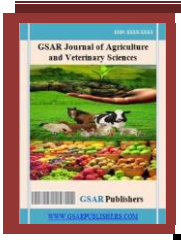

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PREVALENCE, MOLECULAR CHARACTERIZATION, AND ANTIBIOTIC RESISTANCE PATTERNS OF *SALMONELLA* SPECIES ISOLATED FROM RETAIL CHICKEN MEAT IN THE FEDERAL CAPITAL TERRITORY, NIGERIA

By

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Abstract

Salmonella species contaminate a wide range of animal products and remain among the leading causes of foodborne illnesses globally. Poultry meat is widely consumed in Nigeria because of its nutritional value; however, it is also recognized as a major vehicle for the transmission of foodborne pathogens to humans. This study investigated the prevalence, antibiotic resistance patterns, and molecular characterization of Salmonella species in retail chicken meat across the Federal Capital Territory (FCT), Nigeria. A cross-sectional study design was employed, and 165 raw chicken meat samples were collected from retail markets in three Area Councils of the FCT: Abuja Municipal Area Council (AMAC), Bwari, and Kuje. Isolation and identification of Salmonella were carried out using standard culture and biochemical methods, followed by 16S rRNA Gene-Based Molecular Identification. Antimicrobial susceptibility testing was performed using the disk diffusion method against seven commonly used antibiotics. Data were analysed using descriptive statistics. The overall prevalence of Salmonella was 18.8%, with prevalence rates of 12.7%, 20.0%, and 23.6% in AMAC, Bwari, and Kuje, respectively, indicating a significant public health concern. All isolates were identified as Salmonella enterica subsp. enterica, with predominant serovars including Montevideo and Typhimurium. High resistance to nitrofurantoin and erythromycin was observed, consistent with global trends, and multiple drug-resistant Salmonella serovars were detected. The prevalence recorded in this study was higher than previously reported values in the FCT. Salmonella detection was significantly associated with weak regulatory control, underscoring the need for stricter enforcement of food safety regulations. Continuous surveillance of Salmonella in poultry meat and routine antimicrobial susceptibility testing are recommended to mitigate the public health risks associated with foodborne salmonellosis.

Keywords: *Salmonella enterica; Poultry meat; Antimicrobial resistance; Molecular characterisation; Foodborne disease; Nigeria*

I. Introduction

Meat is a nutrient-rich food that provides high-quality proteins, essential vitamins, and minerals with greater bioavailability than many other food sources (McAfee *et al*., 2010). Poultry meat, in particular, is widely consumed because of its affordability and nutritional value. However, poultry meat quality is complex and influenced by multiple interacting factors, including genetics, feeding practices, husbandry, pre-slaughter handling, slaughter procedures, processing, storage, and distribution (Dragan *et al*., 2015). Failures at any of these stages may result in carcass contamination, deterioration of meat quality, and increased public health risks.

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In developing countries, improper food processing and handling, poor sanitation, weak enforcement of food safety regulations, limited public awareness, and inadequate infection control measures significantly contribute to the burden of foodborne diseases (World Health Organization [WHO], 2004). Meat products have been widely recognized as major vehicles for the transmission of foodborne pathogens to humans (Eurosurveillance Editorial Team, 2013), and foodborne infections constitute a substantial global health and economic burden (Nazzal, 2021).

Among foodborne pathogens, *Salmonellaspecies* remain one of the most important causes of bacterial food poisoning worldwide. Since their first isolation, concerns about *Salmonella* infections have continued to increase because of their significant impact on human health, food safety, and national economies (Nair *et al*., 2018). *Salmonellaspecies* are of considerable zoonotic importance due to their ubiquitous distribution, wide host range, increasing number of serotypes, complex pathogenesis, and intricate epidemiological links among animals, humans, and the environment (Díaz-Torres *et al*., 2020).

Salmonella serotypes are broadly classified into typhoidal and non-typhoidal groups based on the clinical syndromes they cause (Smith *et al*., 2016). Typhoidal*Salmonella*, including *Salmonella Typhi* and *Salmonella Paratyphi*, are responsible for enteric fever, whereas non-typhoidal*Salmonella* serotypes, such as *Salmonella Typhimurium* and *Salmonella Enteritidis*, commonly cause gastroenteritis and invasive infections. Non-typhoidal*Salmonella* (NTS) infections occur worldwide and are typically self-limiting in developed countries; however, in sub-Saharan Africa, NTS infections are endemic and represent a major cause of bacteraemia, particularly among children and immunocompromised individuals (Majowicz*et al*., 2010). The burden of invasive NTS infections is further exacerbated in regions with high prevalence of malaria, malnutrition, and HIV (Mandomando*et al*., 2009).

Globally, *Salmonella* infections are estimated to cause approximately 1.3 billion cases of gastroenteritis and several million deaths annually, making them a major public health concern (Kurtz *et al*., 2017). Poultry meat has been consistently identified as an important reservoir of *Salmonella*, with transmission commonly occurring through improper handling of raw poultry products and consumption of undercooked meat (Adeyanju*et al*., 2014).

The growing problem of antimicrobial resistance further complicates the control and treatment of *Salmonella* infections. Resistant bacteria are increasingly detected in food products and environmental sources as a result of extensive antimicrobial use in human medicine, veterinary practice, and food-animal production (Rossi, 2011). The emergence and spread of multidrug-resistant *Salmonella* strains pose a serious threat to effective disease management and public health safety.

Given the public health significance of *Salmonella* contamination in poultry meat and the increasing concern over antimicrobial resistance, this study aimed to determine the prevalence, molecular characterisation, and antibiotic resistance patterns of *Salmonellaspecies* isolated from retail chicken meat in markets within the Federal Capital Territory (FCT), Nigeria.

Materials and Methods

Study Area

This study was conducted in the Federal Capital Territory (FCT), Nigeria. The FCT comprises six Area Councils: Abuja Municipal Area Council (AMAC), Gwagwalada, Kuje, Bwari, Abaji, and Kwali. The territory is located at latitude 9.0578°N and longitude 7.4951°E in the northern hemisphere and covers an estimated land area of approximately 7,315 km², with moderate climatic conditions (Alu*et al*., 2021). It shares boundaries with Niger State to the west and north, Kaduna State to the northeast, Nasarawa State to the east, and Kogi State to the southwest. The estimated population of the FCT was 1,406,239 according to the 2022 population census (Bashir *et al*., 2021).

However, the study was restricted to retail chicken meat markets within AMAC, Bwari, and Kuje Area Councils (Figure 1).

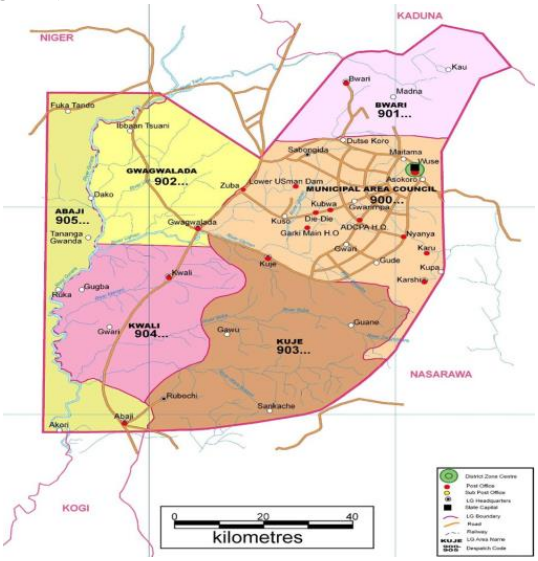

Figure 1: Map of the Federal Capital Territory of Nigeria showing the study locations

Source: Andrews, 2018

Study Design

A cross sectional study design was employed and simple random sampling approach was used in selecting the 3 Area Councils. Each Area Council had an equal chance of being selected from the sampling frame.Using a prevalence rate of 11.1% Salmonella species in retailed meat in Calabar metropolis (Ukut*et al*., 2010), the following sample size was determined using the Thrusfield formula of 2005:

$$n = \frac{Z^2 \times P (1 - P)}{d^2}$$ (Thrusfield, 2005)

Where:

n = required sample size

Z = confidence interval at 95% (standard value of 1.96)

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P = previous prevalence: 11.1% (Ukut*et al*. 2010)
d = desired absolute precision (5%)

Therefore:

$$n = \frac{(1.96)^2 \times 0.111 (1 - 0.111)}{0.05^2}$$

$$n = 152$$

Note: The sample size was increased to 165 to avoid bias.

Sample Collection

A total of 165 raw chicken meat samples (1 g each) were aseptically collected from retail markets and chicken selling points over a two-month period (June–July 2022). Five different markets or selling points were sampled in each Area Council and designated as M1–M5. Sample collection was carried out twice weekly using a systematic sampling technique. Each sample was placed in a sterile, labelled container and transported in an ice-packed Coleman flask to the Namiroch Advanced Laboratory, Kwali, Abuja, under a maintained cold chain. Laboratory analyses were initiated immediately upon arrival.

Isolation and Identification of *Salmonella*

Isolation and identification of *Salmonella* species were performed following the Int+
ernational Organization for Standardization protocol ISO 6579:2010 for food microbiology (Puig*et al*., 2013; World Health Organization (WHO), 2010).

Non-selective Pre-enrichment

Upon arrival at the laboratory, 1 g of each chicken meat sample was homogenised in 9 mL of buffered peptone water using a sterile pestle and mortar to obtain a 1:10 dilution. The homogenates were incubated at 37°C for 18–24 hours for non-selective pre-enrichment (Kim *et al*., 2012; Adeyanju*et al*, 2014).

Selective Enrichment

Following pre-enrichment, 0.1 mL of each culture was inoculated into 10 mL of Rappaport–Vassiliadis Soya Peptone (RVS) broth (Oxoid, England). The inoculated broths were incubated at 41.5 ± 0.5°C for 18–24 hours to selectively enrich *Salmonella* species (Puig*et al*., 2013).

Selective Agar Plating

A sterile 10 µL wire loop was used to streak a loopful of the RVS culture onto prepared and solidified Brilliant Green Agar (BGA) plates (LabM, UK). The plates were incubated at 37°C for 18–24 hours. Presumptive *Salmonella* colonies were identified based on characteristic colour changes of the medium from yellow to red or pink (Adeyanju*et al*, 2014).

Sub-culturing and Preservation

Suspected colonies were sub-cultured onto nutrient agar plates (LabM, UK) and incubated at 37°C for 18–24 hours. Distinct colonies were transferred onto nutrient agar slants and stored at 4°C for further biochemical confirmation and molecular analysis.

Biochemical Tests

Presumptive *Salmonella* isolates recovered from retail chicken meat samples were subjected to standard biochemical tests for preliminary identification prior to molecular confirmation.

Antibiotic Sensitivity Test

Antimicrobial susceptibility testing of confirmed *Salmonella* isolates was performed using the Kirby–Bauer disk diffusion method in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI, 2021). Briefly, each *Salmonella* isolate was sub-cultured on nutrient agar and incubated at 37°C for 18–24 hours. A few well-isolated colonies were then emulsified in sterile normal saline, and the turbidity of the suspension was adjusted to match the 0.5 McFarland standard.

Using a sterile swab, the standardized bacterial suspension was evenly inoculated onto the surface of Mueller–Hinton agar plates. Antibiotic-impregnated discs were aseptically placed on the inoculated agar surface using sterile forceps, ensuring adequate spacing between discs to avoid overlapping zones of inhibition. The antibiotics tested were selected based on their common use in human and veterinary medicine and included amoxicillin/clavulanic acid, ceftazidime, ciprofloxacin, gentamicin, erythromycin, nitrofurantoin, and sulphamethoxazole/trimethoprim.

The inoculated plates were incubated aerobically at 37°C for 18–24 hours. Following incubation, the diameters of the zones of inhibition around each antibiotic disc were measured in millimetres using a calibrated ruler. Isolates were classified as susceptible, intermediate, or resistant based on CLSI interpretative criteria (CLSI, 2021). Multidrug resistance (MDR) was defined as resistance to three or more classes of antimicrobial agents (Magiorakos*et al*., 2012).

Determination of Multiple Antibiotic Resistance Index (MARI)

The Multiple Antibiotic Resistance Index (MARI) was calculated for each confirmed Salmonella isolate to assess the level of exposure of the isolates to antimicrobial agents and to evaluate the potential public health risk associated with antimicrobial misuse. The MARI was determined using the formula:

$$MARI = a/b$$

Where“a” represents the number of antibiotics to which a given isolate exhibited resistance, and “b” represents the total number of antibiotics tested against that particular isolate (Krumperman, 1983).

In this study, antimicrobial susceptibility testing was performed against seven commonly used antibiotics; therefore, the value of b was fixed at seven for all isolates. A MARI value greater than 0.2 was interpreted as indicative of isolates originating from high-risk sources where antibiotics are frequently used or misused, whereas values ≤ 0.2 suggested low-risk sources with limited antibiotic exposure (Krumperman, 1983; Singh et al., 2012).

The MARI values obtained were used to identify multidrug-resistant Salmonella isolates and to support interpretation of resistance patterns observed among isolates recovered from retail chicken meat.

DNA Extraction

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Genomic DNA extraction was carried out at InqabaBiotec Laboratory, Ibadan, Nigeria, using the ZymoBIOMICS™ DNA Miniprep Kit, following the manufacturer's instructions. Briefly, 250 µL of each *Salmonella* culture was lysed using mechanical bead beating, followed by centrifugation, filtration, DNA binding, washing, and elution steps as specified in the kit protocol. Purified DNA was eluted in 50 µL of DNase/RNase-free water and stored at appropriate temperatures for downstream molecular analysis.

Primers and PCR Amplification

Universal primers targeting the 16S rRNA gene were used for molecular identification of *Salmonellaspecies*, as previously described by Pradhab et al. (2011). The forward primer (27F) and reverse primer (1492R) were obtained from InqabaBiotec, South Africa. Primer sequences and target regions are presented in Table 3.1.

Table 3.1: Primer Sequence Obtained for Molecular Analysis

27F (Forward Primer)	1492R (Reverse Primer)
Sequence:5'-AGAGTTTGATCMTGGCTCAG-3'	Sequence:5'-TACGGYTACCTTGTTACGACTT-3'
Primer targets the 5' end of the 16S rRNA gene.	Primer targets the 3' end of the 1 rRNA gene

Next-Generation Sequencing (NGS)

Extracted genomic DNA samples were shipped to InqabaBiotec Laboratories, South Africa, for Next-Generation Sequencing (NGS). Amplification of the 16S rRNA gene (V1–V9 region) was performed using primers 27F and 1492R (Pradhab*et al*., 2011). Amplicons were barcoded using PacBio M13 barcodes and pooled equimolarly following quantification. AMPure PB bead-based purification was conducted prior to library preparation. SMRTbell libraries were prepared according to the manufacturer's protocol and sequenced on the PacBio Sequel IIe system. Sequence data were analysed using SMRT Link software and compared with reference sequences in the National Center for Biotechnology Information (NCBI) database for taxonomic assignment.

Data Analysis

Data generated from laboratory analyses were summarised using descriptive statistics, tables and percentages. Statistical analyses were conducted using SPSS version 25.

II. Result

Prevalence of *Salmonella species*

The results revealed that 31 out of 165 samples tested positive for *Salmonella species*, indicating a prevalence rate of 18.8%. (See *Table: 2*).

Area-specific prevalence rates showed variation among the three Area Councils. In AMAC, 7 out of 55 samples (12.7%) were positive for *Salmonella*. In Bwari, 11 out of 55 samples (20.0%) were positive, while Kuje recorded the highest prevalence, with 13 out of 55 samples (23.6%) testing positive (Table 2).

Further analysis of individual market sampling points revealed differences in contamination levels within each Area Council (Tables 3–5), indicating heterogeneous distribution of *Salmonella* contamination across retail outlets.

Biochemical Tests

Biochemical testing confirmed that all isolates exhibited characteristic reactions consistent with Salmonella enterica, including oxidase negativity, citrate utilisation, and H_2S production on TSI agar (Cheesbrough, 2010; WHO, 2010) (Table 4.1).

Table 4.1: Overall Prevalence of Salmonella in AMAC, BWARI and KUJE Area Councils

Locations	No. of Samples	Salmonella Positives
AMAC	55	7 (12.7%)
Bwari	55	11 (20%)
Kuje	55	13 (23.6%)
Total	**165**	**31 (18.8%)**

Figure 2: Prevalence of *Salmonella* in retail chicken meat across some Area Councils of the Federal Capital Territory, Nigeria

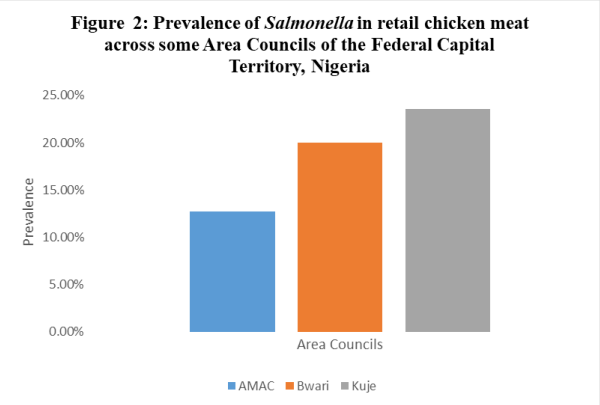

Table 4.2: Prevalence of Salmonella in AMAC, BWARI and KUJE Area Councils

LOCATIONS						TOTAL	PREVALENCE
Sample Points in AMAC	**M-1**	**M-2**	**M-3**	**M-4**	**M-5**		
No. of Samples	11	11	11	11	11	**55**	
Salmonella Positives	2	1	1	1	2	**7**	**12.7%**
Sample Points in Bwari	**M-1**	**M-2**	**M-3**	**M-4**	**M-5**		
No. of Samples	11	11	11	11	11	**55**	
Salmonella	2	1	2	4	2	**11**	**20%**

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Positives							
Sample Points in Kuje	**M-1**	**M-2**	**M-3**	**M-4**	**M-5**		
No. of Samples	11	11	11	11	11	**55**	
Salmonella Positives	4	2	2	3	2	**13**	**23.6%**

***Table 4.3*: Summary of Biochemical Reactions of *Salmonella* Isolates from Retail Chicken Meat**

Biochemical Test	Observed Reaction	Interpretation
Gram staining	Gram-negative rods	Consistent with Enterobacteriaceae
Oxidase test	Negative	Typical of *Salmonella spp*.
Catalase test	Positive	Characteristic of *Salmonella spp*.
Indole test	Negative	Differentiates from indole-positive enterics
Urease test	Negative	Excludes urease-producing bacteria
Citrate utilisation (Simmons citrate)	Positive	Indicative of Salmonella enterica
Triple Sugar Iron (TSI) agar	Alkaline slant / Acidic butt (K/A) with H_2S ± gas	Characteristic Salmonella reaction
Hydrogen sulfide (H_2S) production	Positive	Diagnostic feature of Salmonella
Lactose fermentation	Negative	Confirms non-lactose fermenter

Antibiotic Susceptibility Profile of *Salmonella* Isolates

High resistance rates were observed for nitrofurantoin and erythromycin, with 29 isolates (93.5%) showing resistance to each of these antibiotics. Resistance to amoxicillin/clavulanic acid and ceftazidime was observed in 19 (61.3%)and 18 (58.1%)isolates, respectively.

Lower resistance rates were recorded for gentamicin (3 isolates; 9.7%) and for both ciprofloxacin and sulphamethoxazole/trimethoprim (1 isolate; 3.2%each). Most isolates remained susceptible to ciprofloxacin and sulphamethoxazole/trimethoprim (30 isolates; 96.8%), while susceptibility to gentamicin was observed in 21 isolates (67.7%).

Intermediate susceptibility was recorded for amoxicillin/clavulanic acid and gentamicin in 7 isolates (22.6%)each, and for ceftazidime in 6 isolates (19.4%). Overall, the antibiotic susceptibility profile indicated the presence of multidrug-resistant (MDR) *Salmonella* isolates among the samples analysed (Table 4).

Table 4.4: Antibiotic Susceptibility Profile of Salmonella Isolates from Chicken Meat in FCT

STATUS	AMC	CAZ	CIP	CN	E	F	SXT
RESISTANCE	**19/31 (61.3%)**	**18/31 (58.1%)**	**1/31 (3.2%)**	**3/31 (9.7%)**	**29/31 (93.5%)**	**29/31 (93.5%)**	**1/31 (3.2%)**
INTERMEDIATE	**7/31 (22.6%)**	**6/31 (19.4%)**	**-**	**7/31 (22.6%)**	**-**	**-**	**-**
SENSITIVITY	**5/31 (16.1%)**	**7/31 (22.5%)**	**30/31 (96.8%)**	**21/31 (67.7%)**	**2/31**	**2/31**	**30/31 (96.8%)**

AMC=Amoxicillin/Calvulanic acid, CAZ=Ceftazidime, CIP=Ciprofloxasin, CN=Gentamicin, E=Erythromycin, F=Nitrofurantoin, SXT=Sulphamethoxazole/Trimethoprim

Multiple Antibiotic Resistance Index (MARI)

The calculated MARI values ranged from 0.29 to 0.71, indicating varying degrees of antimicrobial exposure among the isolates.A majority of the isolates exhibited MARI values greater than 0.2, which is indicative of origin from high-risk environments where antibiotics are frequently used or misused.

Molecular Characterisation of *Salmonella* Isolates

Molecular characterisation of presumptive *Salmonella* isolates using 16S rRNA - Based Molecular Identification confirmed that all isolates belonged to *Salmonella enterica* subsp. *enterica*. Sequence analysis revealed the presence of several strains, with a high prevalence of *Salmonella enterica* subsp. *enterica*serovar*Typhimurium* (29%) followed by *Salmonella enterica* subsp. *enterica*serovar*Montevideo*(16%), *Salmonella enterica* strain SA20031245 chromosome (16%) and*Salmonella enterica* strain PNUSAS148096 chromosome (16%) (Table 6).

All sequences showed high query coverage (100%) and percentage identity ranging from 89.7% to 95.4% when compared with reference sequences in the NCBI database. Accession numbers were assigned to each isolate following sequence submission (Table 5).

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Table 4.5 **Salmonellaenterica strains Identified**

S/N	Salmonella*enterica* strains	ACCESSION NO	LENT (bp)	% QUERY COVER	% ID
1	*Salmonella enterica* strain CFSAN029882 chromosome	CP074652.1	4911611	100	95.43
-+2	*Salmonella enterica* strain FDAARGOS_718 chromosome	CP054901.1	4667369	100	95.33
3	*Salmonella enterica* strain PNUSAS148096 chromosome	CP093081.1	4708042	100	94.63
4	*Salmonella enterica* strain SA20031245 chromosome	CP030235.1	4522338	100	94.10
5	*Salmonella enterica* strain 85-0120 chromosome	CP054715.1	4794154	100	89.70
6	*Salmonella enterica* subsp. entericaserovar Montevideo strain FCC0123 chromosome	CP040379.1	4619529	100	89.68
7	*Salmonella enterica* subsp. entericaserovar Typhimurium strain SAP17-8290 chromosome	CP040568.1	4965236	100	89.97

Table 4.6**: Occurrence and distribution of *Salmonellaentericas*trains in the study area**

Salmonella strains	**Area Councils**							
	AMAC		**KUJE**		**BWARI**		**TOTAL**	
	N	%	N	%	N	%	N	%
Salmonella enterica strain CFSAN029882 chromosome	0	0	2	15.4	1	9.1	3	10
Salmonella enterica strain FDAARGOS_718 chromosome	2	28.6	1	7.7	0	0	3	10
Salmonella enterica strain PNUSAS148096 chromosome	1	14.3	0	0	4	36.4	5	16
Salmonella enterica strain SA20031245 chromosome	1	14.3	2	15.4	2	18.2	5	16
Salmonella enterica strain 85-0120 chromosome	0	0	1	7.7	0	0	1	3
Salmonella enterica subsp. entericaserovar Montevideo strain FCC0123 chromosome	1	14.3	3	23.1	1	9.1	5	16
Salmonella enterica subsp. entericaserovar Typhimurium strain SAP17-8290 chromosome	2	28.6	4	30.8	3	27.3	9	29
TOTAL	7	100	13	100	11	100	31	100

Phylogenetic Analysis

Phylogenetic analysis demonstrated that the *Salmonella enterica* strains identified in this study clustered closely with reference *Salmonella* strains retrieved from the GenBank database. The evolutionary relationships indicated a high degree of genetic similarity between the isolates obtained from retail chicken meat and previously reported *Salmonella enterica* strains. Closely related isolates clustered together on the phylogenetic tree, suggesting shared ancestry and potential common contamination sources (Figure 3).

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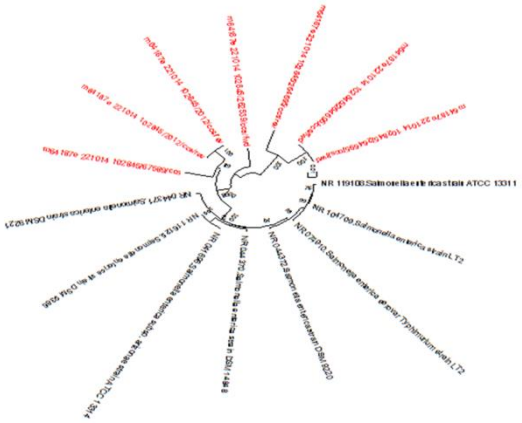

Figure 3: Phylogenetic tree analyses of the identified Salmonella(Sequences, in Red) showing evolutionary relationship with reference Salmonella strains from the GenBank (in Black).

Discussion

The findings of this study demonstrates that *Salmonella enterica* strains are prevalent in retail chicken meat across the three Area Councils investigated in the Federal Capital Territory (FCT), with an overall prevalence rate of 18.8%. This level of contamination represents a significant public health concern and is higher than previously reported values in the FCT. The slaughtering and processing of chicken in the FCT involves halal slaughtering of chicken, de-feathering by scalding in an improvised container usually, a drum. The same hot water is used for the whole day. Feathers are removed by hands and the whole operation takes placeat the point of salein the market. The same tablesare used for de-feathering, evisceration, cutting and packaging without proper cleaning.However, earlier studies conducted in FCT documented markedly lower prevalence rates including 0% from 150 raw chicken meat samples suggesting a possible increase in Salmonella contamination over time or variations attributable to differences in sampling locations, methodologies, and hygiene practices (Bawa*et al*., 2020).

Comparable prevalence rates have been reported in other parts of Nigeria, particularly within the North Central and South West regions, although wide variability exists across studies (Tafida*et al*., 2013; Fashae*et al*., 2010). Higher prevalence rates have also been reported in poultry meat and poultry farms in other regions of Nigeria and Africa, highlighting the persistent challenge of *Salmonella* contamination in poultry production and retail systems (Jibril*et al*., 2020; Kagambèga*et al*., 2013). Globally, similar variations in prevalence have been observed, reflecting differences in poultry management practices, biosecurity measures, and regulatory frameworks (Duc*et al*., 2019).

The observed variation in prevalence among AMAC, Bwari, and Kuje Area Councils may be attributed to differences in hygiene practices, slaughtering procedures, transportation, storage conditions, and levels of regulatory oversight. Cross-contamination during slaughter, dressing, and handling of poultry meat at retail outlets has been identified as a major contributor to *Salmonella* dissemination along the food chain (Adeyanju*et al*., 2014).

The antibiotic susceptibility profile revealed high resistance rates to ntrofurantoin and erythromycin, findings that are consistent with global trends and previous reports from Nigeria and other developing countries (Singh *et al*., 2012; Igbinosa*et al*., 2022). Resistance to amoxicillin/clavulanic acid and ceftazidime was also notable, suggesting widespread exposure of *Salmonellastrains* to commonly used antibiotics in poultry production. These findings raise serious concerns regarding the continued effectiveness of routinely prescribed antimicrobials for the treatment of salmonellosis.

In contrast, most isolates remained susceptible to ciprofloxacin and sulphamethoxazole/trimethoprim, indicating that fluoroquinolones and some combination therapies may still be effective treatment options. Similar susceptibility patterns have been reported in previous studies, although emerging resistanceto fluoroquinolones has been documented and remains a cause for concern (Monte *et al*., 2019). Continued misuse of these critically important antimicrobials could compromise their future effectiveness.

The identification of multidrug-resistant (MDR) *Salmonella serovars* in this study is particularly alarming. The MDR patterns observed are consistent with reports linking indiscriminate antimicrobial use in poultry farming to the selection and spread of resistant strains (Nair *et al*., 2018). Such strains can be transmitted to humans through contaminated poultry meat, posing a serious threat to public health.

Molecular analysis confirmed that all isolates belonged to *Salmonella enterica subsp. enterica*, with a predominance of *Salmonella enterica* subsp. *enterica*serovar*Typhimurium* (29%) followed by *Salmonella enterica* subsp. *enterica*serovar*Montevideo*(16%)**,** *Salmonella enterica* strain SA20031245 chromosome (16%) and*Salmonella enterica* strain PNUSAS148096 chromosome (16%) These serovars are widely recognised for their association with foodborne outbreaks and human infections worldwide (Timme*et al*., 2013). Their detection in retail chicken meat underscore the potential for zoonotic transmission and reinforces the role of poultry products as important reservoirs of pathogenic *Salmonella*.

Phylogenetic analysis revealed that the *Salmonella* isolates clustered closely with reference strains retrieved from public databases, indicating high genetic similarity and suggesting shared contamination sources or transmission routes. Similar genetic relatedness among *Salmonella* isolates from human, animal, and environmental sources have been reported previously, pointing to interconnected epidemiological pathways (Akinyemi*et al*., 2023).

Public Health Implications

The high prevalence of *Salmonella*, coupled with the detection of multidrug-resistant strains, poses a substantial public health risk, particularly in settings where poultry meat is frequently consumed and food safety practices are

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suboptimal. The circulation of pathogenic and resistant *Salmonella serovars* in retail markets increases the likelihood of foodborne outbreaks and limits treatment options, thereby exacerbating the overall disease burden (World Health Organization, 2019).

Conclusion

This study demonstrates a substantial prevalence (18.8%) of Salmonella contamination in retail chicken meat sold across some Area Councils of the Federal Capital Territory (FCT), Nigeria. All isolates were identified as *Salmonella enterica subsp. enterica*, with predominant strains including *SalmonellaTyphimurium* which are of significant public health importance. The detection of high resistance rates to nitrofurantoin and erythromycin, alongside the presence of multidrug-resistant (MDR) *Salmonella serovars*, underscores the growing challenge of antimicrobial resistance in the poultry production and retail chain.

The higher prevalence observed in this study compared with earlier reports from the FCT suggests a possible increase in contamination levels or persistent gaps in hygiene practices, regulatory enforcement, and antimicrobial stewardship. Poor sanitation, inadequate awareness of foodborne diseases, and weak regulatory control are possible key factors associated with *Salmonella* contamination. Collectively, these findings highlight a significant food safety and public health risk associated with the consumption of retail poultry meat in the FCT.

Recommendations

Based on the findings of this study, the following recommendations are proposed:

1. Enhanced Surveillance:

Continuous and routine surveillance of *Salmonella species* in poultry meat should be strengthened to monitor prevalence trends, identify circulating serovars, and detect emerging antimicrobial resistance patterns.

2. Antimicrobial Stewardship:

Regular antimicrobial susceptibility testing should be conducted prior to antibiotic administration in poultry production to promote rational drug use and reduce the emergence and spread of multidrug-resistant *Salmonella strains*.

3. Improved Hygiene and Sanitation:

Poultry meat handlers, processors, and retailers should be trained and sensitised on good hygiene practices, including proper slaughtering, handling, storage, and waste disposal, to minimise contamination and cross-contamination.

4. Regulatory Enforcement:

Relevant regulatory agencies should enforce strict compliance with established food safety standards and guidelines governing poultry production, processing, transportation, and retail sales.

5. Public Awareness and Education:

Public health authorities should intensify awareness campaigns targeting poultry farmers, retailers, and consumers on the risks of foodborne salmonellosis, antimicrobial resistance, and the importance of thorough cooking of poultry products.

6. Policy Development:

Policies regulating the use of antibiotics in animal husbandry should be reviewed and strengthened, with emphasis on restricting non-therapeutic use and promoting alternatives to antibiotics where feasible.

Conflict of Interest

Authors have declared that no conflict of interests exist

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