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Environmental Contamination of Poultry Farms by Foodborne Multiple Antibiotics Resistant (MAR) *Salmonella* and *Escherichia coli* Isolates in Ido LGA Ibadan Nigeria

[1]Adegor, E. C., [2]Agbato, O. A., [3]Oladele- Bukola, M. O., [2]Okuneye, O. J., [2]Fagbohun, A. F., [2]Orakwue, O. K., [2]Emikpe, O. O., [2]Adekunle, O. F., [2]Akanbi, I. F., [2]Olurinde, S. Y., [2]Oyedepo, M. O., [2]Boluwade, O., [2*]Fasanmi, O. G., Odunsi O.O.[4]

1. Department of Public Health, National Open University of Nigeria, Abuja, Nigeria
2. Federal College of Animal Health & Production Technology, Moor Plantation, Ibadan, Nigeria
3. Institute of Agricultural Research & Training, Obafemi Awolowo University, Moor Plantation, Ibadan
4. Federal College of Animal health & Production Technology, Moor Plantation, Ibadan

Abstract: Antimicrobial resistance among food-borne bacteria from poultry farms is a growing public health concern in Nigeria. Despite this, data on antibiotic susceptibility profiles of bacterial isolates from poultry farms in Ido Local Government Area, Oyo State, Nigeria remain scarce. This study investigated the antibiograms of *Salmonella* spp. and *Escherichia coli* isolates recovered from selected poultry farms in the study area. A total of 160 samples comprising faeces, feed, soil, and water were collected from five poultry farms. Bacterial isolation was carried out on selective and differential media including Salmonella-Shigella Agar (SSA) and Eosin Methylene Blue (EMB) Agar. Isolates were confirmed by Gram staining and biochemical tests. Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method on Mueller-Hinton Agar, following Clinical and Laboratory Standards Institute guidelines. Six antibiotics were tested: Oxytetracycline, Gentamicin, Enrofloxacin, Ciprofloxacin, Trimethoprim, and Ampicillin. A total of 68 *Salmonella* spp. and 90 *E. coli* isolates were recovered, with faecal samples yielding the highest number of isolates for both organisms. Among *Salmonella* isolates, the highest resistance prevalence were recorded for Enrofloxacin (64.7%), Gentamicin (58.8%), and Oxytetracycline (52.9%). *E. coli* isolates showed critically high resistance to Ampicillin (77.8%), followed by Gentamicin (37.8%) and Oxytetracycline (24.4%). The resistance patterns observed for *Salmonella* isolates (0.50) indicate Multiple Antibiotic Resistance (MAR) indices, consistent with isolates from environments under heavy antibiotic selection pressure. These findings highlight the urgent need for antimicrobial stewardship, regulatory intervention, and routine surveillance of antibiotic resistance in the poultry production sector of Ido LGA and Oyo State.

Keywords: Antibiogram, *Salmonella*, *Escherichia coli*, Poultry farms, Ido LGA, MAR index

INTRODUCTION

Foodborne diseases constitute a major public health burden globally, with bacterial pathogens being the leading aetiological agents (Havelaar *et al.*, 2015; WHO, 2023). Globally, it is estimated that approximately 600 million cases of foodborne illness occur annually, resulting in 420,000 deaths, with children under the age of five bearing a disproportionate share of this burden (WHO, 2023). The economic cost of foodborne diseases

extends beyond morbidity and mortality, imposing significant losses on healthcare systems and agricultural economies worldwide (Pires *et al.,* 2019).

Poultry and poultry products serve as one of the most significant reservoirs and transmission vehicles for food-borne bacterial pathogens, including *Salmonella* spp., *Campylobacter* spp., *Escherichia coli*, *Staphylococcus aureus*, and *Listeria monocytogenes* (Antunes *et al.,* 2016; Bintsis, 2017). These organisms are frequently implicated in outbreaks of gastroenteritis and systemic infections in both developed and developing nations (Tack *et al.,* 2020). In Nigeria, the poultry industry is a vital component of the agricultural sector, providing a major source of animal protein and livelihood for millions of people (Osei-Tutu *et al.,* 2019; FAO, 2021).

The emergence and spread of antimicrobial resistance (AMR) among food-borne bacterial pathogens has attracted significant global attention (Van Boeckel *et al.,* 2019; Murray *et al.,* 2022). The widespread and often indiscriminate use of antibiotics as growth promoters and prophylactics in poultry production has been identified as a key driver of resistance selection and dissemination (Manyi-Loh *et al.,* 2018). Resistant strains originating from poultry farms can reach human populations through consumption of contaminated meat, direct contact with birds or farm workers, and environmental pathways such as contaminated water and soil (Friedman *et al.,* 2017; Rhouma *et al.,* 2021).

Despite the recognized importance of antibiotic resistance surveillance, there remains a paucity of data on the antibiotic susceptibility profiles of food-borne bacterial isolates from poultry farms in many parts of Oyo State, including the study area, Ido LGA (Olatoye, 2010; Adetunji and Isola, 2011). This knowledge gap hampers effective surveillance, risk assessment, and the formulation of evidence-based antimicrobial stewardship policies in the region (Essack *et al.,* 2018; Akinyemi *et al.,* 2020). This study however was designed to isolate and characterize food-borne bacteria from selected poultry farm environments in Ido LGA, to determine their antibiograms and idemtify AMR, as a contribution to the body of knowledge on AMR in Nigeria poultry production systems.

MATERIALS AND METHODS

Study Area

The study was conducted on selected poultry farms located within Ido Local Government Area (LGA), Ibadan, Nigeria. Ido LGA is a peri-urban settlement situated on the outskirts of Ibadan, the Oyo State capital, and is characterized by a considerable concentration of poultry farming activities ranging from small-scale backyard operations to medium-scale commercial farms. The area lies within the derived guinea savannah agroecological zone of southwestern Nigeria. A total of five poultry farms were selected for the study based on their willingness to participate and accessibility.

Study Duration

The study was carried out over a period of eight weeks. This included the phases of sample collection, laboratory analysis, microbial isolation and identification, antimicrobial susceptibility testing, and statistical data analysis.

Materials Used

The following materials and equipment were used during the course of the research:

- Sterile swab sticks (for surface and faecal sample collection)
- Spatula
- Labeled sterile sampling envelopes and containers
- Permanent markers (for sample identification)
- Cold box with ice packs (for sample preservation during transport)
- Growth media: MacConkey agar, Salmonella-Shigella agar, Nutrient agar, Eosin Methylene Blue (EMB) agar, and Mueller-Hinton agar, Mannitol reagent.
- Autoclave (for media sterilization)
- Incubator set at 37°C
- Compound microscope (for microbial identification)
- Microscope slides and cover slips
- Sterile inoculating loops and blades
- Hand gloves and face masks
- Distilled water and normal saline
- pH meter and laboratory glasswares
- Commercially available multi-disk antibiotic discs (Rapid Labs®)

All materials were sterilized appropriately before use to prevent cross-contamination of samples.

Sample Collection and Preservation

A total of one hundred and sixty (160) samples were collected from three important locations across the five poultry farms. Thirty two (32) samples were obtained from each farm, comprising eight sample types collected in equal numbers: (i) faeces from birds, (ii) soil from the farm environment, (iii) water from the source supplied to the birds, and (iv) feed from the feed mill. Faecal samples were collected directly from the floor of the pens using sterile spatulas and deposited into pre-labelled sterile sampling envelopes. Soil samples were collected from three points within each farm and pooled. Water samples were collected in sterile bottles. Feed samples were collected from the feed troughs and milling area.

All samples were collected using pre-labeled sterile dispensing envelopes and containers, immediately placed into sterile containers, and stored in a cold box containing ice packs to maintain a low temperature during transport. Samples were thereafter transported to the Veterinary Microbiology Laboratory, University of Ibadan immediately after collection to preserve their integrity and to prevent deterioration.

Laboratory Analysis

Upon arrival at the laboratory, samples were homogenized where necessary and serially diluted in sterile normal saline. Swabs were streaked onto selective and differential culture media, including Nutrient Agar (NA) for total viable bacterial count, MacConkey Agar (MCA) for isolation of Gram-negative enteric bacteria, Salmonella-Shigella Agar (SSA) for presumptive isolation of *Salmonella* spp., and Eosin Methylene Blue (EMB) Agar for identification of *E. coli*. Inoculated plates were incubated at 37°C for 18–24 hours under aerobic conditions.

Isolation and Identification of Bacterial Isolates

Bacterial colonies were observed for their morphological characteristics, including size, shape, colour, and surface texture. Presumptive colonies with characteristic appearances on each selective medium were sub-cultured on Nutrient Agar to obtain pure cultures. Pure isolates were subjected to Gram staining to determine cell morphology and Gram reaction. Biochemical characterization was performed using the following tests: catalase test, oxidase test, indole test, Triple Sugar Iron (TSI) test, urease test, and citrate utilization test. Results of the biochemical tests were interpreted in combination with colonial and microscopic morphology to confirm the identity of bacterial isolates according to standard microbiological keys.

Microscopy and Microbial Count

Microscopy was carried out on Gram-stained slides to observe the shape and arrangement of bacterial cells. For microbial enumeration, total viable counts (TVC) was determined using serial dilution and plate count techniques. Colony-forming units per gram (CFU/g) was calculated to estimate the bacterial load.

Microbial Enumeration

Total viable counts (TVC) were determined using the pour plate technique following serial dilution of samples in sterile normal saline. Colony-forming units per gram or millilitre (CFU/g or CFU/mL) were calculated to estimate the bacterial load in each sample type. Counts were performed after 24–48 hours of incubation at 37°C.

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed on confirmed *Salmonella* spp. and *E. coli* isolates using the Kirby-Bauer disk agar diffusion method according to the Clinical and Laboratory Standards Institute (CLSI, 2022) protocol on Mueller-Hinton agar (MHA). A standard inoculum of each isolate was prepared by suspending colonies in sterile normal saline and adjusting the turbidity to match a 0.5 McFarland standard (approximately 1.5×10^8 CFU/mL). The inoculum was evenly inoculated onto the surface of MHA plates using sterile swabs. Commercially available multi-disk antibiotic discs (Rapid Labs®) comprising Gentamicin (10 µg), Ciprofloxacin (5 µg), Oxytetracycline (10 µg), Enrofloxacin (5 µg), Trimethoprim (5 µg), and Ampicillin (10 µg) were placed on the inoculated MHA plates using

sterile forceps. Plates were allowed to stand for 15 minutes for pre-diffusion and thereafter incubated at 37°C for 18–24 hours. Following incubation, the diameters of zones of inhibition (ZOI) were measured in millimetres using a transparent ruler and interpreted as Sensitive (S), Intermediate (I), or Resistant (R) according to CLSI (2022) breakpoints.

Determination of Multiple Antibiotic Resistance (MAR) Index

The Multiple Antibiotic Resistance (MAR) index for each bacterial isolate was calculated using the formula proposed by Krumperman (1983):

$$\text{MAR index} = a / b$$

Where **a** is the number of antibiotics to which the isolate was resistant and **b** is the total number of antibiotics tested. Isolates with a MAR index > 0.2 were considered to have originated from a high-risk source of antibiotic contamination (Krumperman, 1983).

Statistical Analysis

Data obtained from the study were expressed as frequencies, percentages, and means with standard deviations. The prevalence of each bacterial isolate and resistance phenotype was calculated as a percentage of the total number of samples examined. All data for bacterial counts were subjected to one-way analysis of variance (ANOVA) using SPSS version 25.0 (IBM Corp., Armonk, NY). Duncan's multiple range test was used as a post-hoc comparison of means found to be statistically significant at $p < 0.05$.

RESULTS AND DISCUSSION

Table 1 shows the Salmonella count in faeces, soil and water samples collected from the poultry environment. Water recorded the highest count ($0.330 \pm 0.010 \times 10^5$ cfu/ml), which was significantly higher ($p < 0.05$) than the counts in faeces ($0.200 \pm 0.020 \times 10^5$ cfu/ml) and soil ($0.202 \pm 0.021 \times 10^5$ cfu/ml). Faeces and soil did not differ significantly from each other, and both had a contamination level of 1.00. Water was therefore about 1.65 times more contaminated than either of them.

Table 1: Determination of levels of salmonella environmental contamination among poultry farms in Oluyole LGA

	Bacterial count (x 10^5/cfu/ml)	Level of contamination
Sample collected		
Faeces	0.200±0.020b	1.00
Soil	0.202±0.021b	1.00
Water	0.330±0.010a	1.65

[b]mean values that are in the same column with different superscripts are significantly different @ p<0.05

Table 2 presents the *E. coli* counts in the three environmental components. Faeces ($0.350 \pm 0.020 \times 10^5$ cfu/ml) and water ($0.340 \pm 0.010 \times 10^5$ cfu/ml) have similar counts that

were significantly higher ($p < 0.05$) than that of soil ($0.295 \pm 0.021 \times 10^5$ cfu/ml). Faeces and water were about 1.20 and 1.17 times more contaminated than soil, respectively.

Table 2: Determination of levels of *E.coli* environmental contamination among poultry farms in Ibadan

	Bacterial count (x 10^5/cfu/ml)	Level of contamination
Sample collected		
Faeces	0.350 ± 0.020^a	1.20
Soil	0.295 ± 0.021^b	1.00
Water	0.340 ± 0.010^a	1.17

[b]mean values that are in the same column with different superscripts are significantly different @ $p<0.05$

Table 3 shows the total food-borne bacterial count. Faeces had the highest count ($4.520 \pm 0.120 \times 10^5$ 5 cfu/ml), which was significantly higher ($p < 0.05$) than the counts in soil ($3.375 \pm 0.150 \times 10^5$ cfu/ml) and water ($3.320 \pm 0.125 \times 10^5$ cfu/ml). Soil and water did not differ significantly and both had a contamination level of 1.00, so faeces was about 1.40 times more contaminated than either.

Table 3: Determination of levels of total food-borne bacteria environmental contamination among poultry farms in Oluyole LGA

	Bacterial count (x 10^5/cfu/ml)	Level of contamination
Sample collected		
Faeces	4.520 ± 0.120^a	1.40
Soil	3.375 ± 0.150^b	1.00
Water	3.320 ± 0.125^b	1.00

[ab]mean values that are in the same column with different superscripts are significantly different @ $p<0.05$

The prevalence of *Salmonella* spp. and *E. coli* isolates recovered from the various sample types collected from the five poultry farms in Ido LGA, Oyo State is presented in Table 4. A total of 68 *Salmonella* isolates and 90 *E. coli* isolates were recovered from the 160 samples examined. Among the four sample types, faeces yielded the highest number of isolates for both *Salmonella* (35.3%) and *E. coli* (33.3%). Feed samples from the feed mill accounted for 20.6% *Salmonella* and 17.8% *E. coli* isolates. Environmental water samples yielded 26.5% *Salmonella* and 22.2% *E. coli* isolates, while soil samples yielded 17.6% *Salmonella* and 26.7% *E. coli* isolates.

The antimicrobial susceptibility patterns of the 68 *Salmonella* spp. and 90 *E. coli* isolates to six antibiotics are shown in Table 5. Among *Salmonella* isolates, Trimethoprim and Ampicillin recorded the highest proportions of sensitive isolates, while Enrofloxacin and Gentamicin showed the highest numbers of resistant isolates. For *E. coli* isolates, Ciprofloxacin and Trimethoprim showed the highest sensitivity pattern, while Ampicillin recorded the highest resistance (35 isolates), followed by Gentamicin.

Table 4: Prevalence of *Salmonella* spp. and *E. coli* isolates from some poultry farms in Ido LGA, Oyo State

Location of Sample	Components of Location	Salmonella spp. n (%)	E. coli n (%)
Bird	Faeces	24 (35.3)	30 (33.3)
Feed Mill	Feed	14 (20.6)	16 (17.8)
Environment	Soil	12 (17.6)	24 (26.7)
	Water	18 (26.5)	20 (22.2)
Total		68	90

Table 5: Antimicrobial susceptibility of *Salmonella* spp. and *E. coli* isolates from Ido LGA, Oyo State

Antimicrobial		Salmonella(68)			E. coli(90)	
agents	S	I	R	S	I	R
Oxytetracycline	20	12	36	38	30	22
Gentamicin	12	16	40	32	24	34
Enrofloxacin	18	6	44	60	20	10
Ciprofloxacin	44	8	16	70	10	10
Trimethoprim	54	6	8	64	8	18
Ampicillin	50	10	28	16	4	70
S: Sensitive I: Intermediate R: Resistant						

Table 6 presents the percentage of *Salmonella* spp. and *E. coli* isolates resistant to each of the six antibiotics tested. Among *Salmonella* isolates, Enrofloxacin recorded the highest resistance rate (64.7%), followed by Gentamicin (58.8%) and Oxytetracycline (52.9%). Ciprofloxacin, Trimethoprim, and Ampicillin recorded relatively lower resistance rates of 23.5%, 11.8%, and 11.8%, respectively. Conversely, among *E. coli* isolates, Ampicillin recorded the highest resistance prevalemce (77.8%), followed by Gentamicin (37.8%) and Oxytetracycline (24.4%). Enrofloxacin and Ciprofloxacin showed the lowest resistance rates (11.1%).

Table 6: Percentage antimicrobial resistance of *Salmonella* spp. and *E. coli* isolates from Ido LGA, Oyo State

Antimicrobial agents	Salmonella Resistant Isolates (%)	E. coli Resistant Isolates (%)
Oxytetracycline	18 (52.9)	11 (24.4)
Gentamicin	20 (58.8)	17 (37.8)
Enrofloxacin	22 (64.7)	5 (11.1)
Ciprofloxacin	8 (23.5)	5 (11.1)
Trimethoprim	4 (11.8)	9 (20.0)
Ampicillin	4 (11.8)	35 (77.8)

Table 7 shows the bacterial isolates with MAR indices in the sampled poultry farms at Ido LGA, Oyo state, considering a prevalence of resistance of ≥ 50%, the MAR index of Salmonella isolates (0.5) is greater than for E. coli (0.17), thereby posing a high risk.

Table 7: Salmonella and Escherichia coli MAR indices of poultry farms in Ido LGA

Bacterial isolate MAR index	Number of antibiotics isolates are resistant to (a)	Number of antibiotics tested (b)	a/b =
Salmonella sp.	3	6	0.50
Escherichia coli	1	6	0.17

NB: At Resistance prevalence of ≥ 50%

DISCUSSION

This study investigated the contamination of poultry environment with food borne bacteria and the antibiograms of *Salmonella* spp. and *Escherichia coli* isolates recovered from faeces, feed, soil, and water samples collected from five poultry farms in Ido Local Government Area, Oyo State, Nigeria. From all the samples collected, *Salmonella* and *Eschericia coli* were isolated and confirmed, giving an overall bacterial recovery rate that underscores the widespread distribution of these pathogens in the poultry farm environment of the study area, similar to the submissions of Fashae *et al.* (2010) and Olatoye et al. (2010).

With respect to sample type, faecal samples yielded the highest number of isolates for both *Salmonella* spp. and *E. coli*. This finding is consistent with the observation that the gastrointestinal tract of poultry serves as the primary reservoir for these food-borne pathogens, and that faecal shedding constitutes the principal route of environmental contamination on poultry farms (Fashae *et al.,* 2010). The higher prevalence of *E. coli* compared to *Salmonella* is expected, given that *E. coli* is a normal commensal of the avian intestinal tract and is therefore more abundantly shed in faeces (Croxen *et al.,* 2013). Environmental samples, including soil and water, also yielded appreciable numbers of both pathogens, indicating that farm environments serve as important secondary reservoirs for these organisms, likely through faecal contamination of soil and water sources (Zhu *et al.,* 2013; Manyi-Loh *et al.,* 2018).

The antimicrobial susceptibility testing revealed significant resistance among both *Salmonella* spp. and *E. coli* isolates to several of the antibiotics tested. Among *Salmonella* isolates, the highest resistance prevalence were recorded for Enrofloxacin (64.7%), Gentamicin (58.8%), and Oxytetracycline (52.9%), hence there is Multiple Antibiotic Resistance (MAR) in this case. The high rate of resistance to Enrofloxacin, a fluoroquinolone, is particularly disturbing from a public health perspective, as fluoroquinolones such as Ciprofloxacin are the drugs of choice for the treatment of severe and invasive salmonellosis in humans (Fashae *et al.,* 2010; Raufu *et al.,* 2014). This finding corroborates the report of Raufu *et al.* (2014), who documented the persistence of fluoroquinolone-resistant *Salmonella enterica* serovar Kentucky in poultry farms across multiple states in Nigeria, attributed to the widespread and unsupervised use of enrofloxacin and related compounds in Nigeria poultry production.

The high resistance of *Salmonella* isolates to Gentamicin (58.8%) and Oxytetracycline (52.9%) is also significant, given that aminoglycosides and tetracyclines are among the most commonly used antibiotic classes in Nigerian poultry farming (Olatoye, 2010; Adetunji and Isola, 2011). The extensive use of these agents as growth promoters and for prophylaxis has created strong selective pressure driving resistance rates to levels that severely compromise their clinical utility (Van Boeckel *et al.,* 2014; Manyi-Loh *et al.,* 2018). These findings are in

agreement with those of Fashae *et al.* (2010), who reported high rates of resistance to tetracycline and aminoglycoside antibiotics among *Salmonella* isolates from broiler chickens in Ibadan, Oyo State.

For *E. coli* isolates however, the most striking finding was the critically high resistance rate to Ampicillin (77.8%), consistent with widespread beta-lactam resistance among *E. coli* from poultry farms in southwestern Nigeria (Adetunji and Isola, 2011; Adesiji *et al.,* 2019). Beta-lactam resistance in Gram-negative bacteria such as *E. coli* is commonly mediated by the production of beta-lactamase enzymes, including extended-spectrum beta-lactamases (ESBLs), which hydrolyse the beta-lactam ring of penicillins and cephalosporins (Bush and Bradford, 2020). The high prevalence of Ampicillin resistance observed in this study suggests that ESBL-producing strains may be present among the *E. coli* isolates, warranting further molecular investigation. This is consistent with the report of Adesiji *et al.* (2019), who detected ESBL-producing *E. coli* in over 40% of poultry farm isolates in southwestern Nigeria.

Gentamicin resistance was also notable among *E. coli* isolates (37.8%), while Oxytetracycline resistance was recorded at 24.4%. These findings reflect the patterns of antibiotic use in the study area, where tetracyclines and aminoglycosides are frequently administered without adequate veterinary oversight (Adesokan *et al.,* 2015). In contrast, *E. coli* isolates showed considerably lower resistance to Ciprofloxacin (11.1%) and Enrofloxacin (11.1%), and relatively modest resistance to Trimethoprim (20.0%). The retained sensitivity of *E. coli* isolates to Ciprofloxacin and Trimethoprim suggests that these agents may retain some clinical utility for treatment of *E. coli*-associated infections in the study area, though this should be confirmed with updated susceptibility data given the dynamic nature of resistance development.

The MAR index provides a useful summary measure of the overall resistance burden of bacterial isolates and the likely antibiotic-use environment from which they originate (Krumperman, 1983). Based on the resistance rates recorded in the present study, the MAR index of the isolates especially Salmonella exceeds 0.2, indicating that the poultry farms in Ido LGA represent high antibiotic-use environments with consequently high selective pressure for resistance (Krumperman, 1983; Olatoye, 2010). This is consistent with the widespread and unregulated use of antibiotics in Oyo State poultry farms, where the majority of farmers obtain antibiotics over the counter without veterinary prescription and administer them without professional guidance (Adesokan *et al.,* 2015; Manyi-Loh *et al.,* 2018).

The observation of multidrug resistance among isolates from this study is a matter of serious public health concern, given the potential for resistant strains to spread from poultry farms to human populations through consumption of contaminated poultry products, direct contact with animals or farm workers, and environmental pathways (Marshall and Levy, 2011; Rhouma *et al.,* 2021). The One Health framework, which recognizes the interconnectedness of human, animal, and environmental health, is particularly applicable to the findings of this study, illustrating how antibiotic misuse in animal agriculture can generate resistance reservoirs that ultimately threaten human therapeutic options (Zinsstag *et al.,* 2011; Mackenzie and Jeggo, 2019). The present findings therefore underscore the urgent need for evidence-based antimicrobial stewardship policies and regulatory interventions in the poultry sector of Ido LGA and the broader Oyo State region.

CONCLUSION

The investigation demonstrated widespread contamination across all monitored environmental media (faeces, soil, and water), confirming the presence and persistence of public health pathogens, including *Salmonella*, *Escherichia coli, Clostridium, Staphylococcus*, and *Shigella* species.

The comparative assessment identified faeces as the primary contamination reservoir, generating the highest total foodborne bacterial load and peak concentrations of *Salmonella spp.* and *E. coli, among other bacteria.* Drinking water served as a major cross-contamination vehicle, harboring the highest Salmonella load alongside elevated *E. coli* levels. Soil acted as a persistent environmental sink.

Salmonella isolates exhibited a multiple antibiotic resistance (MAR) profile by showing significant resistance across three tested classes of antibiotics (enrofloxacin, gentamicin, and oxytetracycline). On the contrary, *E. coli* isolates displayed a narrower resistance spectrum, driven primarily by critically high resistance to ampicillin.

The findings of this study confirm that poultry farms in Ido LGA harbour antibiotic-resistant *Salmonella* spp. and *E. coli* isolates with resistance profiles that raise serious public health concerns. These results highlight the urgent need for antimicrobial stewardship, regulatory intervention, and routine surveillance of antibiotic resistance in the poultry production sector of Ido LGA and Oyo State. It is hereby recommended that the sales and administration of antibiotics to poultry farms without valid veterinary prescription should be strictly regulated by relevant government agencies. Routine antibiogram surveillance of poultry farms in Ido LGA and across Oyo State should be conducted periodically by veterinary researchers to monitor trends in antimicrobial resistance.. Agricultural extension agents should educate farmers on the consequences of antibiotic misuse, the importance of responsible antibiotic stewardship, and the adoption of good biosecurity and farm management practices to reduce the need for antibiotic use.

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