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Detection of Antibiotic Resistance Genes in *Salmonella* Strains Isolated from Fecal Samples of Dogs and Cats in Hanoi, Vietnam

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ABSTRACT

Salmonella belongs to the family *Enterobacteriaceae* and is a common pathogen that causes disease in humans and animals. Dogs and cats are potential sources of zoonotic diseases, including those caused by *Salmonella* spp. The current study aimed to investigate the prevalence and antibiotic resistance of *Salmonella* strains in fecal samples from dogs and cats collected at veterinary clinics in Hanoi, Vietnam. From November 2024 to December 2025, 161 fecal samples from dogs and cats were collected from 12 veterinary clinics in Hanoi, Vietnam, for *Salmonella* isolation. Fecal samples were cultured in peptone buffer water (PBW) and on selective media such as Rappaport-Vassiliadis soybean (RVS) broth and xylose lysine deoxycholate (XLD) agar; suspected *Salmonella* colonies were confirmed by biochemical tests, including sugar fermentation, H_2S, and IMViC reactions. Antibiotic susceptibility was tested by agar diffusion, and genes implicated in antimicrobial resistance were detected by PCR amplification. The results showed that 11 (6.8%) of 161 fecal samples were *Salmonella*-positive; *Salmonella* was detected in 9 of 92 (9.8%) dog fecal samples and 2 of 69 (2.9%) cat fecal samples. The isolates exhibited the highest resistance to tetracycline (90.0%), followed by streptomycin (81.2%). Resistance to chloramphenicol and trimethoprim/sulfamethoxazole was 45.5%; for nalidixic acid, amoxicillin/clavulanic acid, doxycycline, gentamicin, and cefotaxime, resistance rates ranged from 27.3% to 36.4%. The isolates showed similar resistance rates to neomycin, kanamycin, and ciprofloxacin at 18.2%. Twelve antibiotic resistance genes, including bla_{TEM}, *aadA1*, *aadA2*, *aphA1-1AB*, *aac (3')-IV*, *sul1*, *cmlA1*, *floR*, *tetA*, *tetB*, *qnrA*, and *qnrS*, were amplified in the antibiotic-resistant *Salmonella* strains, whereas bla_{PSE-1}, bla_{OXA-1}, *tetG*, *qnrB*, and *aac (6')-ib-cr* were not detected. The results of the current study underscore the importance of monitoring antibiotic resistance in *Salmonella* spp. in companion animals to protect public health.

Keywords: Antibiotic resistance gene, Cat, Dog, *Salmonella*

INTRODUCTION

Salmonella belongs to the family *Enterobacteriaceae*, and to date, more than 2500 *Salmonella* serovars have been identified across different hosts. These serovars are common pathogens that cause disease in humans and animals (Majowicz et al., 2010; Knodler et al., 2019). Dogs and cats are potential sources of zoonotic diseases, including those caused by *Salmonella* spp. (Leonard et al., 2012). However, transmission of *Salmonella* from dogs and cats to humans, in particular, has not received adequate attention (Bataller et al., 2020). Furthermore, studies on antibiotic and multidrug resistance, as well as the mechanisms underlying resistance in bacteria of dog and cat origin, are very limited (Leonard et al., 2012; Srisanga et al., 2017). In addition, the emergence and increase of multidrug-resistant *Salmonella* are significantly impacting treatment efficacy and leading to high mortality rates (WHO, 2016; Divek et al., 2018). Antibiotic resistance is projected to cause approximately 10 million deaths per year by 2050 and cost over $100 trillion worldwide (WHO, 2016).

In Vietnam, approximately 6.48 million dogs and 5.58 million cats are kept for various purposes, many of which are considered pets (Kirin Capital, 2023). Pet dogs and cats often live in the same area as their owners, and close interaction between pets and owners creates a potential pathway for disease transmission to humans (Pedersen et al., 2007; Leonard et al., 2012). However, studies on diseases in dogs and cats in Vietnam often focus on viral diseases such as rabies virus (RABV; Nguyen et al., 2011; Harada et al., 2026), canine distemper virus (CDV; Truong et al., 2022; Van et al., 2025), canine parvovirus type 2 (CPV-2; Hoang et al., 2019; Bui et al., 2023), and feline leukemia virus (FPV; Minh et al.,

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2023), and have not yet focused on bacterial infections such as *Escherichia coli* and *Salmonella* spp., as well as antibiotic resistance and the mechanisms of antibiotic resistance in these bacteria.

Numerous studies conducted in many countries have shown that *Salmonella* strains isolated from dogs and cats are resistant to many antibiotics and carry multiple antibiotic resistance genes (Kiflu et al., 2017; Srisanga et al., 2017; Yildiz and Demirbilek, 2024; Zhao et al., 2024). Currently, information on antibiotic resistance in bacteria, including *Salmonella*, isolated from dogs and cats in Vietnam is limited, highlighting the need for studies of pet-derived bacteria to support strategies to control zoonotic transmission. The present study aimed to determine the prevalence and antibiotic susceptibility of *Salmonella* strains isolated from dogs and cats in Northern Vietnam and to identify antibiotic resistance genes in antibiotic-resistant isolates.

MATERIALS AND METHODS

Ethical approval

The present study was conducted by collecting fecal samples from dogs and cats at veterinary clinics, in accordance with the animal welfare and safety procedures of the Committee on Animal Research and Ethics (CARE) at the Faculty of Veterinary Medicine, Vietnam National University of Agriculture, Vietnam (Approval No. CARE-2024/06). Before the study, ethical considerations were addressed, and pet owners' consent was obtained.

Sampling

From November 2024 to December 2025, 161 fecal samples from dogs (n = 92) and cats (n = 69) were randomly collected from twelve veterinary clinics in Hanoi, Vietnam. Healthy dogs and cats were those brought to the clinics for vaccinations, grooming, and deworming. Unhealthy dogs and cats were included in the study based on typical gastrointestinal symptoms such as diarrhea and were being treated at the clinics. The samples were collected according to the guidelines of QCVN 01-83:2011/BNNPTNT of the Ministry of Agriculture and Rural Development (MARD, 2011). Briefly, fresh fecal samples were carefully collected from each animal using rectal swabs with sterile cotton swabs. Each sample was placed in a separate sample bag and labeled with information such as age, gender, history of diarrhea, and history of antibiotic treatment. The samples were then placed in an ice box and transported to the Department of Veterinary Microbiology and Infectious Diseases, Faculty of Veterinary Medicine, Vietnam National University of Agriculture, for analysis within 24 hours.

Isolation of *Salmonella* spp.

Salmonella isolation from fecal samples followed the method described in the previous study (Bataller et al., 2020), with some modifications. In the laboratory, each fecal sample was homogenized with buffer peptone water (BPW; Merck, Germany) at a 1:9 ratio and incubated at 37°C for 18-24 hours for pre-enrichment. Next, 0.1 mL of the pre-enriched culture in BPW was added to 10 mL of Rappaport-Vassiliadis soya broth (RVS; Merck, Germany) and incubated at 42.5°C for 24-48 hours. Then, a loopful of RVS broth was streaked onto xylose lysine deoxycholate agar (XLD; Merck, Germany) and incubated at 37°C for 24 hours. Black colonies suspected of being *Salmonella* were selected from each plate and cultured on nutrient agar slants (NA; Merck, Germany). A single colony was randomly selected and subjected to biochemical tests, including sugar fermentation, H2S test, IMViC reactions in triple sugar iron (TSI) agar, Tryptone broth (TB), Methyl-red Voges-Proskauer (VP-MR) broth, and Simmons citrate agar (SCA, Merck, Germany). All isolates were stored in brain heart infusion broth (BHI; Merck, Germany) supplemented with 50% glycerol at -80°C for subsequent experiments.

Antibiotic susceptibility test

The antibiotic susceptibility test was performed according to the guidelines of the Clinical and Laboratory Standards Institute (CLSI, 2020). The agar diffusion method was performed on Mueller-Hinton agar (MHA, Merck, Germany) following Bauer et al. (1966). A total of 12 antibiotic agents (Oxoid, UK) from seven classes were used, including penicillins (amoxicillin/clavulanic acid [AMC, 20/10µg]), cephalosporins (cefotaxime [CTX, 30µg]), quinolones (ciprofloxacin [CIP, 5µg], nalidixic acid [NAL, 30µg]), tetracyclines (doxycycline [DOX, 30µg], tetracycline [TET, 30µg]), aminoglycosides (gentamicin [GEN, 10µg], kanamycin [KAN, 30µg], neomycin [NEO, 30µg], streptomycin [STM, 10µg]), phenicols (chloramphenicol [CHL, 30µg]), and sulfonamides (trimethoprim/sulfamethoxazole [STX, 1.25/23.75µg]). Briefly, a standardized suspension of the isolates was applied to MHA plates. Antibiotic disks were then placed on the inoculated agar surface and incubated at 37°C for 16 to 18 hours. *Escherichia coli* ATCC 25922 was used for quality control. An isolate was classified as resistant or multidrug-resistant to antibiotics based on the definition of Magiorakos et al. (2012).

Detection of antibiotic-resistant genes

DNA was extracted using the TopPURE® Genomic DNA Extraction Kit (ABT, Vietnam) according to the manufacturer's instructions. The following genes implicated in antimicrobial resistance [bla_{PSE-1}, bla_{OXA-1}, and bla_{TEM} for β-*lactam*-resistant strains; *aadA1*, *aadA2, aac(3')-IV,* and *aphA-1AB* for aminoglycoside-resistant strains; *catA1*, *cmlA1*, and *floR* for chloramphenicol-resistant strains; *sul1* for sulfonamide-resistant strains; *tetA*, *tetB*, and *tetG* for tetracyclines-resistant strains; and the plasmid-mediated quinolone resistance (PMQR) including *qnrA*, *qnrB*, *qnrS*, and *aac(6')-ib-cr* for quinolone-resistant strains] were detected by PCR amplification. The specific primers are presented in Table 1, and PCR reaction conditions were based on previous studies (Ng et al., 1999; Guerra et al., 2004; Robicsek et al., 2006; Platell et al., 2011). The reaction components included 12.5 µl of GoTag® Green Master Mix (Promega, USA), 1 µl each of the forward and reverse primers (10 µM), 8.5 µl of purified water, and 2 µl of template DNA. PCR products were electrophoresed with a 100 bp DNA ladder on a 1.5% agarose gel supplemented with RedSafe™ Nucleic Acid Staining Solution (Intron, Korea). The desired PCR product was visualized and photographed using the Gelpic100 system (Phusa Biochem, Vietnam).

Data analysis

The data were entered and calculated in Microsoft Excel 2016.

Table 1. Primers used in the present study to detect antibiotic-resistant genes

Antibiotic group	Primers		Sequences (5' ⟶ 3')	PCR products (bp)	Reference
β-lactam	bla_{TEM}	F	TTGGGTGCACGAGTGGGT	503	Guerra et al. (2004)
		R	TAATTGTTGCCGGGAAGC		
	bla_{OXA-1}	F	AGCAGCGCCAGTGCATCA	708	Guerra et al. (2004)
		R	ATTCGACCCCAAGTTTCC		
	bla_{PSE-1}	F	CGCTTCCCGTTAACAAGTAC	419	Guerra et al. (2004)
		R	CTGGTTCATTTCAGATAGCG		
Aminoglycosides	*aadA1-like*	F	GTGGATGGCGGCCTGAAGCC	526	Guerra et al. (2004)
		R	ATTGCCCAGTCGGCAGCG		
	aadA2	F	TGTTGGTTACTGTGGCCGTA	381	Ng et al. (1999)
		R	GCTGCGAGTTCCATAGCTTC		
	aac(3')-IV	F	GTTACACCGGACCTTGGA	674	Guerra et al. (2004)
		R	AACGGCATTGAGCGTCAG		
	aphA1-1AB	F	AAACGTCTTGCTTTCGAGGC	461	Guerra et al. (2004)
		R	CAAACCGTTATTCATTCGTGA		
Sulphonamides Chloramphenicol	*sul1*	F	CTTCGATGAGAGCCGGCGGC	436	Guerra et al. (2004)
		R	GCAAGGCGGAAACCCGCGCC		
	cmlA1	F	TGTCATTTACGGCATACTCG	435	Guerra et al. (2004)
		R	ATCAGGCATCCCATTCCCAT		
	floR	F	CACGTTGAGCCTCTATAT	868	Guerra et al. (2004)
		R	ATGCAGAAGTAGAACGCG		
Tetracyclines	*tetA*	F	GCTACATCCTGCTTGCCT	210	Guerra et al. (2004)
		R	CATAGATCGCCGTGAAGA		
	tetB	F	TTGGTTAGGGGCAAGTTTTG	600	Guerra et al. (2004)
		R	GTAATGGGCCAATAACACCG		
	tetG	F	GCTCGGTGGTATCTCTGC	500	Guerra et al. (2004)
		R	AGCAACAGAATCGGGAAC		
Quinolones	*qnrA*	F	ATTTCTCACGCCAGGATTTG	516	Robicsek et al. (2006)
		R	GATCGGCAAAGGTTAGGTCA		
	qnrB	F	GATCGTGAAAGCCAGAAAGG	469	Robicsek et al. (2006)
		R	ACGATGCCTGGTAGTTGTCC		
	qnrS	F	ACGACATTCGTCAACTGCAA	417	Robicsek et al. (2006)
		R	TAAATTGGCACCCTGTAGGC		
	aac(6')-Ib-cr	F	ATGACTGAGCATGACCTTGC	519	Platell et al. (2011)
		R	TTAGGCATCACTGCGTGTTC		

RESULTS

Isolation of *Salmonella* species

After biochemical testing, 11 of 161 samples (6.8%) were *Salmonella*-positive. Of these, the *Salmonella* isolation rates from dog and cat fecal samples were 9.8% and 2.9%, respectively (Table 2). For fecal samples from dogs and cats with diarrhea and from healthy dogs and cats, the rates were 6 (8.2%) of 73 samples and 5 (5.7%) of 88 samples, respectively.

Antibiotic resistance of *Salmonella* species

The antibiotic resistance rates of eleven *Salmonella* strains are shown in Table 3. Tetracycline resistance was the most common (90.0%), followed by streptomycin (81.2%). Resistance to chloramphenicol and trimethoprim/sulfamethoxazole was also recorded at 45.5% for each antibiotic. Resistance to other antibiotics, including nalidixic acid, amoxicillin/clavulanic acid, doxycycline, gentamicin, and cefotaxime, ranged from 27.3% to 36.4%. The isolates were resistant to neomycin, kanamycin, and ciprofloxacin at a similar rate of 18.2%.

Detection of antibiotic resistance genes

The results of detecting antibiotic resistance genes in *Salmonella* strains are presented in Table 4 and Figures 1 and 2. Twelve antibiotic resistance genes [bla_{TEM}, *aadA1, aadA2, aphA1-1AB, aac (3')-IV, sul1, cmlA1, floR, tetA, tetB, qnrA,* and *qnrS*] were amplified from the antibiotic-resistant *Salmonella* strains, whereas bla_{PSE-1}, bla_{OXA-1}, *tetG, qnrB,* and *aac (6')-ib-cr* were not detected. The *sul1* gene was found in all (100%) of the five trimethoprim/sulfamethoxazole-resistant isolates. The *tetA* and *tetB* genes were detected in 7 (70.0%) and 3 (30.0%) of the ten tetracycline-resistant isolates, respectively. Aminoglycoside resistance genes such as *aadA1* and *aadA2* were detected in 8 (88.9%) and 4 (44.4%) of the nine streptomycin-resistant isolates, respectively; three (33.3%) of the streptomycin-resistant isolates carried both genes simultaneously. The *aphA1-1AB* and *aac (3')-IV* genes were amplified in one (50.0%) of the two kanamycin-resistant isolates and in two (50.0%) of the four gentamicin-resistant isolates, respectively. All chloramphenicol-resistant isolates carried at least one resistance gene, with 4 (80.0%) and 3 (60.0%) of the five isolates carrying the *cmlA1* and *floR* genes, respectively; of these, two (40.0%) isolates carried both genes simultaneously. The *qnrS* and *qnrA* genes were detected in two (66.7%) and one (33.3%) of the three quinolone-resistant isolates. The bla_{TEM} gene was found in all (100%) of the five β-*lactam*-resistant isolates, including three strains co-resistant to amoxicillin/clavulanic acid and cefotaxime, and two strains resistant to one of these antibiotics.

Table 2. Prevalence of *Salmonella* spp. in dog and cat fecal samples collected at veterinary clinics in Hanoi, Vietnam, during November 2024-December 2025

Oder	Type of samples	Cat fecal samples		Dog fecal samples	
		Number	Positive number (%)	Number	Positive number (%)
1	Healthy	38	1 (2.6)	50	4 (8.0)
2	Diarrhea	31	1 (3.2)	42	5 (11.9)
3	Total	69	2 (2.9)	92	9 (9.8)

Table 3. Antibiotic resistance of *Salmonella* strains isolated from dog and cat fecal samples collected at veterinary clinics in Hanoi, Vietnam, during November 2024-December 2025

Order	Antibiotics	Sensitive number (%)	Intermediate number (%)	Resistance number (%)
1	Amoxicillin / clavulanic acid	7 (63.6)	0 (0.0)	4 (36.4)
2	Cefotaxime	6 (54.5)	1 (9.1)	4 (36.4)
3	Ciprofloxacin	8 (72.7)	1 (9.1)	2 (18.2)
4	Doxycycline	5 (45.5)	2 (18.2)	4 (36.4)
5	Kanamycin	7 (63.6)	2 (18.2)	2 (18.2)
6	Gentamicin	5 (45.5)	2 (18.2)	4 (36.4)
7	Nalidixic acid	7 (63.6)	1 (9.1)	3 (27.3)
8	Neomycin	8 (72.7)	1 (9.1)	2 (18.2)
9	Chloramphenicol	5 (45.5)	1 (9.1)	5 (45.5)
10	Streptomycin	2 (18.2)	0 (0.0)	9 (81.8)
11	Tetracycline	1 (9.1)	0 (0.0)	10 (90.9)
12	Trimethoprim / Sulfamethoxazole	4 (36.4)	2 (18.2)	5 (45.5)

Table 4. Antibiotic resistance phenotypes and associated resistance genes in *Salmonella* strains isolated from dog and cat fecal samples collected at veterinary clinics in Hanoi, Vietnam, from November 2024 to December 2025

Order	Code	Antibiotic resistant phenotypes	Antibiotic resistant genotypes
1	D14-061024	STM	-
2	D55-101224	STM, TET	*aadA1*, *tetA*
3	D43-120125	STM, DOX, TET	*aadA2*, *tetA*
4	D71-150325	CHL, STM, TET	*cmlA1*, *aadA1*, *tetA*
5	D08-110125	CHL, STM, TET	*cmlA1*, *aadA1*, *tetA*
6	D58-101224	NAL, GEN, STM, TET, STX	*qnrS*, *aadA1*, *tetB*, *sul1*
7	M02-161125	AMC, CTX, GEN, KAN, DOX, TET	bla_{TEM}, *aphA1-1AB*, *tetB*
8	D31-171124	CTX, CHL, GEN, STM, DOX, TET, STX	bla_{TEM}, *cmlA1*, *floR*, *aac(3)-IV*, *aadA1*, *tetA*, *sul1*
9	D23-090325	AMC, CTX, NEO, STM, DOX, TET, STX	bla_{TEM}, *aadA1*, *aadA2*, *tetB*, *sul1*
10	M14-111024	AMC, CIP, NAL, CHL, NEO, STM, TET, STX	bla_{TEM}, *qnrS*, *floR*, *aadA1*, *aadA2*, *tetA*, *sul1*
11	D62-110225	AMC, CTX, CIP, NAL, CHL, KAN, GEN, STM, TET, STX	bla_{TEM}, *qnrA*, *cmlA1*, *floR*, *aadA1*, *aadA2*, *aac(3)-IV*, *tetA*, *sul1*

AMC: Amoxycillin/clavulanic acid, CTX: Cefotaxime, CIP: Ciprofloxacin, DOX: Doxycycline, KAN: Kanamycin, GEN: Gentamicin, NAL: Nalidixic acid, NEO: Neomycin, CHL: Chloramphenicol, STM: Streptomycin, TET: Tetracycline, STX: Trimethoprim/Sulfamethoxazole; '-': Not detected

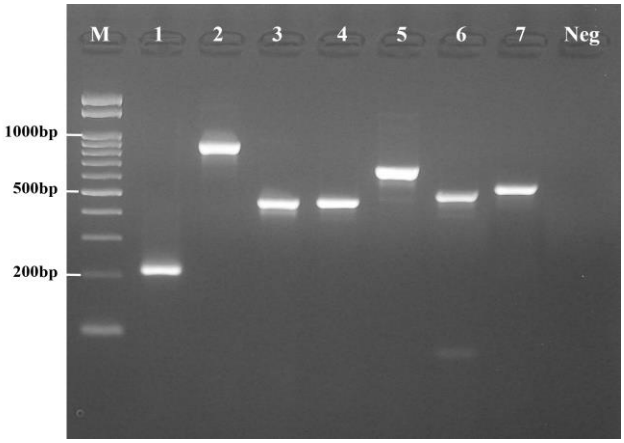

Figure 1. Antibiotic-resistant genes in the *Salmonella* strain D31-171124. M: Marker (100 bp), Lanes 1-7: *tetA* (210 bp), *floR* (868 bp), *cmlA1* (435 bp), *sul1* (436 bp), *aac(3)-IV* (674 bp), bla_{TEM} (503 bp), *aadA1* (526 bp), Neg: Negative control

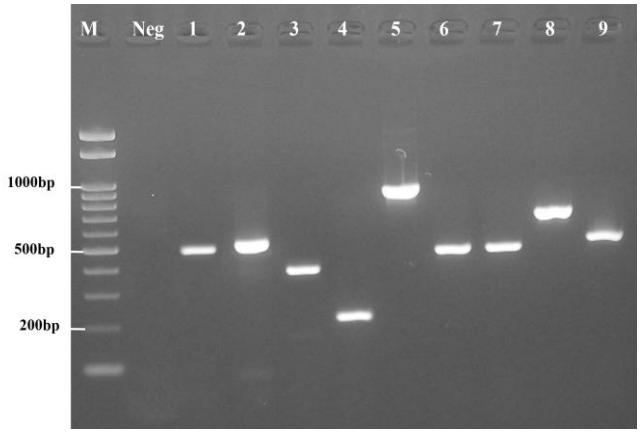

Figure 2. Antibiotic-resistant genes in the *Salmonella* strain D62-110225. M: Marker (100 bp), Neg: Negative control, Lanes 1-9: bla_{TEM} (503 bp), *aadA1* (526 bp), *aadA2* (381 bp), *tetA* (210 bp), *floR* (868 bp), *cmlA1* (435 bp), *sul1* (436 bp), *aac(3)-IV* (674 bp), *qnrA* (516 bp)

DISCUSSION

The higher *Salmonella* isolation rate from dog fecal samples than from cat fecal samples aligns with previous studies in the United States (Reimschuessel et al., 2017) and China (Wei et al., 2020), which reported isolation rates of 2.5-9.47% and 0.6–1.77%, respectively. The isolation rate from dog fecal samples in the current study was similar to rates of 9.47% in China (Wei et al., 2020), 10.5% in Iran (Salehi et al., 2012), and 11.7% in Ethiopia (Kiflu et al., 2017). However, these rates were lower than the 23.0% *Salmonella*-positive rate in dog fecal samples reported in a previous study conducted in Canada (Leonard et al., 2011). Notably, the prevalence of *Salmonella* in dog feces was only 0.23% in the UK (Lowden et al., 2015), 1.0% in Turkey (Bagcigil et al., 2007), and 2.5% in the United States (Reimschuessel et al., 2017). The isolation rates in cat fecal samples in the current study are consistent with positive rates of 0.5%, 0.6%, and 1.77–3.7% in studies conducted in South Africa (Gelaw et al., 2018), the United States (Reimschuessel et al., 2017), and China (Wei et al., 2020; Zhao et al., 2024), respectively. Overall, the isolation rates of *Salmonella* in both dogs and cats vary across countries and regions, which can be explained by differences in sample size, sampling methods and strategies, feeding habits, pet hygiene conditions, sampling season, and geographical and climatic differences between study areas (Sanchez et al., 2002; Seepersadsingh et al., 2010; Wei et al., 2020).

The tetracycline resistance rate among *Salmonella* strains from dogs and cats was similar to the 92.0% reported in a previous study conducted in China (Wei et al., 2020). However, lower resistance rates, such as 11.1%, 32.0%, 59.5%,

and 60.0%, have been reported in previous studies from Turkey, Thailand, Ethiopia, and Iraq (Kiflu et al., 2017; Srisanga et al., 2017; Yildiz and Demirbilek, 2024; Najim et al., 2025). The doxycycline resistance rate was similar to the 30.9% recorded in a study conducted in Ethiopia (Kiflu et al., 2017). However, in a similar study conducted in Turkey, the rate was reported to be 11.1% (Yildiz and Demirbilek, 2024). In the present study, resistance to streptomycin, trimethoprim/sulfamethoxazole, chloramphenicol, gentamicin, and kanamycin in *Salmonella* strains generally matched the rates of 44.6-76.0%, 38.9-41.5%, 44.7-51.7%, 29.6-64.0%, and 32.1-38.9%, respectively, observed in previous studies conducted in China (Wei et al., 2020; Zhao et al., 2024). However, lower rates of resistance to streptomycin (25.4-38.1%), trimethoprim/sulfamethoxazole (9.5-28.0%), chloramphenicol (7.1-17.2%), gentamicin (2.4-20.0%), and kanamycin (0.0-2.4%) have also been observed in dog- and cat-derived *Salmonella* strains in previous studies conducted in Ethiopia (Kiflu et al., 2017), Thailand (Srisanga et al., 2017), Turkey (Yildiz and Demirbilek, 2024), and Iraq (Najim et al., 2025). The neomycin resistance rate (18.6%) was lower than the rate (50.0%) recorded in a study conducted in Turkey (Yildiz and Demirbilek, 2024).

Resistance to amoxicillin/clavulanic acid aligns with the 26.2% rate reported in a study from Ethiopia (Kiflu et al., 2017). However, a previous study in Iraq reported a 48.0% resistance rate among dog-derived *Salmonella* strains (Najim et al., 2025). Notably, in previous studies in China (Wei et al., 2020) and Turkey (Yildiz and Demirbilek, 2024), all dog- and cat-derived *Salmonella* strains were susceptible to amoxicillin. The rate of cefotaxime resistance was lower than the 44.0-52.0% observed in another study conducted in China (Zhao et al., 2024). In the present study, the isolates showed resistance to ciprofloxacin and nalidixic acid at rates of 18.2% and 27.3%, respectively. Resistance to these antibiotics among dog- and cat-derived *Salmonella* strains varied across countries, ranging from susceptibility to 2.4% in Ethiopia and Thailand (Kiflu et al., 2017; Srisanga et al., 2017), 22.2-44.4% in Turkey (Yildiz and Demirbilek, 2024), and 25.8-80.0% in China (Wei et al., 2020; Zhao et al., 2024). Antibiotic resistance in *Salmonella* strains can depend on location, region, season, antibiotic susceptibility testing method, and source of isolation (Aga et al., 2025; Zhang et al., 2026). The varying rates of resistance across localities and regions highlight the role of antibiotic management and use policies in reducing antibiotic resistance in livestock (Osivand et al., 2025).

The amplification rates of tetracycline and sulfonamide resistance genes in the current study are consistent with previous research in China (Zhao et al., 2024), in which the *tetA* and *sul1* genes were found in 45.9-53.3% and 52.2–83.6% of tetracycline- and sulfonamide-resistant *Salmonella* strains isolated from dogs and cats, respectively. However, in a similar study conducted in Thailand, only 20.0% of sulfonamide-resistant strains carried the *sul1* gene, and 51.1% of tetracycline-resistant strains carried either the *tetA* or *tetB* gene, with 21.3% carrying both the *tetA* and *tetB* genes (Srisanga et al., 2017). The widespread distribution of sulfonamide (*sul1*, *sul2*, *sul3*) and tetracycline (*tetA*, *tetB*, *tetC*, *tetG*) resistance genes in antibiotic-resistant *Salmonella* strains from various sources has been noted worldwide, including Bangladesh, China, and Thailand (Zhu et al., 2017; Das et al., 2022; Puangseree et al., 2025). These findings may explain the high rates of resistance to these antibiotic classes in *Salmonella* globally (Zhao et al., 2024). Furthermore, the screening rates for aminoglycoside and chloramphenicol resistance genes are consistent with the study by Srisanga et al. (2017) conducted in Thailand, which reported that aminoglycoside-resistant *Salmonella* strains carried the *aadA1* gene alone and both *aadA1* and *aadA2* genes simultaneously at rates of 80.0% and 20.0%, respectively; the *cmlA1* gene was detected at a rate of 60.7% in chloramphenicol-resistant strains.

The prevalence of plasmid-mediated quinolone resistance (PMQR) genes in quinolone-resistant *Salmonella* strains aligns with a study from China (Zhao et al., 2024), which reported that 17.6%, 60.3-67.4%, and 38.2-44.1% of quinolone-resistant strains carried the *qnrA*, *qnrS*, and *aac(6')-Ib-cr* genes, respectively. In contrast, in Thailand, only 4.9% of quinolone-resistant *Salmonella* strains carried the *qnrS* gene, and other PMQR genes were not detected (Srisanga et al., 2017). The amplification of the bla_{TEM} gene in β-l*actam*-resistant *Salmonella* strains was higher than the 40.0-55.4% rates detected in drug-resistant strains in previous studies in China and Thailand (Srisanga et al., 2017; Zhao et al., 2024). In the present study, the absence of the bla_{OXA-1} and bla_{PSE-1} genes may be due to the small sample size. However, in the aforementioned studies by Srisanga et al. (2017) and Zhao et al. (2024), the bla_{PSE-1} and bla_{OXA} genes were also amplified in only two (3.2%) of 62 ampicillin-resistant strains and ten (3.0%) of 334 β-*lactam*-resistant strains.

CONCLUSION

The present study provided initial insights into the prevalence and antibiotic resistance of *Salmonella* spp. in dog and cat feces collected from veterinary clinics in Northern Vietnam. Despite limitations, including a small sample size, a narrow sampling scope, and an unclear link between infection rates and variables such as breed and age, the findings indicate that, even with low fecal infection levels, dogs and cats can still transmit *Salmonella* to humans through close contact. Some isolated strains may also show resistance to multiple antibiotics and harbor various resistance genes, increasing the

risk of spreading these genes within the community. Larger studies are necessary to identify resistance genes, including plasmids and mutations, and to examine their connection to resistance patterns and multidrug-resistant strains. Additionally, monitoring antibiotic use in animals at veterinary clinics is crucial to reducing antibiotic resistance.

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Authors' contributions

Chu Thi Thanh Huong designed the investigation and methodology and contributed to writing the manuscript. Nguyen Van Phuong, Nguyen Manh Tuong, and Truong Lan Oanh collected the samples and participated in the experiments. Truong Ha Thai provided supervision and methodological support and contributed primarily to writing. All authors revised and approved the final edition of the manuscript.

Availability of data and materials

All data are included in the submitted paper and will be available upon reasonable request from the corresponding author.

Competing interests

The authors declare no conflicts of interest.

Ethical considerations

The present study was originally written without copying any data from published studies or books. No AI tools were used to prepare the current study. All authors accept responsibility for the originality of the data and the manuscript, both at the time of submission and after final revision for publication.

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