



Research article

Prevalence, antimicrobial susceptibility profiles, and selected resistance genes of *Salmonella* spp. isolated from ducks in the Mekong Delta, Vietnam

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Abstract

This study assessed the occurrence of *Salmonella* spp. in ducks sampled at selected sites in the Mekong Delta, Vietnam, and characterized antimicrobial susceptibility and selected antimicrobial resistance genes (ARGs) in the recovered isolates. Of 514 cloacal swabs collected at farms, smallholder households, and live-bird trading sites, 58 were positive (11.28%; 95% CI: 8.68–14.34), yielding 83 representative isolates. Positivity was numerically higher in semi-intensive and intensive systems than in scavenging systems, although the association was not statistically significant ($P = 0.077$). Resistance was most common to amoxicillin (84.34%) and amoxicillin/clavulanic acid (59.04%), followed by sulfamethoxazole/trimethoprim (31.33%), cefotaxime (21.69%), and doxycycline (20.48%). Sixty-eight isolates (81.93%) were resistant to at least two agents, whereas 11 (13.25%) met the class-based definition of multidrug resistance. At least one of the five tested ARGs was detected in 55 isolates (66.27%). The most frequent gene was *aac(3)-IV* (46.99%), followed by *sul1* (22.89%), *dfra1* (15.66%), *tetA* (13.25%), and *blaTEM* (7.23%). The mismatch between phenotypic resistance and detection of the selected genes indicates that the five-gene panel captured only part of the resistance background. Overall, antimicrobial-resistant *Salmonella* was present in the sampled duck production settings, supporting continued surveillance, improved biosecurity, and prudent antimicrobial use.

Keywords: Antimicrobial resistance, Duck production, Food safety, Mekong Delta, *Salmonella*

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INTRODUCTION

Duck production is an important component of agricultural livelihoods and food supply in the Mekong Delta of Vietnam. Ducks are commonly raised under scavenging, semi-intensive, and intensive conditions. These systems differ in bird density, contact with shared water sources, farm hygiene, and movement through live-bird markets, all of which may influence the circulation of enteric bacteria. Among these bacteria, *Salmonella* spp. remains a major foodborne pathogen associated with poultry and poultry-derived products (World Health Organization, 2018).

In Vietnam, *Salmonella* has been detected in poultry, farm environments, slaughterhouses, and retail markets, suggesting that the organism can persist at several points along the production and food supply chain (Nguyen et al., 2021; Nguyen et al., 2023). Ducks are relevant to this problem because they may carry and shed *Salmonella* without obvious clinical signs, allowing contaminated fecal material to enter farm environments, waterways, and market settings. This carrier state can make on-farm detection difficult and may contribute to continued environmental contamination (Kabir, 2010; EFSA Panel on Biological Hazards, 2019).

Antimicrobial resistance (AMR) in *Salmonella* is a concern in food-animal production because antimicrobial use can select for resistant populations (Uddin et al., 2021). Studies from Thailand have reported variable *Salmonella* occurrence and resistance patterns in meat goats, chicken meat, pork, and broiler production chains (Chamlakhorn et al., 2021; Vidayanti et al., 2021; Wongsrichai et al., 2021; Buawiratler et al., 2023). In Vietnam, resistant *Salmonella* has been identified in ducks, other poultry, farm environments, and duck carcasses (Nguyen et al., 2018; Nguyen et al., 2021; Nguyen et al., 2023). However, recent studies that examine sample-level occurrence, phenotypic susceptibility, and selected ARGs together in ducks from the Mekong Delta are scarce. Such information is useful because ducks may shed *Salmonella* without obvious clinical signs and move between household, farm, water-associated, and live-bird market environments (Kabir, 2010; EFSA Panel on Biological Hazards, 2019).

The present study therefore aimed to estimate the sample-level prevalence of *Salmonella* spp. among ducks from different production settings in the Mekong Delta and to characterize antimicrobial susceptibility and selected resistance determinants in the recovered isolates. The five PCR targets represented several well-described resistance mechanisms: *bla*TEM encodes a β -lactamase; *tetA* is associated with tetracycline efflux; *sul1* and *dfrA1* encode resistant variants of enzymes in the folate synthesis pathway; and *aac(3)-IV* encodes an aminoglycoside-modifying enzyme (Partridge et al., 2018; Vu et al., 2021; Das et al., 2022; Chu et al., 2024). These targets are commonly included in food-animal *Salmonella* surveillance and allow comparison with regional studies. The study provides a current reference for *Salmonella* occurrence and selected AMR characteristics in ducks sampled at these sites.

MATERIALS AND METHODS

Ethical approval

The study protocol was reviewed and approved by the Animal Ethics Committee of Can Tho University under approval code CTU-AEC24030. Cloacal swab collection was performed by trained personnel using a minimally invasive procedure, and no experimental treatment was imposed on the sampled ducks. Farm access and sample collection were conducted with permission from flock owners.

Sample collection and preparation

A total of 514 cloacal swab samples were obtained from ducks across the Mekong Delta, southern Vietnam, from February 2025 to March 2026. At the time of sampling, these sites were administratively located in Dong Thap, Hau Giang, and Soc Trang provinces. Because administrative boundaries in this region were subsequently reorganized, the sampling locations are reported using geographic coordinates to avoid ambiguity. The sampling sites included Tra Quyt market, Soc Trang (9.7054721°N, 105.8982169°E); Vi Thanh market, Hau Giang (9.7767095°N, 105.4600610°E); Mot Ngan town, Hau Giang (9.9099982°N, 105.6344354°E); and the Thap Muoi area, Dong Thap (10.5205625°N, 105.8388125°E), as illustrated in Figure 1.



Figure 1 Map of the Mekong Delta region in Vietnam showing the specific sampling locations. Red dots indicate the sampling sites in Dong Thap, Hau Giang, and Soc Trang provinces.

For each duck, age group, farming system, and fecal status were recorded as separate epidemiological variables. Categories within each variable were mutually exclusive, but every duck contributed information to all three variables. Ducks were grouped as <30 days ($n = 175$) or ≥ 30 days ($n = 339$), broadly corresponding to the starter and grower/finisher phases, respectively. Farming systems were classified as scavenging ($n = 64$), semi-intensive ($n = 210$), or intensive ($n = 240$), and fecal status as normal or diarrheic. Each variable was examined separately in relation to *Salmonella* positivity. Cloacal swabs were collected following TCVN 10782:2015 (Ministry of Science and Technology, 2015), placed in Cary-Blair transport medium, maintained at 4–8°C, and transported to the laboratory for microbiological examination within 12 h.

Isolation and identification of *Salmonella* spp.

Isolation and identification of *Salmonella* spp. were performed according to ISO 6579-1:2017 (International Organization for Standardization, 2017), with CHROMagar*Salmonella* Plus used as the chromogenic selective medium. Briefly, each cloacal swab was inoculated into 9 mL of buffered peptone water and incubated at 37°C for 18–24 h for pre-enrichment. After incubation, 0.1 mL of the pre-enrichment culture was transferred into 10 mL of Rappaport-Vassiliadis broth and incubated at 41.5°C for 24 h for selective enrichment.

A loopful of selective enrichment broth was streaked onto CHROMagar*Salmonella* Plus and incubated at 37°C for 24 h. Presumptive

Salmonella colonies were identified by their characteristic appearance on the chromogenic medium and purified on nutrient agar. For each positive sample, one or more colonies with the expected chromogenic appearance were selected for further testing, yielding 83 isolates from 58 positive samples. Biochemical confirmation was performed using Triple Sugar Iron agar, Urea agar, and the IMViC test series. Confirmed isolates were preserved in Nutrient Broth (NB) containing 20% glycerol at -80°C . Before antimicrobial susceptibility testing and PCR analysis, isolates were subcultured on Nutrient Agar (NA) at 37°C for 18–24 h to ensure viability and optimal growth.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was performed by the Kirby–Bauer disk diffusion method on Mueller–Hinton agar, as described by [Bauer et al. \(1966\)](#). Bacterial suspensions were prepared from fresh cultures and adjusted to a 0.5 McFarland standard. The nine-agent panel represented four antimicrobial classes used in regional poultry-associated *Salmonella* surveillance and was selected to support comparison with previous studies ([Nguyen et al., 2021](#); [Vidayanti et al., 2021](#); [Chu et al., 2024](#)): amoxicillin (AML, 10 μg), amoxicillin/clavulanic acid (AMC, 20/10 μg), cefotaxime (CTX, 30 μg), ceftriaxone (CRO, 30 μg), ceftazidime (CAZ, 30 μg), doxycycline (DOX, 30 μg), sulfamethoxazole/trimethoprim (SXT, 23.75/1.25 μg), gentamicin (GEN, 10 μg), and kanamycin (KAN, 30 μg).

After incubation, inhibition zones were measured and interpreted as susceptible, intermediate, or resistant according to published guidelines ([Clinical and Laboratory Standards Institute, 2023](#)). Only isolates classified as resistant were included in the resistance-profile analysis. Resistance to at least two individual antimicrobial agents was described as multi-agent resistance. Multidrug resistance (MDR) was defined as resistance to at least one agent in three or more antimicrobial classes, following [Magiorakos et al. \(2012\)](#). These in vitro classifications were not intended as treatment recommendations.

Genomic DNA extraction and detection of antimicrobial resistance genes

Genomic DNA was extracted from confirmed *Salmonella* isolates using the boiling lysis method described by [Chen and Kuo \(1993\)](#). Briefly, bacterial colonies were suspended in sterile nuclease-free water, heated at 100°C , and centrifuged. The supernatant containing crude DNA was collected and stored at -20°C until PCR analysis.

Five selected antimicrobial resistance genes (*bla*TEM, *dfr*A1, *tet*A, *sul*1, and *aac*(3)-IV) were examined by PCR. The targets were associated with resistance to β -lactams, trimethoprim, tetracyclines, sulfonamides, and aminoglycosides, respectively. PCR reactions were carried out in a final volume of 12.5 μL containing 2 $\times$ PCR Master Mix, forward and reverse primers, nuclease-free water, and DNA template. Positive and negative controls were included in every run. Primer sequences, expected amplicon sizes, and source references are listed in [Table 1](#).

Table 1 Primer sequences and predicted product sizes for PCR detection of selected antimicrobial resistance genes in *Salmonella* spp.

Antimicrobial group	Target gene	Primer sequence (5'-3')	Product size (bp)	Reference
β-lactam	<i>blaTEM</i>	F: TACGATACGGGAGGGCTTAC R: TTCCTGTTTTTCTCACCCA	716	Deb et al., 2020
Trimethoprim	<i>dfrA1</i>	F: CAATGGCTGTTGGTTGGAC R: CCGGCTCGATGTCTATTGT	253	Herrera-Sánchez et al., 2020
Tetracycline	<i>tetA</i>	F: GGCGGTCTTCTTCATCATGC R: CGGCAGGCAGAGCAAGTAGA	502	Das et al., 2022
Sulfonamide	<i>sul1</i>	F: TCACCGAGGACTCCTTCTT R: CAGTCCGCCTCAGCAATATC	331	Vu et al., 2021
Aminoglycoside	<i>aac(3)-IV</i>	F: GATGGGCCACCTGGACTGAT R: GCGCTCACAGCAGTGGTCAT	462	Chen et al., 2004

F: forward; R: reverse; bp: base pair.

Gene-specific cycling conditions are summarized in Table 2. PCR products were separated by agarose gel electrophoresis, stained, and visualized under UV illumination. An isolate was considered positive when an amplicon of the expected size was observed. Gene-detection frequencies were calculated at the isolate level. The *blaTEM* gene was included as a marker associated with aminopenicillin resistance, not as a proxy for all β-lactam resistance mechanisms.

Table 2 PCR thermal cycling conditions for the detection of antimicrobial resistance gene

Gene	Initial denaturation	Denaturation	Annealing	Extension	Final extension
<i>blaTEM</i>	94°C, 3 min	94°C, 1 min, 25 cycles	50°C, 1 min, 25 cycles	72°C, 1 min, 25 cycles	72°C, 10 min
<i>tetA</i>	95°C, 4 min	95°C, 1 min, 35 cycles	64°C, 1 min, 35 cycles	72°C, 1 min, 35 cycles	72°C, 7 min
<i>sul1</i>	95°C, 10 min	95°C, 30 s, 30 cycles	55°C, 1 min, 30 cycles	72°C, 1 min, 30 cycles	72°C, 7 min
<i>dfrA1</i>	94°C, 5 min	94°C, 30 s, 35 cycles	54°C, 1 min, 35 cycles	72°C, 1 min, 35 cycles	72°C, 10 min
<i>aac(3)-IV</i>	95°C, 10 min	95°C, 30 s, 30 cycles	55°C, 1 min, 30 cycles	72°C, 1 min, 30 cycles	72°C, 7 min

Statistical analysis

Data were entered and checked in Microsoft Excel before statistical analysis. The prevalence of *Salmonella* was calculated as the proportion of positive samples among the total number of samples examined. Exact 95% confidence intervals for prevalence estimates were calculated using the exact binomial method via R software version 4.2.2 (R Core Team, 2022).

Associations between *Salmonella* positivity and age group, farming system, and fecal status were examined separately in univariable contingency-table analyses. Pearson's chi-square test was used when its assumptions were met. Fisher's exact test, or the Fisher–Freeman–Halton exact test for larger tables, was used when expected cell counts were small. Statistical significance was set at $P < 0.05$.

Antimicrobial susceptibility results and selected ARG profiles were summarized descriptively at the isolate level. Because 83 isolates were obtained from 58 positive samples and some samples contributed more than one isolate, isolate-level resistance and gene-detection frequencies were not treated as host-level prevalence. The factors shown in Table 3 were also analyzed separately: categories within a factor were mutually exclusive, but each duck contributed data to the analyses of age group, farming system, and fecal status.

Table 3 Univariable associations between epidemiological factors and sample-level *Salmonella* positivity among ducks in the Mekong Delta (n = 514)

Factor	Category	No. of samples	No. positive	Prevalence (%)	95% CI	P-value
	Total	514	58	11.28	8.68-14.34	
Age	<30 days	175	23	13.14	8.52-19.07	0.339
	≥30 days	339	35	10.32	7.30-14.07	
Farming system	Scavenging	64	3	4.69	0.98-13.09	0.077
	Semi-intensive	210	21	10.00	6.30-14.88	
	Intensive	240	34	14.17	10.01-19.23	
Fecal status	Diarrhea	176	21	11.93	7.54-17.66	0.738
	Normal	338	37	10.95	7.83-14.77	

CI: confidence interval. Each epidemiological factor was analyzed separately. Categories within a factor were mutually exclusive, but each duck contributed data to the analyses of age group, farming system, and fecal status. Pearson's chi-square test was used when assumptions were met; exact tests were used when expected cell counts were small.

RESULTS

Prevalence and epidemiological distribution of *Salmonella* spp.

Salmonella spp. was detected in 58 of the 514 cloacal swab samples, giving a sample-level prevalence of 11.28% (95% CI: 8.68–14.34) (Table 3).

No significant difference in *Salmonella* positivity was observed between ducks aged <30 days and those aged ≥30 days. The prevalence was 13.14% in ducks aged <30 days and 10.32% in ducks aged ≥30 days ($P = 0.339$). Similarly, *Salmonella* prevalence did not differ significantly between ducks with diarrheic feces and those with normal feces, with positive rates of 11.93% and 10.95%, respectively ($P = 0.738$).

Salmonella positivity was lowest in scavenging systems (4.69%) and higher in semi-intensive (10.00%) and intensive systems (14.17%). The association was not statistically significant ($P = 0.077$), and the comparison was limited by the unbalanced group sizes (scavenging, $n = 64$; intensive, $n = 240$).

Antimicrobial susceptibility profiles

Antimicrobial susceptibility testing was performed on 83 representative *Salmonella* isolates using nine antimicrobial agents (Table 4). The highest resistance rates were observed for amoxicillin (84.34%) and amoxicillin/clavulanic acid (59.04%). Resistance to third-generation cephalosporins was lower, with resistance rates of 21.69% for cefotaxime, 14.46% for ceftriaxone, and 4.82% for ceftazidime.

Table 4 Antimicrobial susceptibility profiles of *Salmonella* isolates from ducks (n = 83 isolates)

Antimicrobial group	Antimicrobial agent (code)	Susceptible n (%)	Intermediate n (%)	Resistant n (%)
β-lactams	Amoxicillin (AML)	12 (14.46)	1 (1.20)	70 (84.34)
	Amoxicillin/clavulanic acid (AMC)	21 (25.30)	13 (15.66)	49 (59.04)
	Cefotaxime (CTX)	52 (62.65)	13 (15.66)	18 (21.69)
	Ceftriaxone (CRO)	64 (77.11)	7 (8.43)	12 (14.46)
	Ceftazidime (CAZ)	75 (90.36)	4 (4.82)	4 (4.82)
Tetracycline	Doxycycline (DOX)	59 (71.08)	7 (8.43)	17 (20.48)
Sulfonamide/trimethoprim	Sulfamethoxazole/trimethoprim (SXT)	55 (66.27)	2 (2.41)	26 (31.33)
Aminoglycosides	Gentamicin (GEN)	60 (72.29)	17 (20.48)	6 (7.23)
	Kanamycin (KAN)	59 (71.08)	16 (19.28)	8 (9.64)

Resistance was also detected to sulfamethoxazole/trimethoprim and doxycycline, with rates of 31.33% and 20.48%, respectively. Resistance to aminoglycosides was comparatively low, with 9.64% of isolates resistant to kanamycin and 7.23% resistant to gentamicin. Among the tested agents, ceftazidime showed the highest susceptibility rate (90.36%).

Phenotypic antimicrobial resistance profiles and multidrug resistance

Table 5 shows the number of antimicrobial agents to which each of the 83 isolates was resistant. Four isolates (4.82%) were susceptible to all tested agents, whereas 68 (81.93%) were resistant to at least two agents.

Table 5 Distribution of phenotypic resistance levels and common resistance profiles among *Salmonella* isolates from ducks (n = 83 isolates)

Resistance level	Dominant phenotype(s)	No. of isolates	Percentage (%)
Susceptible	No resistance detected	4	4.82
Resistant to 1 agent	DOX	6	7.23
	AML	3	3.61
	Other single-resistance profiles	2	2.41
Resistant to 2 agents	AML+AMC	22	26.51
	AML+SXT	5	6.02
	Other double-resistance profiles	4	4.82
Resistant to 3 agents	AML+AMC+SXT	6	7.23
	AML+CTX+CRO	3	3.61
	AML+AMC+CRO	2	2.41
	AML+AMC+KAN	2	2.41
	AML+AMC+DOX	2	2.41
	Other triple-resistance profiles	5	6.02
Resistant to ≥4 agents	AML+AMC+DOX+SXT	4	4.82
	Other profiles resistant to ≥4 agents	13	15.66
Total		83	100.00

AML: amoxicillin; AMC: amoxicillin/clavulanic acid; CTX: cefotaxime; CRO: ceftriaxone; CAZ: ceftazidime; DOX: doxycycline; SXT: sulfamethoxazole/trimethoprim; GEN: gentamicin; KAN: kanamycin.

The largest group consisted of isolates resistant to two antimicrobial agents (31/83, 37.35%), followed by isolates resistant to three agents (20/83, 24.10%). Seventeen isolates (20.48%) were resistant to four or more antimicrobial agents. Although 37 isolates (44.58%) were resistant to three or more individual agents, 11 isolates (13.25%) met the strict MDR definition of resistance to at least one agent in three or more antimicrobial classes.

The condensed resistance profiles are presented in Table 5. The most common resistance phenotype was AML+AMC, which was detected in 22 isolates (26.51%). Other observed profiles included AML+SXT, AML+AMC+SXT, AML+CTX+CRO, AML+AMC+CRO, AML+AMC+KAN, and AML+AMC+DOX. Among isolates resistant to four or more agents, the AML+AMC+DOX+SXT phenotype was observed in four isolates (4.82%), while other profiles resistant to ≥4 agents accounted for 13 isolates (15.66%).

Detection of antimicrobial resistance genes

Of the 83 isolates, 55 (66.27%) carried at least one of the five tested ARGs (Table 6). The most frequent gene was *aac(3)-IV*, detected in 39 isolates (46.99%), followed by *sul1* in 19 (22.89%), *dfrA1* in 13 (15.66%), *tetA* in 11 (13.25%), and *blaTEM* in six (7.23%). Percentages for individual genes are not additive because an isolate could carry more than one target. In the co-occurrence analysis (Table 7), 30 isolates (36.14%) carried one target, 17 (20.48%) carried two, and eight (9.64%) carried three. The most common two-gene profiles were *sul1* + *aac(3)-IV* and *aac(3)-IV* + *dfrA1*, each found in five isolates (6.02%).

Table 6 Frequency of selected antimicrobial resistance genes among *Salmonella* isolates from ducks (n = 83 isolates)

Antimicrobial group	Antimicrobial resistance gene	No. of positive isolates	Frequency (%)
β-lactam	<i>blaTEM</i>	6	7.23
Trimethoprim	<i>dfrA1</i>	13	15.66
Tetracycline	<i>tetA</i>	11	13.25
Sulfonamide	<i>sul1</i>	19	22.89
Aminoglycoside	<i>aac(3)-IV</i>	39	46.99
Any tested ARG	At least one of the five tested genes	55	66.27

Percentages are not additive because an isolate may carry more than one selected antimicrobial resistance gene.

Table 7 Co-occurrence patterns of selected antimicrobial resistance genes among *Salmonella* isolates from ducks (n = 83 isolates)

Number of ARGs	Genotypic profile (ARG combinations)	No. of isolates	Percentage (%)
0 genes	No tested ARGs detected	28	33.73
1 gene	<i>aac(3)-IV</i>	17	20.48
	<i>sul1</i>	5	6.02
	<i>tetA</i>	3	3.61
	<i>blaTEM</i>	3	3.61
	<i>dfrA1</i>	2	2.41
2 genes	<i>sul1</i> + <i>aac(3)-IV</i>	5	6.02
	<i>aac(3)-IV</i> + <i>dfrA1</i>	5	6.02
	<i>sul1</i> + <i>dfrA1</i>	2	2.41
	<i>tetA</i> + <i>aac(3)-IV</i>	2	2.41
	<i>aac(3)-IV</i> + <i>blaTEM</i>	2	2.41
	<i>tetA</i> + <i>dfrA1</i>	1	1.20
3 genes	<i>sul1</i> + <i>tetA</i> + <i>aac(3)-IV</i>	4	4.82
	<i>sul1</i> + <i>aac(3)-IV</i> + <i>dfrA1</i>	3	3.61
	<i>tetA</i> + <i>aac(3)-IV</i> + <i>blaTEM</i>	1	1.20
Total		83	100.0

DISCUSSION

Salmonella was detected in 58 of 514 cloacal swabs (11.28%) collected at selected sites in the Mekong Delta. These 58 samples yielded 83 isolates, many of which were resistant to more than one antimicrobial agent; about two-thirds carried at least one of the five selected ARGs. Because some samples yielded more than one isolate, the prevalence estimate applies to samples, whereas susceptibility and gene results describe the isolate collection.

The observed prevalence was close to the 11.67% reported by Ly and Nguyen (2010) in ducks from the Mekong Delta. This similarity should not be taken to mean that regional prevalence has remained unchanged, as the studies differed in sampling locations, sample types, production systems, study periods, and laboratory methods. Our result is also consistent with reports that poultry and poultry-associated environments can maintain *Salmonella* along production and market chains in the region (Nguyen et al., 2021).

Salmonella positivity was similar in ducks with normal and diarrheic feces. Fecal appearance alone is therefore unlikely to be a useful field screening criterion. Only fecal status was recorded, not a full clinical examination, so the comparison should not be interpreted as one between clinically healthy and diseased birds. Even so, the recovery of *Salmonella* from ducks with normal feces supports including birds without obvious fecal abnormalities in surveillance (Kabir, 2010; EFSA Panel on Biological Hazards, 2019).

Positivity rose numerically from scavenging to semi-intensive and intensive systems, but the association was not significant. The small scavenging group and unbalanced sample sizes limit the comparison, and no causal relationship can be inferred. Stocking density, confinement, hygiene, bird movement, and access to shared water may affect transmission, but these factors were not measured directly in this study (EFSA Panel on Biological Hazards, 2019). A balanced, repeated-sampling design would be needed to assess the effect of production intensity more reliably.

Resistance was dominated by the β -lactam agents, particularly amoxicillin and amoxicillin/clavulanic acid. Similar β -lactam resistance has been reported in *Salmonella* from ducks, other poultry, farm environments, and food-related sources in Vietnam (Nguyen et al., 2018; Nguyen et al., 2021; Vu et al., 2021). Studies from Thailand have also found substantial aminopenicillin resistance in isolates from chicken meat and pork (Vidayanti et al., 2021; Wongsrichai et al., 2021). Resistance to cefotaxime, ceftriaxone, and ceftazidime was less frequent than resistance to amoxicillin, but the presence of resistant isolates remains relevant to AMR surveillance.

Resistance to sulfamethoxazole/trimethoprim and doxycycline was also present, whereas resistance to gentamicin and kanamycin was uncommon. Ceftazidime had the highest proportion of susceptible isolates. These in vitro results should not be used to guide treatment without clinical assessment, diagnostic testing, antimicrobial-stewardship considerations, and applicable veterinary guidelines.

The proportion of isolates resistant to at least two agents should not be confused with the proportion meeting the MDR definition. Although 81.93% were resistant to at least two agents, only 13.25% were resistant to at least one agent in three or more antimicrobial classes (Magiorakos et al., 2012). Many profiles combined several β -lactams, increasing the number of drugs involved without adding another antimicrobial class. Reporting both measures therefore gives a more accurate picture of the resistance pattern.

Published AMR and MDR estimates for duck- and waterfowl-associated *Salmonella* vary widely because studies differ in sample source, production system, geographic setting, antimicrobial panel, laboratory criteria, and MDR definition (Chen et al., 2020; Chu et al., 2024; El Mansy et al., 2025). The MDR proportion reported here should therefore be considered in relation to the nine-agent panel and the class-based definition used. Even though only 13.25% met the strict MDR definition, the frequent multi-agent phenotypes warrant continued surveillance of duck-associated isolates in the Mekong Delta.

At least one selected ARG was detected in 66.27% of isolates. PCR confirms that a target DNA sequence is present, but it does not show whether the gene is expressed, functional, present in a particular genomic context, or responsible for the observed phenotype. A limited panel will therefore miss resistance mechanisms involving other genes or regulatory pathways, and some disagreement between genotype and phenotype is expected (McDermott et al., 2016).

The clearest mismatches involved amoxicillin and aminoglycosides. Amoxicillin resistance was detected in 84.34% of isolates, whereas *bla*TEM was found in only 7.23%, showing that *bla*TEM alone could not explain the phenotype. Other β -lactamases, regulatory changes, altered membrane permeability, or methodological factors may be involved, but this study did not test them. Likewise, *aac*(3)-IV was detected in 46.99% of isolates, while only 7.23% were resistant to gentamicin. Detection of the gene does not establish that it is expressed or functional under the test conditions. These results point to unresolved resistance mechanisms rather than identifying a specific alternative mechanism (McDermott et al., 2016).

The presence of *sul1* and *dfrA1* is biologically consistent with resistance to the components of sulfamethoxazole/trimethoprim, although paired genotype-phenotype analysis was not performed and agreement could not be quantified. The

most frequent two-gene profiles were *sul1* + *aac(3)-IV* and *aac(3)-IV* + *dfrA1*. Resistance genes may occur on mobile genetic elements such as integrons and plasmids and can be co-selected (Partridge et al., 2018; Chu et al., 2024). However, co-occurrence within the same isolate does not demonstrate physical linkage. Integron or plasmid characterization, or whole-genome sequencing, would be needed to establish the genomic context of these combinations.

Overall, the gene data add context to the phenotypic results but do not explain them fully. A broader ARG panel, additional β -lactamase and AmpC targets, paired genotype–phenotype analysis, and sequence confirmation of representative amplicons would improve molecular interpretation. Serovar identification would add epidemiological detail, although it would not by itself resolve gene–phenotype mismatches.

Antimicrobial-resistant *Salmonella* in cloacal swabs has implications for food safety and veterinary public health because fecal shedding can contaminate rearing areas, shared water, transport environments, and live-bird trading sites. This study did not trace transmission to people, duck products, or the wider environment; it therefore identifies a potential source of contamination rather than a demonstrated transmission pathway. Non-typhoidal *Salmonella* remains an important foodborne hazard associated with poultry and poultry-derived products (World Health Organization, 2018).

Continued AMR monitoring in duck production should include birds with normal feces. Practical control measures include prudent antimicrobial use, routine cleaning, reduced fecal contamination, careful management of shared water sources, and biosecurity practices that limit pathogen movement among birds, households, farms, and markets. These measures are consistent with international recommendations for AMR control in food-producing animals (World Organisation for Animal Health, 2024).

Several limitations should be noted. Sampling was confined to selected sites and was not designed to represent all duck production systems in the Mekong Delta. Group sizes were unbalanced, and the analysis did not account for possible clustering of ducks within farms, households, flocks, or trading sites. The reported prevalence therefore describes the sampled ducks and should not be interpreted as a probability-based estimate for the entire region.

The isolate collection also requires caution because 83 isolates came from 58 positive samples and some samples contributed more than one isolate. Isolate-level frequencies do not represent host-level prevalence or 83 independent ducks. Serovars were not identified, only five ARGs were screened, amplicons were not sequence-confirmed, and paired genotype–phenotype analysis was not undertaken. Future studies should use broader molecular characterization, more balanced sampling, and an analytical approach that reflects the sampling hierarchy.

CONCLUSIONS

Salmonella spp. was found in cloacal swabs from ducks at selected sites in the Mekong Delta, including birds with normal feces. Resistance was concentrated in amoxicillin and amoxicillin/clavulanic acid, and at least one of the five selected ARGs was detected in about two-thirds of the isolate collection. The limited agreement between resistance phenotypes and the selected genes indicates that important resistance determinants remain uncharacterized. The results support continued surveillance and practical measures to improve hygiene, biosecurity, and antimicrobial stewardship in duck production. They should be interpreted in light of the selected-site sampling, unbalanced groups, recovery of multiple isolates from some positive samples, lack of serovar data, and limited molecular testing.

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CONFLICT OF INTEREST

The authors declare no financial or personal conflicts of interest. ChatGPT (OpenAI) was used during manuscript revision for language editing and content structuring. All AI-assisted outputs were critically reviewed and verified by the authors, who take full responsibility for the accuracy and integrity of the final manuscript.

AUTHOR CONTRIBUTIONS

Pham Ngoc Thao Vy: Conceptualization (supporting); Methodology (equal); Investigation (lead); Formal analysis (lead); Writing – original draft (lead).

Nguyen Trong Ngu: Methodology (equal); Investigation (supporting); Data curation (lead); Writing – review & editing (equal).

Bui Thi Le Minh: Conceptualization (lead); Supervision (lead); Validation (lead); Project administration (lead); Writing – review & editing (equal). All authors approved the final manuscript.

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