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Phenotypic and Genomic Detection of *Salmonella* spp. in Broiler Chicken Meat Across Distribution Chains in Surabaya, Indonesia

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Abstract: This study aimed to investigate *Salmonella* spp. contamination in broiler chicken meat obtained from traditional markets, modern markets, and poultry slaughterhouses in Surabaya, East Java, using phenotypic and genomic approaches. A total of 15 broiler chicken meat samples were analyzed. Phenotypic identification was performed through colony morphology observation, Gram staining, and biochemical testing, while genomic confirmation was conducted using Polymerase Chain Reaction (PCR) targeting the *invA* gene. The results showed that two samples (13.33%) obtained from traditional markets were positive for *Salmonella* spp., whereas all samples collected from modern markets and poultry slaughterhouses tested negative. These findings indicate variation in contamination levels among different distribution sources, with a higher risk of *Salmonella* spp. contamination in broiler chicken meat sold in traditional markets. Therefore, strengthened surveillance and improved hygiene and sanitation practices are essential to ensure food safety and protect public health. This study provides comparative evidence of *Salmonella* spp. contamination across different broiler chicken distribution channels through the integration of phenotypic identification and molecular confirmation.
Keywords: *Salmonella* spp.; broiler chicken meat; phenotypic identification; *invA* gene; food safety

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INTRODUCTION

Food availability is one of the most fundamental human needs and requires careful attention in terms of both quality and quantity (Pathiassana & Zharrido, 2021). An adequate supply of safe and nutritious food contributes not only to public health, productivity, and well-being but also to broader social and economic development (Choi et al., 2023). In this context, food safety has become a major consumer concern, emphasizing the need to ensure that food products are free from pathogenic microorganisms and safe for consumption (Sriwulan et al., 2022). In Indonesia, animal protein is an important component of the daily diet, with chicken meat being one of the most widely consumed sources (Maya et al., 2023). Broiler chicken meat is particularly preferred because of its high protein content, favorable fat composition, and digestibility (Sihotang et al., 2023). Broilers also offer production advantages, including rapid growth and efficient feed conversion (Mar'i, 2025). However, the high nutrient content of chicken meat also provides a suitable medium for the growth of pathogenic microorganisms, thereby increasing the risk of contamination that may threaten consumer health (Glendinning et al., 2019).

One of the major food safety concerns in poultry products is contamination by *Salmonella* spp., an important foodborne pathogen associated with salmonellosis (Pavelquesi et al., 2023). Salmonellosis may cause clinical symptoms such as diarrhea, abdominal pain, vomiting, and fever (Yanestria, 2019). Previous research has shown that broiler chickens are susceptible to contamination by harmful

microorganisms that can cause food poisoning (Ramadani et al., 2023). Transmission of *Salmonella* commonly occurs through the consumption of unhygienic food, either as a result of direct contamination or cross-contamination during handling and processing (Andari and Yudhayanti, 2022). This risk is particularly relevant in developing countries, where food safety surveillance systems often remain limited and face multiple implementation challenges (Jayaweera et al., 2020).

Salmonella contamination may occur at various stages of the broiler chicken production and distribution chain, including farming, transportation, slaughtering at poultry slaughterhouses, distribution, and retail sale (Voss, 2019). Several factors may serve as critical control points, including feed, water, and housing conditions at the farm level (Gosling et al., 2022), transportation conditions (Elsayed, 2019), and evisceration during slaughtering (Zeng et al., 2021). In addition, inadequate cold chain management during distribution (Necidova et al., 2024) and poor hygiene practices at the market level (Nopriani et al., 2020) may further increase the likelihood of bacterial contamination. These conditions highlight the need to evaluate contamination not only at a single point in the supply chain but also across different distribution channels.

Although many studies have investigated *Salmonella* spp. contamination in chicken meat, several methodological limitations remain. Phenotypic identification through culture and biochemical testing enables the observation of bacterial morphology and growth characteristics, but it may be limited in sensitivity, specificity, and detection speed (Vargas et al., 2023). In contrast, molecular identification using Polymerase Chain Reaction (PCR) provides a faster, more specific, and more sensitive approach for detecting *Salmonella* spp. (Jayaweera et al., 2020; Melati et al., 2022). Previous studies by Shofia et al. (2023) and Darmawan et al. (2020) relied primarily on phenotypic approaches without molecular confirmation, which may limit the comprehensiveness of the findings. Conversely, studies based solely on molecular detection often provide limited information on bacterial phenotypic characteristics. Therefore, combining phenotypic and molecular approaches is necessary to obtain more reliable and comprehensive detection of *Salmonella* spp.

In addition to methodological limitations, previous studies have not sufficiently compared *Salmonella* spp. contamination across multiple poultry distribution channels, including traditional markets, modern markets, and poultry slaughterhouses, within a single urban setting. In Surabaya, comparative data across these distribution sources remain limited, despite differences in hygiene practices, handling procedures, and cold chain implementation that may influence contamination levels. Such comparative information is important for identifying potential contamination patterns and critical points within the local broiler chicken meat supply chain.

Based on this background, this study aimed to identify the presence of *Salmonella* spp. in broiler chicken meat obtained from traditional markets, modern markets, and poultry slaughterhouses in Surabaya, East Java. This study also aimed to describe the phenotypic characteristics of suspected isolates, confirm the presence of *Salmonella* spp. using PCR targeting the *invA* gene, and compare contamination levels among distribution locations. The study refers to the Indonesian National Standard SNI 9159:2023, which requires *Salmonella* spp. to be absent in 25 g of chicken meat (Apriyanti et al., 2020). The contribution of this study lies in the integration of phenotypic identification and molecular confirmation, as well as in its comparative assessment of *Salmonella* spp. contamination across different broiler chicken meat distribution channels in Surabaya. These findings support food safety, salmonellosis prevention, and contamination control in broiler meat supply chains.

METHOD

Research Design

This study employed an exploratory descriptive design with an observational approach to detect and identify *Salmonella* spp. contamination in broiler chicken meat. The exploratory component involved collecting broiler chicken carcass samples from three distribution points in Surabaya: a traditional market, a modern market, and a poultry slaughterhouse. The descriptive component was used to characterize the occurrence of *Salmonella* spp. contamination based on phenotypic and genomic identification in accordance with the SNI 9159:2023 standard.

The study was conducted from December 2025 to January 2026 and consisted of two main stages: sample collection and laboratory analysis. All collected samples were analyzed at the Gastro Laboratory, Institute of Tropical Disease, Airlangga University, which is equipped with facilities for microbiological and molecular testing. The research procedures were performed systematically through bacterial isolation, phenotypic identification using morphological and biochemical assays, and genomic confirmation using polymerase chain reaction (PCR) targeting the *invA* gene. The overall workflow included sample collection, cold-chain transportation, bacterial isolation, phenotypic testing, and molecular analysis, all of which were designed to ensure accurate and comprehensive detection of *Salmonella* spp.

Research Samples

The samples used in this study were fresh whole broiler chicken carcasses. The carcasses had been defeathered and eviscerated, with the heads, feet, and internal organs removed, and had not undergone further processing, freezing, or preservation. Therefore, the samples were classified as raw, retail-ready carcasses.

Samples were obtained from three distribution locations in Surabaya, namely one traditional market, one modern market, and one poultry slaughterhouse. These locations were selected to represent differences in hygiene, sanitation, and cold-chain management practices. Sampling was conducted using a simple random sampling technique by selecting available broiler chicken carcasses at each location without prior selection based on physical appearance or seller preference. A total of 15 samples were collected, comprising five samples from each distribution category.

The sample size was determined based on the considerations of an exploratory study and the minimum sampling requirements for microbiological testing according to SNI 9159:2023. Sampling was carried out in the morning between 5:00 and 9:00 AM using aseptic procedures, including the use of gloves and sterile containers, to prevent cross-contamination. This sampling period was selected to ensure sample freshness immediately after processing and distribution.

After collection, the samples were placed in a cooler box maintained at approximately 4°C using ice packs to preserve microbiological conditions during transportation. The samples were then transported to the laboratory on the same day for analysis. Each sample was assigned an identification code according to its collection location to facilitate data recording and analysis. Thus, the samples were intended to represent broiler chicken meat distributed through different marketing channels in Surabaya.

Research Instruments and Procedures

The instruments used in this study included standard microbiological and molecular laboratory equipment, such as Petri dishes, test tubes, incubators, microscopes, autoclaves, micropipettes, thermal cyclers, and electrophoresis apparatus. The materials used included selective and enrichment media, namely

Xylose Lysine Deoxycholate (XLD) agar, Buffered Peptone Water (BPW), and Selenite broth, as well as reagents for biochemical testing and PCR analysis. The procedures followed the SNI 9159:2023 and SNI 2897:2008 standards to ensure methodological validity, standardization, and scientific accountability.

The procedure began with sterilization of laboratory equipment using an autoclave at 121°C for 15 minutes. Samples were then collected aseptically and subjected to bacterial isolation through pre-enrichment in BPW, selective enrichment in Selenite broth, and inoculation onto XLD agar. From each presumptive positive sample, three representative colonies were selected, resulting in a total of nine isolates for biochemical testing. This step was performed to capture potential intra-sample variation among colonies with similar morphological characteristics.

Colonies suspected to be *Salmonella* spp. were further examined phenotypically through morphological observation, Gram staining, and biochemical tests, including Triple Sugar Iron Agar (TSIA), Lysine Iron Agar (LIA), motility, indole, urease, citrate, methyl red (MR), and Voges–Proskauer (VP) tests. Isolates showing results consistent with *Salmonella* spp. were subsequently confirmed genomically using PCR targeting the *invA* gene.

The primers used for PCR amplification were as follows: forward primer 5'-GTG AAA TTA TCG CCA CGT TCG GGC AA-3' and reverse primer 5'-TCA TCG CAC CGT CAA AGG AAC C-3'. DNA extraction was performed using the boiling method. PCR amplification was carried out under optimized conditions, consisting of initial denaturation at 95°C for 5 minutes, followed by 35 cycles of denaturation at 95°C for 30 seconds, annealing at 60°C for 30 seconds, and extension at 72°C for 30 seconds, with a final extension at 72°C for 5 minutes.

The amplified PCR products were analyzed using 1.5% agarose gel electrophoresis and visualized under UV transillumination. The presence of a DNA band at approximately 284 bp was interpreted as positive for *Salmonella* spp. A known *Salmonella* spp. strain was used as the positive control, while nuclease-free water was used as the negative control to validate the PCR results and prevent false-positive amplification.

Data Analysis

Data were analyzed descriptively to determine the presence and characteristics of *Salmonella* spp. contamination in broiler chicken meat samples collected from different distribution locations. Phenotypic identification data were analyzed based on the consistency of colony morphology and biochemical test results with the typical characteristics of *Salmonella* spp., in accordance with SNI 2897:2008.

Genomic identification data were analyzed based on the presence of a specific DNA band resulting from amplification of the *invA* gene, with an expected amplicon size of approximately 284 bp. A sample was considered positive when it exhibited phenotypic characteristics consistent with *Salmonella* spp. and was confirmed by PCR through the presence of the target DNA band. Conversely, a sample was considered negative when it did not meet both criteria.

The results were further compared across sampling locations to examine the distribution of *Salmonella* spp. contamination in traditional markets, modern markets, and poultry slaughterhouses. This analysis was intended to provide a comprehensive overview of contamination patterns and differences in microbiological conditions among distribution channels. The findings were then interpreted qualitatively in relation to the research objectives and applicable food safety standards, thereby providing a basis for drawing conclusions and formulating recommendations.

RESULTS AND DISCUSSION

Salmonella spp. Contamination Status in Broiler Chicken Meat

Salmonella spp. contamination was detected in 2 out of 15 samples (13,33%), all originating from traditional markets. Samples were classified as positive only when both phenotypic and PCR results were consistent (Table 1). This approach aims to improve identification accuracy and minimize the possibility of errors due to similarities in characteristics with other enteric bacteria.

Table 1. Contamination status of chicken meat from traditional markets, modern markets, and poultry slaughterhouses in Surabaya, East Java

Sample Code	Sampling location	Contamination Status	Contamination percentage
PT DA 1	Traditional Market	Negative	
PT DA 2	Traditional Market	Negative	
PT DA 3	Traditional Market	Positive	40 %
PT DA 4	Traditional Market	Negative	
PT DA 5	Traditional Market	Positive	
PM DA 6	Modern Market	Negative	
PM DA 7	Modern Market	Negative	
PM DA 8	Modern Market	Negative	0%
PM DA 9	Modern Market	Negative	
PM DA 10	Modern Market	Negative	
RPHU DA 11	Poultry Slaughterhouses	Negative	
RPHU DA 12	Poultry Slaughterhouses	Negative	
RPHU DA 13	Poultry Slaughterhouses	Negative	0%
RPHU DA 14	Poultry Slaughterhouses	Negative	
RPHU DA 15	Poultry Slaughterhouses	Negative	
Total	**All Locations**	**2/15 positive**	**13.33%**

Based on Table 1, phenotypic and molecular identification consistently confirmed that 2 out of 15 samples were positive for Salmonella spp., namely PT DA 3 and PT DA 5, resulting in an overall contamination percentage of 13.33%. Both positive samples originated from traditional markets, with a contamination percentage of 40% (2/5 samples). This pattern suggests that contamination is strongly associated with retail-level handling conditions rather than upstream processing at slaughterhouses. Traditional markets typically lack controlled temperature management and have higher exposure to environmental contaminants, which may facilitate post-processing contamination of chicken meat.

The detection of contamination only in traditional market samples in this study may indicate differences in handling, hygiene, or sanitation conditions during distribution and selling processes. Traditional markets generally have more open selling environments, higher exposure to flies, repeated contact between meat and selling surfaces, and less controlled storage temperatures compared to modern markets and poultry slaughterhouses. These conditions may increase the risk of bacterial contamination during the selling process. However, these findings are limited to the samples analyzed in this study. *Salmonella* contamination status was determined through sequential identification stages, including presumptive testing using XLD selective media, colony morphology observation, Gram staining, biochemical testing, and molecular confirmation using the PCR method. These procedures were conducted to improve the accuracy of *Salmonella* spp. identification.

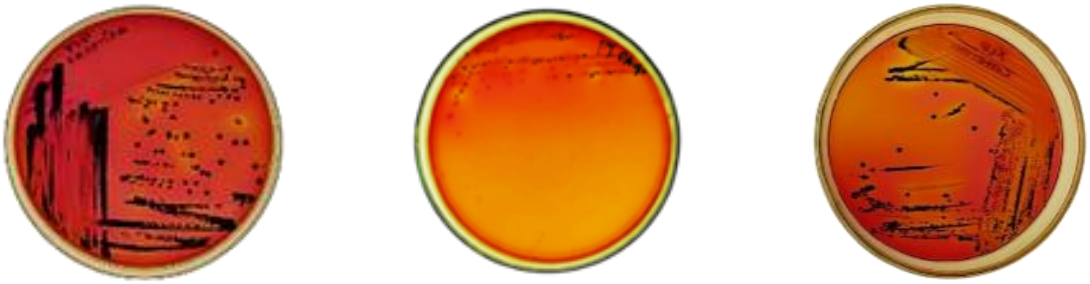
The contamination percentage of *Salmonella spp.* in traditional markets in this study was 40%, which was higher than the findings reported by Anjelifa et al. (2025),

where 29.17% of broiler chicken meat samples from traditional markets were confirmed positive for *Salmonella* based on selective media isolation, Gram staining, and biochemical tests. Candra et al. (2022) also reported the presence of *Salmonella* spp. contamination in chicken meat sold in traditional markets in West Surabaya. Studies conducted in other countries have similarly reported *Salmonella* contamination in poultry products marketed to consumers, including studies from the United States and Qatar (Thames et al. 2022 ; Al-Hadidi et al. 2022). Differences in contamination levels among studies may be influenced by sanitation conditions, meat handling practices, product distribution, sample size, and the identification methods used. Variations in contamination levels compared with previous studies also reflect differences in sampling design, market hygiene standards, and regional food safety enforcement systems, suggesting that Salmonella prevalence is highly context-dependent.

This study had several limitations, including the relatively limited number of samples and the sampling locations, which only covered several traditional markets, modern markets, and poultry slaughterhouses in Surabaya, East Java. In addition, this study focused only on phenotypic identification and molecular confirmation using PCR without serotype identification or antimicrobial resistance testing. Therefore, further studies with a broader sample coverage and more comprehensive molecular analyses are needed to provide a more comprehensive understanding of the distribution and characteristics of *Salmonella spp.* in broiler chicken meat.

Presumptive Detection of *Salmonella* spp. on XLD Medium

Based on the results of the presumptive test using XLD medium (Figure 1), not all samples exhibited the characteristic colony features of *Salmonella* spp.; isolates PT DA3, PT DA4, and PT DA5 displayed the characteristic colony features of *Salmonella* spp., with red colonies featuring a black spot in the center. This characteristic is a hallmark of *Salmonella* spp. on the selective differential XLD medium. XLD medium functions through a selective mechanism due to its sodium deoxycholate content, which inhibits Gram-positive bacteria, and acts differentially based on the bacteria's ability to ferment sugars and produce hydrogen sulfide (H_2S). The red color of the colonies indicates that the bacteria do not predominantly ferment lactose or sucrose, resulting in an alkaline pH of the medium due to the decarboxylation of lysine. Meanwhile, the formation of black spots indicates H_2S production that reacts with ferric ammonium citrate to form ferrous sulfide. However, these results are still presumptive because some other enteric bacteria may also exhibit similar characteristics, so further testing is required for confirmation.



Bakterial isolate PT DA3 | Bakterial isolate PT DA4 | Bakterial isolate PT DA5

Figure 1. Results of the presumptive test for *Salmonella* spp. in chicken meat suspected of being positive on XLD medium

These findings are consistent with previous reports indicating that *Salmonella* spp. colonies on XLD medium are generally red with a black center due to H_2S production (Anjelifa et al., 2025; Sedeik et al., 2019). Wahyuni et al. (2022) also reported that XLD medium is effective as an initial screening step for *Salmonella* spp. in poultry products. However, some studies indicate that bacteria such as *Proteus* spp. can also produce H_2S, potentially leading to false-positive results during the presumptive stage. Therefore, morphological, biochemical, and molecular tests are necessary to improve identification accuracy (Nofrianti et al., 2022).

Morphological and Gram Characteristics of *Salmonella* spp.

Observations of colony morphology on XLD medium (Table 2 and Figure 2) indicate that all suspected isolates share uniform characteristics: circular form, convex elevation, entire margin, and a red color with a black center. Additionally, Gram staining results (Figure 3) show that all isolates are rod-shaped (bacilli) and Gram-negative. The pink color in the Gram stain results from the thin peptidoglycan layer in Gram-negative bacteria, which is unable to retain the crystal violet-iodine complex during the decolorization process, thereby allowing it to absorb the counterstain safranin. This combination of colony morphological characteristics and Gram staining properties supports the initial hypothesis that the isolates obtained are *Salmonella* spp.

Table 2. Morphology of suspected *Salmonella* spp. colonies in broiler chicken meat

Isolat	Form	Elevation	Margin	Color
PT DA3	Circular	Convex	Entire	Red color with a black center
PT DA4	Circular	Convex	Entire	Red color with a black center
PT DA5	Circular	Convex	Entire	Red color with a black center

Figure 2. XLD medium in Which *Salmonella* spp. was suspected to be present in the PT DA5 isolate

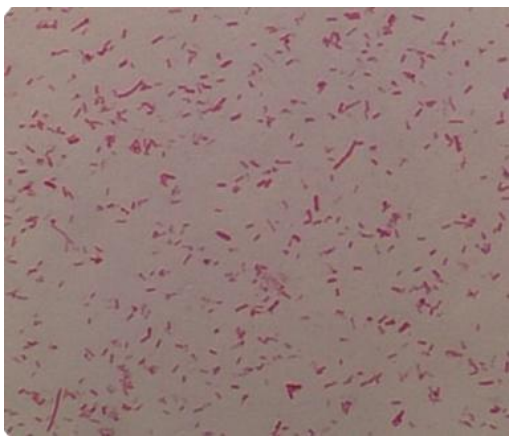


Figure 3. Result of gram staining of *Salmonella* spp.

These findings are consistent with previous studies indicating that *Salmonella* spp. exhibit round colonies with circular form and have a Gram-negative bacillary morphology (Sedeik et al., 2019; Wahyuni et al., 2022). Furthermore, Atmanto et al. (2022) and Amin et al. (2023) explain that the complex structure of the Gram-negative cell wall underlies the differences in Gram staining. However, several other enteric bacteria, such as *Escherichia coli*, also share similar morphological and Gram characteristics; therefore, identification at this stage is not yet sufficiently specific and requires confirmation through biochemical and molecular testing.

Phenotypic Identification via Biochemical Tests

To confirm phenotypic identification, suspected *Salmonella* spp. isolates obtained from XLD medium were subsequently tested using a series of biochemical tests. At this stage, three colonies with similar morphology were selected from each suspected sample (PT DA3, PT DA4, and PT DA5) for biochemical testing, resulting in a total of nine test isolates. This is because each XLD plate yielded multiple colonies with similar presumptive Salmonella characteristics, and three representative colonies were selected from each sample to capture possible intra-sample variation among isolates. Each isolate was then tested using biochemical parameters, including the indole, motility, citrate, urease, Methyl Red (MR), Voges-Proskauer (VP), Triple Sugar Iron Agar (TSIA), and Lysine Iron Agar (LIA) tests, as presented in Table 3. These tests aimed to evaluate the physiological characteristics and metabolic capabilities of each isolate, allowing for the selection of isolates with reaction patterns most consistent with the characteristic traits of *Salmonella* spp. prior to further molecular confirmation.

Table 3. Biochemical test results for three isolates suspected to be *Salmonella* spp.

Sampel Code	Biochemical Test							
	Indol	**Motil**	**Citrate**	**Urease**	**MR**	**VP**	**TSIA**	**LIA**
Positive control	-	+	-	-	+	-	K/A + H_2S	K/K
PT DA3 (1)	+	+	-	-	+	-	K/A	K/K
PT DA3 (2)	-	+	-	-	+	-	K/A + H_2S	K/K
PT DA3 (3)	-	+	-	-	+	-	K/A + H2S	K/K
PT DA4 (1)	-	+	-	+	+	-	K/A + H_2S	K/K
PT DA4 (2)	+	+	+	+	+	-	K/H + H2S	K/K
PT DA4 (3)	-	+	-	+	+	-	K/K	K/K
PT DA5 (1)	+	+	-	-	+	-	K/A	K/K
PT DA5 (2)	+	+	-	+	+	-	K/A	K/K
PT DA5 (3)	-	+	-	-	+	-	K/A + H_2S	K/K

Description: TSIA = Triple Sugar Iron Agar; LIA = Lysine Iron Agar; MR = Methyl Red; VP = Voges-Proskauer; K/A=alkali/asam; (+)=positive; (–)=negative

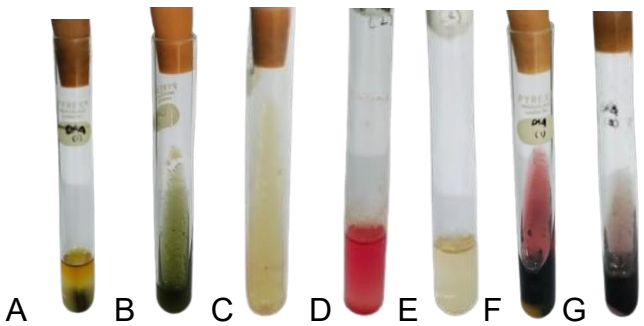


Figure 3. Characteristics of *Salmonella* spp. in the PT DA 3 (3) isolate based on biochemical tests (A: SIM; B: Citrate; C: Urease; D: MR; E: VP; F: TSIA; G: LIA)

The results of the biochemical tests (Table 3) show that only three isolates namely PT DA3 (2), PT DA3 (3), and PT DA5 (3) exhibited characteristics consistent with *Salmonella* spp., whereas isolate PT DA4 did not match the typical characteristics of *Salmonella* spp. These isolates exhibited a characteristic pattern of indole-negative, motility-positive, citrate-negative, urease-negative, MR-positive, and VP-negative, as well as a TSIA K/A pattern with H_2S production. This pattern reflects *Salmonella's* metabolic ability to ferment glucose without fermenting lactose and sucrose, and to produce H_2S gas. Variations in results for other isolates suggest the possibility of other enteric bacteria with similar characteristics, such as *Proteus* spp. or *Enterobacter* spp., thereby underscoring the importance of biochemical testing as a screening step prior to molecular confirmation.

These results are consistent with the study by Indriyani et al. (2019), which stated that *Salmonella* spp. exhibit a TSIA K/A pattern with H_2S, as well as Amiruddin et al. (2017), who reported negative indole and positive motility as characteristic features of Salmonella. Other studies also indicate that a positive MR test and a negative VP test are characteristic indicators of mixed acid fermentation in *Salmonella* spp. (Anjelifa et al., 2025). However, the presence of variation among isolates suggests that biochemical tests have limitations in terms of specificity, necessitating their combination with molecular methods to ensure accurate identification.

Genomic Confirmation and Distribution of *Salmonella* spp. Contamination

Molecular confirmation results using PCR (Figure 4.4) showed that three isolates, namely PT DA3 (2), PT DA3 (3), and PT DA5 (3), produced a DNA band of approximately 284 bp corresponding to the invA target gene. The DNA band aligned with the positive control, indicating that amplification was optimal and specific. The absence of a band in the negative control confirms that no contamination occurred during the PCR process. Based on these results, the three isolates were confirmed to be positive for *Salmonella* spp. genomically. Although three isolates were confirmed positive by PCR, these isolates originated from only two samples (PT DA3 and PT DA5), resulting in a final contamination rate of 2/15 samples (13.33%). Furthermore, based on Table 3, out of a total of 15 samples, only two samples were confirmed positive, and all were from traditional markets, while modern markets and RPHU showed negative results.

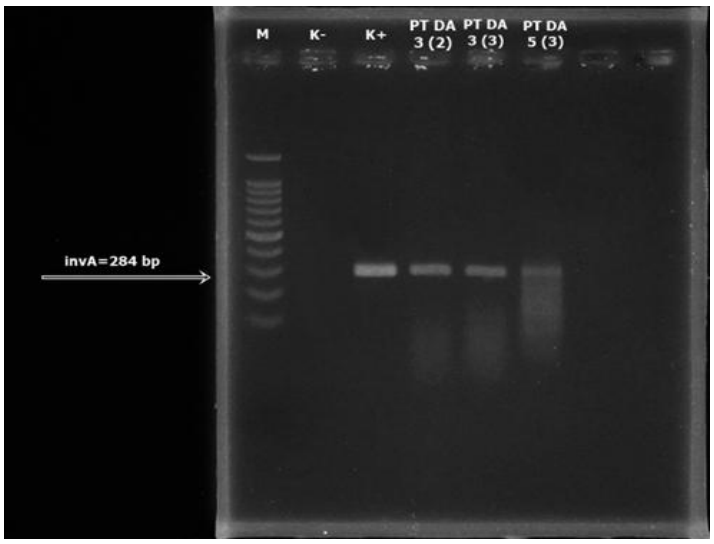


Figure 4. Visualization of PCR results via electrophoresis (M: marker; K-: negative control; K+: positive control; PT DA3 (2), PT DA3 (3) & PT DA5 (3): DNA template)

These findings are supported by studies by Jayaweera et al. (2020) and Melati et al. (2022), which indicate that PCR targeting the invA gene exhibits high sensitivity and specificity in detecting *Salmonella* spp. Additionally, studies by Voss (2019) and Zeng et al. (2021) indicate that *Salmonella* contamination occurs more frequently in distribution chains with poor sanitation, such as traditional markets. Differences in results between traditional and modern markets were also reported by Chea et al. (2022), who attributed this to better implementation of hygiene, sanitation, and cold chain practices in modern markets.

Detection of *Salmonella* spp. in broiler chicken meat from traditional markets indicates that contamination is associated with the retail (post-processing) stage rather than upstream production at slaughterhouses (Voss, 2019; Zeng et al., 2021). This is supported by the absence of positive samples from modern markets and poultry slaughterhouses, while all positive isolates were obtained from traditional market samples. Such findings are associated with limited temperature control during display, repeated exposure of carcasses to ambient conditions, and intensive handling during selling activities, which increase the potential for cross-contamination (Elsayed, 2019; Nopriani et al., 2020). In contrast, modern markets and slaughterhouses generally apply standardized hygiene practices and cold-chain management that help reduce bacterial proliferation and contamination risks after processing (Gosling et al., 2022; Necidova et al., 2024; Chea et al., 2022).

CONCLUSION

This study demonstrates that *Salmonella* spp. contamination in broiler chicken meat in Surabaya, East Java, was detected in 2 out of 15 samples (13.33%), all of which originated from traditional markets, while samples from modern markets and poultry slaughterhouses were negative. The presence of *Salmonella* spp. was confirmed through both phenotypic identification and PCR targeting the invA gene. These findings indicate a potential public health risk of *Salmonella* transmission through poultry meat sold in traditional markets, which may contribute to foodborne illness if proper hygiene and sanitation practices are not implemented. Therefore, strengthening hygiene control, sanitation practices, and cold chain management in traditional markets is essential to improve food safety. Future studies are recommended to include larger sample sizes, broader geographical coverage, and additional analyses such as serotyping and antimicrobial resistance profiling to provide a more comprehensive understanding of *Salmonella* spp. contamination in poultry meat distribution chains.

RECOMMENDATION

Further research is recommended to explore alternative methods for sample processing, such as quantitative approaches, serotype identification, and the use of advanced molecular techniques, in order to improve the accuracy of detection and understanding of the characteristics of *Salmonella* spp. These approaches are expected to yield more comprehensive data and support the development of more effective strategies for controlling contamination in poultry-derived food products.

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REFERENCES

Apriyanti, A.A., Sudiarta, I.W., dan Singapurwa, N.M. (2020). Analisis Cemaran Mikrobiologi Pada Daging Ayam Broiler Yang Beredar di Pasar Tradisional Kecamatan Denpasar Barat. *Jurnal Gema Agro*, *25(2*), 115-127.

Al-Hadidi, S., Al mana, H., Eltai, N. O. (2022). Retail chicken carcasses as a reservoir of multidrug-resistant *Salmonella*. *Microbial Drug Resistance, 28*(7), 1013–1021.

Amin, S. S., Ghozali, Z., Rusdiana, M., & Efendi, S. (2023). Identifikasi Bakteri dari Telapak Tangan dengan Pewarnaan Gram Identification of Bacteria from Palms with Gram Stain. *CHEMVIRO: Jurnal Kimia dan Ilmu Lingkungan*, 1(1), 30–35.

Amiruddin RR, Darniati, Ismail. (2017). Isolasi Dan Identifikasi *Salmonella* sp. Pada Ayam Bakar Di Rumah Makan Kecamatan Syiah Kuala Kota Banda Aceh. *JIMVET*. 1(3): 265–274

Andari S. dan Yudhayanti D. (2022). Isolasi Dan Identifikasi *Salmonella* sp. Pada Daging Ayam Segar Yang Dijual di Pasar Legi Ponorogo. *Jurnal Delima Harapan*, 9 (2), 101-108.

Anjelifa, R., Rusidah, Y., Kurnia, S. D., Sholikhati, A., Mundriyastutik, Y., dan Adi, A. S. (2025). Isolasi dan Identifikasi *Salmonella* sp. Pada Daging Ayam Broiler di Pasar Tradisional X. *Jurnal Pangan dan Gizi*, 15(1), 1–12.

Atmanto, Y. K. A. A., Asri, L. A., & Kadir, N. A. (2022). Media Pertumbuhan Kuman. *Jurnal Medika Hutama*, 04(01), 3069– 3075.

Chea, R., Nguyen-Viet, H., Tum, S., Unger, F., Lindahl, J., Grace, D., Ty, C., Koam, S., Sina, V., Sokchea, H., Pov, S., Heng, T., Phirum, O., dan Dang-Xuan, S. (2022). Experimental Cross-Contamination of Chicken Salad with *Salmonella enterica* serovars Typhimurium and London During Food Preparation in Cambodian Households. *PLoS ONE*, 17 (8).

Choi, J., Kong, B., Bowker, B. C., Zhuang, H., dan Kim, W. K. (2023). Nutritional Strategies to Improve Meat Quality and Composition in the Challenging Conditions of Broiler Production: a review. *Animals*, 13(8), 1386.

Darmawan, A., Muslimin, L., Arifah, S., dan Mahatmi, H. (2020). Kontaminasi *Salmonella* spp. pada Daging Ayam Broiler Yang Dijual di Beberapa Pasar Tradisional di Makassar. *Indonesia Medicus Veterinus*, 9(2), 168-176.

Elsayed, M., El-Gohary, F., Zakaria, A., dan Gwida, M. (2019). Tracing of *Salmonella* Contaminations Throughout an Integrated Broiler Production Chain in Dakahlia Governorate, Egypt. *Pakistan Veterinary Journal*, 39(4).

Engki Zelpina, Septa Walyani, Aji Barbora Niasono, Fitri Hidayati. (2020). Dampak infeksi *Salmonella* sp. Dalam Daging Ayam dan Produknya Terhadap Kesehatan Masyarakat. *Jurnal of Health Epidemiology and Communicable Diseases,* 6(1): 25-32.

Fatchiyah, F., Rohmah, R. N., Triprisila, L. F., Virgirinia, R. P., Rahayudi, B., Kurnianingsih, N., dan Razis, A. F. (2022). The Expression of Myoz1 and ApoB is Positively Correlated with Meat Quality of Broiler Chicken. *Veterinary Medicine International*, (1), 3266076.

Glendinning, L., Stewart, R., Pallen, M., Watson, K., & Watson, M. (2019). Assembly of Hundreds of Novel Bacterial Genomes from the Chicken Caecum. *Genome Biology*, 21(1), 34.

Gosling R., Oastler C., Nichols C., Jackson G., Wales A.D., dan Davies R.H. Investigations into *Salmonella* Contamination in Feed Mills Producing Rations for the Broiler Industry in Great Britain. (2022). *Veterinary Sciences*, 9 (7), 307.

Indrawati, Y., Datta, F. U., dan Detha, A. I. (2023). Studi Literatur Pengaruh Penambahan Bakteri Asam Laktat Dalam Pakan Formulasi Lokal Atau Pakan Komersial Terhadap Profil Mikrobiota *Salmonella* sp. Pada Saluran Pencernaan Ayam Broiler. *Jurnal Veteriner Nusantara*, 6(2), 382-394.

Indriyani, D. P., Tyasningsih, W., dan Praja, R. N. (2019). Isolation and Identification of *Salmonella* from Meat in Banyuwangi Abattoir. *Jurnal Medik Veteriner*, 2 (2), 83-88.

Jayaweera, T. S. P., Ruwandeepika, H. A. D., Deekshit, V. K., Vidanarachchi, J. K., Kodithuwakku, S. P., Karunasagar, I., dan Cyril, H. W. (2020). Isolation and Identification of *Salmonella* spp. from Broiler Chicken Meat in Sri Lanka and their Antibiotic Resistance. *Journal of Agricultural Sciences–Sri Lanka*, 15(3).

Li, H., Li, L., Chi, Y., Tian, Q., Zhou, T., Han, C., Zhu, Y., dan Zhou, Y. (2020). Development of a standardized Gram stain procedure for bacteria and inflammatory cells using an automated staining instrument. *MicrobiologyOpen*, 9(9).

Liur, I. J. (2020). Kualitas kimia dan mikrobiologis daging ayam broiler pada pasar tradisional Kota Ambon. *Al-Hayat: Journal of Biology and Applied Biology*, 3(2), 59-66.

Mar'i, S. (2025). Studi Efektivitas Pakan Konsentrat Dalam Optimasi Pertambahan Berat Badan Ayam Broiler di Masa Pembesaran. *ARMADA: Jurnal Penelitian Multidisiplin,* 3(1), 1-6.

Maya, N. P., Febriyantiningrum, K., Selomashar, M., dan Nurfitria, N. (2023). Deteksi Cemaran Bakteri *Eschericia coli* Pada Daging Ayam Broiler di Upt Laboratorium Kesehatan Hewan Dinas Peternakan Provinsi Jawa Timur di Tuban. *Biology Natural Resources Journal*, 1(2), 56-62.

Melati, R. P., Nurjanah, S., dan Rahayu, W. P. (2022). Desain Primer Gen Virulensi invA untuk Identifikasi dan Sekuensing *Salmonella* pada Sampel Karkas Ayam. *Jurnal Ilmu Produksi dan Teknologi Hasil Peternakan*, 10(2), 91-97.

Necidova, L., Zouharova, A., Harustiakova, D., Bursova, S., Bartakova, K., Golian, J. (2024). The Effect of Cold Chain Distruption on The Microbiological Profile of Chield Chicken Meat. *Journal of microbiology, biotechnology and food sciences. Poultry science*, 103(12), 104290.

Nissa, L. I. K., Rahayu, Y. P., Mambang, D. E. P., dan Daulay, A. S. (2023). Prevalensi bakteri *Salmonella* sp. pada daging ayam potong di pasar tradisional, pasar modern, dan merek terkenal di kota Medan. *Journal of Pharmaceutical and Sciences,* 1842-1853.

Nuchchanart, W., Pikoolkhao, P., dan Saengthongpinit, C. (2022). Development of a Lateral Flow Dipstick Test for the Detection of 4 Strains of *Salmonella* spp. in Animal Products and Animal Production Environmental Samples Based on Loop-mediated Isothermal Amplification. *Animal Bioscience,* 36 (4), 654 - 670.

Nofrianti, F. F., Novita, A., Jamin, F., Ismail, Farida, dan Eka Sari. (2022). Deteksi Cemaran *Salmonella* sp. pada Bakso Bakar yang di Jual di Kopelma Darussalam Banda Aceh Detection of *Salmonella* Sp. Contamination in Grilled Meatballs Sold in Kopelma Darussalam Banda Aceh. *Jurnal Ilmiah Mahasiswa Veteriner (JIMVET),* 6 (3), 162-168.

Nopriani, P., Wardani, H., S., dan Kurniawan, A. (2020). Association Between Food Handlers Hygiene and Food Sanitation to the Contamination of *Salmonella* Sp. on Sempol. *Advances in Health Sciences Research*, 29, 109-113.

Pathiassana, M. T., & Izharrido, B. (2021). Penilaian skor keamanan pangan pada UMKM rumah makan ABC di Kabupaten Sumbawa. *Jurnal Pengolahan Pangan,* 6(2), 61-70.

Pavelquesi, S. L. S., de Oliveira Ferreira, A. C. A., Rodrigues, L. F. S., de Souza Silva, C. M., da Silva, I. C. R., dan Orsi, D. C. (2023). Prevalence and Antimicrobial Resistance of *Salmonella* spp. Isolated from Chilled Chicken Meat Commercialized at Retail in Federal District, Brazil. *Journal of Food Protection*, 86(9), 100130.

Ramadani, A., Rahayu, Y. P., Nasution, M. P., & Yuniarti, R. (2023). Analisis Cemaran Bakteri *Staphylococcus aureus* Pada Daging Ayam Krispy Pinggir Jalan dan Fast Food di Daerah Teladan Kota Medan. *Journal of Pharmaceutical and Sciences*, 6 (3), 1265–1272.

Ratnaningtyas, S., Wahyudi, D., Wulansari, D., & Utami, W. P. (2023). Deteksi Cemaran *Salmonella* Sp. Pada Komoditas Tuna, Tongkol Dan Cakalang (Ttc) Yang Dijual di Pasar Inpres di Daerah Istimewa Yogyakarta. *Klorofil,* 7(1), 2023.

Reema, N. E., Sunil, B., Menon, K. V., Sethulekshmi, C., Vijay, D., Irshad, A., dan Gleeja, V. L. (2025). Occurrence and Distribution of *Salmonella* in a Broiler Chicken Processing Line in Thrissur district, Kerala. *Journal of Veterinary and Animal Sciences*, 56(1), 129-135.

Reta, G. G., Lopes, S. M., Martins de Aquino, N. S., dan Tondo, E. C. (2023). Quantification of *Salmonella* Transfer in Cross-contamination Scenarios Found in Chicken Slaughterhouses*. Food microbiology*, 116, 104347.

Risnanda, K. R., Masfufatun, M., Listyawati, A. F., Kuntaman, K., dan Sudibya, A. (2023). Prevalence of Enterobacteriaceae Producing Extended Spectrum Beta-Lactamase (ESBL) in Broiler Meat (*Gallus domesticus*) Sold in Regional Markets of West Surabaya. *Biology, Medicine, & Natural Product Chemistry*, 12(2), 607-610.

Safitri, Hidayati NA, Hertati R. 2019. Prevalensi Bakteri Salmonella Pada Ayam Potong Yang Dijual Di Pasar Tradisional Pangkalpinang. *Ekotonia: Jurnal Penelitian Biologi, Botani, Zoologi dan Mikrobiologi*. Vol 4(1).

Sedeik M.E., Nahed A. El-shall1, Ashraf M. Awad, Sally M. Elfeky, Mohamed E. Abd El-Hack. (2019). Isolation, conventional and molecular characterization of *Salmonella* spp. from newly hatched broiler chicks. *AMB Express*, 9 (316).

Shanmugaraj C., Archana Anokhe, dan Vinay Kalia. (2021). Determination of Fermentation Pathway by Methyl Red and Voges Proskauer (MRVP) Test. *AgriCos e-Newsletter*, 2 (11).

Shofia, Y. R., Agustin, A. L. D., Supriadi, S., & Ningtyas, N. S. I. I. (2023). Deteksi Bakteri *Salmonella* sp. pada Daging Ayam Bbroiler Yang Dijual di Pasar Rakyat Kota Mataram. *Mandalika Veterinary Journal*, 3(1), 35-46.

Sihotang, N., Sinaga, K., dan Rusdhi, A. (2023). Deteksi Bakteri Patogen Pada Daging Ayam di Pasar Tradisional Hamparan Perak. *Journal of Pharmaceutical and Sciences,* 640-648.

Simanjuntak, M. (2017). Pengaruh Penambahan Tepung Daun Kemangi (*Acimum* spp.) Dalam Pakan Terhadap Performans Ayam Broiler. *Jurnal Hutan Pulau-Pulau Kecil,* 1(3), 172-182.

Sipayung S.M., Rahayu W. P., Nurjanah S. (2023). Prevalensi Cemaran Bakteri Indikator Sanitasi dan Patogen Pada Daging Ayam dan Produk Olahannya di

Indonesia: Sistematika review dan Meta Analisis. *Jurnal Mutu Pangan*, 10 (2), 116-127.

Siswantoro, D., Mubarok, R. A., Prasetyo, A. F., Hertamawati, R. T., dan Kusuma, S. B. (2022). Contamination of *Salmonella* sp. Bacteria on Broiler Chicken Meat. *Jurnal Ternak (Animal Science Journal),* 13(1), 36-41.

SNI. 2023. SNI 9159:2023. Batas Maksimum Cemaran Mikroba Dalam Pangan. *Badan Standar Nasional.*

Sousa, J. M., Barbosa, A., Araújo, D., Castro, J., Azevedo, N. F., Cerqueira, L., & Almeida, C. (2024). Evaluation of Simultaneous Growth of *Escherichia coli* O157: H7, *Salmonella* spp., and Listeria Monocytogenes in Ground Beef Samples in Different Growth Media. *Foods,* 13(13), 2095.

Sriwulan, S., Murtadho I. I., Mawardi I.I., Andayani H. D., Alina Y., dan Nurfitria N. (202). Angka Lempeng Total Bakteri Ikan Kuniran Dan Ikan Tongkol Asap di Pasar Baru Tuban. *Biol. Nat. Resour. J.,* 1 (1), 29–33.

Sun, T., Liu, Y., Qin, X., Aspridou, Z., Zheng, J., Wang, X., dan Dong, Q. (2021). The Prevalence and Epidemiology of Salmonella in Retail Raw Poultry meat in China: A Systematic Review and Meta-analysis. *Foods,* 10(11), 2757.

Thames, A., Author, B., Author, C., Author, D., & Author, E. (2022). The prevalence of *Salmonella* and Campylobacter on broiler meat at different stages of commercial poultry processing. *Animals*, 12(18), 2460.

Tuhumury, F. D. A., Kaihena, M., & Seumahu, C. A. (2022). Analisa total bakteri *Salmonella* spp. Pada Produk Ikan Cakalang Asap Yang Dijual Pada Beberapa Pasar di Kota Ambon. *Bioscientist: Jurnal Ilmiah Biologi*, 10(2), 682-694.

Tkachuk, S., Bogatko, N., Hrynevych, N., dan Savchuk, L. (2023). Expert Evaluation of Meat of Broiler Chickens for Sale on the Agricultural Market. *Scientific Reports of the National University of Life and Environmental Sciences of Ukraine,* 5(19).

Turner, D. (2020). Sampling Methods in Research Design. *Headache: The Journal of Head and Face Pain*, 60 (1).

Ubaidillah, U., dan Haryati, H. (2023). Faktor Risiko Kontaminasi *Salmonella* Spp. Pada Daging Ayam Broiler (*Gallus gallus Domestica*) Yang Dijual di Pasar Banguntapan. *Surya Medika: Jurnal Ilmiah Ilmu Keperawatan dan Ilmu Kesehatan Masyarakat*, 18(1), 31-40.

Vargas, D. A., Betancourt-Barszcz, G. K., Blandon, S. E., Applegate, S. F., Brashears, M. M., Miller, M. F., Gragg, S. E., dan Sanchez-Plata, M. X. (2023). Rapid Quantitative Method Development for Beef and Pork Lymph Nodes Using BAX® System Real Time *Salmonella* Assay. *Foods (Basel, Switzerland),* 12(4), 822.

Voss-Rech, D., Kramer, B., Silva, V. S., Rebelatto, R., Abreu, P. G., Coldebella, A., & Vaz, C. S. L. (2019). Longitudinal Study Reveals Persistent Environmental *Salmonella* Heidelberg in Brazilian Broiler Farms. *Veterinary Microbiology*, 233, 118-123.

Wahyuni S., Erina, M. Daud AK, Fakhrurrazi, M. Jalaluddin, Teuku Zahrial Helmi. (2022). Isolasi *Salmonella* sp. dan Prevalensinya pada Tembolok (Ingluviens) Ayam Buras dan Ayam Ras di Pasar Ayam Peunayong Kota Banda Aceh. *Jurnal Sain Veteriner*, Vol. 40. No. 3. Hal 314-322.

Wang, M., Qazi, I. H., Wang, L., Zhou, G., dan Han, H. (2020). Salmonella Virulence and Immune Escape. *Microorganisms,* 8(3), 407.

Yanestria, S., Rahmaniar, R., Wibisono, F., dan Effendi, M. (2019). Detection of InvA Gene of Salmonella from Milkfish (*Chanos chanos*) at Sidoarjo Wet Fish Market, Indonesia, Using Polymerase Chain Reaction Technique. *Veterinary World,* 12, 170 - 175.

Zain, R., Hidanah, S., Damayanti, R., & Warsito, S. H. (2021). Detection of *Salmonella* sp. on Bulk Meatballs and Packaged Meatballs at Sepanjang Market, Sidoarjo. *Journal of Applied Veterinary Science and Technology*, 2(2), 31-36.

Zeng, H., De Reu, K., Gabriël, S., Mattheus, W., De Zutter, L., dan Rasschaert, G. (2021). *Salmonella* Prevalence and Persistence in Industrialized Poultry Slaughterhouses. *Poultry Science,* 100(4), 100991.

Zulfiati, A. (2018). Isolasi Mikroba Penghasil Antibiotik Dari Pasir Pantai Lemo-Lemo Kabupaten Bulukumba Dalam Menghambat Beberapa Bakteri Patogen. *Jurnal Kesehatan*, 13(1).