Journal of Applied Biology & Biotechnology Vol. 13(2), pp. 258-265, March-April, 2025
Available online at http://www.jabonline.in
DOI: 10.7324/JABB.2025.226516

Antibiotic resistance of *Salmonella* from raw chicken meat at retail markets in Vinh Long Province

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ARTICLE INFO

Article history:
Received on: October 29, 2024
Accepted on: December 12, 2024
Available Online: January 25, 2025

Key words:
Chicken meat, food poisoning, multiple resistances, retail market, *Salmonella*

ABSTRACT

Salmonellosis is one of the most prevalent foodborne illnesses worldwide. This study aimed to evaluate the prevalence and antibiotic susceptibility of *Salmonella* isolates derived from raw chicken meat sold at various retail markets in Vinh Long Province, Vietnam. The results indicated that 100% of the chicken meat samples contained high densities of *Salmonella* spp. A total of 21 *Salmonella* isolates were obtained from these samples during this investigation. Using PCR techniques and 16S rRNA gene sequencing, three bacterial strains (SP5_7, SP8_8, and SP9_9) were identified as *Salmonella* spp., with similarities of 95.31%, 97.89%, and 93.60%, respectively. The antibiogram results revealed that the *Salmonella* isolates were highly sensitive to ampicillin-sulbactam (90%), sulfamethoxazole-trimethoprim (67%), and doxycycline (52%), and were completely sensitive to gentamicin. Conversely, significant resistance was observed against ampicillin (86%), tetracycline (71%), amoxicillin (62%), and ciprofloxacin (57%). Notably, 86% of the strains exhibited multiresistance to three to ten antibiotics, with the highest proportion (19%) showing resistance to three antibiotics. Furthermore, 18 out of the 21 strains presented a multiple antibiotic resistance (MAR) index >0.2, indicating frequent exposure to antibiotics. These findings underscore the necessity for stricter control measures in the sale of fresh chicken in markets to mitigate the spread of *Salmonella* in the environment.

1. INTRODUCTION

In Vietnam, consumers can easily purchase chicken meat (slaughtered and unprocessed) at retail markets or supermarkets. However, ensuring food hygiene and safety for chicken meat before, during, and after the slaughter process is a significant concern due to bacterial contamination from various sources. Most retail markets receive chicken meat from small, manual slaughterhouses with unsanitary conditions, posing a high risk of contamination from water sources and chicken feces at both the slaughterhouse and the point of sale [1]. Among the bacteria that cause foodborne illnesses, *Salmonella* is particularly dangerous, causing severe gastrointestinal diseases and is often associated with chickens produced and processed without adequate food hygiene and safety measures [2].

Salmonella spp. are rod-shaped, nonsporulating, gram-negative bacteria [3]. They are the primary source of food poisoning globally and can cause significant illness in both humans and animals [4]. According to the Centers for Disease Control and Prevention, *Salmonella* infections affect approximately 1.35 million people annually, resulting in about 420 deaths [5]. In Vietnam, *Salmonella* has been responsible for a series of food poisoning outbreaks in recent years [6]. Currently, over 2,500 *Salmonella* serovars have been identified in humans and animals, with approximately 10% isolated from poultry [7].

Among animal-derived food products, chicken meat is considered healthy due to its relatively high protein content and low-fat content [8]. However, raw chickens are a crucial source of *Salmonella* spp. infection in humans [9]. Poultry meat is linked to about 30% of foodborne salmonellosis infections globally [10]. Nontyphoid *Salmonella* spp. typically cause mild infections leading to diarrhea, which usually resolves on its own and rarely progresses to septicemia and meningitis [11]. In contrast, typhoid *Salmonella* spp. can cause severe symptoms, including fever, headache, and fatigue [12].

The pervasive use of antibiotics in veterinary, human, and agricultural medicine has led to the emergence and increase of antibiotic-resistant microorganisms, adversely impacting sustainable food production, agriculture, and the environment. Previous studies have documented antibiotic resistance in various bacterial species that cause diseases in humans [13], poultry [14], and other important animals in aquaculture, including shrimp and fish [15, 16]. Genes for antibiotic resistance can be transferred from bacteria containing these genes to other bacteria

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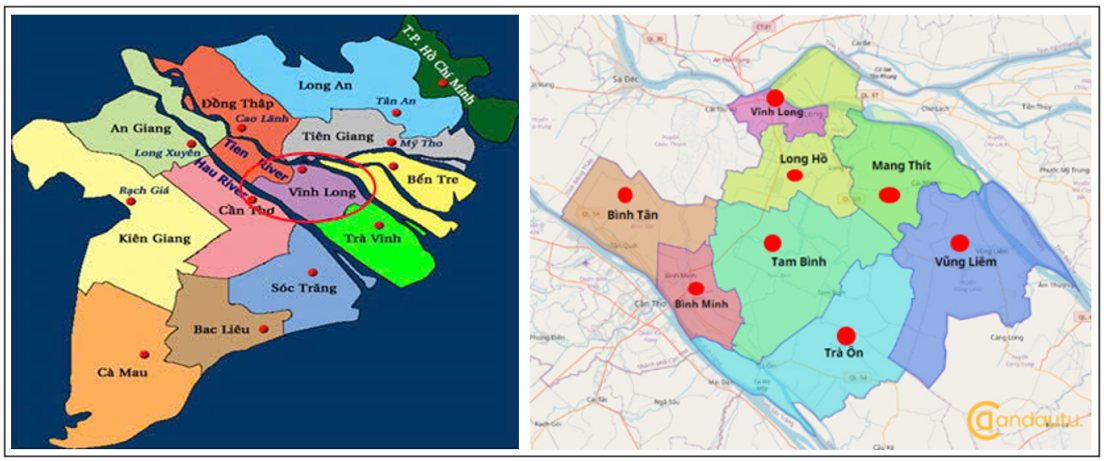

Figure 1. Chicken meat samples were obtained from retail markets in Vinh Long Province (red circles).

in the surrounding environment [17]. Treating bacterial infections has become increasingly challenging due to rising antibiotic resistance [18]. The overuse of antibiotics in veterinary and clinical medicine, as well as animal husbandry, has been linked to the development of antibiotic-resistant *Salmonella* isolates [19]. Various antibiotic-resistant *Salmonella* isolates have been collected from animal-derived products, especially poultry meat, and the surrounding environment [20,21]. Numerous studies globally and in Vietnam have recorded multidrug-resistant *Salmonella* spp. in chicken meat [22,23]. However, data on the antibiotic susceptibility of *Salmonella* in chicken meat from retail markets are limited.

Ensuring food safety for chicken meat in Vietnam is a significant concern due to the high risk of bacterial contamination, particularly from *Salmonella* spp. This study aimed to evaluate the antibiotic resistance and contamination rates of *Salmonella* originating from raw chicken meat at different retail markets in Vinh Long Province. The primary objectives were to determine the prevalence of *Salmonella,* characterize their antibiotic susceptibility, and identify potential sources of contamination. Using advanced molecular techniques like PCR and 16S rRNA gene sequencing, this research provides a detailed and precise identification of *Salmonella* strains, offering novel insights into the bacterial contamination landscape in this region. These findings reveal that *Salmonella* contamination in chicken meat is prevalent and that many strains exhibit significant antibiotic resistance. These results highlight the urgent need for stricter sanitary practices in both slaughterhouses and retail markets to mitigate the spread of antibiotic-resistant bacteria. This study not only adds valuable data to the existing body of knowledge but also has significant implications for public health and food safety. These findings support the development of effective strategies and policies to control bacterial contamination and manage antibiotic resistance, ultimately safeguarding consumer health.

2. MATERIALS AND METHODS

2.1. Study Design

The investigation was conducted between January and December 2023. In total, 83 samples of chicken meat were collected from different retail marketplaces in Vinh Long province. In a controlled environment, samples were collected in sterile plastic bags.

2.2. Collection and Testing of Chicken Meat Samples

Samples of raw chicken meat were collected from small retail markets in Vinh Long Province (Fig. 1). From each market, three samples of fresh chicken meat, including muscle, skin, and liver, were randomly selected. These samples were stored in foam boxes with ice, and then transported immediately by private vehicle to the laboratory for analysis of bacterial density and isolation of *Salmonella*.

2.3. Determination of *Salmonella* Densities

Salmonella bacterial densities in the chicken meat samples were determined using the Vietnamese standard (TCVN) 10780-1:2017 as a guide. Briefly, chicken muscle, skin, and liver samples were pooled and homogenized with sterilized distilled water. The homogenized sample was agitated at 120 rpm for 30 minutes, followed by serial dilution to 10^{-6}. Aliquots (0.1 ml) of each dilution were spread onto *Salmonella Shigella* agar (SS-agar, HiMedia, India). After 24 hours of incubation at 37°C, the bacterial colonies were counted. The bacterial population was determined using the following formula (log CFU/g): CFU/g = dilution level plated × number of colonies counted/volume plated [24].

2.4. *Salmonella* Isolation

Salmonella was isolated from the diluted samples. Specifically, 100 µl of each sample was spread on SS agar and incubated at 37°C. Selective colonies were picked and repeatedly cultured in appropriate media to obtain pure colonies. The colony morphology, motility, Gram stain, and catalase activity of the isolated bacterial strains were examined [25].

2.5. Antibiotic Sensitivity of *Salmonella* Isolates

The antibiotic susceptibility of the isolates was evaluated according to Bauer *et al.* [26]. Twelve antibiotics were tested: ceftazidime (30 µg), levofloxacin (5 µg), ampicillin (AMP/10 µg), doxycycline (DOX/30 µg), kanamycin (KAN/30 µg), gentamicin (GEN/10 µg), tetracycline (TET/30 µg), sulfamethoxazole-trimethoprim (SXT/23.75/1.25 µg), ciprofloxacin (CIP/5 µg), amoxicillin (AMO/10 µg), and AMP-sulbactam (AMS/10 µg). Colonies were dissolved in sterile 0.85% NaCl to match the turbidity of a McFarland standard, creating a suspension with a density of 10^8 CFU/ml. A 100 µl aliquot of the bacterial suspension was spread onto TSA media. The plates containing the antibiotic discs were incubated at 37°C for 24 hours.

The inhibition zones were then measured and evaluated according to the Clinical and Laboratory Standards Institute [27] guidelines for susceptibility (S), intermediate (I), and resistance (R). Resistance to three or more antibiotic classes was classified as multidrug resistance [28]. *Escherichia coli* ATCC® 25922 was used as a quality control.

2.6. Multiple Antibiotic Resistance (MAR) Indices

The MAR index for each bacterial strain was calculated using the formula MAR = R/E, where R represents the number of antibiotics to which the strain is resistant, and E represents the total number of antibiotics tested. A MAR value greater than 0.2 indicates frequent antibiotic use, while a value less than 0.2 indicates infrequent or nonuse of antibiotics [29].

2.7. Identification of *Salmonella*

Bacterial DNA extraction followed the method of Sambrook *et al.* [30], with slight modifications. *Salmonella* isolates were enriched in Luria Bertani media (LB media, Himedia, India) and shaken at 110 rpm at room temperature. Two milliliters of bacterial culture were centrifuged at 13,000 rpm for 5 minutes. The bacterial biomass was then resuspended in 1 ml of lysis buffer (1 M Tris-HCl, 0.5 mM EDTA, 5 M NaCl, 0.1% SDS, pH 8.0) and incubated for 30 minutes at room temperature. The supernatant was precipitated with 95% ethanol and resuspended in 70% ethanol. DNA samples meeting the purity and concentration requirements were stored in 100 µl of 0.1X TE solution (10 mM Tris-HCl, 1 mM EDTA, pH 8.0) at −80°C for PCR.

2.8. PCR Reaction

To amplify the 16S rRNA gene fragment of the bacterial isolates, the primer pairs 27F and 1492R were used [31]. PCRs were performed in a 12.5 µl volume containing distilled water, 1X PCR Buffer, 1.5 mM $MgCl_2$, 150 µM dNTPs, 20 pmol of each primer, 2.0 U *Taq* DNA polymerase, and the DNA sample. The PCR conditions were as follows: initial denaturation at 94°C for 5 minutes, followed by 30 cycles of denaturation at 94°C for 1 minute, primer annealing at 63°C for 1 minute, extension at 72°C for 2 minutes, and a final extension at 72°C for 10 minutes. The PCR products were electrophoresed on a 1.5% agarose gel, photographed using the Analytik Jena gel imaging system, and sequenced at Macrogen Company (Korea) for bacterial species identification.

2.9. Data Analysis

Descriptive statistical methods were employed to analyze the data, determining the average values and percentages of resistant, susceptible, intermediate, and sensitive bacterial strains, along with the overall bacterial population. The similarity of the DNA sequences of the isolated bacteria to known *Salmonella* spp. in the NCBI database was assessed using the BLASTn program. For the alignment of bacterial sequences with reference sequences, the CLUSTAL W program was utilized [32].

To construct a phylogenetic tree, the neighbor-joining method, a distance-based algorithm widely used for reconstructing phylogenies, was applied. This method was implemented with bootstrap values calculated from 1,000 replicates to ensure the robustness and reliability of the tree. The phylogenetic analysis was performed using MEGA6 software [33], which provided a detailed evolutionary relationship among the isolated *Salmonella* isolates and reference strains from the database. This comprehensive analysis not only confirmed the identity of the isolated strains but also offered insights into their genetic relatedness and evolutionary lineage.

Table 1. Bacterial population of *Salmonella* spp. on chicken at traditional markets.

Sample collection location	Number of samples	Bacterial densities (log CFU/g)
Vinh Long City	12	2.96 ± 0.03^{a}
Long Ho district	9	2.68 ± 0.12^{b}
Tam Binh district	8	2.81 ± 0.06^{ab}
Tra On district	10	2.75 ± 0.11^{ab}
Vung Liem district	11	2.74 ± 0.10^{ab}
Mang Thit district	12	2.73 ± 0.05^{ab}
Binh Minh district	10	2.64 ± 0.08^{b}
Binh Tan district	11	2.73 ± 0.07^{b}

*Note: mean ± standard deviation; different letters followed by numbers in the same column show significant differences ($p < 0.05$).

3. RESULTS

3.1. Bacterial Population of *Salmonella* in Chickens

The study revealed that all 83 chicken meat samples collected from various retail markets were contaminated with high densities of *Salmonella* spp. (Table 1). The bacterial densities ranged from 2.64 ± 0.08 to 2.96 ± 0.03 log CFU/g, with statistically significant differences observed between the surveyed markets.

Notably, the highest bacterial density was recorded in Vinh Long City (2.96 ± 0.03 log CFU/g), which could be attributed to higher market activity and possibly less stringent sanitary conditions. In contrast, the lowest density was found in Binh Minh (2.64 ± 0.08 log CFU/g), suggesting relatively better hygiene practices or lower market turnover. The bacterial densities in other districts, such as Long Ho (2.68 ± 0.12 log CFU/g) and Binh Tan (2.73 ± 0.07 log CFU/g), also showed considerable contamination but were significantly different from the highest and lowest values ($p < 0.05$).

These results indicate that while *Salmonella* contamination is a widespread issue across all markets, certain locations present relatively high bacterial loads, highlighting the need for targeted interventions to improve food safety standards. The significant variation in bacterial densities across different markets underscores the impact of local hygiene practices and the need for consistent and effective sanitary measures across all retail locations to mitigate health risks associated with *Salmonella* in chicken meat.

3.2. Isolation of *Salmonella* Isolates

Twenty-one *Salmonella* isolates were obtained from pooled samples of chicken muscle, liver, and skin and cultured on SS-agar media (Fig. 2A). The bacterial colonies on the SS-agar medium were colorless, with a black center, raised, intact, and small (Fig. 2B). The colony size ranged from 3–5 mm after 24–48 hours of incubation at 37°C. All the isolated strains were motile, gram-negative, and short rod-shaped (Fig. 2C), and all the strains were positive for catalase (Fig. 2C).

3.3. Antibiotic Susceptibility of *Salmonella* Isolates

The results demonstrated that *Salmonella* spp. strains exhibited varying degrees of sensitivity and resistance to different antibiotics (Fig. 3). The strains were most sensitive to AMS (90%), SXT (67%), and DOX (52%).

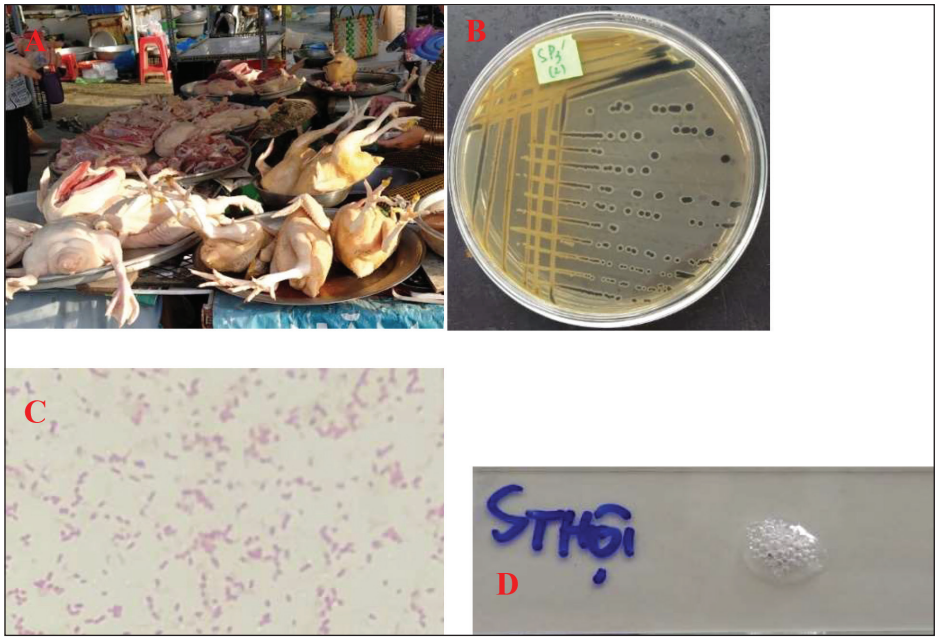

Figure 2. S*almonella* strains isolated on SS-agar medium with A. chicken meat samples from the retail market; B. *Salmonella* spp. was grown on SS agar media; C. gram stain results; D. catalase activity of the isolated strain.

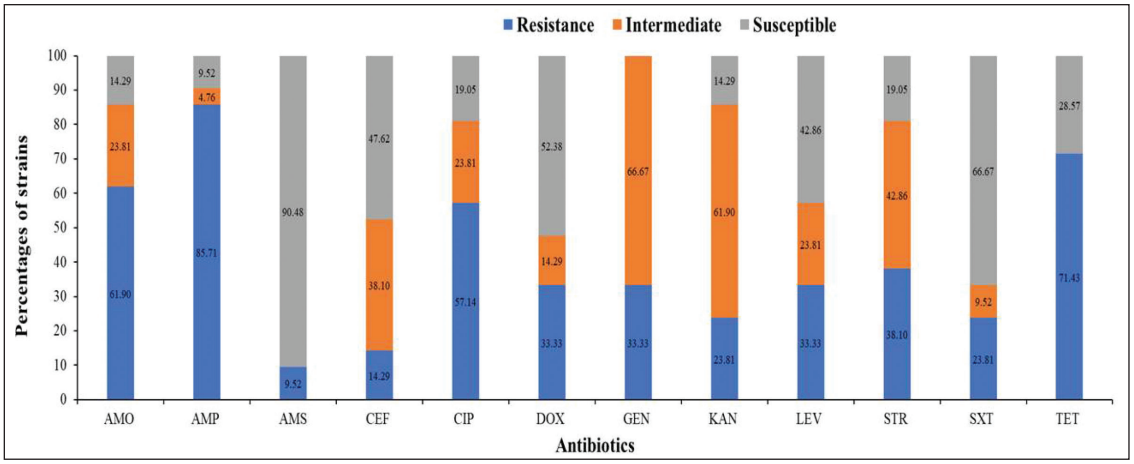

Figure 3. Proportion of *Salmonella* isolates susceptible to antibiotics. Note: AMO, AMP, AMS, CEF, CIP, DOX, GEN, KAN, LEV, STR, SXT, and TET.

However, these strains were completely resistant to GEN. Significant resistance was observed against AMP (86%), TET (71%), AMO (62%), and CIP (57%), with the lowest resistance observed for AMS (8%). These findings indicate significant variation in the susceptibility of *Salmonella* strains to different antibiotics, emphasizing the challenge posed by antibiotic resistance in bacterial infections. The high sensitivity to AMS suggests its potential effectiveness in treating infections caused by these strains. In contrast, the complete resistance to GEN and high resistance to antibiotics such as TET, AMP, CIP, and AMO highlight the pressing necessity for ongoing observation and prudent use of antibiotics to manage and control the spread of resistant *Salmonella* strains. The varying levels of resistance and susceptibility observed underscore the importance of implementing stringent antibiotic stewardship programs and enhancing hygiene practices in poultry production and processing environments. This approach can help mitigate the risk of antibiotic-resistant bacterial infections and ensure food safety for consumers.

3.4. Multidrug Resistance in Bacteria

Research has indicated that 86% of *Salmonella* spp. strains exhibit multidrug resistance (Fig. 4). The most common resistance pattern involved three antibiotics, with the highest rate of 19%. This was followed by resistance to four, five, eight, and nine antibiotics, each at 14%, while the lowest resistance was observed with six antibiotics at 10%. Additionally, out of the 21 bacterial strains identified in the present study, 20 presented multidrug-resistant phenotypes (Table 2). Notably, two strains, STH_10 and SVL_21, exhibited the same resistance phenotype to AMP and TET.

The high prevalence of MAR among *Salmonella* isolates highlights a critical public health issue. The diversity in resistance patterns suggests that these bacteria have been exposed to multiple antibiotics, resulting in the selection of resistant strains. The most common resistance to these three antibiotics underscores the need for stringent antibiotic usage policies and the importance of regular surveillance

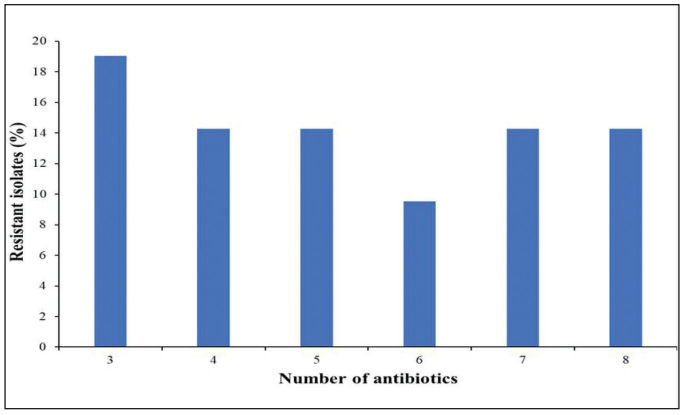

Figure 4. Multidrug resistance rate of isolated S*almonella* strains.

to monitor resistance trends. The identification of common resistance phenotypes, such as AMP-TET, provides valuable information for developing targeted treatment strategies and informs public health interventions to mitigate the spread of resistant isolates.

3.5. MAR Indices of *Salmonella*

The results demonstrated that the multidrug resistance index of *Salmonella* isolates ranged from 0.17 to 0.67 (Table 2). Notably, the majority of bacterial strains (eighteen out of twenty-one) presented a MAR index >0.2, indicating frequent exposure to antibiotics. The highest multidrug resistance indices were observed in strains SP8_8, SP9_9, and SBM_20, each with a MAR index of 0.67.

The high MAR indices observed among the *Salmonella* isolates suggest widespread and frequent use of antibiotics, leading to significant multidrug resistance. Strains exhibiting the highest MAR indices, such as SP8_8, SP9_9, and SBM_20, pose a substantial public health risk due to their potential resistance to multiple commonly used antibiotics. These results underline the importance of enforcing strict antibiotic stewardship and improving antibiotic usage monitoring in poultry production and retail settings. The presence of multidrug-resistant phenotypes underscores the need for developing and implementing effective antibiotic management policies to mitigate the spread of resistant strains and ensure food safety.

3.6. *Salmonella* Identification via PCR

The findings demonstrated that the 16S rRNA gene segment was effectively amplified from all the isolated bacterial strains via PCR, resulting in a product size of approximately 1,500 bp (Fig. 5).

The sequencing results indicated that three strains, SP5_7, SP8_8, and SP9_9, shared 95.31%, 97.89%, and 93.60% similarity, respectively, with *S. enterica* strain KS7 (KT270313.1), *S. enterica* strain GS-31 16S (OP382468.1), and *S. enterica* isolate SV68221 (LR792423.1) from GenBank. Phylogenetic tree analysis revealed that these three bacterial isolates were genetically closely related and grouped with known *Salmonella* strains in the GenBank database (Fig. 6). These results confirm the identity of the isolated strains as *Salmonella* spp. and highlight their genetic similarity to previously characterized strains. The effective amplification and sequencing of the 16S rRNA gene segment provide solid evidence for the presence and identification of *Salmonella* in the samples, supporting the conclusion that these isolates belong to the same phylogenetic group as other *Salmonella* strains recorded in GenBank. This genetic information is crucial for understanding the epidemiology and potential pathogenicity of these isolates, contributing to broader efforts in monitoring and controlling *Salmonella* contamination in food products.

Table 2. Phenotypes and multi-resistance indexes of *Salmonella* isolates.

Bacterial isolates	Multiple antibiotic resistance phenotype	MAR index
SP3_4	AMP-CIP-TET	0.25
SP4_6	AMP-GEN-TET	0.25
STH_12	AMO-AMP-DOX	0.25
SMT_19	AMP-STR-TET	0.25
SP3_3	AMO-AMP-CEF-CIP	0.33
SP4_5	AMO-AMP-CIP-LEV	0.33
STH_13	AMP-CIP-DOX-GEN	0.33
SP2_2	AMP-CIP-GEN-LEV-STR	0.42
STO_16	AMO-AMP-DOX-KAN-TET	0,42
STB_17	AMO-AMP-CIP-DOX-TET	0.42
STH_11	AMO-AMP-CEF-DOX-GEN-STR	0.50
SLH_18	AMO-AMP-CIP-KAN-LEV-TET	0.50
SP1_1	AMO-CIP-KAN-LEV-STR-SXT-TET	0.58
STA_14	AMO-AMP-DOX-GEN-STR-SXT-TET	0,58
STN_15	AMO-AMP-AMS-CIP-DOX-LEV-TET	0.58
SP8_8	AMO-AMP-CEF-CIP-KAN-STR-SXT-TET	0.67
SP9_9	AMO-CIP-GEN-KAN-LEV-STR-SXT-TET	0.67
SBM_20	AMO-AMP-AMS-CIP-LEV-STR-SXT-TET	0.67

*Note: AMO (amoxicillin), AMP (ampicillin), AMS (ampicillin-sulbactam), CEF (ceftazidime), CIP (ciprofloxacin), DOX (doxycycline), GEN (gentamicin), KAN (kanamycin), LEV (levofloxacin), STR (streptomycin), SXT (sulfamethoxazole-trimethoprim), TET (tetracycline).

4. DISCUSSION

Salmonella spp. are critical indicators of contamination in fresh meat, and their presence is prohibited by Vietnamese standards (TCVN 7046:2009). However, this study indicates an increased frequency of *Salmonella* infection in chicken meat sold at traditional markets, with significant differences observed among the surveyed markets. Specifically, the highest contamination density was recorded in Vinh Long city, while the lowest was found in Binh Minh ($p < 0.05$). These results surpass those of earlier research; for example, Huong *et al.* [34] reported a 48.9% contamination rate in chicken meat from retail markets in Hanoi, and Manh *et al.* [35] reported a 41.7% contamination rate in Ben Tre city. Additionally, a study in Egypt by El-Aziz [36] detected *S. typhimurium* in 44% of fresh chicken meat, 40% of liver, and 48% of heart samples. The high contamination rates observed in the present study may be attributed to poor hygienic conditions throughout the chicken production chain like storage conditions or the hygiene practices at the markets, including inadequate sanitation of water sources [37]. Furthermore, the high rate of *Salmonella* contamination in this study might be the result of possible limitations, such as the representativeness of the poultry meat samples or the sampling size; the samples were not taken from a variety of market types, such as supermarkets, small retail stores, or wet markets; and there are variations in the handling procedures or hygiene standards among market vendors during transportation.

Regarding antibiotic resistance, the results revealed that *Salmonella* strains exhibited high resistance rates to AMP (86%), TET (71%), AMO (62%), and CIP (57%). These findings align with those of Akinola *et al.* [38], who reported significant resistance in *Salmonella*

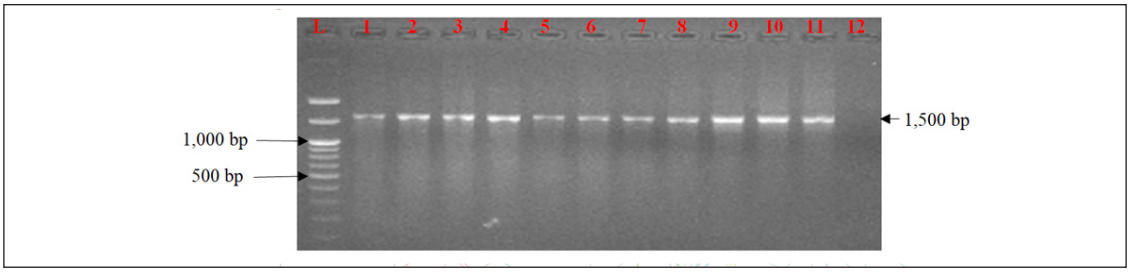

Figure 5. Amplification of the 16S rRNA gene segment of representative *Salmonella* isolates via PCR. Note: L: 100 bp DNA standard ladder; Lanes 1-11: bacterial strains SP5_7, SP3_4, SP4_6, STH_12, SMT_19, SP3_3, SP4_5, STH_13, STO_16, SP8_8, and SP9_9, respectively; Lane 12: Negative control.

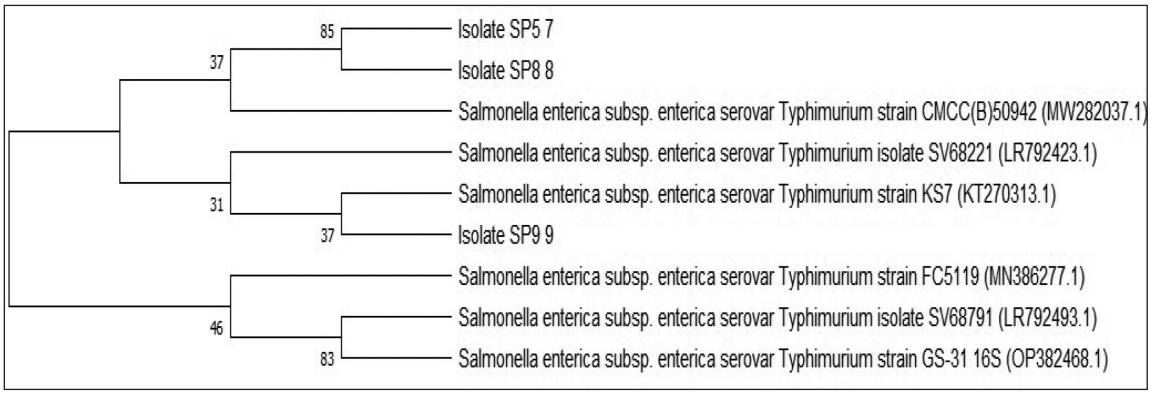

Figure 6. Phylogenetic tree showing isolates belonging to the same group as S*almonella* spp. in Genbank.

strains from broilers and egg-laying chickens in South Africa to AMP (56%), TET (69%), and CIP (30%). Similar patterns of resistance have been observed in other regions. For example, Kanaan [39] reported that *Salmonella* isolates from frozen and raw chickens in Iraq exhibited high resistance to nalidixic acid (73.7%), TET (63.2%), and SXT (63.2%). In Morocco, *Salmonella* isolates were resistant to TET (57.50%), CIP (57.50%), and KAN (27.50%), but no resistance to GEN was detected [40]. In Vietnam, Nhat *et al.* [41] reported resistance rates of 68.8% for AMP, 67.7% for TET, and 57.3% for trimethoprim in *Salmonella* isolates from pig and poultry meat. Additionally, Huong *et al.* [42] demonstrated high resistance rates to AMP (59.5%), TET (83.8%), and streptomycin (89.2%) in *Salmonella* strains from poultry farms in North Vietnam. Antibiotic resistance is likely a result of the indiscriminate use of antimicrobials as growth promoters and medicinal agents on farms [43]. Resistance can originate at various stages, from breeding sites [44] to animal feed [45], and within farming environments for broilers and egg-laying chickens [46]. This ultimately leads to the circulation of drug-resistant bacteria in products, presenting a serious risk to consumer health [47]. Many previous studies established a relationship between agricultural antibiotic use and resistance patterns in foodborne pathogens [48,49].

The multidrug resistance phenomenon of *Salmonella* has been extensively documented in prior research [50]. In the current investigation, 86% of *Salmonella* isolates exhibited multidrug resistance, which is greater than the 29.4% reported by Fanissa *et al.* [51] in chicken meat from traditional markets in Indonesia. In Malaysia, Sukri *et al.* [52] reported that all *Salmonella* isolates from raw chicken and contact surfaces in wet markets were multidrug resistant to erythromycin, penicillin, TET, and chloramphenicol. Similarly, Zhang *et al.* [53] reported an 81.1% multidrug resistance rate in *Salmonella* spp. from chicken meat in China. Furthermore, Ali *et al.* [54] revealed that 86% of *Salmonella* strains from retail chickens in Ethiopia were resistant to 2–7 antibiotics. Guran *et al.* [55] illustrated that 86.3% of *Salmonella* strains from organic chickens in Turkey were multidrug resistant. In summary, the high rate of multidrug resistance and *Salmonella* infection found in this study highlights the critical need for improved hygienic procedures in the retail and chicken production industries. These findings call for stringent antibiotic stewardship and continuous monitoring to mitigate the spread of resistant strains and ensure consumer safety; for instance, suggestions for better farm management techniques, surveillance, or legislative adjustments may be helpful.

5. CONCLUSION

This study revealed that all tested chicken meat samples from traditional markets in Vinh Long were heavily contaminated with *Salmonella* spp., with significant variations in contamination levels across different markets. Three bacterial strains (SP5_7, SP8_8, and SP9_9) were confirmed as *Salmonella* spp. through PCR techniques and 16S rRNA gene sequencing. The antibiogram results revealed extensive resistance to multiple antibiotics, with a multidrug resistance rate of 86%, and a majority of the strains exhibited frequent antibiotic exposure, as indicated by a MAR index >0.2. The novel application of advanced molecular techniques in this study provides important new information about the state of bacterial contamination and emphasizes the critical need for focused interventions and improved sanitary practices in slaughterhouses and retail markets. Future research should concentrate on stringent antibiotic stewardship programs and continuous surveillance to manage and control the spread of antibiotic-resistant *Salmonella* strains, ensuring the sustainability of poultry farming practices and safeguarding public health.

6. AUTHOR CONTRIBUTIONS

All authors made substantial contributions to conception and design, acquisition of data, or analysis and interpretation of data; took part in drafting the article or revising it critically for important intellectual content; agreed to submit to the current journal; gave final approval of the version to be published; and agree to be accountable for all aspects of the work. All the authors are eligible to be an author as per the international committee of medical journal editors (ICMJE) requirements/guidelines.

7. FUNDING

There is no funding to report.

8. CONFLICTS OF INTEREST

The authors report no financial or any other conflicts of interest in this work.

9. ETHICAL APPROVALS

This study does not involve experiments on animals or human subjects.

10. DATA AVAILABILITY

All the data is available with the authors and shall be provided upon request.

11. PUBLISHER'S NOTE

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12. USE OF ARTIFICIAL INTELLIGENCE (AI)-ASSISTED TECHNOLOGY

The authors declares that they have not used artificial intelligence (AI)-tools for writing and editing of the manuscript, and no images were manipulated using AI.

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How to cite this article:
Quach TCV, Nguyen TT. Antibiotic resistance of *Salmonella* from raw chicken meat at retail markets in Vinh Long Province. J Appl Biol Biotech 2025;13(2):258–265. DOI: 10.7324/JABB.2025.226516