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Prevalence, Genetic Diversity, and Antimicrobial Resistance of *Salmonella Enterica* Isolated from Broiler Chicken Farms in Dormaa Ahenkro, Ghana

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ABSTRACT

Salmonella enterica (*S. enterica*) remains one of the most important bacterial agents linked to foodborne illness, particularly in regions with expanding poultry production. The present study aimed to investigate the occurrence, antimicrobial resistance, and genetic characteristics of *S. enterica* isolated from broiler chicken farms in Dormaa Ahenkro, Ghana. One hundred samples (cloacal swabs, feed, water, and litter) were collected from five farms and examined through culture, biochemical tests, antimicrobial susceptibility assays, and molecular confirmation of the *invasion gene A* (*invA*). Twenty-eight isolates (28%) were confirmed as *Salmonella*, all of which exhibited resistance to amoxicillin. Resistance to the antibiotics Ceftazidime, Gentamicin, Imipenem, and Aztreonam tested ranged from 4-25%. Nineteen isolates amplified the *invA* gene, and sixteen out of 19 submitted samples were successfully sequenced and confirmed as *S. enterica* with 93.85-99.80% identity. Phylogenetic and haplotype analyses demonstrated substantial genetic diversity, suggesting localized evolutionary divergence. The present findings highlight the presence of multidrug-resistant *Salmonella* within broiler production systems, emphasizing the need for improved biosecurity and responsible antimicrobial use to safeguard public health. Broiler chicken farms serve as an essential food source in many Ghanaian communities, yet they can harbour bacteria that pose risks to consumers. It was observed that *Salmonella* contamination in birds and their surroundings in Dormaa Ahenkro. Notably, *Salmonella* strains seen in these studies were also resistant to commonly used antibiotics, underscoring the need for stronger hygiene practices, prudent antibiotic use, and consistent monitoring to limit the spread of drug-resistant strains from farms to the wider population. Improving control measures will enhance food safety and support the sustainability of poultry production in Ghana.

Keywords: Antimicrobial resistance, Broiler chicken, Molecular characterization, *Salmonella*, One Health

INTRODUCTION

Poultry production continues to play a central role in food security across Africa, contributing 2.5 million metric tons annually and supporting rural livelihoods (Mottet and Tempio, 2017; FAO, 2023). However, the sector faces significant threats from foodborne pathogens such as *Salmonella enterica* (*S. enterica*), a leading cause of gastrointestinal disease globally that contaminates poultry through feed, litter, drinking water, housing environments, and bird-to-bird transmission (Kulkarni et al., 2019).

Globally, non-typhoidal *S. enterica* causes 93.8 million human infections and 155,000 deaths annually, with poultry serving as the primary transmission vehicle (Ramtahal et al., 2022). Different poultry-related serovars make broiler farms a very important place to watch (EFSA, 2019; CDC, 2022). While many countries, such as the UK, Germany, and the United States, have established monitoring systems, Sub-Saharan Africa, including Ghana, remains data-deficient on non-typhoidal *Salmonella* prevalence and antimicrobial resistance (AMR) in poultry systems (Andoh et al., 2016; FAO, 2021a).

Dormaa Ahenkro, a major poultry-producing area in Ghana's Brono Region, lacks comprehensive baseline data on broiler farm contamination. The insufficient data on *S. enterica* strains hinder effective control measures and pose a threat to public health (Thye et al., 2025). The present study aimed to address these critical gaps by investigating *S. enterica* prevalence, AMR profiles, and genetic characteristics in Dormaa Ahenkro broiler farms, providing essential evidence for targeted farm-level interventions and national One Health strategies.

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MATERIALS AND METHODS

Ethical approval

Ethical clearance was obtained from the Research and Ethics Committee of the School of Agriculture and Technology, University of Energy and Natural Resources, Sunyani, Ghana. The study design and protocol were approved with the following certificate number, SOAT/ECE/015/2025.

Study area and sample collection

A cross-sectional study was conducted from April to August 2025 across five broiler farms purposively selected, targeting active producers representing typical area operations in Dormaa Ahenkro, Bono Region, Ghana. According to the 2020 population and housing census, 1.8 million poultry birds were reared by 200 registered farmers (Veterinary Service Department, Dormaa Ahenkro, 2020). A total of 100 samples comprising 25 each of cloacal swabs, feed, water, and litter were collected using sterile cotton swabs for cloaca (inserted 2-3 cm, rotated, placed in Amies transport medium), sterile bags for feed/litter (100g composite), and sterile bottles for water (100 ml). All were sealed and labelled with farm ID/sample type/date, transported in a cooler at 4-8˚C, and processed within 24 hours for isolation of *Salmonella* on Xylose Lysine Deoxycholate (XLD) agar.

Culturing, isolation, and identification of *Salmonella*

To identify *S. enterica* in cloacal swab, feed, litter, and water samples, standard microbiological culture followed by biochemical confirmation (ISO 6579-1:2017) was employed. *Salmonella* isolation and identification involved pre-enrichment in Buffered Peptone Water (BPW), followed by selective enrichment in Modified Semi-solid Rappaport Vassiliadis broth at 42˚C for 24 hours. *S. Enteritidis* ATCC 13076 served as the positive control. Ten mls of BPW was used for cloacal swabs, and 25 g of all other samples were inoculated into 225 mL of BPW and incubated at 37˚C for 18-24 hours. Selective plating was performed on XLD agar to isolate presumptive *Salmonella* colonies, with the positives appearing as red or pink colonies, typically with black centers. Colonies were then subjected to biochemical confirmation using Triple Sugar Iron (TSI) agar (red slant/yellow butt ± gas/H_2S after 18-24 hours), citrate utilization (positive), and indole test (blue color change on Simmons agar; Andoh et al., 2016). All media were purchased from Oxoid Limited, Basingstoke, UK.

Antimicrobial susceptibility testing

The Kirby-Bauer disk diffusion method (Bauer et al., 1966) was used to assess susceptibility to five antibiotic classes: Penicillin (Amoxicillin [AML 10 µg]), carbapenems (Imipenem [IMP 10 µg]), monobactams (Aztreonam [ATM 30 µg]), cephalosporins (Ceftazidime [CAZ 30 µg]), and aminoglycosides (Gentamicin [CN 30 µg]). Antibiotic susceptibility testing utilized commercially purchased disks from UK OXOID (Thermo Scientific, Basingstoke, UK). Isolates were prepared to a 0.5 McFarland turbidity standard and tested on Mueller-Hinton agar (Oxoid, UK). Zones of inhibition were interpreted using European Committee on Antimicrobial Susceptibility Testing 2025 (EUCAST) clinical breakpoints, and isolates resistant to at least three antibiotic classes were classified as multidrug-resistant (Magiorakos et al., 2012). A cotton swab was used to spread the standardized *Salmonella* suspension evenly across the entire surface of the Mueller-Hinton agar in three different directions, creating an even bacterial lawn. After allowing the plates to dry for 10 minutes, antibiotic discs were then gently placed on the surface of the inoculated agar plates using sterile forceps. The inoculated agar plates were left undisturbed to dry at room temperature for approximately 10 minutes. Following this, antibiotic discs were aseptically positioned on the agar surface with sterile forceps, ensuring gentle and precise placement (Ogodo et al., 2022). It was also ensured that enough and even spacing was considered to prevent the antibiotic disc from overlapping its zone of inhibition. After which, the plates were incubated at 37˚C for 16-24 hours. Results were interpreted according to European Committee on Antimicrobial Susceptibility Testing (EUCAST) breakpoints and classified into the following categories, including Resistant and Susceptible.

Measurement of inhibition zones

The diameter of each inhibition zone was measured using a calibrated ruler and recorded in millimeters. Antimicrobial susceptibility outcomes were assessed in accordance with EUCAST 2025 interpretive criteria and stratified into three distinct response groups. Isolates classified as Susceptible (S) are expected to respond to the tested antimicrobial agent when administered at conventional therapeutic dosages. The Intermediate (I) category reflects situations in which treatment efficacy can be achieved by increasing drug exposure, either through dose adjustment or improved penetration at the site of infection. Isolates designated as Resistant (R) are not expected to respond to therapy, as effective antimicrobial activity cannot be achieved within safe and clinically attainable concentration ranges. All

susceptibility profiles were recorded for individual isolates, and isolates indicating resistance to three or more antibiotic classes were considered multidrug-resistant (MDR).

Molecular confirmation and characterization

Extraction of Genomic DNA was performed from purified isolates using the crude lysate boiling method (Adzitey et al., 2025), in which a colony was lysed in 30 µL molecular-grade water at 99°C. PCR targeting the *invasion* gene A (*invA*; 285 bp) was performed in a 25 µL reaction mixture which contained a 13.75 µL of nuclease-free water, 2.5 µL of 10x PCR buffer, 1.5 µL of 25 mM $MgCl_2$, 1.0 Taq polymerase (5 U/µL), 3.75 Template DNA lysate 0.5 µL of 10 mM dNTPs, 1.0 µL each of forward primers (5'-GTGAAATTATCGCCACGTTCGGGCAA-3') and reverse primers (5'-TCATCGCACCGTCAAAGACC-3') targeting the *invA* gene (Adzitey et al., 2025). PCR cycling conditions included initial denaturation at 94°C for 5 minutes, followed by 40 cycles of denaturation at 94°C for 30 seconds, annealing at 64°C for 30 seconds, and extension at 72°C for 30 seconds. Amplicons were visualized by electrophoresis on a 1% agarose gel (CSL-AG500, Cleaver Scientific Ltd, UK) stained with ethidium bromide (Sigma-Aldrich, USA; 0.5 µg/mL), using a 100 bp DNA ladder as the molecular size marker, and imaged under UV transillumination (Bio-Rad, USA). Additionally, amplicons were subjected to Sanger sequencing using an Applied Biosystems 3500 Genetic Analyzer thermocycler (Thermo Fisher Scientific, USA), and the resulting sequences were edited, aligned, and compared with those in the National Centre for Biotechnology Information (NCBI) database for species confirmation.

Data, sequence, and phylogenetic analyses

Descriptive statistics represented in tables and graphs were inferred using Microsoft Office Suite 2021. Cleaned sequences were analysed using Molecular Evolutionary Genetics Analysis (MEGA; Kumar et al., 2018) for phylogenetic reconstruction, and Population Analysis with Reticulate Trees (POPART) and DNA Sequence Polymorphism (DNAsP; Leigh and Bryant, 2015) were applied to determine haplotype variation, nucleotide diversity, and mutation patterns. Neutrality tests, including Tajima's D, Fu's Fs, Fu and Li's D*, and Fu and Li's F, were calculated using DnaSP version 6 (Rozas et al., 2017) to assess signatures of population expansion, selection, or demographic history. BLAST searches from NCBI were performed to determine relatedness to global strains.

RESULTS

Prevalence

Out of 100 samples examined, 28% were verified as *Salmonella* positive. All sample sources recorded contamination (Figure 1), with feed recording the highest prevalence at 36% (9/25), followed by cloacal swabs at 28% (7/25). Litter and water revealed lower prevalence rates of 24% each (6/25). Despite the observed differences, prevalence among the sample sources was not statistically significant ($p > 0.05$).

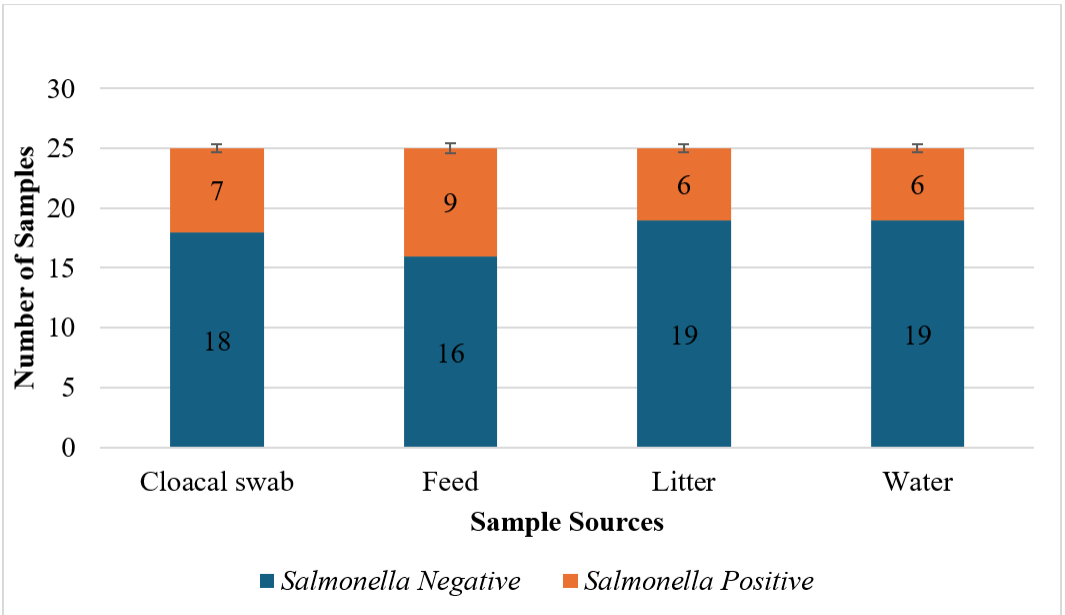

Figure 1. Occurrences of *Salmonella enterica* isolated from litter, cloacal swabs, drinking water, and feed samples in broiler chicken farms located in Dormaa Ahenkro from April to September 2025

Antimicrobial resistance profiles

All 28 *Salmonella* isolates indicated 100% resistance to amoxicillin (Table 1), with breakpoints defined in Table 2 (EUCAST, 2025). Resistance rates to ceftazidime, gentamicin, imipenem, and aztreonam ranged from 4% to 25%. Isolate BW05 (water sample, Farm B) was resistant to all tested antibiotic classes and was identified as an MDR isolate.

Table 1. Antibiogram profile of *Salmonella enterica* isolated from Dormaa Ahenkro broiler chicken farms from April to September 2025

Antibiotic name	Samples type	Resistant	Sensitive
Ceftazidime	Feed, cloacal swabs, litter, and water	1 (4%)	27 (96%)
Gentamicin	Feed, cloacal swabs, litter, and water	2 (8%)	26 (92%)
Amoxicillin	Feed, cloacal swabs, litter, and water	28 (100%)	0 (0%)
Imipenem	Feed, cloacal swabs, litter, and water	4 (16%)	24 (84%)
Aztreonam	Feed, cloacal swabs, litter, and water	2 (8%)	26 (92%)

Table 2. Antibiotic breakpoints with disk diffusion test based on EUCAST 2025

Antibiotic	Susceptible (≥ mm)	Intermediate (mm)	Resistance (≤ mm)
Ceftazidime	18	15-17	≤14
Gentamicin	15	13-14	≤12
Amoxicillin	18	14-17	≤13
Imipenem	23	20-22	≤19
Aztreonam	21	17-20	≤16

Table 3. Antibiotic resistance profile of *Salmonella enterica* samples isolated from broiler chicken farms in Dormaa Ahenkro from April to September 2025

Sample ID	Ceftazidime	Gentamicin	Amoxicillin	Imipenem	Aztreonam
A-FE04	28 mm (S)	29 mm (S)	11 mm (R)	29 mm (S)	33 mm (S)
B-FS05	30 mm (S)	29 mm (S)	6 mm (R)	26 mm (S)	37 mm (R)
B-W05	12 mm (R)	16 mm (S)	6 mm (R)	10 mm (R)	18 mm (R)
C-LT01	29 mm (S)	26 mm (S)	12 mm (R)	15 mm (R)	35 mm (S)
C-LT03	29 mm (S)	22 mm (S)	6 mm (R)	26 mm (S)	36 mm (S)
C-LT04	30 mm (S)	25 mm (S)	6 mm (R)	24 mm (S)	33 mm (S)
C-W01	25 mm (S)	26 mm (S)	16 mm (R)	24 mm (S)	34 mm (S)
C-W04	25 mm (S)	24 mm (S)	6 mm (R)	24 mm (S)	32 mm (S)
C-FE02	22 mm (S)	15 mm (S)	6 mm (R)	15 mm (R)	16 mm (R)
D-W01	24 mm (S)	25 mm (S)	16 mm (R)	27 mm (S)	30 mm (S)
D-W02	28 mm (S)	26 mm (S)	11 mm (R)	28 mm (S)	33 mm (S)
D-FE02	25 mm (S)	25 mm (S)	16 mm (R)	32 mm (S)	31 mm (S)
D-FE03	26 mm (S)	28 mm (S)	13 mm (R)	34 mm (S)	37 mm (S)
D-FE04	26 mm (S)	24 mm (S)	16 mm (R)	33 mm (S)	36 mm (S)
D-FE05	32 mm (S)	30 mm (S)	16 mm (R)	28 mm (S)	38 mm (S)
D-LT02	27 mm (S)	22 mm (S)	6 mm (R)	18 mm (I)	36 mm (S)
D-FS02	25 mm (S)	22 mm (S)	12 mm (R)	24 mm (S)	36 mm (S)
D-FS03	27 mm (S)	26 mm (S)	17 mm (R)	33 mm (S)	35 mm (S)
D-FS04	27 mm (S)	22 mm (S)	6 mm (R)	24 mm (S)	36 mm (S)
D-FS05	26 mm (S)	28 mm (S)	12 mm (R)	28 mm (S)	36 mm (S)
E-FE02	26 mm (S)	34 mm (S)	18 mm (R)	26 mm (S)	35 mm (S)
E-FE03	28 mm (S)	30 mm (S)	18 mm (R)	26 mm (S)	32 mm (S)
E-W01	28 mm (S)	27 mm (S)	17 mm (R)	32 mm (S)	34 mm (S)
E-W02	29 mm (S)	28 mm (S)	6 mm (R)	31 mm (S)	36 mm (S)
E-LT02	26 mm (S)	20 mm (S)	6 mm (R)	22 mm (S)	35 mm (S)
E-LT03	26 mm (S)	26 mm (S)	17 mm (R)	32 mm (S)	32 mm (S)
E-FE04	24 mm (S)	27 mm (S)	16 mm (R)	29 mm (S)	33 mm (S)
E-FS01	25 mm (S)	24 mm (S)	13 mm (R)	28 mm (S)	34 mm (S)

FE: Feed, CS: Cloacal swabs, LT: Litter, W: Water, S: Susceptible (standard dosing), I: Susceptible with increased exposure, R: Resistant, A, B, C, D, and E represent the farms. Results were interpreted using EUCAST 2025 breakpoints for disk diffusion (mm inhibition zones).

PCR, molecular confirmation, and characterization of *Salmonella enterica*

A uniform fragmentation length of 285 bp was produced using the partial *invA* gene primers. Nineteen isolates were PCR-positive for the *invA* gene. Sixteen isolates were successfully sequenced, which yielded a clear, readable 285 bp band of the target *invA* gene. While the three remaining isolates failed to produce clear bands on gel electrophoresis and were discarded. The Nucleotide BLAST algorithm from NCBI identified all 16 isolates as *Salmonella enterica subsp*. Comparing them to earlier data in the GenBank, with a 93.85 to 99.80% identification rate (Table 3). The identified isolates were AFE04, CLT03, CLT04, CW04, DFE03, DW02, DFS04, DFE05, DLT02, DW01, DFE0, EFE02, EFE03, EW02, ELT03, and EFE04. BLAST analysis indicated that the sequences shared high similarity with *Salmonella* isolates from Egypt, Nigeria, Zambia, and France.

Haplotype analysis of *Salmonella enterica's InvA* gene (285 bp) across 16 sequences (Figure 2) identified 19 segregating (polymorphic) sites (S = 6.7%), of which 14 were singleton mutations. A total of 25 mutations (Eta) were detected, yielding 15 haplotypes with high haplotype diversity (Hd = 0.959 ± 0.00129) and nucleotide diversity (π = 0.043). Average pairwise nucleotide differences were k = 12.3. Neutrality tests indicated a Tajima's D value of -1.92870, which was statistically significant ($P < 0.05$), indicating an excess of low-frequency polymorphisms probably caused by recent population growth or purifying selection. Fu's Fs statistic was 2.404, while Fu and Li's D (-1.87464) and F (-2.20404) statistics were negative but not statistically significant ($P > 0.05$), pointing to a similar trend of excess rare alleles, but without strong statistical support.

Table 4. *Salmonella enterica* subsp. *enterica* GenBank deposits compared to the sequences of bacteria in the present study

Sample ID	Identical to	GenBank accession number	Country	Identity (%)	Host
A-FE04	*Salmonella*	PQ720689	Egypt	98.80	Poultry
C-LT03	*Salmonella*	PQ720689	Egypt	98.80	Poultry
C-LT04	*Salmonella*	MZ683411	Nigeria	98.80	Poultry
C-W04	*Salmonella*	MF678530	Egypt	93.85	Poultry
D-FE03	*Salmonella*	MT478121	Egypt	93.85	Poultry
D-W02	*Salmonella*	KJ718884	Egypt	99.21	Poultry
D-FS04	*Salmonella*	PQ720689	Egypt	98.80	Poultry
D-FE05	*Salmonella*	PP921862	Zambia	99.21	Poultry
D-LT02	*Salmonella*	MT478121	Egypt	98.79	Poultry
D-W01	*Salmonella*	MT478121	Egypt	99.60	Poultry
D-FE04	*Salmonella*	KX524162	Egypt	96.28	Poultry
E-FE02	*Salmonella*	KX524162	Egypt	94.05	Poultry
E-FE03	*Salmonella*	MT478121	Egypt	97.98	Poultry
E-W02	*Salmonella*	MT478121	Egypt	98.39	Poultry
E-LT03	*Salmonella*	KX524156	Egypt	98.00	Poultry
E-FE04	*Salmonella*	KX524162	Egypt	98.02	Poultry

FE: Feed, CS: Cloacal swabs, LT: Litter, W: Water, A, B, C, D, and E represent the sample sources.

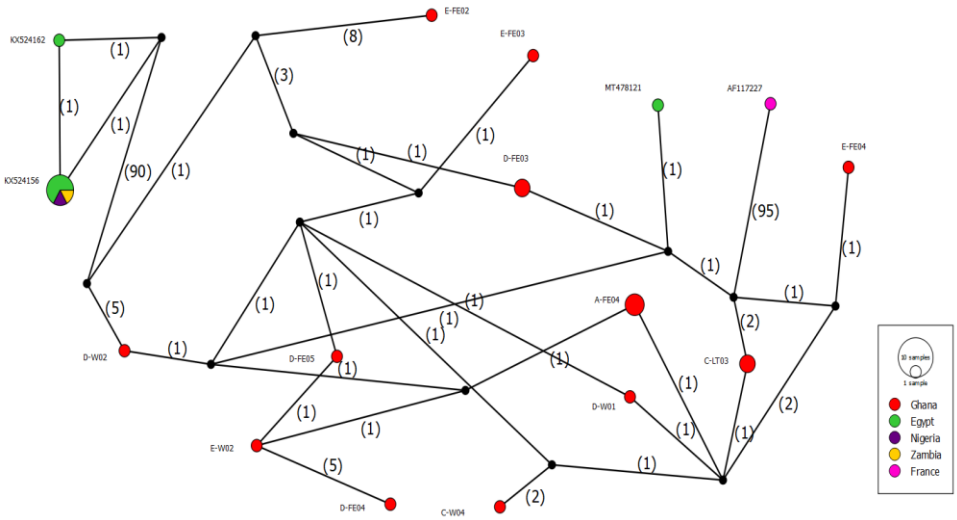

Figure 2. Haplotype network of *Salmonella enterica* based on the *invasion gene A* gene sequences (~285bp) isolated from broiler chicken farms in Dormaa Ahenkro from April to September 2025

Phylogenetic analysis based on the partial *invasion gene A*

Phylogenetic analysis of *S. enterica* conducted in MEGA X (Kumar et al., 2018) revealed a Ghanaian clade encompassing all 16 local *S. enterica* isolates, with strong support (bootstrap = 100 at root node) and differentiating them from reference sequences from Egypt, Nigeria, Zambia, and France (Figure 3). In the Ghanaian isolates, sub-lineages like DFE03, DLT02, DW02, and EW02 formed a group with robust support (bootstrap = 78). On the other hand, other internal branches had less support (bootstraps = 50-72). Egyptian and Nigerian genomes formed distinct clusters (bootstrap = 92); the Zambian isolate formed a distinctive lineage (bootstrap = 88); and the French isolate served as the basal reference.

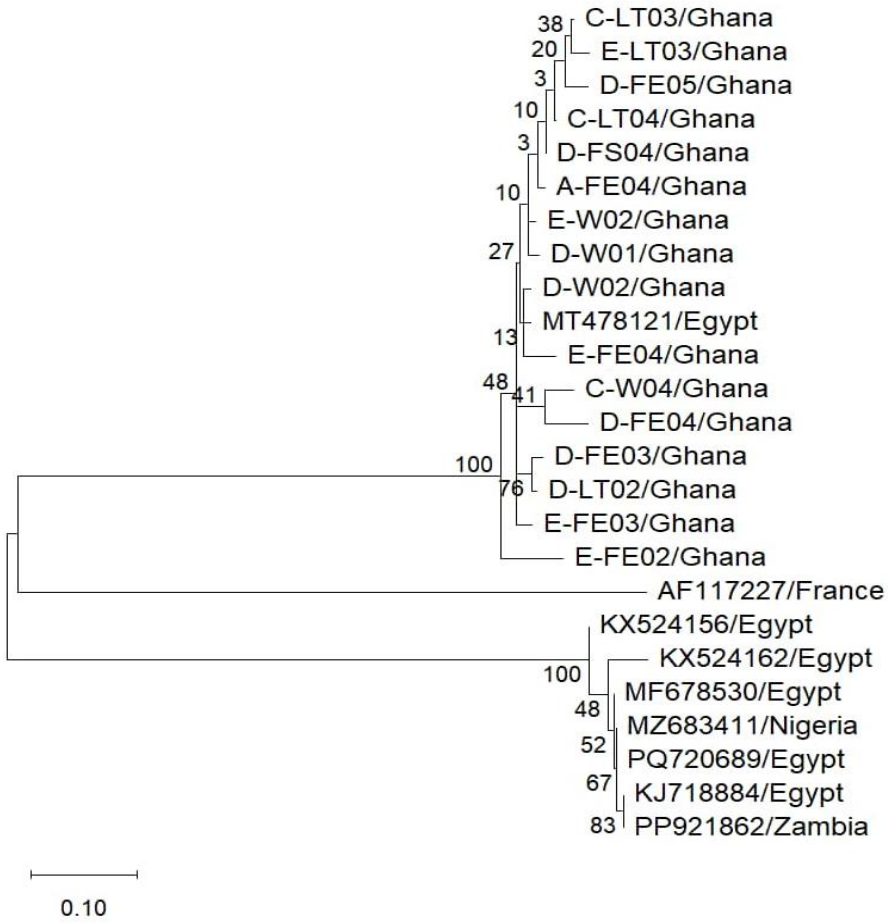

Figure 3. Maximum-likelihood phylogenetic tree of *Salmonella enterica* isolated from broiler chicken farms (April-September 2025) based on partial *invasion* gene A sequences from GenBank and the present study. The phylogenetic tree was constructed in MEGA 12 using the Tamura-Nei model with 100 bootstrap replications

DISCUSSION

Salmonella was identified in 28% of broiler chicken farms in the present study from Dormaa Ahenkro. Isolates were confirmed through molecular characterization using the *invA* gene, which verified the identity of *S. enterica* in 19 out of 28 presumptive isolates (67.9%), which is consistent with previous work in which phenotypic identification was confirmed molecularly through the *invA* gene and aligns with studies that document false positives from biochemical and serological methods due to cross-reactivity and non-specific agglutination (Grimont and Weill, 2007; Foley et al., 2013; El-Baz et al., 2017). The observed 28% farm-level prevalence is consistent with similar findings from other regions within Ghana. For example, a 25% farm-level prevalence of *Salmonella* was reported in Accra, Ghana (Andoh et al., 2016), along with a 44% overall prevalence in commercial poultry and a 6-10% prevalence in the environment on Ashanti-region farms (Andoh et al., 2021). Another study in the Accra Plains, Ghana, found that 32.4% of poultry environmental samples were contaminated with *Salmonella* and highlighted that farming conditions and biosecurity practices are key factors driving contamination (Adzitey et al., 2025). *Salmonella* detected in food-producing animals serves as a direct reservoir for zoonotic transmission, posing a considerable risk to food safety and public health in

Dormaa Ahenkro and surrounding communities (Feasey et al., 2012). The current study confirmed the presence of *Salmonella. enterica* in broiler chicken farms and their surrounding environment in Dormaa Ahenkro Municipality, Ghana, detecting the *invA* gene with 28% farm-level prevalence consistent with regional studies in Ghana and West Africa (Andoh et al., 2016; FAO, 2021a;b; Baah, 2023). The isolates exhibited complete resistance to amoxicillin, with no susceptible strains detected, which is consistent with reports of excessive β-lactam use in Ghanaian poultry production. The high MDR prevalence observed is consistent with WHO and FAO recommendations for antibiotic stewardship (FAO, 2021a; WHO, 2021; Ferreira et al., 2022). The identification of extensively drug-resistant (XDR) isolate B-W05 (resistant to ≥ 4 antibiotic classes) suggests potential zoonotic transmission risks and limited treatment options, consistent with the need for improved biosecurity and surveillance in broiler farms (WHO, 2021). Furthermore, the combination of PCR and partial *invA* gene sequencing enabled robust bacteriological identification of *S. enterica* in feed, water, litter, and cloacal swabs collected from broiler chicken farms in Dormaa Ahenkro, Ghana. It is important to note that the *invA* gene is a single, highly conserved virulence gene involved in invasion across *Salmonella* serovars and is not expected to reflect the full range of whole-genome diversity (Rahn et al., 1992; Nhung et al., 2022). The high haplotype and nucleotide diversity within *invA* likely result from micro-epidemiological variation among closely related strains rather than deep phylogenetic divergence across serotypes.

Overall, the phylogenetic tree supports regional structuring and diversification of *S. enterica* populations in Ghana, with Ghanaian isolates forming distinct clusters rather than mixing closely with isolates from other African countries or Europe (Feasey et al., 2012). The observed genotypic clustering indicates regional diversification of *S. enterica* lineages in sub-Saharan Africa. The findings from the present study suggest that local transmission and farm-level dynamics may be more influential than international spread in shaping the current *S. enterica* population in Ghanaian poultry. The Centers for Disease Control and Prevention (CDC, 2011) and Bugarel et al. (2017) have reported that *S. enterica* ranks among the most concerning foodborne pathogens due to its frequent association with multidrug resistance. In Ghana, *S. enterica* has been isolated from human clinical cases, including invasive bloodstream infections in children and invasive nontyphoidal *Salmonella* (iNTS) disease involving *S. Enteritidis* and *S. Typhimurium*, indicating circulation in the human population and emphasizing the zoonotic threat posed by poultry-associated serovars (Feasey et al., 2012; Ablordey et al., 2018; Park, 2019). However, due to the limited number and diversity of isolates in the present study, it is currently not possible to confirm that *S. Enteritidis* is the most common serovar in Ghana. *S. Enteritidis* has also been reported in other African countries, including Nigeria and Zambia, where it has been detected in poultry and associated with human infections (Akinyemi et al., 2021), underscoring the transboundary nature of *Salmonella* and antimicrobial resistance challenges in the region. The One Health framework offers a valuable approach for interpreting the present findings on *Salmonella* and antimicrobial resistance in poultry (WHO, 2021; FAO, 2021b). The discovery of zoonotic *S. enterica* in Ghanaian broiler farms, coupled with near-universal resistance to widely used antibiotics such as amoxicillin (100%), highlights the interconnectedness of human, animal, and environmental health (OIE, 2020; WHO, 2021; FAO, 2021b). Multidrug-resistant *Salmonella* in poultry products can reach consumers through contaminated meat and eggs. Previous studies in Ghana have linked poultry-derived *S. Enteritidis* and other non-typhoidal serovars to a substantial proportion of reported salmonellosis and invasive bloodstream infections, although the exact attribution fraction remains to be determined and would benefit from dedicated source-attribution and One Health genomic studies (Feasey et al., 2012; Ablordey et al., 2018; Park, 2019). On-farm antimicrobial use, farm hygiene, and environmental contamination are likely to contribute to the emergence and spread of resistant *Salmonella* strains that threaten both animal productivity and human food safety (Andoh et al., 2016; FAO, 2021b; WHO, 2021) Within this context, the One Health operational framework encourages countries to coordinate surveillance and control measures across veterinary, public-health, and environmental sectors to prevent and contain zoonotic infections, manage antimicrobial resistance, and strengthen food-safety systems (OIE, 2020; FAO, 2021b; WHO, 2021; Mumford, 2023). Integrating laboratory-based AMR monitoring in poultry, routine carcass and environmental sampling along the value chain, and clinical reporting of human salmonellosis would allow earlier detection of resistant strains such as those identified in the present study and support evidence-based regulation of antimicrobial use (FAO, 2021b; WHO, 2021).

CONCLUSION

The present study found *Salmonella enterica* in 28% of samples from broiler farms in Dormaa Ahenkro, with all 28 isolates exhibiting complete resistance to amoxicillin; isolate B-W05 also revealed resistance to all four antibiotics tested, qualifying as multidrug-resistant (MDR). Limited funding prevented whole-genome sequencing for serovar identification, traditional antisera serotyping, and expanding sampling beyond 100 purposively selected samples across five farms. The *invA* PCR (285 bp) confirmed species identity but did not provide serovar or full genomic details. Future adequately funded research should prioritize Whole Genome Sequencing for serotyping, resistance profiling, and source

attribution across +500 samples from Ghana's major poultry regions, integrating human clinical isolates for One Health transmission studies. Routine surveillance, strict antimicrobial stewardship, farmer biosecurity training, and combined molecular-traditional serotyping will control environmental contamination and reduce zoonotic risks along the poultry value chain. Note that population growth, globalization of trade, ecological change, and advances in technology make such integrated approaches increasingly essential for improving public health at local and global levels. It is recommended that a larger study with broader sampling from multiple sources, such as farms, processing plants, markets, and human cases, would be necessary to draw definitive conclusions.

DECLARATIONS

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Authors' contributions

Moses Addo Nartey has contributed to conceptualization, data curation, methodology, writing, original draft, validation, and supervision. Abdul Lateef Sulemana contributed to investigation, methodology, visualization, writing, original draft, and software procedures. Francis Addy contributed to resources, writing, editing, and formal analysis. Peter Asiedu contributed to visualization, writing, and editing. Bernard Ato Hagan contributed to data curation, resources, and project administration. Bismark Kyei contributed to writing, and editing. Frederick Adzitey contributed to resources, writing, editing, and supervision. All authors have read and approved the final edition of the manuscript.

Availability of data and materials

The data to support the present study's findings are available upon reasonable request to the corresponding author.

Conflicts of interests

The authors declared no conflict of interest.

Ethical considerations

The authors have checked the ethical considerations, including issues such as plagiarism, consent for publication, misconduct, data fabrication and/or falsification, as well as double publication and/or submission redundancy. The authors confirm that no AI tools were used in conducting and preparing this study.

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