

| RESEARCH ARTICLE

Antimicrobial Susceptibility Profiles of Zoonotic *Campylobacter* spp and *Salmonella enterica* Recovered from Poultry Droppings in the Selected Poultry Farms of Aluu Community, Rivers State, Nigeria

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| ABSTRACT

Poultry production plays a vital role in food security and economic development, but it is increasingly associated with the emergence of zoonotic pathogens and antimicrobial resistance (AMR). This study determined the occurrence and antimicrobial susceptibility profiles of *Campylobacter* species and *Salmonella enterica* isolated from poultry droppings in selected farms in Aluu Community, Rivers State, Nigeria. A cross-sectional laboratory-based study was conducted using 120 fresh poultry dropping samples. Isolation and identification followed ISO standard procedures, while antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method in accordance with CLSI guidelines. The results revealed that *Campylobacter* species were the most prevalent (28.3%), followed by *Salmonella enterica* (23.3%), with mixed infection observed in 8.3% of samples. Nearly half of the samples (48.4%) yielded no target organisms. *Salmonella enterica* showed high susceptibility to ciprofloxacin (82.1%) and gentamicin (75.0%) but exhibited marked resistance to tetracycline and ampicillin (67.9% each). Similarly, *Campylobacter* isolates were highly susceptible to azithromycin (85.3%) and erythromycin (79.4%) but demonstrated high resistance to tetracycline (67.7%) and ciprofloxacin (52.9%). Multidrug resistance was observed in 41.9% of isolates. The study highlights poultry droppings as important reservoirs of zoonotic bacteria and antimicrobial-resistant organisms. The high prevalence of resistance underscores the need for strengthened antimicrobial stewardship, improved farm hygiene, and integrated One Health surveillance to mitigate public health risks associated with poultry production systems.

| KEYWORDS

Poultry droppings, *Salmonella enterica*, *Campylobacter* spp., antimicrobial resistance, multidrug resistance

| ARTICLE INFORMATION

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1. Introduction

Poultry production is one of the fastest-growing sectors of animal agriculture worldwide and serves as a major source of animal protein and income, particularly in low- and middle-income countries. In Nigeria, the poultry industry contributes significantly to food security, employment generation, and economic development. However, the rapid expansion and intensification of poultry farming have been accompanied by increasing concerns regarding the emergence and dissemination of zoonotic bacterial pathogens and antimicrobial resistance (AMR) within poultry production systems (Mebrahtu et al., 2025).

Among the bacterial pathogens associated with poultry, *Campylobacter* species and *Salmonella enterica* are recognized as two of the most important foodborne zoonotic agents of global public health significance. These organisms commonly colonize the intestinal tract of apparently healthy birds and are frequently shed in large numbers through poultry droppings, thereby contaminating poultry houses, feed, water, soil, and surrounding environments (WHO, 2020). Poultry droppings therefore constitute an important reservoir and transmission source of these pathogens to humans, domestic animals, and the wider environment.

Campylobacter, particularly *Campylobacter jejuni* and *Campylobacter coli*, is regarded as one of the leading causes of bacterial gastroenteritis globally. Human infection usually results from the consumption of contaminated poultry products, untreated water, or through direct contact with infected birds and contaminated environments. Clinical manifestations range from mild diarrhoea to severe abdominal pain, fever, and, in rare cases, post-infectious complications such as Guillain -Barré syndrome and reactive arthritis (Mohan et al., 2025). Similarly, *Salmonella enterica* is responsible for millions of cases of foodborne infections worldwide and remains a major cause of gastroenteritis, septicaemia, and mortality, particularly among children, the elderly, and immunocompromised individuals (WHO, 2025).

The widespread and often indiscriminate use of antimicrobial agents in poultry production for therapeutic, prophylactic, and growth-promoting purposes has accelerated the development and dissemination of antimicrobial-resistant bacteria. Antibiotics such as tetracyclines, fluoroquinolones, aminoglycosides, β -lactams, and sulphonamides are frequently administered in poultry farms, often without adequate veterinary supervision. Continuous exposure of bacteria to these drugs creates selective pressure that favours the emergence of resistant strains capable of persisting in poultry and their environments (Mebratu et al., 2025).

Antimicrobial resistance has become one of the most serious threats to global health in the twenty-first century. Recent global surveillance reports have demonstrated a worrying increase in resistance among major bacterial pathogens, including foodborne organisms such as *Salmonella* and *Campylobacter*. The increasing occurrence of multidrug-resistant strains has significantly reduced treatment options, increased healthcare costs, prolonged hospitalization, and contributed to higher morbidity and mortality rates worldwide (WHO, 2025). In Africa, weak antimicrobial stewardship programmes, unrestricted access to antibiotics, and inadequate surveillance systems further exacerbate the problem of antimicrobial resistance.

Poultry production systems in Nigeria are particularly vulnerable to the emergence and spread of antimicrobial-resistant bacteria because of poor biosecurity practices, overcrowding, inadequate sanitation, and indiscriminate antibiotic usage. Poultry droppings are commonly disposed of in open environments or used as organic manure without prior treatment, creating opportunities for the dissemination of resistant pathogens and resistance genes into the environment and food chain. Consequently, poultry farmers, farm workers, and nearby communities are at an increased risk of exposure to zoonotic pathogens and antimicrobial-resistant bacteria.

Although several studies have reported the occurrence of *Campylobacter* and *Salmonella* in poultry and poultry products in Nigeria, there remains limited information regarding the antimicrobial susceptibility profiles of these pathogens in poultry droppings from farms located in Aluu Community, Rivers State. Local epidemiological data are essential for understanding resistance trends, guiding antibiotic stewardship programmes, and developing effective public health interventions aimed at reducing the burden of foodborne diseases and antimicrobial resistance.

Therefore, this study was designed to determine the antimicrobial susceptibility profiles of zoonotic *Campylobacter* species and *Salmonella enterica* recovered from poultry droppings in selected poultry farms in Aluu Community, Rivers State, Nigeria. The findings of this study will provide valuable baseline data on the occurrence and resistance patterns of these important foodborne pathogens and contribute to ongoing efforts toward antimicrobial resistance surveillance and the implementation of the One Health approach in Nigeria.

2. Literature Review

2.1 Overview Of Zoonotic Foodborne Pathogens In Poultry

Poultry production is one of the fastest-growing livestock sectors globally, providing an affordable source of high-quality animal protein. However, intensive poultry farming has also increased the emergence and dissemination of zoonotic bacterial pathogens capable of infecting humans through direct contact with birds, contaminated poultry products, or environmental exposure (FAO, 2025; Oloso et al., 2024). Among these pathogens, *Campylobacter* species and *Salmonella enterica* remain the leading bacterial causes of foodborne gastroenteritis worldwide (Kaakoush et al., 2024; Antunes et al., 2023). Their ability to colonize the intestinal tract of apparently healthy chickens without causing clinical disease enables them to persist within poultry

farms and contaminate poultry droppings, litter, drinking water, equipment, and processing environments (Whitman, 2024). Consequently, poultry serves as an important reservoir for human infections, making effective surveillance essential for protecting both animal and public health (WHO, 2024; FAO, 2025).

The increasing burden of antimicrobial resistance among these zoonotic pathogens has further complicated disease management. Resistant strains originating from poultry may be transmitted to humans through the food chain or environmental contamination, thereby reducing treatment options for severe infections (WHO, 2024; EFSA, 2025). This growing concern has prompted the adoption of the One Health approach, which recognizes the interconnectedness of human, animal, and environmental health in controlling antimicrobial resistance (FAO, 2025; WOA, 2024).

2.2 *Campylobacter* Species as Zoonotic Pathogens

Campylobacter jejuni and *Campylobacter coli* are recognized as the most important species responsible for human campylobacteriosis (Kaakoush et al., 2024). These Gram-negative, curved, microaerophilic bacteria naturally inhabit the intestinal tract of poultry, where they establish asymptomatic colonization (Whitman, 2024). Their presence in poultry droppings contributes significantly to environmental contamination and facilitates transmission to humans through handling of birds, contaminated meat, water, and farm environments (Kaakoush et al., 2024).

Human infection commonly manifests as diarrhea, abdominal pain, fever, nausea, and vomiting. Although infections are usually self-limiting, severe complications such as bacteremia, reactive arthritis, and Guillain-Barré syndrome may occur in susceptible individuals (Kaakoush et al., 2024). The infectious dose of *Campylobacter* is remarkably low, making even minimal contamination sufficient to initiate infection (Whitman, 2024).

Several investigations conducted in Nigeria and other African countries have reported a high prevalence of *Campylobacter* in poultry farms, highlighting the role of poultry as a major reservoir (Oloso et al., 2024). Recent systematic reviews further indicate that poultry contributes the highest proportion of *Campylobacter* infections among food-producing animals worldwide (Kaakoush et al., 2024).

2.3 *Salmonella enterica* as a Major Foodborne Pathogen

Salmonella enterica is among the most significant bacterial pathogens affecting both humans and animals (Antunes et al., 2023). Numerous serovars of *S. enterica*, particularly non-typhoidal *Salmonella*, are frequently associated with poultry production systems (Whitman, 2024). Chickens often carry these organisms asymptotically, continuously shedding bacteria in their feces and contaminating the surrounding environment (Antunes et al., 2023).

Human salmonellosis is commonly acquired through consumption of contaminated poultry meat, eggs, or foods contaminated during processing. Clinical symptoms include diarrhea, fever, abdominal cramps, nausea, and vomiting, while invasive infections may occur in immunocompromised individuals, children, and the elderly (Antunes et al., 2023).

Studies conducted across Africa have consistently demonstrated the widespread occurrence of *Salmonella enterica* in poultry farms and poultry products (Oloso et al., 2024). In Nigeria, antimicrobial-resistant and virulent strains have been isolated from poultry droppings, emphasizing the importance of proper waste disposal and biosecurity measures to reduce environmental contamination and disease transmission (WHO, 2024; Oloso et al., 2024).

2.4 Poultry Droppings as Reservoirs of Zoonotic Bacteria

Poultry droppings constitute one of the principal reservoirs of zoonotic microorganisms within poultry production systems (Whitman, 2024). Fresh fecal materials harbor numerous pathogenic bacteria that can persist for extended periods under favorable environmental conditions. Poor disposal of poultry waste facilitates contamination of soil, surface water, vegetables, animal feed, and farm equipment, thereby increasing opportunities for pathogen dissemination (FAO, 2025; Oloso et al., 2024).

In many developing countries, poultry manure is frequently utilized as organic fertilizer without adequate composting. This practice may introduce viable pathogenic bacteria into agricultural soils and water bodies, creating additional exposure pathways for humans and livestock (FAO, 2025). Farm workers, poultry handlers, and nearby communities remain particularly vulnerable through occupational exposure to contaminated droppings (WHO, 2024).

Environmental persistence of *Campylobacter* and *Salmonella* underscores the importance of routine microbiological monitoring of poultry waste, especially in regions where poultry farming is expanding rapidly and biosecurity measures remain inadequate (Whitman, 2024; FAO, 2025).

2.5 Antimicrobial Resistance in *Campylobacter* Species

Antimicrobial resistance among *Campylobacter* species has become an important global public health concern (Mohan et al., 2025). Although uncomplicated infections generally resolve without antimicrobial therapy, severe or prolonged cases require treatment with macrolides or fluoroquinolones. Unfortunately, increasing resistance to these antibiotics has been documented worldwide (Kaakoush et al., 2024; Mohan et al., 2025).

The emergence of resistant *Campylobacter* strains has largely been attributed to indiscriminate antibiotic use in poultry production for disease prevention, treatment, and growth promotion. Resistance mechanisms include chromosomal mutations, acquisition of resistance genes, and active efflux pumps that reduce antibiotic effectiveness (Mohan et al., 2025).

Studies from Nigeria have reported resistance of poultry-derived *Campylobacter* isolates to nalidixic acid, chloramphenicol, streptomycin, and several other commonly used antibiotics, although susceptibility patterns vary among geographical locations (Oloso et al., 2024). These findings emphasize the need for continuous surveillance to guide empirical therapy and antimicrobial stewardship (CDC, 2024; WHO, 2024).

2.6 Antimicrobial Resistance in *Salmonella enterica*

The increasing occurrence of multidrug-resistant *Salmonella enterica* has become one of the greatest challenges confronting food safety and public health (Antunes et al., 2023; WHO, 2024). Resistant strains have emerged due to prolonged exposure to antibiotics used extensively in veterinary medicine, often without laboratory confirmation or veterinary supervision (WOAH, 2024).

Resistance has frequently been reported against tetracycline, ampicillin, sulfonamides, aminoglycosides, and several β -lactam antibiotics. More recently, resistance to fluoroquinolones and third-generation cephalosporins has raised serious concerns because these antibiotics are widely used in treating invasive salmonellosis (Antunes et al., 2023; EFSA, 2025).

The spread of resistance genes through plasmids, transposons, and integrons facilitates rapid dissemination of multidrug resistance within poultry farms (Mebrahtu et al., 2025). Nigerian studies have demonstrated that poultry-derived *Salmonella enterica* isolates often possess both antimicrobial resistance determinants and virulence genes, increasing their potential threat to public health (Oloso et al., 2024).

2.7 Factors Contributing to Antimicrobial Resistance in Poultry Farms

Several management practices contribute to the development and spread of antimicrobial-resistant bacteria within poultry production systems. These include indiscriminate antibiotic administration, self-medication by farmers, inappropriate dosing, poor adherence to withdrawal periods, overcrowding, inadequate sanitation, poor biosecurity, and unrestricted access to antimicrobial agents (FAO, 2025; WOA, 2024).

In Nigeria, antibiotics are commonly administered prophylactically or incorporated into feed and drinking water without proper veterinary guidance. Such practices exert selective pressure that promotes the survival and multiplication of resistant bacterial populations. Resistant organisms are subsequently disseminated through poultry droppings, contaminated equipment, farm workers, insects, rodents, and surface runoff (Oloso et al., 2024; WHO, 2024).

Improving antimicrobial stewardship, strengthening farm biosecurity, implementing vaccination programs, and enhancing farmer education have been identified as effective strategies for reducing antimicrobial resistance in poultry production systems (FAO, 2025; CDC, 2024; WOA, 2024).

2.8 Knowledge Gap

Although numerous studies have investigated antimicrobial resistance among poultry-associated bacteria in different parts of Nigeria, available information remains unevenly distributed across geographical regions (Oloso et al., 2024). Relatively few studies have specifically examined the antimicrobial susceptibility profiles of zoonotic *Campylobacter* species and *Salmonella enterica* simultaneously from poultry droppings in Rivers State, particularly within Aluu Community.

Furthermore, antimicrobial resistance patterns continue to evolve due to changing antibiotic usage practices, making periodic local surveillance essential (WHO, 2024; EFSA, 2025). Generating location-specific susceptibility data will provide valuable evidence for antimicrobial stewardship, support veterinary and public health interventions, and contribute to the implementation of One Health strategies aimed at controlling antimicrobial-resistant zoonotic pathogens (FAO, 2025; WOA, 2024).

The present study therefore seeks to determine the antimicrobial susceptibility profiles of zoonotic *Campylobacter* spp. and *Salmonella enterica* recovered from poultry droppings collected from selected poultry farms in Aluu Community, Rivers State, Nigeria. The findings will provide current baseline information for researchers, clinicians, veterinarians, policymakers, and poultry producers in developing effective measures for the prevention and control of antimicrobial-resistant foodborne pathogens.

3. Materials and Methods

3.1 Study Area

The study was conducted in Aluu Community, located in Ikwerre Local Government Area of Rivers State, Nigeria. Aluu lies approximately between latitude 4°54'–4°57'N and longitude 6°54'–6°58'E within the tropical rainforest belt of the Niger Delta region. The area experiences a humid tropical climate characterized by two distinct seasons: the rainy season, which extends from March to October, and the dry season, which occurs between November and February. Annual rainfall ranges from 2,000 to 2,500 mm, while the average temperature varies between 25 and 32°C. Poultry farming constitutes an important agricultural activity in the community, with numerous small- and medium-scale farms rearing broilers and layers under intensive and semi-intensive management systems.

3.2 Study Design

A cross-sectional laboratory-based study was carried out to determine the antimicrobial susceptibility profiles of zoonotic *Campylobacter* species and *Salmonella enterica* isolated from poultry droppings obtained from selected poultry farms in Aluu Community, Rivers State, Nigeria. The study involved the collection of fresh poultry droppings, bacteriological isolation and identification of target organisms, and determination of their antibiotic susceptibility patterns.

3.3 Selection of Poultry Farms

Selected poultry farms within Aluu Community were visited following permission obtained from the farm owners. Farms included in the study were those actively involved in commercial poultry production and had maintained poultry populations for not less than six months before sample collection. Information regarding farm management practices, flock size, and antibiotic usage was obtained through oral interviews with the farm managers.

3.4 Sample Size Determination

The sample size was determined using the formula described by Cochran for prevalence studies:

$$n = \frac{Z^2 P(1-P)}{d^2}$$

Where:

- (n) = minimum sample size;
- (Z) = standard normal deviate at 95% confidence interval (1.96);
- (P) = estimated prevalence of *Salmonella* and *Campylobacter* in poultry from previous studies;
- (d) = margin of error set at 5%.

A total of 120 fresh poultry droppings were collected from selected poultry farms during the study period.

3.5 Sample Collection

Freshly voided poultry droppings were aseptically collected using sterile spatulas and transferred into sterile universal containers. Samples were properly labelled with the date, farm identification number, and sample code. The samples were immediately placed in an ice-packed insulated container and transported to the Microbiology Laboratory within four hours of collection for bacteriological analysis. All procedures were performed according to standard microbiological protocols described by the International Organization for Standardization (ISO, 2023).

3.6 Isolation and Identification of *Salmonella enterica*

Isolation of *Salmonella enterica* was carried out according to the procedures outlined in ISO 6579-1:2023. Briefly, one gram of each poultry dropping sample was homogenized in 9 mL of buffered peptone water and incubated at 37°C for 18–24 h for pre-enrichment. Following pre-enrichment, 1 mL of the culture was transferred into Rappaport–Vassiliadis Soy Peptone broth and incubated at 42°C for 24 h. A loopful of the enriched culture was streaked onto Xylose Lysine Deoxycholate (XLD) agar and Hektoen Enteric agar and incubated aerobically at 37°C for 24 h. Presumptive *Salmonella* colonies appeared as red colonies with black centres on XLD agar. Representative colonies were purified and subjected to Gram staining and biochemical characterization, including Triple Sugar Iron agar, citrate utilization, urease production, indole production, motility test, and lysine decarboxylase test. Final identification of isolates was confirmed according to the criteria described in Bergey's Manual of Systematic Bacteriology (Whitman, 2024).

3.7 Isolation and Identification of *Campylobacter* Species

Isolation of *Campylobacter* species was performed according to the methods described by ISO 10272-1:2023 with slight modifications. Approximately one gram of each sample was inoculated into Bolton enrichment broth supplemented with selective antibiotics and incubated under microaerophilic conditions at 42°C for 48 h. Following enrichment, aliquots of the culture were streaked onto modified charcoal cefoperazone deoxycholate agar (mCCDA) and incubated at 42°C for 48 h in a microaerophilic atmosphere consisting of approximately 5% oxygen, 10% carbon dioxide, and 85% nitrogen. Suspected colonies were examined for colony morphology, Gram reaction, motility, oxidase test, and catalase test. Curved or spiral Gram-negative rods that were oxidase- and catalase-positive were presumptively identified as *Campylobacter* species.

3.8 Preservation of Bacterial Isolates

Pure bacterial isolates were maintained on nutrient agar slants at 4°C for short-term storage and subsequently preserved in tryptic soy broth containing 20% glycerol at –20°C until further analysis.

3.9 Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar in accordance with the recommendations of the Clinical and Laboratory Standards Institute (CLSI, 2025). Bacterial suspensions equivalent to 0.5 McFarland turbidity standard (approximately 1.5×10^8 CFU/mL) were prepared from pure cultures. Sterile cotton swabs were used to inoculate the surface of Mueller–Hinton agar plates uniformly.

The antibiotic discs used for *Salmonella enterica* included:

- Ciprofloxacin (5 µg)
- Gentamicin (10 µg)
- Tetracycline (30 µg)
- Ampicillin (10 µg)
- Ceftriaxone (30 µg)
- Chloramphenicol (30 µg)

For *Campylobacter* species, the antibiotics tested included:

- Erythromycin (15 µg)
- Azithromycin (15 µg)
- Ciprofloxacin (5 µg)
- Tetracycline (30 µg)
- Gentamicin (10 µg)
- Chloramphenicol (30 µg).

The inoculated plates were incubated under appropriate conditions, after which the diameters of inhibition zones were measured in millimetres and interpreted as susceptible, intermediate, or resistant according to CLSI (2025) guidelines.

3.10 Quality Control

Quality assurance procedures were maintained throughout the study. Media sterility and performance tests were conducted before use. Reference strains, including *Salmonella enterica* ATCC 14028 and *Campylobacter jejuni* ATCC 33560, were used as quality control organisms during antimicrobial susceptibility testing following CLSI recommendations (CLSI, 2025).

3.11 Data Analysis

Data obtained from the study were entered into Microsoft Excel and analysed using the Statistical Package for Social Sciences (SPSS) version 27. Descriptive statistics, including frequencies, percentages, means, and standard deviations, were calculated. Differences in antimicrobial resistance patterns among isolates were determined using the Chi-square test, and statistical significance was accepted at a probability value of less than 0.05 ($p < 0.05$).

3.12 Ethical Considerations

Permission to conduct the study was obtained from the management of the selected poultry farms before sample collection. All laboratory procedures were performed in accordance with institutional biosafety guidelines and internationally accepted standards for handling potentially pathogenic microorganisms.

4. Results

4.1 Distribution of *Salmonella enterica* and *Campylobacter* Species Isolated from Poultry Droppings

Out of the 120 poultry dropping samples examined, *Campylobacter* species had the highest occurrence with a prevalence of 28.3%, followed by *Salmonella enterica* (23.3%). Mixed isolation of both organisms was observed in 8.3% of the samples, while nearly half of the samples (48.4%) yielded no target bacterial pathogens.

Table 4.1: Distribution of *Salmonella enterica* and *Campylobacter* Species Isolated from Poultry Droppings

Bacterial Isolate	Number of Positive samples (n=120)	Prevalence (%)
<i>Salmonella enterica</i>	28	23.3
<i>Campylobacter</i> spp	34	28.3
Mixed Isolation (<i>Salmonella</i> + <i>Campylobacter</i>)	10	8.3
No Growth of Target Organisms	58	48.4

4.2 Antimicrobial Susceptibility Profile of *Salmonella enterica* Isolates (n = 28)

Salmonella enterica isolates demonstrated high susceptibility to ciprofloxacin (82.1%), gentamicin (75.0%), and ceftriaxone (71.4%). However, substantial resistance was observed against tetracycline (67.9%), ampicillin (67.9%), and trimethoprim-sulfamethoxazole (50.0%), indicating widespread resistance to commonly used antibiotics.

Table 4.2: Antimicrobial Susceptibility Profile of *Salmonella enterica* Isolates (n = 28)

Antibiotic	Sensitive	Intermediate	Resistant
Ciprofloxacin (5 µg)	23 (82.1)	2 (7.1)	3 (10.8)
Gentamicin (10 µg)	21 (75.0)	3 (10.7)	4 (14.3)
Tetracycline (30 µg)	7 (25.0)	2 (7.1)	19 (67.9)
Ampicillin (10 µg)	6 (21.4)	3 (10.7)	19 (67.9)
Ceftriaxone (30 µg)	20 (71.4)	3 (10.7)	5 (17.9)
Chloramphenicol (30 µg)	18 (64.3)	2 (7.1)	8 (28.6)

4.3 Antimicrobial Susceptibility Profile of *Campylobacter* Species (n = 34)

The *Campylobacter* isolates were highly susceptible to azithromycin (85.3%), erythromycin (79.4%), and gentamicin (73.5%). Conversely, high levels of resistance were observed against tetracycline (67.7%) and ciprofloxacin (52.9%), suggesting emerging resistance to fluoroquinolones and tetracyclines among poultry-associated *Campylobacter* strains.

Table 4.3: Antimicrobial Susceptibility Profile of *Campylobacter* Species (n = 34)

Antibiotic	Sensitive n (%)	Intermediate n (%)	Resistant n (%)
Erythromycin (15 µg)	27 (79.4)	2 (5.9)	5 (14.7)
Azithromycin (15 µg)	29 (85.3)	1 (2.9)	4 (11.8)
Ciprofloxacin (5 µg)	12 (35.3)	4 (11.8)	18 (52.9)
Tetracycline (30 µg)	8 (23.5)	3 (8.8)	23 (67.7)
Gentamicin (10 µg)	25 (73.5)	2 (5.9)	7 (20.6)
Chloramphenicol (30 µg)	20 (58.8)	3 (8.8)	11 (32.4)

4.4 Multidrug Resistance Pattern of Bacterial Isolates

A high prevalence of multidrug resistance (41.9%) was observed among the bacterial isolates recovered from poultry droppings. Only 16.2% of the isolates were susceptible to all antibiotics tested. The findings indicate that poultry droppings constitute an important reservoir of antimicrobial-resistant zoonotic pathogens and may pose a significant public health risk.

Table 4.4: Multidrug Resistance Pattern of Bacterial Isolates

Resistance Pattern	Number of Isolates	Percentage (%)
Resistant to one antibiotic	11	17.7
Resistant to two antibiotics	15	24.2
Resistant to three or more antibiotics (MDR)	26	41.9
Fully susceptible isolates	10	16.2
Total	62	100

5. Discussion

The findings of this study demonstrate that poultry droppings constitute an important reservoir of zoonotic bacterial pathogens, particularly *Campylobacter* species and *Salmonella enterica*, and further highlight the growing challenge of antimicrobial resistance within poultry production systems. Of the 120 poultry dropping samples examined, *Campylobacter* species were the most frequently isolated organisms, with a prevalence of 28.3%, while *Salmonella enterica* accounted for 23.3% of the isolates. Additionally, co-contamination with both pathogens was detected in 8.3% of the samples, indicating the simultaneous circulation of multiple enteric pathogens within the poultry environment.

The higher prevalence of *Campylobacter* compared with *Salmonella* agrees with the established epidemiological role of poultry as the principal reservoir of thermophilic *Campylobacter*, particularly *Campylobacter jejuni* and *Campylobacter coli*. These organisms colonize the intestinal tract of birds without causing apparent disease and are continuously shed in faeces, thereby facilitating environmental contamination and increasing the risk of transmission to humans through direct contact, contaminated water, and poultry products. Recent reports by the World Health Organization (WHO, 2024) and the Food and Agriculture Organization (FAO, 2025) identified poultry as the major source of human campylobacteriosis worldwide and emphasized the increasing burden of antimicrobial-resistant *Campylobacter* originating from food animals. Similar prevalence rates have been reported in recent studies conducted in Nigeria, Kenya, and other low- and middle-income countries, where poor farm sanitation, inadequate biosecurity measures, and intensive production systems favour the persistence and dissemination of the organism (Mughini-Gras et al., 2024; Olosolo et al., 2024).

The prevalence of *Salmonella enterica* observed in this study also confirms the continuing importance of poultry as a significant reservoir of salmonellosis-associated pathogens. The occurrence of *Salmonella* in nearly one-quarter of the examined samples is comparable to reports from several African and Asian countries, where prevalence rates ranging between 15% and 35% have been documented in poultry farms (Antunes et al., 2023; EFSA, 2025). The persistence of *Salmonella* within poultry production systems has been attributed to several factors, including contaminated feed, poor hygiene practices, inadequate waste disposal, and unrestricted access to veterinary antimicrobials. These factors contribute to the establishment and maintenance of infection cycles within farms and increase the potential for dissemination into the food chain.

The detection of both *Campylobacter* and *Salmonella* in the same samples is of considerable public health importance. Co-contamination of poultry waste with multiple enteric pathogens may amplify environmental dissemination and increase opportunities for horizontal gene transfer among bacterial populations, particularly the transfer of antimicrobial resistance determinants. Contaminated poultry litter is increasingly recognized as an important vehicle for the spread of zoonotic pathogens and resistance genes into soil and water systems, thereby creating additional routes of human exposure (FAO, 2025; WHO, 2025). Consequently, the presence of mixed infections in poultry droppings represents a potential threat not only to food safety but also to environmental and public health.

The absence of the target organisms in approximately half of the samples may reflect differences in management practices among farms, including variations in bird age, stocking density, sanitation measures, prior antimicrobial exposure, and environmental conditions. Previous studies have shown that the microbial composition of poultry faeces can vary considerably depending on husbandry practices and seasonal influences, which may account for differences in pathogen recovery rates (CDC, 2024).

The antimicrobial susceptibility profile of *Salmonella enterica* isolates revealed high susceptibility to ciprofloxacin, gentamicin, and ceftriaxone. The observed effectiveness of ciprofloxacin and ceftriaxone is encouraging because these agents remain among the recommended drugs for the treatment of invasive salmonellosis. Similar susceptibility patterns have been reported by the World Organisation for Animal Health (WOAH, 2024), which noted that third-generation cephalosporins and fluoroquinolones continue to retain therapeutic efficacy against many *Salmonella* strains despite emerging resistance trends. Nevertheless, the high levels of resistance observed against tetracycline and ampicillin are alarming and reflect the extensive and often indiscriminate use of these antimicrobials in poultry production. Tetracyclines and β -lactam antibiotics have been widely employed for disease prevention, treatment, and growth promotion in many developing countries, creating strong selective pressure for the emergence and persistence of resistant bacteria (CDC, 2024).

Resistance to trimethoprim-sulfamethoxazole was also substantial, indicating a gradual decline in the effectiveness of this antimicrobial combination. Recent genomic investigations have shown that poultry-associated *Salmonella* frequently harbour resistance genes such as *tetA*, *tetB*, *blaTEM*, and *sul1*, which confer resistance to tetracyclines, β -lactams, and sulfonamides, respectively (EFSA, 2025). The presence of these resistance determinants within poultry environments is of significant concern because they can be transferred to other bacterial species through mobile genetic elements, thereby accelerating the spread of antimicrobial resistance.

The antimicrobial susceptibility profile of *Campylobacter* species demonstrated high sensitivity to azithromycin and erythromycin, findings that are consistent with current treatment recommendations that identify macrolides as the first-line drugs for the management of human campylobacteriosis (WHO, 2024). Several recent studies have reported sustained susceptibility of *Campylobacter* isolates to macrolides despite increasing resistance to other antimicrobial classes (Kaakoush et al., 2024; WHO, 2025). However, the high resistance observed against ciprofloxacin is particularly concerning. Fluoroquinolones were previously considered highly effective against *Campylobacter* infections, but resistance has increased dramatically worldwide and is now recognized as a major challenge in both veterinary and human medicine. This resistance is primarily associated with mutations in the *gyrA* gene and the extensive use of fluoroquinolones in animal production systems (EFSA, 2025).

Similarly, the high level of resistance to tetracycline suggests widespread dissemination of the *tet(O)* resistance gene among poultry-associated *Campylobacter* isolates. Comparable findings have been documented in recent studies from Africa and Asia, where resistance rates exceeding 60% have been reported (FAO, 2025; WHO, 2024). The increasing resistance to fluoroquinolones and tetracyclines threatens the effectiveness of available treatment options and underscores the need for continuous surveillance and prudent antimicrobial use.

The multidrug resistance profile observed in this study further highlights the magnitude of the antimicrobial resistance problem. Approximately 41.9% of all bacterial isolates were resistant to three or more antimicrobial agents and therefore met the criteria for multidrug resistance. This prevalence is comparable to recent global reports identifying poultry production systems as major reservoirs of multidrug-resistant zoonotic bacteria and antimicrobial resistance genes (CDC, 2024; EFSA, 2025). The emergence of multidrug-resistant isolates is largely driven by inappropriate antimicrobial practices, including prophylactic administration, self-prescription by farmers, and the use of antibiotics as growth promoters. Such practices facilitate the selection and propagation of resistant organisms that can subsequently be transmitted to humans through direct contact with poultry, contaminated food products, or environmental exposure.

Collectively, the findings of this study demonstrate that poultry droppings are important reservoirs of both zoonotic pathogens and antimicrobial resistance determinants. The high prevalence of antimicrobial resistance and multidrug-resistant isolates among *Salmonella enterica* and *Campylobacter* species highlights the critical need for coordinated interventions within the framework of the One Health approach. Strengthening antimicrobial stewardship programmes, improving farm hygiene and biosecurity, and implementing integrated surveillance systems are essential measures for mitigating the public health risks associated with antimicrobial-resistant pathogens in poultry production systems.

6. Conclusion

This study demonstrated that poultry droppings from selected poultry farms in Aluu Community, Rivers State, harbour significant populations of zoonotic bacterial pathogens, particularly *Campylobacter* spp. and *Salmonella enterica*. The recovery of these organisms from a substantial proportion of the samples confirms that apparently healthy poultry can serve as important reservoirs of enteric pathogens with the potential to contaminate the farm environment and pose serious risks to animal and human health. The findings reinforce the role of poultry production systems as critical points in the transmission of foodborne pathogens through direct contact, environmental exposure, and the food chain.

The antimicrobial susceptibility results revealed a concerning pattern of resistance among the bacterial isolates. High resistance rates to commonly used antibiotics, particularly tetracycline, ampicillin, and ciprofloxacin, together with the considerable occurrence of multidrug-resistant isolates, suggest that antimicrobial misuse or overuse within poultry production may be contributing to the selection and persistence of resistant bacterial populations. The presence of multidrug-resistant *Campylobacter* spp. and *Salmonella enterica* in poultry droppings raises significant public health concerns because these organisms may disseminate resistance determinants to other bacteria and reduce the effectiveness of antibiotics commonly used for treating human infections.

Overall, the findings emphasize the need for continuous microbiological surveillance and routine antimicrobial resistance monitoring in poultry farms to detect emerging resistance trends and guide appropriate intervention strategies. Strengthening farm biosecurity, promoting good hygiene and waste management practices, enforcing prudent antimicrobial use through effective antimicrobial stewardship programmes, and improving farmer education are essential measures for limiting the spread of resistant zoonotic pathogens. In addition, collaboration among veterinarians, public health professionals, regulatory agencies, researchers, and poultry producers within a One Health framework is critical for addressing the growing challenge of antimicrobial resistance. The baseline data generated by this study contribute valuable local evidence for informing public health policies, supporting antimicrobial stewardship initiatives, and developing sustainable strategies for the prevention and control of antimicrobial-resistant foodborne pathogens in Rivers State, Nigeria, and comparable poultry-producing regions.

7. Recommendations

1. Routine surveillance programmes should be established for the monitoring of *Salmonella*, *Campylobacter*, and antimicrobial resistance patterns in poultry farms.
2. The indiscriminate use of antibiotics in poultry production should be strictly regulated, and antimicrobial stewardship programmes should be strengthened.
3. Poultry farmers should be educated on appropriate biosecurity practices, hygienic waste disposal, and responsible antimicrobial use.
4. The use of antibiotics as growth promoters should be discouraged, and alternative strategies such as vaccination, probiotics, and improved farm management practices should be encouraged.
5. Government agencies and veterinary authorities should implement policies that promote the prudent use of antimicrobials and strengthen regulatory oversight of veterinary drug distribution.
6. Integrated One Health surveillance programmes involving human, animal, and environmental health sectors should be developed to monitor and control the dissemination of antimicrobial-resistant pathogens.
7. Further molecular studies should be conducted to characterize the resistance genes and transmission pathways of antimicrobial-resistant *Salmonella* and *Campylobacter* isolates within poultry production systems.

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