (2006) stated that the emergence of antibiotic-resistant strains is a problem caused by many factors, possibly due to the inappropriate use of antibiotics in treatment or as supplements in animal feed. Research by Liu et al. (2022) demonstrated that the antibiotic resistance of pig-derived *E. coli* was varied and multi-drug resistant, with the highest resistance to six antibiotics being 26.35%. The isolated strains were resistant to tetracyclines, penicillin, and chloramphenicol, which were commonly used for disease prevention in pig farms, and less resistant to quinolones

and aminoglycosides, which are not used in pig farms in Beijing, China.

On the other hand, the high resistance of *E. coli* strains to antibiotics in the slaughterhouse could be due to several reasons. The unhygienic slaughter environment could be a source of storing and spreading resistant *E. coli* strains from pigs' feces and digestive tract substances or be contaminated by pigs imported from different sources. Wang et al. (2021) indicated that the hygiene of slaughterhouses was an essential issue causing *E. coli* contamination in the pig slaughtering process in China. In Hau Giang province, the examined slaughterhouse was a medium-sized semi-industrial type, and most of the process steps were done by humans. Thus, *E. coli* contamination from pigs' feces could occur during slaughtering. The reports of *E. coli* isolated from pig slaughterhouses were resistant to many antibiotics, such as 100.00% to streptomycin in Indonesia (Sudarwanto et al., 2017) or oxytetracycline (64.00%), followed by streptomycin, sulphonamide, ampicillin, chloramphenicol, trimethoprim sulfamethoxazole, ceftiofur, amoxicillin clavulanic acid, aztreonam, and nitrofurantoin in the United Kingdom (Yang et al., 2020).

This study also showed that *E. coli* strains isolated from pigs' feces in Hau Giang province showed multidrug resistance. This phenomenon could be due to the use of antibiotics on farms or contamination from the diverse origin of pigs' feces in the slaughterhouse. In this study, those *E. coli* strains frequently resisted ampicillin and streptomycin. This could be proof of the resistance of *E. coli* strains linked to the long-term use of those antibiotics for domestic animals in the examined region. There is a direct relationship between antimicrobial resistance and antimicrobial use (Varga et al., 2009). In China, the reports of antibiotic-resistance *E. coli* showed that 80.67% of *E. coli* strains isolated from the pig slaughterhouses were multi-drug resistant (MDR) strains multidrug resistance (Fang et al., 2018), and 91% of isolates resistant to crucial drugs, including colistin, carbapenems, and tigecycline in pig farms (Peng et al., 2022). In Thailand, the antibiograms of amoxicillin-trimethoprim/sulfamethoxazole, amoxicillin-doxycillin-trimethoprim/sulfamethoxazole, amoxicillin-gentamycin-trimethoprim/sulfamethoxazole, and amoxicillin-doxycillin-gentamycin-trimethoprim/ sulfamethoxazole were found frequently in multidrug-resistance *E. coli* isolated in pig farms (Mitchaothai and Srikijkasemwat, 2021).

The present study showed that *E. coli* strains isolated from pigs' feces could harbor diverse antibiotic-resistance genes. Compared to the antimicrobial susceptibility test results, the prevalence of examined antibiotic-resistance genes was consistent. Gene *blaampC* and *aadA1* encoding for resistance of β -lactam and aminoglycoside antibiotics, respectively, were highly detected in those *E. coli* strains in

this study. Moreover, those *E. coli* strains isolated from pigs' feces on the farms and the slaughterhouse also harbored multiple antibiotic-resistance genes; gene *blaampC* was found in most of the patterns. The patterns' results also reflected the consistency of the antimicrobial susceptibility test and the prevalence of antibiotic-resistance genes in case of resistance to ampicillin with streptomycin popularly. It indicated that these genes were related to the antimicrobial susceptibility of *E. coli* strains to ampicillin and streptomycin. Conversely, although tetracycline and bactrim had low resistance in the antimicrobial susceptibility test, genes *tetA* and *sulIII* were detected to be relatively high in those *E. coli* strains isolated from pigs' feces on the farms and the slaughterhouse in Hau Giang province. It revealed that other factors could also affect the antibiotic-resistance expression of *E. coli* strains. Several antibiotic-resistant genes are considered silent resistance genes, which are not expressed frequently or at low levels, even when exposed to antibiotics (Stasiak et al., 2021). Poirel et al. (2018) have found that the number of antibiotic resistance genes is increasing due to the horizontal and vertical transfer of antibiotic resistance genes among Enterobacteria, in which *E. coli* takes a role as a donor and recipient of antibiotic resistance genes; thus, it can acquire antibiotic resistance genes from other bacteria but can also transfer its antibiotic resistance genes to other bacteria. According to Mazurek et al. (2018), a study on the complexity of antibiotic resistance of *E. coli* in the city of Zielona Góra, Poland, also showed that *E. coli* isolated from pig feces had the presence of *tetA* (54.00%) and *sulIII* (45.00%). In pig farms in Brazil, most *E. coli* strains are resistant to antimicrobials and carry genes of resistance to quinolones, fluoroquinolones, and ESBLs, and because of that, these findings are essential for public health (Brisola et al., 2019). In Thailand, multidrug-resistant (MDR) *E. coli* was found in a high proportion of fecal samples isolated from diarrheic piglets from pig farms in Thailand, and several isolates harbored colistin-resistance genes *mcr-1* and *mcr-3*. Moreover, it provides informative scientific evidence regarding bacterial antibiotic resistance in pig farms and raises public health awareness regarding transmitting antibiotic-resistance genes from animals to humans (Nguyet et al., 2022). Thus, the management of using antibiotics on farms is essential to prevent the presence and spreading of antibiotic-resistant *E. coli* strains in the husbandry environment and slaughterhouses.

In this study, *E. coli* strains were isolated from healthy pigs; thus, the prevalence of adhesive antigens required to penetrate and cause diseases was low. However, the presence of F18 and F41 in *E. coli* strains isolated from pigs' feces on the farms was more frequent than in the slaughterhouse. Those *E. coli* strains could be infected among pigs on farms, while those *E. coli* strains in the slaughterhouse could be contaminated from the

slaughtering process. Although that, the prevalence of F18 and F41 indicated that pathogenic *E. coli* strains have survived in pigs on the farms and the slaughterhouse. If those pathogenic *E. coli* strains were transmitted to pigs on the farms or contaminated on porks to consumers, they could cause severe diseases. Dubreuil et al. (2016) indicated that the presence of adhesive antigens, including F4, F5, F6, F18, and F41, could increase the severity of diseases in animals. The F18 Enterotoxigenic *Escherichia coli* (ETEC) could severely impact piglets' growth performance, intestinal function, and immune responses (Becker et al., 2020), while *E. coli* F41 strains were mainly found in human gastroenteritis cases in Qatar (Peters et al., 2019). Therefore, the prevalence of pathogenic *E. coli* on farms and slaughterhouses is requested to prevent diseases in animals and humans.

CONCLUSIONS AND RECOMMENDATIONS

The *E. coli* strains isolated from pigs' feces on the farms and the slaughterhouse in Hau Giang province, Vietnam, showed a relatively high rate of antibiotic resistance, especially resistance to β -lactam and aminoglycoside antibiotics used frequently in swine production there. Moreover, those *E. coli* strains also harbored many antibiotic-resistance genes with several patterns and pathogenic adhesive antigens. It indicated a potential risk for causing diseases in pigs and humans and difficulty in the treatments. Further research should be conducted to clarify the overview of antibiotic resistance and pathogenicity of *E. coli* isolated from pigs on farms and slaughterhouses; then, a comprehensive approach can be applied to protect animals' and humans' health in this region.

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NOVELTY STATEMENT

Escherichia coli is one of the most pathogenic bacteria that causes diseases and failure treatments in animals and humans, especially antibiotic-resistant strains. Moreover, *E. coli* can be transmitted via food products like pork or indirect or direct contact with pigs' feces. The unhygienic conditions of farms and slaughterhouses are potentially causing infection between animals and humans. Research on antibiotic resistance and adhesive genes in *E. coli* isolated from pigs in farms and slaughterhouses is essential to evaluate the risk and protect animal and human health,

particularly foodborne diseases.

AUTHOR'S CONTRIBUTION

Nguyen Khanh Thuan, Bui Thi Le Minh, and Ngo Van Thong conceptualized, designed, and supervised the research. Nguyen Khanh Thuan critically reviewed the study. Nguyen Ho Thanh Tuyen, Nguyen Lam Truong, and Pham Minh Thien collected samples and processed the data. Nguyen Khanh Thuan, Bui Thi Le Minh, and Ngo Van Thong analyzed and interpreted the data generated. All authors revised and approved the final manuscript.

CONFLICT OF INTEREST

The authors have declared no conflict of interest.

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