



# Prevalence and Antibiotic Resistance of *Salmonella* spp. in Pigeons Farmed at Bac Ninh Province, Vietnam

Chu Thi Thanh Huong<sup>1</sup> , Truong Lan Oanh<sup>2</sup> , Vu Thi Thu Tra<sup>2</sup> , and Truong Ha Thai<sup>1\*</sup>

<sup>1</sup>Department of Veterinary Microbiology and Infectious Diseases, Faculty of Veterinary Medicine, Vietnam National University of Agriculture, Gia Lam, Hanoi, Vietnam

<sup>2</sup>Department of Veterinary Public Health, Faculty of Veterinary Medicine, Vietnam National University of Agriculture, Gia Lam, Hanoi, Vietnam

\*Corresponding author's E-mail: ththai@vnua.edu.vn

## ABSTRACT

Pigeons are known to be the potential reservoir for several pathogenic microorganisms, including *Salmonella*, *E. coli*, *Chlamydia* spp., and *Cryptococcus* spp. This study aimed to determine the prevalence and antibiotic resistance of *Salmonella* in fecal samples from pigeons raised in Northern Vietnam. From January to December 2024, 128 fresh fecal samples were collected from 32 different pigeon farms in Bac Ninh province, Vietnam, for *Salmonella* isolation. Fecal samples were cultured on peptone buffer and selective media such as rappaport-vassilidis soybean broth and xylose lysine deoxycholate agar; suspected *Salmonella* colonies were confirmed by biochemical tests and *InvA* gene identification. Results showed that 40 out of 128 samples (31.3%) were positive for *Salmonella*. The isolated *Salmonella* strains were tested for antibiotic susceptibility by agar diffusion method for ampicillin, meropenem, cefotaxime, ceftazidime, doxycycline, tetracycline, gentamicin, streptomycin, nalidixic acid, ciprofloxacin, norfloxacin, sulfonamide, and trimethoprim/sulfamethoxazole. The isolates exhibited the highest resistance rate to tetracycline (67.5%), followed by ampicillin and sulfonamide (62.5%). Cefotaxime, streptomycin, and trimethoprim/sulfamethoxazole were resistant at rates of 52.0%, 47.5%, and 45.0%, respectively. Resistance to ciprofloxacin, gentamicin, doxycycline, nalidixic acid, and chloramphenicol ranged from 20.0% to 35.0%. No *Salmonella* strains were observed to be resistant to ceftazidime, meropenem, and norfloxacin. The current results indicated that 92.5% (37/40) isolates were resistant to at least one antibiotic, with 26 different antibiotic resistance patterns. Twenty-eight (70.0%) strains were identified as multidrug-resistant (MDR), with resistance to 3-4 antibiotic classes, and 5-6 antibiotic classes and 7 antibiotic classes found in 11 (27.5%), 12 (30.0%), and 5 (12.5%) of the isolates, respectively. Overall, the findings of the current study indicated a high prevalence of antibiotic-resistant *Salmonella* in pigeon farms, with many strains identified as MDR.

**Keywords:** Antibiotic resistance, *InvA*, Pigeon, *Salmonella*

## INTRODUCTION

*Salmonella enterica* is a species of Gram-negative bacteria, a member of the *Enterobacteriaceae* family, and over 2,500 different serotypes have been identified (Grimont and Weill 2007). Notably, animals infected with *Salmonella*, including rats, wild animals, poultry, and cattle, are important sources of *Salmonella* infection in humans (Zhang et al., 2024).

Globally, pigeons (*Columba livia*) are highly valued for the high nutritional content of their meat and eggs. Therefore, the domestic pigeon farming industry has developed into an important part of the poultry industry in many countries around the world (Karim et al., 2020; Wang et al., 2025). In Vietnam, pigeons are increasingly raised for meat due to the low cost of housing, food, and veterinary care. The increasing raising and trading of pigeons unintentionally leads to the risk of spreading infectious diseases, including diseases transmitted from animals to humans (Pedersen et al., 2007). Pigeons are known to be potential hosts for several pathogenic microorganisms, including *Salmonella*, *Escherichia coli*, *Chlamydia* spp., and *Cryptococcus* spp. (Tanaka et al., 2005; Vasconcelos et al., 2018; Karim et al., 2020). Furthermore, due to close contact with humans, pigeons are considered one of the important sources of *Salmonella* infection in humans (Teske et al., 2013; de Oliveira et al., 2018). For example, *Salmonella* strains in pigeon meat can infect humans through the food chain or can be transmitted through direct contact and feces (Teske et al., 2013; de Oliveira et al., 2018).

The use of any antibiotic creates selective pressure favorable to antibiotic-resistant bacteria (Olesen et al., 2020). Therefore, the use and misuse of antibiotics in many countries and regions have made antibiotic resistance a global concern, frequently mentioned in scientific literature (Muteeb et al., 2023; Nammi et al., 2025). Furthermore, the lack of treatment options due to antibiotic resistance is one of the most discussed issues related to human health. Additionally, the misuse and overuse of antibiotics to treat *Salmonella* infections has led to the emergence of multidrug-resistant (MDR) bacteria (Walther et al., 2017; Xu et al., 2021). To date, studies on the prevalence and antibiotic resistance of bacteria in pigeon farms in Vietnam are limited. Therefore, further studies are needed to clarify the potential risks of bacterial infections, including *Salmonella* spp., to pigeons and human health in Vietnam. This study aimed to determine the prevalence and antibiotic resistance of *Salmonella* spp. in fecal samples isolated from pigeons raised in Northern Vietnam.

ORIGINAL ARTICLE  
Received: December 29, 2026  
Revised: January 28, 2026  
Accepted: February 29, 2026  
Published: March 25, 2026

## MATERIALS AND METHODS

### Ethical approval

The present study was conducted by collecting samples in accordance with the guidelines outlined in the Helsinki declaration and the animal welfare and safety procedures of the Committee on Animal Research and Ethics (CARE), Faculty of Veterinary Medicine, Vietnam National University of Agriculture, Vietnam (Approval No. CARE-2024/01). The authors considered farmers' ethical concerns and consent before conducting the study.

### Sampling

In this study, 128 fresh fecal samples were randomly collected from 32 different pigeon farms, as suggested by local veterinarians; each farm is raising at least 1000 pairs of breeding pigeons, in Bac Ninh province, Vietnam, from January to December 2024. 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 by using sterile spoons. Each sample was placed in a separate sterile sample bag, labeled, stored at 4°C in a dry ice box, and immediately transported to the laboratory of the Department of Veterinary Microbiology and Infectious Diseases, Faculty of Veterinary Medicine, National University of Agriculture, Vietnam, for analysis within 24 hours.

### Salmonella isolation

The isolation of *Salmonella* from fecal samples was performed according to the method described in the previous study (Bupasha et al., 2020) with some modifications. Approximately one gram of substance from fecal samples was homologized with buffer peptone water (BPW; Merck, Germany) following the ratio 1:9 and incubated at 37°C within 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 (RVS) broth (Merck, Germany), followed by further incubation at 42.5°C for 24 hours. A loopful of culture broth was then sampled from the selective enrichment RVS broth, streaked onto xylose lysine deoxycholate agar (XLD; Merck, Germany), and incubated at 37°C for 24 hours. Presumptive black colonies 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 such as indole, sugar fermentation, and H<sub>2</sub>S test, IMViC reaction in Tryptone broth (TB), triple sugar iron agar (TSI), Methyl-red Voges-Proskauer broth (VP-MR broth), and Simmons citrate agar (SCA, Merck, Germany), respectively. All isolates were kept in brain heart infusion broth (BHI; Merck, Germany) supplemented with 50% glycerol at -20°C for subsequent experiments.

### Salmonella confirmation

DNA was extracted using the TopPURE® Genomic DNA Extraction Kit (ABT, Vietnam) according to the manufacturer's instructions. The specific primers (Oliveira et al., 2003) corresponding to the following nucleotide sequence based on the *invA* gene, a biomarker for *Salmonella* spp. (Forward: 5'-GTGAAATTATCGCCACGTTCCGGC-3' and Reverse: 5'-TCATCGCACCGTCAAAGGAACC-3'). An expected PCR product of 284 bp was used. The PCR reaction conditions included an initial denaturation at 94°C for 5 minutes, followed by 35 denaturation cycles at 94°C for 30 seconds, annealing at 55°C for 30 seconds, and extension at 72°C for 45 seconds, followed by a final extension at 72°C for 10 minutes on a thermocycler (Gene Atlas, Antec Bio, Japan). 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. The PCR products were electrophoresed on 1.5% agarose gel supplemented with RedSafe™ Nucleic Acid Staining Solution (Intron, Korea).

### Antimicrobial susceptibility test

Antibiotic susceptibility test was examined according to the guidelines of the Clinical and Laboratory Standards Institute (CLSI, 2024). Agar diffusion method was performed on Mueller-Hinton agar (MHA, Merck, Germany) following Bauer et al. (1966) and 14 different antibiotic agents (Oxoid, UK) belong to eight groups were used, including penicillines (ampicillin [10 µg]), carbapenems (meropenem [10 µg]); cephalosporins (cefotaxime [30 µg], ceftazidime [30 µg]); tetracyclines (doxycycline [30 µg]; tetracycline [30 µg]); aminoglycosides (gentamicin [10 µg], streptomycin [10 µg]); phenicols (chloramphenicol [30 µg]); quinolones (nalidixic acid [30 µg], ciprofloxacin [5 µg], norfloxacin [10 µg]); sulfonamides (sulfonamides [300 µg], trimethoprim/sulfamethoxazole [1.25/23.75 µg]). The *Escherichia coli* ATCC 25922 strain is used for quality control. An isolate was determined to be resistant or multidrug-resistant to antibiotics based on the definition of Magiorakos et al. (2012).

### Data analysis

The data was entered and calculated using Microsoft Excel 2016 software.

## RESULTS

After conducting biochemical and molecular tests, 31.3% (40/128) of fecal samples were *Salmonella*-positive (Figure 1). Antibiotic resistance rates of the isolated *Salmonella* strains were presented in Table 1. The isolates exhibited the highest resistance rate to tetracycline (67.5%), followed by ampicillin and sulfonamides (62.5%). Cefotaxime, streptomycin, and trimethoprim/sulfamethoxazole were resistant at rates of 52.0%, 47.5%, and 45.0%, respectively. The *Salmonella* strains showed resistance to ciprofloxacin (20.0%), gentamicin (25.0%) and doxycycline (25.0%), nalidixic acid (32.5%), and

chloramphenicol (35.0%). No *Salmonella* strains were found to be resistant to ceftazidime, meropenem, and norfloxacin. The antibiotic resistance patterns of the *Salmonella* isolates are presented in Table 2. The *Salmonella* strains exhibited 26 different antibiotic resistance patterns. Of which, resistance to 1-2 and 3-5 antibiotics was found in eight and twelve of the isolates, respectively. There were eleven and six of the isolates that exhibited resistance to 6-8 and 9-11 kinds of antibiotics, respectively. The results in Table 3 indicated that 92.5% (37/40) *Salmonella* isolates were resistant to at least one antibiotic, of which 70.0% (28/40) isolates were identified as MDR. Among the MDR isolates, resistance to 3-4 antibiotic classes, 5-6 antibiotic classes, and  $\geq 7$  antibiotic classes was found in eleven (27.5%), twelve (30.0%), and five (12.5%) out of the *Salmonella* isolates, respectively.

**Table 1.** Antibiotic resistance status of the isolated *Salmonella* spp. from fecal samples of pigeons farmed in Bac Ninh, Vietnam, in 2024

Antibiotic groups	Antibiotic	Resistance n (%)	Intermediate n (%)	Susceptible n (%)
Beta-lactams	Ampicillin	25 (62.5)	2 (5.0)	13 (32.5)
	Ceftazidime	0 (0.0)	0 (0.0)	40 (100)
	Cefotaxime	21 (52.5)	1 (2.5)	18 (45.0)
	Meropenem	0 (0.0)	3 (7.5)	37 (92.5)
aminoglycosides	Gentamicin	10 (25.0)	2 (5.0)	28 (70.0)
	Streptomycin	19 (47.5)	3 (7.5)	18 (45.0)
Quinolones	Nalidixic acid	13 (32.5)	4 (10.0)	23 (57.5)
	Ciprofloxacin	8 (20.0)	3 (7.5)	29 (72.5)
	Norfloxacin	0 (0.0)	2 (5.0)	38 (95.0)
Tetracyclines	Doxycycline	10 (25.0)	2 (5.0)	28 (70.0)
	Tetracycline	27 (67.5)	3 (7.5)	10 (25.0)
Phenicol	Chloramphenicol	14 (35.0)	3 (7.5)	23 (57.5)
Sulfonamides	Sulfonamides	25 (62.5)	1 (2.5)	16 (40.0)
	Trimethoprim/Sulfamethoxazole	18 (45.0)	2 (5.0)	20 (50.0)

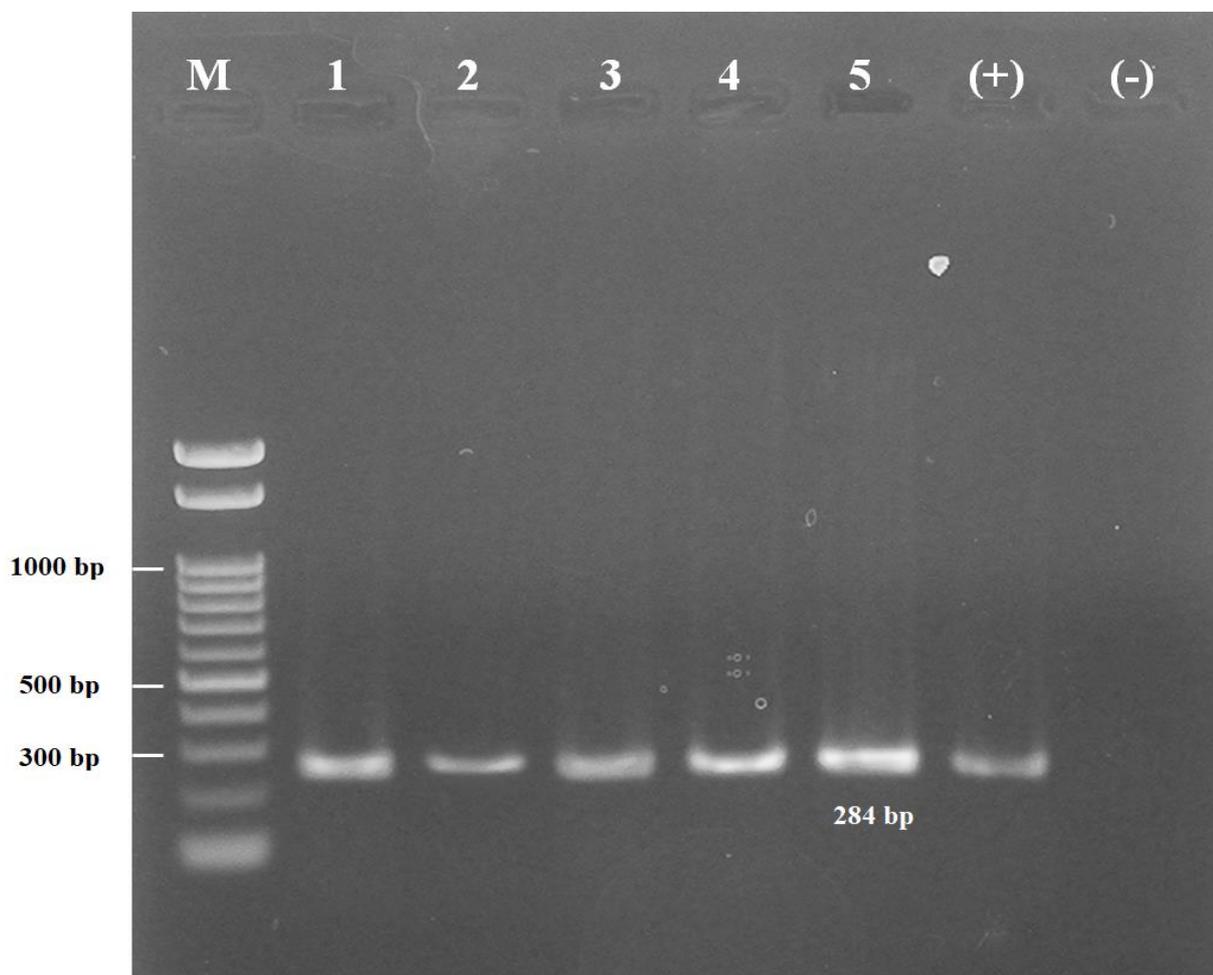
**Table 2.** Antibiotic resistance patterns of the isolated *Salmonella* spp. from fecal samples of pigeon farmed in Bac Ninh, Vietnam, in 2024

Order	Antibiotic resistance patterns	Number of antibiotic resistances	Number of strains
1	Susceptible	0	3
2	AMP	1	1
3	TET	1	4
4	SXT, TET	2	3
5	SUL, SXT, TET	3	1
6	SUL, SXT, STM, TET	4	1
7	AMP, CTX, CHL, STM	4	1
8	AMP, CTX, SUL, DOX	4	2
9	AMP, SUL, STM, GEN	4	1
10	AMP, CTX, CHL, STM, GEN	5	1
11	AMP, CTX, SUL, TET, DOX	5	1
12	AMP, CTX, CHL, SUL, SXT	5	2
13	AMP, CTX, SXT, STM, NAL	5	1
14	AMP, SUL, STM, TET, NAL	5	1
15	AMP, CHL, SUL, SXT, TET, DOX	6	2
16	AMP, CTX, SUL, SXT, STM, TET	6	2
17	AMP, CTX, CHL, SUL, GEN, TET, DOX	7	1
18	AMP, CHL, SUL, SXT, STM, GEN, TET, DOX	8	1
19	AMP, CTX, CHL, SUL, STM, GEN, TET, NAL	8	2
20	AMP, CTX, SUL, STM, GEN, TET, NAL, CIP	8	1
21	AMP, CTX, SUL, STM, TET, DOX, NAL, CIP	8	1
22	AMP, CTX, SUL, SXT, STM, TET, DOX, NAL	8	1
23	AMP, CTX, CHL, SUL, STM, TET, DOX, NAL, CIP	9	2
24	AMP, CTX, SUL, STM, GEN, TET, DOX, NAL, CIP	9	1
25	AMP, CTX, SUL, SXT, STM, TET, DOX, NAL, CIP	9	1
26	AMP, CHL, SUL, SXT, STM, GEN, TET, DOX, NAL, CIP	10	1
27	AMP, CTX, CHL, SUL, SXT, STM, GEN, TET, DOX, NAL, CIP	11	1

AMP: Ampicillin; CTX: Cefotaxime; CHL: Chloramphenicol; CIP: Ciprofloxacin; DOX: Doxycycline; GEN: Gentamicin; NAL: Nalidixic acid; NOR: Norfloxacin; STM: Streptomycin; STX: Trimethoprim/Sulfamethoxazole; SUL: Sulfonamides; TET: Tetracycline

**Table 3.** Number of the multi-drug resistant *Salmonella* strains isolated from fecal samples of pigeons farmed in Bac Ninh, Vietnam in 2024

Order	Number of antibiotic resistance groups	Number of exhibited strains	
		Number	Percentage
1	Susceptible	3	7.5
2	Resistance to 1 - 2 classes	9	22.5
3	Resistance to 3 - 4 classes	11	27.5
4	Resistance to 5 - 6 classes	12	30.0
5	Resistance to $\geq 7$ classes	5	12.5

**Figure 1.** Agarose gel electrophoresis of *invA* gene in *Salmonella* strains isolated from fecal samples of pigeons farmed in Bac Ninh, Vietnam, in 2024. M: DNA maker (100 bp), Lane 1-5: *invA* positive (284 bp), (+): positive control, (-): negative control.

## DISCUSSION

In this study, the *invA* gene was amplified in all isolates *Salmonella*, in agreement with the studies conducted in Egypt (El-Sebay et al., 2017; Hagag et al., 2022), Indonesia (Wibisono et al., 2021), and Iran (Mashayekh et al., 2022). The *invA* gene is widely used to identify *Salmonella* species in various samples and is associated with intestinal invasion in animals (Oliveira et al., 2003; El-Sebay et al., 2017). The *invA* gene is also a suitable marker for molecular analyses and preliminary phylogenetic analysis of *Salmonella* in epidemiological studies (McWhorter et al., 2019; Fadipe and Hölzle, 2025). The rate of *Salmonella*-positive (31.1%) is consistent with rates ranging from 22.22% to 37.5% in cloacal swab and fecal samples of pigeons in previous studies in Bangladesh (Hosain et al., 2012; Karim et al., 2020; Bupasha et al., 2021). However, the isolation rates of *Salmonella* species were only about 0.81% and 2.0% in pigeons in other studies in Brazil and Egypt (Ruben et al., 2018; Hagag et al., 2022), respectively. In addition, *Salmonella* was detected in pigeon organ samples ranging from 3.5% in Egypt (Yousef and Mamdouh et al., 2016), 5.47% in Poland (Kaczorek-Lukowska

*et al.*, 2021), 8.0% in India (Dutta *et al.*, 2013), 14.9% in China (Zhang *et al.*, 2024), to 28.57% in Bangladesh (Raman *et al.*, 2016). The prevalence of *Salmonella* in pigeons varied across studies in different countries, which may be related to different sampling methods. However, the high positive rate of *Salmonella* in pigeon fecal samples in this study may be due to poor sanitary conditions and inadequate hygiene practices, as well as cross-contamination between high-density cages at the farms. Therefore, this underscores the need for stricter hygiene measures at pigeon farms in the study area.

Antibiotics are the most common therapy for treating bacterial diseases, including *Salmonella* infections in pigeons (Tang *et al.*, 2023; Zhang *et al.*, 2024). In veterinary medicine, the widespread and continuous use of antibiotics has exacerbated antibiotic resistance in bacterial strains derived from animals and livestock (Tang *et al.*, 2023). High resistance rates of *Salmonella* to tetracycline, ampicillin, sulfonamide, and streptomycin have been noted in previous studies in India (Dutta *et al.*, 2013), Bangladesh (Karim *et al.*, 2020; Bupasha *et al.*, 2021), and China (Zhang *et al.*, 2024). The high levels of resistance to these antibiotics may be due to their widespread use in the treatment and prevention of diseases in both veterinary and human medicine worldwide (Bupasha *et al.*, 2021). In the current study, 32.5% of the *Salmonella* isolates were resistant to nalidixic acid. The results of the current study are lower than previous reports conducted in India (Dutta *et al.*, 2013) and Bangladesh (Saifullah *et al.*, 2016; Bupasha *et al.*, 2021), which reported that 50.0-72.4% of the isolates were resistant to this antibiotic, respectively. The rate of *Salmonella* resistance to ciprofloxacin was similar to that in previous studies, as about 10.0% in China (Zhang *et al.*, 2024), and 28.6% in Egypt (Yousef and Mamdouh *et al.*, 2016). However, another study in Bangladesh (Saifullah *et al.*, 2016; Karim *et al.*, 2020) and India (Dutta *et al.*, 2013) reported that all *Salmonella* strains isolated from pigeons were susceptible to this antibiotic. All *Salmonella* strains in the present study were susceptible to norfloxacin. However, approximately 8.33%, 15.6%, and 20.0-29.0% of *Salmonella* strains derived from pigeons in previous studies in India (Dutta *et al.*, 2013), Poland (Kaczorek-Łukowska *et al.*, 2021), and Egypt (Yousef and Mamdouh *et al.*, 2016), respectively, exhibited resistance to norfloxacin.

The gentamicin resistance rate in this study was consistent with the rate of 22.0% in Bangladesh (Saifullah *et al.*, 2016). However, resistance to gentamicin of *Salmonella* varied significantly between countries, ranging from 8.33% in India (Dutta *et al.*, 2012) to 100% in China (Zhang *et al.*, 2024). Similarly, the trimethoprim/sulfamethoxazole resistance of *Salmonella* strains was reported to be under 10.0% in China (Zhang *et al.*, 2024), ranging from 21.8% to 25.0% in Poland and India (Dutta *et al.*, 2012; Kaczorek-Łukowska *et al.*, 2020), approximately 50.0% to 55.6% in Egypt (Yousef and Mamdouh *et al.*, 2016; Hagag *et al.*, 2022), and up to 86.2% in Bangladesh (Saifullah *et al.*, 2016). The rate of doxycycline resistance was consistent with the rate of 22.2% in a previous study conducted in Egypt (Hagag *et al.*, 2022), but lower than the rate of 37.5% in a study conducted in Poland (Kaczorek-Łukowska *et al.*, 2020). In the current study, chloramphenicol, a drug banned for use in livestock and veterinary medicine in Vietnam, was resistant by 35.0% of the isolates. This may be due to the widespread use of other phenicol antibiotics, such as florfenicol and thiamphenicol, in livestock and veterinary medicine in Vietnam. The rate of cefotaxime resistance was 52.5%, which could be comparable to results from previous studies conducted in India (Dutta *et al.*, 2012), in Egypt (Yousef and Mamdouh *et al.*, 2016; Hagag *et al.*, 2022), and Bangladesh (Bupasha *et al.*, 2020). Conversely, all isolates were susceptible to ceftazidime and meropenem, consistent with those reported by Zhang *et al.* (2024) in China. This could be due to the limited use of these two drugs in animal husbandry and veterinary medicine because their high cost makes them inaccessible in Vietnam.

The frequent use of antibiotics in livestock and veterinary medicine for disease prevention and treatment is a significant factor leading to the emergence of antibiotic-resistant bacteria, which are then transmitted to humans through the food chain (Hosain *et al.*, 2012; Tang *et al.*, 2023). In this study, approximately 70% of the isolated *Salmonella* strains were identified as multidrug-resistant (MDR). However, this is not surprising given the high rates of MDR in pigeon-derived *Salmonella* strains in previous studies. The proportion of isolates exhibiting MDR ranged from 54.54% to 96.6% in studies conducted in Bangladesh (Bupasha *et al.*, 2020; Karim *et al.*, 2020) and 90.62% in China (Zhang *et al.*, 2024). Currently, due to limited vaccine and antibiotic supplies in the pigeon breeding industry, infections caused by MDR bacteria can lead to ineffective treatment in this species (Kaczorek-Łukowska *et al.*, 2021; Zhang *et al.*, 2024). The situation underscores the need for continuous monitoring of antibiotic resistance in pigeon populations and the cautious use of antibiotics.

## CONCLUSION

The results of the current study indicated a high prevalence of antibiotic-resistant *Salmonella* in pigeon farms of Vietnam. Furthermore, many isolated bacterial strains exhibited resistance to multiple antibiotics. This underscores the need for monitoring measures to limit the indiscriminate use of antibiotics in pigeon farming and thus prevent the spread of antibiotic-resistant bacteria. In addition, more extensive studies on other pigeon diseases are needed to support the management and development of the pigeon farming industry in Vietnam.

## DECLARATIONS

### Funding

This research received internal funding from Vietnam National University of Agriculture, with project code T2024-09-34.

### Acknowledgments

The authors of the current study would like to thank the students who helped with sample transportation and also the local veterinarians in Bac Ninh province for their excellent technical assistance.

### Authors' contributions

Chu Thi Thanh Huong designed the investigation and methodology and contributed to the manuscript. Vu Thi Thu Tra and Truong Lan Oanh participated in doing the experiments and analyzing the data. Truong Ha Thai was responsible for supervision, methodological support, and primarily for writing the manuscript. All authors revised and approved the final edition of the manuscript before publication in the present journal.

### Availability of data and materials

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

### Ethical considerations

This article was written originally without any copy from published articles and books. No AI tools were used for conducting and preparing the current study.

### Competing interests

The authors declared no conflict of interest.

## REFERENCES

- Bauer AW, Kirby WM, Sherris JC, and Turck M (1966). Antibiotic susceptibility testing by a standardized single disk method. *American Journal of Clinical Pathology*, 45(4): 493-496. DOI: <https://www.doi.org/10.1093/ajcp454 ts493>
- Bupasha ZB, Begum R, Karmakar S, Akter R, Bayzid M, Ahad A, and Sarker MS (2021). Multidrug-Resistant *Salmonella* spp. isolated from apparently healthy pigeons in a live bird market in Chattogram, Bangladesh. *World's Veterinary Journal*, 10(4): 508-513. DOI: <https://www.doi.org/10.54203/scil.2020.wvj61>
- Clinical and laboratory standards institute (CLSI) (2024). Performance standards for antimicrobial susceptibility testing, 34th Edition. CLSI supplement M100. Wayne, PA: Clinical and Laboratory Standards Institute, pp. 24-25. Available at: <https://pid-el.com/wp-content/uploads/2024/07/CLSI-M100.pdf>
- de Oliveira MCV, Camargo BQ, Cunha MPV, Saldenberg AB, Teixeira RHF, Matajira CEC, Moreno LZ, Gomes VTM, Christ APG, Barbosa MRF et al. (2018). Free-ranging synanthropic birds (*Ardea alba* and *Columba livia domestica*) as carriers of *Salmonella* spp. and diarrheagenic *Escherichia coli* in the Vicinity of an Urban Zoo. *Vector-Borne Zoonotic Diseases*, 18(1): 65-69. DOI: <https://www.doi.org/10.1089/vbz.2017.2174>
- Dutta P, Borah M, Sarmah R, and Gangil R (2013). Isolation of *Salmonella Typhimurium* from pigeons (*Columba livia*) in Greater Guwahati, its histopathological impact and antibiogram. *Comparative Clinical Pathology*, 22: 147-150. DOI: <https://www.doi.org/10.1007/s00580-013-1789-2>
- El-Sebay NA, Abu Shady HM, El-Rashed El-Zeedy SA and Samy AA (2017). *InvA* gene sequencing of *Salmonella Typhimurium* isolated from Egyptian poultry. *Asian Journal of Scientific Research*, 10 (3): 194-202. DOI: <https://www.doi.org/10.3923/ajsr.2017.194.202>
- Fadipe EO and Hölzle LE (2025). Phylogenetic analysis and public health implications of *Salmonella* strains in Southwestern states of Nigeria using *invA* gene sequences. *Animals*, 15(23): 3399. DOI: <https://www.doi.org/10.3390/ani15233399>
- Grimont PAD and Weill FX (2007). Antigenic formulae of the *Salmonella* serovars, 9<sup>th</sup> Edition. WHO Collaborating Center for Reference and Research on *Salmonella* at Institute Pasteur in France, Paris, pp. 6-9. Available at: [https://www.pasteur.fr/sites/default/files/veng\\_0.pdf](https://www.pasteur.fr/sites/default/files/veng_0.pdf)
- Hagag A, Naguib D, Mohamed A and Elgohary A (2022). Prevalence, virulence genes, and antibiotic resistance of *Escherichia coli* and *Salmonella* spp. isolated from pigeons and humans. *Mansoura Veterinary Medical Journal*, 23(1): 4. DOI: <https://www.doi.org/10.21608/mvmj.2021.88961.1072>
- Hosain MS, Islam MA, Khatun MM and Dey RK (2012). Prevalence and antibiogram profiles of *Salmonella* isolated from pigeons in Mymensingh, Bangladesh. *Microbes Health*, 1(2): 54-57. DOI: <https://www.doi.org/10.3329/mh.v1i2.14090>
- Kaczorek-Lukowska E, Sowińska P, Franaszek A, Dziejulska D, Małaczewska J, and Stenzel T (2021). Can domestic pigeon be a potential carrier of zoonotic *Salmonella*? *Transboundary and Emerging Diseases*, 68(4): 2321-2333. DOI: <https://www.doi.org/10.1111/tbed.13891>
- Karim SJI, Islam M, Sikder T, Rubaya R, Halder J, and Alam J (2020). Multidrug resistant *Escherichia coli* and *Salmonella* spp. isolated from pigeons. *Veterinary World*, 13(10): 2156. DOI: <https://www.doi.org/10.14202/vetworld.2020.2156-2165>
- Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, Harbarth S, Hindler JF, Kahlmeter G, Olsson-Liljequist B et al. (2012). Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. *Clinical Microbiology and Infection*, 18(3): 268-281. DOI: <https://www.doi.org/10.1111/j.1469-0691.2011.03570.x>

- Mashayekh Z, Moradi Bidhendi S and Khaki P (2022). Detection of *invA*, *sivH*, and *agfA* virulence genes in *Salmonella* spp. Isolated from Broiler Breeder Farms in Alborz Province, Iran. Archives of Razi Institute, 77(2):607-614. DOI: <https://www.doi.org/10.22092/ARI.2021.353674.1607>
- McWhorter AR, Tearle R, Moyle TS and Chousalkar KK (2019). *In vivo* passage of *Salmonella Typhimurium* results in minor mutations in the bacterial genome and increases in vitro invasiveness. Veterinary Research, 50: 71. DOI: <https://www.doi.org/10.1186/s13567-019-0688-1>
- Muteeb G, Rehman MT, Shahwan M, and Aatif M (2023). Origin of antibiotics and antibiotic resistance, and their impacts on drug development: A narrative review. Pharmaceuticals, 16(11): 1615. DOI: <https://www.doi.org/10.3390/ph16111615>
- Ministry of agriculture and rural development (MARD) (2011). National technical regulation on animal diseases - General requirements for sample collection, storage and shipment. QCVN 01-83: 2011/BNNPTNT, pp. 5-10. Available at: <https://sgtvt.bacninh.gov.vn/documents/154127/14279228/QCVN+01-83-2011-BNNPTNT.pdf/2a692d85-15d0-445c-969e-8964f5dadcad>
- Nammi J, Pasala R, Andhe N, Vasam R, Poruri AD, and Sherikar RR (2025). Antibiotic misuse: An in-depth examination of its global consequences and public health challenges. Cureus, 17(6): e85941. DOI: <https://www.doi.org/10.7759/cureus.85941>
- Olesen SW, Lipsitch M, and Grad YH (2020). The role of “spillover” in antibiotic resistance. Proceedings of the National Academy of Sciences of the United States of America, 117: 29063-29068. DOI: <https://www.doi.org/10.1073/pnas.2013694117>
- Oliveira SD, Rodenbusch CR, Cé MC, Rocha SL and Canal CW (2003). Evaluation of selective and non-selective enrichment PCR procedures for *Salmonella* detection. Letters in Applied Microbiology. 36(4): 217-21. DOI: <https://www.doi.org/10.1046/j.1472-765x.2003.01294.x>
- Pedersen K and Clark L (2007). A review of Shiga toxin *Escherichia coli* and *Salmonella enterica* in cattle and free-ranging birds: potential association and epidemiological links. Human-Wildlife Conflicts, 1(1): 68-77. DOI: <https://www.doi.org/10.26077/fn01-a919>
- Rahman MM, Rahman MM, Meher MM, Khan MSI, and Anower AKMM (2016). Isolation and antibiogram of *Salmonella* spp. from duck and pigeon in Dinajpur, Bangladesh. Journal of Advanced Veterinary and Animal Research, 3(4): 386-391. DOI: <http://www.doi.org/10.5455/javar.2016.c177>
- Ruben VH, Windleyanne GAB, Elisângela SL, Régis SCT, Isaac NGS, Mariana DB, Alexandre H and William MC (2018). Antimicrobial susceptibility and diarrheagenic diagnosis of *Escherichia coli* and *Salmonella enterica* isolated from feral pigeons (*Columba livia*) captured in Fortaleza, Brazil. Pesquisa Veterinária Brasileira, 38 (11): 2150-2154. DOI: <https://www.doi.org/10.1590/1678-5150-PVB-5633>
- Saifullah MK, Mamun MM, Rubayet RM, Nazir KHMNH, Zesmin K, and Rahman MT (2016). Molecular detection of *Salmonella* spp. isolated from apparently healthy pigeon in Mymensingh, Bangladesh and their antibiotic resistance pattern. Journal of Advanced Veterinary and Animal Research, 3(1): 51-55. DOI: <http://www.doi.org/10.5455/javar.2016.c131>
- Tanaka C, Miyazawa T, Watarai M, and Ishiguro N (2005). Bacteriological survey of feces from feral pigeons in Japan. Journal of Veterinary Medical Science, 67(9): 951-953. DOI: <https://www.doi.org/10.1292/jvms.67.951>
- Tang B, Siddique A, Jia C, Ed-Dra A, Wu J, Lin H, and Yue M (2023). Genome-based risk assessment for foodborne *Salmonella enterica* from food animals in China: A One Health perspective. International Journal of Food Microbiology, 390: 110120. DOI: <https://www.doi.org/10.1016/j.ijfoodmicro.2023.110120>
- Teske L, Ryll M, Rubbenstroth D, Hänel I, Hartmann M, Kreienbrock L, and Rautenschlein S (2013). Epidemiological investigations on the possible risk of distribution of zoonotic bacteria through apparently healthy homing pigeons. Avian Pathology, 42(5): 397-407. DOI: <https://www.doi.org/10.1080/03079457.2013.822468>
- Vasconcelos RH, Teixeira RSdC, Silva INGd, Lopes EdS and Maciel WC (2018). Feral pigeons (*Columba livia*) as potential reservoirs of *Salmonella* spp. and *Escherichia coli*. Arquivos do Instituto Biológico, 85: e0412017. DOI: <https://www.doi.org/10.1590/1808-1657000412017>
- Walther B, Tedin K and Lübke-Becker A (2017). Multidrug-resistant opportunistic pathogens challenging veterinary infection control. Veterinary Microbiology, 200: 71-78. DOI: <https://www.doi.org/10.1016/j.vetmic.2016.05.017>
- Wang J, Lu Q, Yao L, Zhang W, Hu Q, Guo Y, Wen G, Shao H, Luo Q, and Zhang T (2025). Research note: Prevalence and genetic characteristics of pathogenic *E. coli* isolates from domestic pigeons in central China. Poultry Science, 104(2): 104705. DOI: <https://www.doi.org/10.1016/j.psj.2024.104705>
- Wibisono FM, Faridah HD, Wibisono FJ, Tyasningsih W, Effendi MH, Witaningrum AM, and Ugbo EN (2021). Detection of *invA* virulence gene of multidrug-resistant *Salmonella* species isolated from the cloacal swab of broiler chickens in Blitar district, East Java, Indonesia. Veterinary World, 14(12): 3126-3131. DOI: <https://www.doi.org/10.14202/vetworld.2021.3126-3131>
- Xu Y, Zhou X, Jiang Z, Qi Y, Ed-Dra A, and Yue M (2021). Antimicrobial resistance profiles and genetic typing of *Salmonella* serovars from chicken embryos in China. Antibiotics, 10(10): 1156. DOI: <https://www.doi.org/10.3390/antibiotics10101156>
- Yousef S and Mamdouh R (2016). Class I Integron and  $\beta$ -lactamase encoding genes of multidrug resistance *Salmonella* isolated from pigeons and their environments. Cellular and Molecular Biology (Noisy-le-grand), 62(14): 48-54. DOI: <https://www.doi.org/10.14715/cmb/%202016.62.14.8>
- Zhang Y, Lu Z, Zhao H, Li S, Zhuang H, Wang J, Li R, Zheng W, Zhu H, Xie P et al. (2024). Antimicrobial resistance and genomic characterization of *Salmonella* isolated from pigeons in China. Transboundary and Emerging Diseases, 2024: 3315678. DOI: <https://www.doi.org/10.1155/2024/3315678>

**Publisher's note:** [Scienceline Publication](https://www.scienceopen.com) Ltd. remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.



**Open Access:** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third-party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <https://creativecommons.org/licenses/by/4.0/>.

© The Author(s) 2026