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One health dynamics of *Campylobacter* spp. in poultry meat, market environments, and public health risk in Maiduguri, Nigeria: occurrence and antimicrobial resistance

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ABSTRACT

Aim: Purpose of the study was to investigate the occurrence, antimicrobial resistance patterns and associated risk factors of *Campylobacter* spp. across the human–animal–environment interface within a One Health framework in Maiduguri, northeastern Nigeria.

Method and materials: A cross-sectional design was employed between March and December 2025. A total of 520 samples, comprising 400 poultry (live and slaughtered birds) and 120 environmental samples, were collected and analyzed using standard microbiological methods. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method, while a structured questionnaire assessed knowledge, hygiene practices, and antibiotic use among 100 poultry stakeholders.

Results: Overall, 82 (15.8%) samples were positive for *Campylobacter*, with *C. jejuni* (11.0%) predominating over *C. coli* (4.8%). Environmental samples exhibited a higher contamination rate (24.2%) compared to poultry samples (13.3%), with wash water identified as the most contaminated source (35.0%). Significant associations were observed between *Campylobacter* occurrence and poultry species ($p = 0.0242$), sample type ($p < 0.0001$), and bird health status ($p = 0.0319$). High levels of antimicrobial resistance were detected, particularly against vancomycin (84.1%), penicillin (79.3%), and ampicillin (73.2%). Multidrug resistance was prevalent in 72.0% of isolates, with a mean multidrug resistance index of 0.37 ± 0.14. Behavioral assessment revealed poor awareness of *Campylobacter* (9.0%), inadequate hygiene practices, and widespread misuse of antibiotics, including non-prescription use (82.0%) and growth promotion (71.0%).

Conclusion: It was concluded that these findings highlight significant public health risks driven by environmental contamination, poor biosecurity, and antimicrobial misuse. Integrated One Health interventions focusing on hygiene improvement, antimicrobial stewardship, and surveillance are urgently required to mitigate transmission and resistance.

Keywords: Campylobacter, Antimicrobial Resistance, One Health, Poultry, Food Safety Farming

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Introduction

The *Campylobacter* species are among the most important bacterial agents of foodborne gastroenteritis globally, posing substantial public health and socioeconomic burdens, particularly in low- and middle-income countries where food safety systems are often inadequate (Badjo *et al*., 2024 and Severino *et al*., 2025). Among the genus, *Campylobacter jejuni* and *Campylobacter coli* are the most frequently implicated species in human infections, responsible for a wide spectrum of disease ranging from self-limiting diarrhoea to severe inflammatory enteritis. In some cases, infections may result in serious post-infectious complications, including Guillain–Barré syndrome and reactive arthritis (Veronese and Dodi, 2024; Worku *et al*., 2024).

From a One Health perspective, *Campylobacter* spp. are zoonotic pathogens maintained at the interface of animals, humans, and the environment. Poultry remains the principal reservoir, with birds often colonized asymptomatically in their gastrointestinal tract at very high bacterial loads (Njoga *et al*., 2025; Veronese and Dodi, 2025). This silent colonization plays a critical role in environmental contamination and foodborne transmission, particularly during slaughtering, processing and retail handling. Contamination of poultry carcasses commonly occurs through fecal leakage, improper evisceration, contaminated equipment, and water used during processing especially in settings where biosecurity and hygienic standards are poorly enforced (Ahmed and Gulhan, 2022; Popa *et al*., 2025).

In many developing countries, including Nigeria, the poultry value chain is largely dominated by informal systems, particularly open markets where slaughtering, dressing, and retailing are conducted under suboptimal sanitary conditions. These environments act as critical nodes for pathogen amplification and dissemination within human–animal–environment interface (Nyokabi *et al*., 2018; Ovuru *et al*., 2023). Consequently, poultry meat sold in such markets represents an important vehicle for *Campylobacter* transmission to consumers, with significant implications for food safety and public health.

Epidemiological studies have consistently demonstrated the widespread occurrence of *Campylobacter* in poultry meat and associated environments. Reported prevalence varies widely depending on geographic location, production systems, and hygienic practices, with some studies documenting alarmingly high contamination rates in retail poultry products (El-Saadony *et al*., 2023; Kostoglou *et al*., 2023). In Nigeria, investigations conducted in slaughter slabs and open markets have reported high levels of contamination, in some instances exceeding 70–90% positivity in chicken meat samples (Nwankwo *et al*., 2016; Njoga *et al*., 2019; 2025). These findings emphasize the persistent food safety challenges associated with poultry handling and distribution systems.

In addition to their importance as foodborne pathogens, *Campylobacter* spp. has emerged as significant contributors to global burden of antimicrobial resistance (AMR). The widespread and often unregulated use of antimicrobials in poultry production for therapeutic, prophylactic, and growth-promoting purposes has accelerated selection of resistant strains (Bukari *et al*., 2025; Hassen *et al*., 2026). These resistant organisms can be transmitted along food chain and through environmental pathways, ultimately reaching humans and complicating treatment outcomes (Mayyas *et al*., 2025).

Of particular concern is the increasing resistance of *Campylobacter* isolates to critically important antimicrobials used in human medicine, including fluoroquinolones, macrolides, and tetracyclines (Mohan *et al*., 2025). Multidrug-resistant strains have been widely reported in poultry-associated *Campylobacter* populations in several regions, including Nigeria, raising concerns about limited therapeutic options and potential treatment failures in human infections (Woźniak-Biel *et al*., 2018; Bukari *et al*., 2025). This situation is further exacerbated by weak regulatory enforcement, limited antimicrobial stewardship, and inadequate surveillance systems across animal production and food distribution networks.

The burden of *Campylobacter* exposure may be particularly high in urban centers such as Maiduguri, where rapid population growth, high demand for affordable animal protein, and informal meat marketing systems converge. Open markets in such settings often lack adequate refrigeration, sanitation infrastructure, and controlled slaughter practices, thereby creating ideal conditions for bacterial survival, multiplication, and cross-contamination (Okello *et al*., 2025; Njoga *et al*., 2026). Despite these risk factors, there remains limited integrated data on the occurrence and antimicrobial resistance patterns of *Campylobacter* spp. in poultry meat and associated market environments within this region.

From a One Health standpoint, understanding the circulation of *Campylobacter* at the human–animal–environment interface is critical for designing effective control strategies. Localized epidemiological evidence is essential to inform risk mitigation measures, strengthen food safety systems, and guide antimicrobial stewardship interventions.

Therefore, this study aims to investigate the occurrence and antimicrobial resistance profiles of *Campylobacter* spp. in poultry meat obtained from open markets and poultry farms in Maiduguri, Nigeria. The findings are expected to contribute to a better understanding of the One Health dynamics of *Campylobacter* transmission in the region and support evidence-based interventions aimed at improving food safety and reducing the burden of antimicrobial-resistant infections.

Materials and Methods

This study was conducted between March and December 2025 in Maiduguri, the capital and largest urban center of Borno State, located in northeastern Nigeria. The study area lies within the Sudan–Sahel ecological zone, approximately between latitudes 11°46′N and 11°53′N, and longitudes 13°02′E and 13°13′E. The region is characterized by a semi-arid climate, with prolonged dry seasons, high ambient temperatures frequently exceeding 40°C during the hot season, low relative humidity, and a distinct harmattan period marked by dry, dust-laden winds.

Maiduguri has experienced rapid urbanization and population growth in recent years, resulting in increased demand for affordable animal protein, particularly poultry products. These dynamics, coupled with limited cold-chain infrastructure and informal marketing systems, create conditions that may facilitate the persistence and transmission of foodborne pathogens.

The study was conducted across major poultry value chain nodes, including major live bird markets (Monday Market, Custom Market, and Tashan Bama Market), commercial poultry farms, backyard production systems, and poultry slaughter/retail points. These locations were selected due to their central role in poultry aggregation, processing, and distribution, and their significance as potential hotspots for pathogen amplification and transmission within the human–animal–environment interface.

Study Design

A cross-sectional study design was employed to investigate the occurrence and antimicrobial resistance patterns of *Campylobacter* spp. within a One Health framework. The study integrated microbiological sampling across the human–animal–environment interface with a structured assessment of stakeholder practices. Microbiological investigations encompassed samples from live birds (cloacal swabs), slaughtered poultry (carcass swabs and tissue samples), and environmental sources, including processing surfaces and water used for carcass washing. In addition, a structured questionnaire was administered to poultry farmers, live bird sellers, and butchers to evaluate their level of knowledge, hygiene practices, and patterns of antimicrobial use, thereby providing contextual insights into behavioral factors influencing the transmission dynamics and resistance profiles of *Campylobacter* spp.

Study Population and Sampling Strategy

The study population comprised poultry sourced from commercial farms, backyard production systems, and live bird markets, as well as birds presented for slaughter and processing. Both apparently healthy and clinically sick birds were included to ensure a comprehensive representation of infection status across the production and marketing continuum.

A total of 400 poultry samples were collected, consisting of 200 samples from live birds obtained via cloacal swabs—chickens (n = 70), ducks (n = 45), pigeons (n = 45), and turkeys (n = 40)—and 200 samples from slaughtered birds, including carcass swabs and tissue specimens from chickens (n = 140), ducks (n = 15), pigeons (n = 35), and turkeys (n = 10). To evaluate environmental contamination and potential points of cross-transmission, an additional 120 samples were collected from critical control points within slaughter and retail settings, comprising processing tables (n = 30), knives (n = 25), chopping boards (n = 25), and carcass wash water (n = 40).

Sampling was conducted using a non-probability convenience approach, guided by accessibility, operational feasibility, and the intensity of poultry handling activities at selected sites. For the behavioral assessment component, a total of 100 respondents, including poultry farmers, live bird sellers, and butchers, were purposively selected and administered a structured questionnaire to capture data on knowledge, hygiene practices, and antimicrobial usage patterns relevant to the transmission dynamics of *Campylobacter* spp.

Sample Size Determination

The minimum sample size was determined using the standard formula for prevalence studies:

$$N = \frac{Z^2 \times P_{exp}\,(1 - P_{exp})}{d^2}$$

$$N = \frac{1.96^2 \times P_{exp}\,(1 - P_{exp})}{d^2}$$

Where,

N = required sample size
Z = standard normal deviate corresponding to a 95% confidence level (1.96)
P = assumed prevalence (0.5), adopted due to absence of prior data in study area to maximize sample size
d = desired level of precision (0.05)

Using these parameters, a minimum sample size of 384 was obtained. To enhance statistical power, improve representativeness, and account for potential sample loss or laboratory attrition, the sample size was increased to 400 poultry samples. In addition, 120 environmental samples were included to capture contamination at critical control points within the poultry value chain, while 100 respondents were incorporated into the questionnaire survey to strengthen the behavioral and One Health analytical components of the study.

Sample Collection

A total of 520 microbiological samples, comprising 400 poultry and 120 environmental samples, were collected using strict aseptic techniques to ensure sample integrity and minimize contamination. Samples from live birds were obtained as cloacal swabs using sterile cotton-tipped applicators, while samples from slaughtered birds included carcass surface swabs and tissue specimens (intestinal contents and muscle) collected immediately post-slaughter to capture contamination associated with processing activities. Environmental samples were collected from critical control points within slaughter and retail settings, including frequently contacted processing surfaces such as tables, knives, and chopping boards, as well as water used for carcass washing.

All samples were appropriately labeled with unique identifiers and relevant metadata. Samples were immediately placed in sterile containers and transported under cold chain conditions (4–8°C) to the Department of Veterinary Microbiology Postgraduate Research laboratory, University of Maiduguri for bacteriological analysis within 4–6 hours of collection to preserve microbial viability and ensure analytical reliability.

Questionnaire Survey

A structured questionnaire was administered to 100 poultry stakeholders, including farmers, live bird sellers, and butchers, to assess their awareness of *Campylobacter* infection and other foodborne diseases, hygiene practices during poultry handling and processing, and patterns of antimicrobial use. The instrument was pre-tested for clarity and reliability and refined accordingly prior to deployment. It was specifically designed to capture key behavioral and management variables relevant to transmission risk within the One Health framework, thereby providing contextual insights into factors influencing the occurrence and dissemination of *Campylobacter* spp. across the human–animal–environment interface. Where necessary, the questionnaire was administered through interviewer-guided sessions to ensure clarity and completeness of responses. Participation in the survey was voluntary, and informed consent was obtained from all respondents prior to data collection. Confidentiality of participants' information was strictly maintained throughout the study.

Isolation and Identification of Campylobacter spp.

Isolation of *Campylobacter* spp. was performed using standard culture-based microbiological methods optimized for thermophilic species as described by Demiroğlu *et al*. (2022) and Neyaz *et al*. (2024). Briefly, samples were initially enriched in selective enrichment broth (Bolton broth supplemented with selective antibiotics) and incubated under microaerophilic conditions at 42°C for 24–48 hours to enhance the recovery of *Campylobacter* organisms.

Following enrichment, aliquots were streaked onto selective agar media, including modified charcoal cefoperazone deoxycholate agar (mCCDA), and incubated under microaerophilic conditions at 42°C for 24–48 hours. Microaerophilic conditions were generated using commercially available gas-generating systems.

Presumptive identification of *Campylobacter* isolates was based on characteristic colony morphology (grayish, moist, and spreading colonies), Gram staining (Gram-negative curved or spiral rods), and motility patterns (rapid, darting motility under wet mount microscopy). Further confirmation was achieved through standard biochemical tests, including oxidase and catalase reactions.

Species-level differentiation of isolates, particularly *Campylobacter jejuni* and *Campylobacter coli*, was performed using established biochemical assays such as the hippurate hydrolysis test. These procedures were conducted in accordance with recognized microbiological protocols for the isolation and identification of thermophilic *Campylobacter* spp (Vaz *et al*., 2014).

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar supplemented with 5% defibrinated sheep blood, in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI, 2020). This approach was adopted to ensure standardized and internationally comparable interpretation of resistance patterns in *Campylobacter* isolates.

A panel of commercially prepared antibiotic discs (Oxoid, UK) representing commonly used antimicrobials in both human and veterinary medicine was employed. The antibiotics tested included ampicillin (10 µg), penicillin (10 IU), sulphamethoxazole/trimethoprim (25 µg), erythromycin (5 µg), ciprofloxacin (5 µg), streptomycin (10 µg), vancomycin (5 µg), oxacillin (5 µg), gentamicin (10 µg), chloramphenicol (30 µg), tetracycline (5 µg), and amoxicillin/clavulanic acid (30 µg).

Pure bacterial colonies were suspended in sterile saline and standardized to a 0.5 McFarland turbidity standard prior to inoculation. The standardized inoculum was evenly spread onto prepared agar plates to ensure uniform bacterial growth.

A maximum of six antibiotic discs was applied per agar plate to prevent overlapping zones of inhibition and ensure accurate measurement. Plates were incubated under microaerophilic conditions at 37–42°C for 24–48 hours.

Following incubation, zones of inhibition were measured in millimeters and interpreted as susceptible, intermediate, or resistant according to CLSI interpretative breakpoints. These results were used to determine resistance profiles and multidrug resistance patterns among isolates.

Determination of Multidrug Resistance and Multidrug Resistance Index (MDRI)

Multidrug resistance (MDR) was defined as resistance to three or more classes of antimicrobial agents, in line with established international standards for antimicrobial resistance classification.

To further quantify the extent of antimicrobial pressure and the potential risk associated with the sources of isolation, the Multidrug Resistance Index (MDRI) was calculated for each *Campylobacter* isolate using the formula:

$$\text{MDRI} = \frac{a}{b}$$

Where:

a = number of antibiotics to which an isolate exhibited resistance

b = total number of antibiotics tested

The MDRI provides an estimate of the level of antibiotic exposure in the source environment from which the isolates originated. An MDRI value greater than 0.2 was interpreted as indicative of high-risk contamination sources characterized by frequent or indiscriminate use of antimicrobial agents. This threshold was used to assess the epidemiological significance of resistance patterns within the One Health context of the study.

Data Analysis

Data generated from laboratory investigations and questionnaire surveys were systematically entered into Microsoft Excel and subsequently exported to IBM SPSS Statistics (Version 25.0) for analysis.

Descriptive statistical methods were employed to summarize the prevalence of *Campylobacter* spp., distribution across sample sources, and antimicrobial resistance patterns. Results were presented as frequencies and percentages.

Associations between categorical variables, including sample source, management practices, and *Campylobacter* occurrence or resistance profiles, were evaluated using the Chi-square test.

Where applicable, binary logistic regression analysis was performed to identify potential risk factors associated with *Campylobacter* contamination and antimicrobial resistance at the human–animal–environment interface. All statistical tests were conducted at a 95% confidence level, and results were considered statistically significant at $p < 0.05$.

Ethical Considerations

All procedures involving human participants complied with established ethical standards for research involving human subjects. Informed consent was obtained from all respondents prior to questionnaire administration, and participation was entirely voluntary. Confidentiality and anonymity of all participants were strictly maintained throughout the study, and data were used solely for research purposes.

All animal-related procedures, including sample collection from live birds and carcasses, were conducted in accordance with internationally accepted guidelines for the ethical use and handling of animals in research. Care was taken to minimize stress and discomfort to the animals during sampling, and all procedures were performed by trained personnel following standard veterinary biosafety practices.

Results and Discussion

The distribution and prevalence of *Campylobacter* spp. across poultry species and environmental matrices are presented in Table 1. From a total of 520 samples analyzed, 82 (15.8%) yielded *Campylobacter* isolates, comprising 57 (11.0%) *C. jejuni* and 25 (4.8%). Within poultry-derived samples (n = 400), 53 (13.3%) were positive, whereas environmental sources (n = 120) recorded a comparatively higher contamination rate of 29 (24.2%). Among live birds, 36 out of 200 cloacal swabs (18.0%) were positive for *Campylobacter*, with chickens accounting for the highest proportion [16/70 (22.9%)], followed by ducks [9/45 (20.0%)], turkeys [7/40 (17.5%)], and pigeons [4/45 (8.9%)]. Notably, *C. jejuni* predominated across all species, while *C. coli* was not isolated in pigeons (Table 1). In contrast, samples from slaughtered poultry exhibited a markedly lower prevalence, with *Campylobacter* spp. isolated from 17 (8.5%) out of 200 samples. Within this category, turkeys showed the highest contamination rate [3/10 (30.0%)], followed by ducks [4/15 (26.7%)], chickens [9/140 (6.4%)], and pigeons [1/35 (2.9%)].

Environmental sampling revealed considerable contamination across processing points, with wash water demonstrating the highest prevalence [14/40 (35.0%)], followed by processing tables [7/30 (23.3%)], chopping boards [5/25 (20.0%)], and knives [3/25 (12.0%)]. Across all environmental samples, *C. jejuni* remained the dominant species compared to *C. coli* (Table 1).

The analysis of risk factors associated with the occurrence of *Campylobacter* spp. in poultry samples (Table 2). A statistically significant association was observed between poultry species and *Campylobacter* occurrence (χ^2 = 9.421; p = 0.0242). When expressed as a proportion of the total sampled population (n = 400), chickens contributed the highest share of infections [25/400 (6.3%)], followed by ducks [13/400 (3.3%)], turkeys [10/400 (2.5%)], and pigeons [5/400 (1.3%)]. However, when examined within species-specific groups, ducks [13/60 (21.7%)] and turkeys [10/50 (20.0%)] exhibited higher positivity rates compared to chickens [25/210 (11.9%)] and pigeons [5/80 (6.3%). Sample type was identified as a highly significant determinant of *Campylobacter* occurrence (χ^2 = 218.1; $p < 0.0001$). Live birds accounted for a greater proportion of overall infections [36/400 (9.0%)] compared to slaughtered poultry [17/400 (4.3%)]. Out of 200 samples collected from live birds 36 (18.0%) was found to be infected with *Campylobacter*, while 17 (8.5%) out of the 200 samples collected from slaughtered poultry were found infected with *Campylobacter*. The estimated odds ratio (OR = 0.02039) indicates a substantially lower likelihood of recovering *Campylobacter* from slaughtered samples.

Bird health status also showed a significant association with *Campylobacter* detection (χ^2 = 4.603; p = 0.0319). Apparently healthy birds contributed a larger proportion of total positives [35/400 (8.8%)] compared to clinically sick birds [18/400 (4.5%)]. Nonetheless, within-group analysis revealed a higher positivity rate among clinically sick birds [18/90 (20.0%)] than apparently healthy birds [35/310 (11.3%)]. The odds ratio (OR = 0.5091) further suggests a reduced likelihood of *Campylobacter* detection in apparently healthy birds relative to clinically affected ones.

The antimicrobial susceptibility profile of *Campylobacter* isolates recovered from poultry and environmental sources is presented in Table 3. A high level of resistance was observed across multiple antimicrobial classes, with the greatest resistance recorded against vancomycin [69/82 (84.1%)], penicillin [65/82 (79.3%)], ampicillin [60/82 (73.2%)], and oxacillin [58/82 (70.7%)]. Substantial resistance was also noted for tetracycline [55/82 (67.1%)] and sulphamethoxazole/trimethoprim [51/82 (62.2%)]. Moderate resistance levels were observed for streptomycin [48/82 (58.5%)] and ciprofloxacin [41/82 (50.0%)], while comparatively lower resistance rates were detected for erythromycin [30/82 (36.6%)], chloramphenicol [34/82 (41.5%)], and gentamicin [23/82 (28.0%)]. Notably, gentamicin exhibited the highest susceptibility profile, with 50 (61.0%) of isolates remaining sensitive, followed by erythromycin [40 (48.8%)] and chloramphenicol [36 (43.9%)] (Table 3).

The distribution of multidrug resistance (MDR) and the multidrug resistance index (MDRI) among the isolates are summarized in Table 4. Out of the 82 *Campylobacter* isolates, 59 (72.0%) were classified as MDR, exhibiting resistance to three or more antimicrobial classes, while only 23 (28.0%) were non-MDR. The MDRI values ranged from 0.00 to >0.60, with the majority of isolates clustering within the intermediate range of 0.21–0.40 [30 (36.6%)], followed by 0.41–0.60 [25 (30.5%)]. A smaller proportion of isolates exhibited MDRI values between 0.00–0.20 [15 (18.3%)], while 12 (14.6%) demonstrated very high MDRI values (>0.60), indicative of intense antimicrobial selection pressure. The overall mean MDRI was 0.37 ± 0.14 (Table 4).

The specific multidrug resistance phenotypes expressed by the isolates are detailed in Table 5. The most predominant resistance pattern was AMP–PEN–OXA–TET–SXT, observed in 15 (18.3%) isolates, representing concurrent resistance to β-lactams, tetracyclines, and folate pathway inhibitors. This was followed by PEN–OXA–TET–STR–SXT [13 (15.9%)], which additionally incorporates resistance to aminoglycosides, and AMP–PEN–TET–CIP–SXT [10 (12.2%)], reflecting combined resistance to β-lactams, tetracyclines, fluoroquinolones, and folate inhibitors. Other notable patterns included PEN–OXA–STR–CIP–ERY [8 (9.8%)], encompassing resistance across β-lactams, aminoglycosides, fluoroquinolones, and macrolides. Importantly, a subset of isolates [7 (8.5%)] exhibited extensive multidrug resistance, characterized by resistance to six or more antimicrobial classes (AMP–PEN–OXA–TET–STR–SXT).

The knowledge and awareness of *Campylobacter* infection and related food safety concepts among poultry farmers, live bird sellers, and butchers are presented in Table 6. Overall, awareness levels were markedly low across all assessed domains. Only 9 (9.0%; 95% CI: 4.8–16.3) respondents reported awareness of *Campylobacter* infection, while an overwhelming majority of 91 (91.0%; 95% CI: 83.8–95.2) had no prior knowledge of the pathogen. Similarly, knowledge of zoonotic transmission was limited to 13 (13.0%; 95% CI: 7.8–21.0) respondents, with 87 (87.0%) lacking such awareness. Awareness of foodborne diseases was slightly higher but still suboptimal, with 18 (18.0%; 95% CI: 11.7–26.7) respondents demonstrating knowledge compared to 82 (82.0%) who were unaware. In the context of antimicrobial resistance, only 15 (15.0%; 95% CI: 9.3–23.3) participants indicated awareness, whereas 85 (85.0%) had no knowledge of this critical issue. Notably, understanding of the importance of hygiene in disease prevention, although comparatively higher, remained limited, with 22 (22.0%; 95% CI: 15.0–31.1) respondents demonstrating awareness compared to 78 (78.0%) who did not. All assessed knowledge variables showed statistically significant differences (χ^2 range: 62.72–134.5; $p < 0.0001$) (Table 6).

The hygienic practices of poultry handlers in live bird markets and processing environments (Table 7). The findings reveal widespread inadequacies in essential biosecurity and hygiene measures. Only 24 (24.0%; 95% CI: 16.7–33.2) respondents reported adequate hand-washing practices after handling birds, while 76 (76.0%) practiced inadequate hygiene. The use of protective clothing such as gloves and aprons was particularly poor, with just 11 (11.0%; 95% CI: 6.3–18.6) respondents adhering to recommended practices, compared to 89 (89.0%) who did not. Routine cleaning of processing surfaces was adequately practiced by 27 (27.0%; 95% CI: 19.3–36.4) respondents, whereas 73 (73.0%) reported inadequate cleaning. Similarly, only 19 (19.0%; 95% CI: 12.5–27.8) respondents used clean water for carcass washing, and proper waste disposal practices were observed in just 16 (16.0%; 95% CI: 10.1–24.4) cases. All practice indicators were statistically significant (χ^2 range: 42.32–121.7; $p < 0.0001$) (Table 7).

The patterns of antibiotic usage among poultry farmers and handlers are presented in Table 8. The results indicate widespread misuse and poor stewardship of antimicrobial agents. A substantial proportion of respondents, 82 (82.0%; 95% CI: 73.3–88.3), reported using antibiotics without veterinary prescription, while only 18 (18.0%) adhered to professional guidance. Additionally, 71 (71.0%; 95% CI: 61.5–79.0) respondents reported using antibiotics for growth promotion, reflecting non-therapeutic application of these drugs. Compliance with recommended withdrawal periods was notably low, with only 14 (14.0%; 95% CI: 8.5–22.1) respondents adhering to guidelines, compared to 86 (86.0%) who did not. Furthermore, access to veterinary supervision prior to drug administration was limited, as only 21 (21.0%; 95% CI: 14.2–30.0) respondents reported consulting veterinary professionals, while 79 (79.0%) did not. All variables showed strong statistical significance (χ^2 range: 35.28–103.7; $p < 0.0001$) (Table 8).

This present study provides insight into the epidemiology of *Campylobacter* spp. within poultry production systems and associated environments in Maiduguri, Nigeria, highlighting important host, environmental, and management-related drivers of transmission. The overall prevalence of 15.8% observed in this study indicates a substantial burden of *Campylobacter* within the poultry value chain, reinforcing its continued relevance as a foodborne pathogen of public health importance. This finding is consistent with the report of Nwankwo *et al*. (2016), who similarly documented a notable prevalence of the bacterium, with higher isolation rates from both poultry and human samples in Sokoto State, Nigeria.

In a related perspective, Njoga *et al*. (2025) reported the isolation of the organism from poultry sources and further demonstrated a substantial occupational risk of human infection through questionnaire-based assessments among poultry handlers in Enugu State, Nigeria, highlighting the public health relevance of human–animal interfaces in transmission dynamics. The predominance of *Campylobacter jejuni* (11.0%) over *Campylobacter coli* (4.8%) observed in the present study aligns with global epidemiological evidence, where *C. jejuni* is consistently reported as the principal species

Table 1. Distribution and prevalence of *Campylobacter* spp. across poultry species and environmental sources in poultry farms and live bird markets in Maiduguri, Borno State, Nigeria (n = 520)

Sample Category	Sample Source	No. Examined	No. Positive (%)	*C. coli* n (%)	*C. jejuni* n (%)
Live Birds (Cloacal swabs)	Chickens	70	16 (22.9)	5 (7.1)	11 (15.7)
	Duck	45	9 (20.0)	3 (6.7)	6 (13.3)
	Pigeon	45	4 (8.9)	0 (0.0)	4 (8.9)
	Turkeys	40	7 (17.5)	3 (7.5)	4 (10.0)
Total		200	36 (18.0)	11 (5.5)	25 (12.5)
Slaughtered Poultry (Carcass/Tissue)	Chickens	140	9 (6.4)	2 (1.4)	7 (5.0)
	Ducks	15	4 (26.7)	2 (13.3)	2 (13.3)
	Pigeons	35	1 (2.9)	0 (0.0)	1 (2.9)
	Turkeys	10	3 (30.0)	1 (10.0)	2 (20.0)
Total		200	17 (8.5)	5 (2.5)	12 (6.0)
Subtotal (Poultry)	–	400	53 (13.3)	16 (4.0)	37 (9.3)
Environmental Samples	Processing tables	30	7 (23.3)	2 (6.7)	5 (16.7)
	Knives	25	3 (12.0)	0 (0.0)	3 (12.0)
	Chopping boards	25	5 (20.0)	2 (8.0)	3 (12.0)
	Wash water	40	14 (35.0)	5 (12.5)	9 (22.5)
Subtotal (Environment)	–	120	29 (24.2)	9 (7.5)	20 (16.7)
Overall Total	–	520	82 (15.8)	25 (4.8)	57 (11.0)

Table 2. Risk factors associated with the occurrence of *Campylobacter* spp. in poultry samples (n = 400) in Maiduguri, Borno State, Nigeria

Variable	Category	No. Examined	No. Positive (%)	Prevalence (%) 95% CI (LL – UL)	χ^2	p-value	OR
Poultry Species	Chicken	210	25 (11.9)	6.3^{a} (4.3 – 9.1)	9.421	0.0242	-
	Duck	60	13 (21.7)	3.3^{b} (1.9 – 5.5)			
	Pigeon	80	5 (6.3)	1.3^{c} (0.5 – 2.9)			
	Turkeys	50	10 (20.0)	2.5^{d} (1.4 – 4.5)			
Sample Type	Live birds	200	36 (18.0)	9.0^{a} (6.6 – 12.2)	218.1	<0.0001	0.02039
	Slaughtered poultry	200	17 (8.5)	4.3^{b} (2.7 – 6.7)			
Bird Health Status	Apparently healthy	310	35 (11.3)	8.8^{a} (6.4 – 11.9)	4.603	0.0319	0.5091
	Clinically sick	90	18 (20.0)	4.5^{b} (2.9 – 7.0)			

Key: CI= Confidence Interval; LL – UL = Lower limit – Upper limit; χ^2 = Chi – square

^{a,b,c,d} Values with different superscripts indicate significant ($p < 0.05$) difference in prevalence rates

Table 3. Antimicrobial resistance patterns, multidrug resistance (MDR), and multidrug resistance index (MDRI) of *Campylobacter* spp. isolated from poultry and environmental sources in Maiduguri, Borno State, Nigeria (n = 82)

Antimicrobial Agent (Disc Potency)	Antimicrobial Class	Resistant n (%)	Intermediate n (%)	Susceptible n (%)
Ampicillin (10 μg)	β-lactam (penicillin)	60 (73.2)	8 (9.8)	14 (17.0)
Penicillin (10 IU)	β-lactam (penicillin)	65 (79.3)	5 (6.1)	12 (14.6)
Amoxicillin/clavulanic acid (30 μg)	β-lactam (β-lactamase inhibitor)	45 (54.9)	10 (12.2)	27 (32.9)
Oxacillin (5 μg)	β-lactam (penicillinase-resistant)	58 (70.7)	7 (8.5)	17 (20.8)
Tetracycline (5 μg)	Tetracyclines	55 (67.1)	7 (8.5)	20 (24.4)
Chloramphenicol (30 μg)	Phenicols	34 (41.5)	12 (14.6)	36 (43.9)
Gentamicin (10 μg)	Aminoglycosides	23 (28.0)	9 (11.0)	50 (61.0)
Streptomycin (10 μg)	Aminoglycosides	48 (58.5)	7 (8.5)	27 (32.9)
Ciprofloxacin (5 μg)	Fluoroquinolones	41 (50.0)	8 (9.8)	33 (40.2)
Erythromycin (5 μg)	Macrolides	30 (36.6)	12 (14.6)	40 (48.8)
Sulphamethoxazole/trimethoprim (25 μg)	Folate pathway inhibitors	51 (62.2)	6 (7.3)	25 (30.5)
Vancomycin (5 μg)	Glycopeptides	69 (84.1)	4 (4.9)	9 (11.0)

Table 4. Multidrug resistance profile and MDRI distribution of *Campylobacter* spp. isolated from poultry and environmental sources in Maiduguri, Borno State, Nigeria

Parameter	Category	Number of Isolates (%)
MDR Status	MDR (≥3 classes)	59 (72.0)
	Non-MDR (<3 classes)	23 (28.0)
MDRI Range	0.00 – 0.20	15 (18.3)
	0.21 – 0.40	30 (36.6)
	0.41 – 0.60	25 (30.5)
	>0.60	12 (14.6)
Mean MDRI ± SD	—	0.37 ± 0.14

Table 5. Multidrug resistance phenotypes of *Campylobacter* spp. isolated from poultry and environmental sources in Maiduguri, Borno State, Nigeria

Resistance Pattern (Abbreviated)	Antibiotics Included	Frequency (%)
AMP–PEN–OXA–TET–SXT	β-lactams + tetracycline + folate inhibitors	15 (18.3)
PEN–OXA–TET–STR–SXT	β-lactams + aminoglycoside + tetracycline	13 (15.9)
AMP–PEN–TET–CIP–SXT	β-lactams + fluoroquinolone + tetracycline	10 (12.2)
PEN–OXA–STR–CIP–ERY	β-lactams + aminoglycoside + macrolide	8 (9.8)
AMP–PEN–OXA–TET–STR–SXT	Extensive MDR (≥6 classes)	7 (8.5)

Key: AMP = Ampicillin; PEN = Penicillin; AMC = Amoxicillin/clavulanic acid; OXA = Oxacillin; TET = Tetracycline; CHL = Chloramphenicol; GEN = Gentamicin; STR = Streptomycin; CIP = Ciprofloxacin; ERY = Erythromycin; SXT = Sulphamethoxazole/trimethoprim

Table 6. Knowledge and awareness of *Campylobacter* infection and food safety among poultry farmers, live bird sellers, and butchers in Maiduguri, Borno State, Nigeria (n = 100)

Knowledge Variable	Response	Number of Respondents n (%)	95% CI (LL – UL)	χ^2	p-value
Awareness of *Campylobacter* infection	Aware	9 (9.0)	4.8 – 16.3	134.5	<0.0001
	Not Aware	91 (91.0)	83.8 – 95.2		
Knowledge of zoonotic transmission	Aware	13 (13.0)	7.8 – 21.0	109.5	<0.0001
	Not Aware	87 (87.0)	79.0 – 92.2		
Awareness of foodborne diseases	Aware	18 (18.0)	11.7 – 26.7	81.92	<0.0001
	Not Aware	82 (82.0)	73.3 – 88.3		
Knowledge of antibiotic resistance	Aware	15 (15.0)	9.3 – 23.3	98.0	<0.0001
	Not Aware	85 (85.0)	76.7 – 90.7		
Understanding of hygiene importance in disease prevention	Aware	22 (22.0)	15.0 – 31.1	62.72	<0.0001
	Not Aware	78 (78.0)	68.9 – 85.0		

associated with poultry colonization and human campylobacteriosis (WHO, 2020; Taha-Abdelaziz *et al*., 2023; Kuang *et al*., 2025). This dominance may be attributed to its superior colonization capacity within the avian gastrointestinal tract, enhanced environmental adaptability, and greater persistence under processing and handling conditions, which collectively facilitate its transmission along the food chain. However, this finding contrasts with the reports of Nwankwo *et al*. (2016) and Njoga *et al*. (2025), who documented a higher prevalence of *C. coli* compared to *C. jejuni*. These variations may be attributable to differences in study design, sample size, geographical and ecological settings, husbandry practices, as well as variations in laboratory diagnostic approaches and species identification techniques.

Such disparities further highlight the influence of local epidemiological and methodological factors on the distribution patterns of *Campylobacter* species across different study environments.

Table 7. Hygienic practices among poultry handlers in live bird markets and processing environments in Maiduguri, Nigeria (n = 100)

Practice Indicator	Response	Number of Respondents n (%)	95% CI (LL – UL)	χ^2	p-value
Hand washing after handling birds	Adequate Practice	24 (24.0)	16.7 – 33.2	54.08	<0.0001
	Inadequate Practice	76 (76.0)	66.7 – 83.3		
Use of protective clothing (gloves/aprons)	Adequate Practice	11 (11.0)	6.3 – 18.6	121.7	<0.0001
	Inadequate Practice	89 (89.0)	81.4 – 93.8		
Routine cleaning of processing surfaces	Adequate Practice	27 (27.0)	19.3 – 36.4	42.32	<0.0001
	Inadequate Practice	73 73.0)	63.6 – 80.7		
Use of clean water for carcass washing	Adequate Practice	19 (19.0)	12.5 – 27.8	76.88	<0.0001
	Inadequate Practice	81 (81.0)	72.2 – 87.5		
Proper waste disposal practices	Adequate Practice	16 (16.0)	10.1 – 24.4	92.48	<0.0001
	Inadequate Practice	84 (84.0)	75.6 – 89.9		

Key: CI= Confidence Interval; LL – UL = Lower limit – Upper limit; χ^2 = Chi – square

Table 8. Antibiotic usage practices among poultry farmers and handlers in Maiduguri, Nigeria (n = 100)

Practice Indicator	Response	Number of Respondents n (%)	95% CI (LL – UL)	χ^2	P value
Use of antibiotics without veterinary prescription	Yes	82 (82.0)	73.3 – 88.3	81.92	<0.0001
	No	18 (18.0)	11.7 – 26.7		
Use of antibiotics for growth promotion	Yes	71 (71.0)	61.5 – 79.0	35.28	<0.0001
	No	29 (29.0)	21.0 – 38.5		
Observance of recommended withdrawal period	Yes	14 (14.0)	8.5 – 22.1	103.7	<0.0001
	No	86 (86.0)	77.9 – 91.5		
Access to veterinary supervision before drug use	Yes	21 (21.0)	14.2 – 30.0	67.28	<0.0001
	No	79 (79.0)	70.0 – 85.8		

Key: CI= Confidence Interval; LL – UL = Lower limit – Upper limit; χ^2 = Chi – square

The higher contamination observed in environmental samples (24.2%) compared to poultry samples (13.3%) emphasize the critical role of environmental reservoirs in the persistence and dissemination of *Campylobacter*. In particular, the high prevalence in wash water (35.0%) suggests that water used during slaughter and processing may serve as a major vehicle for cross-contamination. This finding aligns with previous reports that identify contaminated water and processing surfaces as key contributors to pathogen spread within live bird markets and slaughter facilities (Whiley *et al.*, 2013; Zhang *et al.*, 2018; Chala *et al.*, 2021; Njoga *et al.*, 2025). The detection of *Campylobacter* on processing tables, chopping boards, and knives further indicates inadequate sanitation practices and highlights the potential for repeated contamination cycles during processing operations.

The comparatively higher prevalence in live birds (18.0%) relative to slaughtered poultry (8.5%) suggests that colonization primarily occurs at the farm or pre-slaughter stage, with partial reduction during processing. However, the persistence of the organism in carcass samples indicates that slaughtering processes in the study area may not be sufficiently effective in eliminating contamination. This observation is consistent with findings from similar settings where traditional slaughter practices, limited biosecurity, and poor hygienic conditions contribute to the survival and spread of *Campylobacter* (Zainol *et al*., 2024; Njoga *et al*., 2025). The significant association between sample type and *Campylobacter* occurrence further supports the notion that intervention strategies should prioritize both pre-harvest and post-harvest control measures.

Species-specific differences observed in this study provide additional epidemiological insights. While chickens contributed the largest proportion of overall infections (6.3%) due to their higher representation in the sample population, ducks and turkeys exhibited higher within-group prevalence rates (21.7% and 20.0%, respectively), suggesting increased susceptibility or exposure in these species. These findings corroborate earlier studies indicating that waterfowl, particularly ducks, may act as important reservoirs of *Campylobacter* due to their frequent contact with contaminated water sources and their capacity to asymptomatically harbor the organism (Ahmed and Gulhan, 2022; Wysok *et al*., 2022). The relatively lower prevalence observed in pigeons may reflect differences in husbandry practices, ecological behavior, or reduced exposure to contaminated environments.

The significant association between bird health status and *Campylobacter* detection highlights the complex interplay between host physiology and pathogen dynamics. Although apparently healthy birds contributed a greater proportion of total positives due to their larger sample size, clinically sick birds exhibited a higher within-group prevalence, suggesting that disease conditions may enhance bacterial shedding or susceptibility. This observation is in agreement with previous reports that stress, immunosuppression, and concurrent infections can increase *Campylobacter* colonization and excretion in poultry (Ahmed and Gulhan, 2022; Mbai *et al*., 2022; Wu *et al*., 2024). Importantly, the detection of *Campylobacter* in apparently healthy birds reinforces its status as a commensal organism in poultry, posing a silent but significant risk for transmission to humans.

The antimicrobial resistance profile observed in this study reveals a concerning pattern of reduced susceptibility among *Campylobacter* isolates from both poultry and environmental sources, with important implications for treatment efficacy and public health. The high levels of resistance to β-lactam antibiotics, including penicillin (79.3%), ampicillin (73.2%), and oxacillin (70.7%), are consistent with the intrinsic and acquired resistance mechanisms widely reported in *Campylobacter* spp., particularly the production of β-lactamases and reduced permeability of the bacterial cell wall (Zenebe *et al*., 2020; Hasan *et al*., 2025). The notably high resistance to vancomycin (84.1%) is expected, given that *Campylobacter* is a Gram-negative organism inherently resistant to glycopeptides due to the outer membrane barrier, and thus this finding primarily reflects intrinsic resistance rather than acquired selective pressure.

The elevated resistance to tetracycline (67.1%) and sulphamethoxazole/trimethoprim (62.2%) suggests extensive and possibly indiscriminate use of these antimicrobials in poultry production systems. Tetracycline resistance in *Campylobacter* has been strongly associated with the presence of the tet (O) gene, often carried on transferable genetic elements, facilitating rapid dissemination within bacterial populations (Alam *et al*., 2023). Similarly, resistance to folate pathway inhibitors may reflect long-term exposure and selective pressure within both veterinary and environmental contexts. These findings align with reports from other low- and middle-income countries where antimicrobial use in animal husbandry is often poorly regulated (Ayandiran *et al*., 2018; Fani *et al*., 2019).

Of particular concern is the moderate to high resistance observed against fluoroquinolones (ciprofloxacin, 50.0%) and macrolides (erythromycin, 36.6%), which are considered critically important antimicrobials for the treatment of human campylobacteriosis (Tramuta *et al*., 2024; Popa *et al*., 2025). Resistance to fluoroquinolones is commonly linked to point mutations in the gyrA gene, while macrolide resistance is associated with mutations in the 23S rRNA gene or the presence of efflux pumps such as CmeABC (Shariati *et al*., 2022; Wang *et al*., 2025). The presence of such resistance patterns in this study raises significant concerns regarding the potential for therapeutic failure, particularly in severe or invasive infections.

In contrast, gentamicin demonstrated the highest level of susceptibility (61.0%), suggesting that aminoglycosides may still retain effectiveness against *Campylobacter* in the study area. However, the emergence of resistance to streptomycin (58.5%), another aminoglycoside, indicates that this class of antibiotics is not entirely spared from resistance development. The relatively moderate susceptibility to chloramphenicol (43.9%) may reflect its limited use in contemporary veterinary practice due to regulatory restrictions, thereby reducing selective pressure.

The high prevalence of multidrug resistance (72.0%) observed in this present study is particularly alarming and indicative of widespread exposure of *Campylobacter* populations to multiple antimicrobial agents. This level of MDR exceeds values reported in some previous studies and underscores the intensity of antimicrobial selection pressure within the local poultry production environment (Gahamanyi *et al*., 2021; Barata *et al*., 2024; Kholeif *et al*., 2025; Mayyas *et al*., 2025). The MDRI distribution further supports this observation, with a mean value of 0.37 ± 0.14, suggesting that isolates originated from high-risk environments where antibiotics are frequently used. MDRI values above 0.2 are generally considered indicative of high-risk contamination sources with significant antimicrobial exposure (Ayandele *et al*., 2020), and the substantial proportion of isolates within the 0.21–0.60 and >0.60 ranges in this study reinforces this concern.

The diversity of multidrug resistance phenotypes observed reflects the complex and multifactorial nature of antimicrobial resistance development in *Campylobacter*. The predominance of resistance patterns involving β-lactams, tetracyclines, and folate pathway inhibitors suggests that these antimicrobial classes are under strong selective pressure within the study setting. The identification of extensive MDR phenotypes, including resistance to six or more antimicrobial classes, is particularly noteworthy and indicative of the emergence of highly resistant strains with limited treatment options. Such patterns have been increasingly reported in regions with unregulated antimicrobial usage and highlight the potential for horizontal gene transfer and co-selection of resistance determinants (Adhikari *et al*., 2025; Mayyas *et al*., 2025).

From a public health perspective, the coexistence of high antimicrobial resistance and environmental contamination observed in this study amplifies the risk of transmission of resistant *Campylobacter* strains through the food chain. Poultry products contaminated with MDR strains may serve as a direct source of infection, while environmental reservoirs may facilitate indirect transmission and persistence. These findings emphasize the urgent need for antimicrobial stewardship programs targeting poultry production, including regulation of antibiotic use, promotion of alternative disease control strategies, and enforcement of withdrawal periods.

The findings of this study reveal substantial gaps in knowledge, suboptimal hygienic practices, and widespread misuse of antibiotics among poultry farmers, live bird sellers, and butchers, all of which have important implications for the persistence and transmission of *Campylobacter* and antimicrobial resistance within the poultry value chain. The consistently low levels of awareness observed across all assessed domains indicate a critical deficiency in risk perception and health literacy among key stakeholders involved in poultry production and processing. Notably, awareness of *Campylobacter* infection was extremely limited (9.0%), suggesting that the pathogen remains largely unrecognized despite its established role as a leading cause of bacterial gastroenteritis globally (WHO, 2020; Njoga *et al*., 2025). This lack of awareness may hinder the adoption of preventive measures and contribute to ongoing transmission within both animal and human populations.

Similarly, the limited knowledge of zoonotic transmission (13.0%) and foodborne diseases (18.0%) underscores a broader disconnect between occupational exposure and perceived health risks. In settings such as live bird markets, where human–animal interactions are frequent and often unregulated, insufficient understanding of zoonotic pathways can significantly increase the likelihood of pathogen transmission (Abebaw and Assefie, 2025; Sparaciari *et al*., 2025). The low level of awareness regarding antimicrobial resistance (15.0%) is particularly concerning, given the growing global burden of resistant infections and the central role of agricultural antibiotic use in driving resistance emergence (Ahmed *et al*., 2024). Even though awareness of hygiene as a preventive measure was relatively higher (22.0%), it remained inadequate, suggesting that knowledge alone where present may not be sufficient to translate into effective practice.

The observed deficiencies in hygienic practices further reinforce the risks associated with low awareness. The majority of respondents reported inadequate hand hygiene, limited use of personal protective equipment, and poor sanitation of processing surfaces. These findings are consistent with previous studies in similar informal poultry systems, where infrastructural limitations, lack of training, and economic constraints contribute to poor compliance with hygiene standards (Grace *et al*., 2024; Melaku *et al*., 2025). The particularly low use of protective clothing (11.0%) and inadequate cleaning of processing surfaces (73.0%) suggest a high potential for cross-contamination during handling and slaughtering processes. Moreover, the limited use of clean water for carcass washing and poor waste disposal practices highlight environmental pathways through which *Campylobacter* and other pathogens may persist and spread.

The patterns of antibiotic usage identified in this study provide further evidence of systemic challenges in antimicrobial stewardship. The high proportion of respondents using antibiotics without veterinary prescription (82.0%) reflects weak regulatory oversight and easy access to antimicrobial agents, a situation commonly reported in many low- and middle-income countries (Nepal *et al*., 2026; Orisile *et al*., 2026). The widespread use of antibiotics for growth promotion (71.0%) and the low compliance with withdrawal periods (14.0%) are particularly problematic, as these practices not only promote the selection of resistant bacteria but also increase the risk of antimicrobial residues entering the food chain. The limited access to veterinary supervision (21.0%) further exacerbates this issue, as farmers and handlers may rely on informal knowledge or peer recommendations when administering drugs.

Conclusion

This study demonstrated that *Campylobacter spp.* was widely distributed across poultry and associated environmental matrices in Maiduguri, with an overall prevalence of 15.8% and a notably higher contamination burden in environmental sources compared to poultry samples. The predominance of *C. jejuni* across all sample types reinforces its central role in poultry-associated campylobacteriosis and highlights its epidemiological importance within the local production and processing continuum. The significantly higher recovery of isolates from live birds relative to slaughtered poultry, coupled with species-specific differences, underscores the influence of host factors and production systems on pathogen dynamics. The detection of substantial environmental contamination, particularly in wash water and processing surfaces, provides strong evidence of critical control failures along the processing chain and highlights the environment as a key reservoir facilitating cross-contamination and transmission. Furthermore, the significant associations observed with poultry species, sample type, and health status emphasize the multifactorial nature of *Campylobacter* occurrence within the production system.

Of particular concern is the high level of antimicrobial resistance observed among isolates, including widespread resistance to commonly used antibiotics and a high prevalence of multidrug resistance (72.0%), with elevated multidrug resistance index values indicative of sustained antimicrobial selection pressure. The diversity of resistance phenotypes, including strains resistant to multiple antimicrobial classes, underscores the growing therapeutic challenge posed by *Campylobacter* in this setting.

Equally critical are behavioral and management factors identified in this study. The findings reveal markedly low levels of knowledge and awareness of *Campylobacter*, food safety, and antimicrobial resistance among poultry handlers, alongside widespread deficiencies in hygienic practices and extensive misuse of antibiotics, including non-prescription use and poor compliance with withdrawal periods. These practices constitute significant drivers of pathogen transmission and antimicrobial resistance emergence within the human–animal–environment interface.

Recommendations

To mitigate burden and transmission of *Campylobacter* within poultry value chain, immediate implementation of integrated control measures is essential. Hygiene and biosecurity practices should be strengthened across all critical points particularly in live bird markets and processing environments through enforcement of minimum sanitary standards, provision of clean water and routine disinfection of equipment and surfaces. Capacity-building programs targeting poultry farmers, traders and processors should be prioritized to improve knowledge of zoonotic diseases, food safety and personal hygiene practices with emphasis on handwashing, use of protective clothing and safe carcass handling. In parallel, farm-level interventions, including improved housing waste management and controlled access to flocks should be promoted to reduce environmental contamination and pathogen circulation.

Addressing antimicrobial resistance requires coordinated One Health–driven strategies that integrate veterinary public health, and environmental sectors. Regulatory frameworks governing antibiotic distribution and use should be strengthened to limit non-prescription access and discourage the use of antimicrobials for growth promotion. Enhanced veterinary oversight alongside antimicrobial stewardship programs, is critical to promote judicious drug use. Routine surveillance systems for antimicrobial resistance and *Campylobacter* occurrence across poultry, humans and environmental sources should be institutionalized to support evidence-based decision-making. Furthermore, investment in diagnostic capacity and future research focusing on molecular characterization and source attribution is recommended to better elucidate transmission pathways and inform targeted interventions aimed at improving food safety and protecting public health.

References

Abebaw B and Assefie S (2025). Knowledge, attitude, and practices to foodborne zoonotic diseases and their associated factors in and around Debre Tabor City, Northwest Ethiopia. Veterinary Medicine International, 8360480. https://doi.org/10.1155/vmi/8360480

Adhikari Y, Bourassa DV, Poudel S, Bailey MA, Zhang L, Buhr RJ and Macklin KS (2025). Antimicrobial resistance pattern in *Campylobacter* strains isolated from both no-antibiotics-ever (NAE) and conventional broiler complexes: genotypic and phenotypic characterization. Poultry Science, 104(10): 105516. https://doi.org/10.1016/j.psj.2025.105516

Ahmed NA and Gulhan T (2022). *Campylobacter* in wild birds: is it an animal and public health concern? Frontiers in Microbiology, 12: 812591. https://doi.org/10.3389/fmicb.2021.812591

Ahmed SK, Hussein S, Qurbani K, Ibrahim RH, Fareeq A, Mahmood KA and Mohamed MG (2024). Antimicrobial resistance: impacts, challenges, and future prospects. Journal of Medicine, Surgery, and Public Health, 2: 100081. https://doi.org/10.1016/j.glmedi.2024.100081

Alam GS, Hassan MM, Ahaduzzaman M, Nath C, Dutta P, Khanom H, Khan SA, Pasha MR, Islam A, Magalhaes RS and Cobbold R (2023). Molecular detection of tetracycline-resistant genes in multi-drug-resistant *Escherichia coli* isolated from broiler meat in Bangladesh. Antibiotics (Basel), 12(2): 418. https://doi.org/10.3390/antibiotics12020418

Ayandele AA, Oladipo EK, Oyebisi O and Kaka MO (2020). Prevalence of multi-antibiotic resistant *Escherichia coli* and *Klebsiella* species obtained from a tertiary medical institution in Oyo State, Nigeria. Qatar Medical Journal, 2020 (1): 9. https://doi.org/10.5339/qmj.2020.9

Ayandiran TO, Falgenhauer L, Schmiede J, Chakraborty T and Ayeni FA (2018). High resistance to tetracycline and ciprofloxacin in bacteria isolated from poultry farms in Ibadan, Nigeria. Journal of Infection in Developing Countries, 12(6): 462–470. https://doi.org/10.3855/jidc.9862

Badjo AOR, Kabore NF, Zongo A, Gnada K, Ouattara A, Muhigwa M, Ouangraoua S, Poda A, Some SA, Schubert G, Eckmanns T, Leendertz FH, Belarbi E and Ouedraogo AS (2024). Burden and epidemiology of *Campylobacter* species in acute enteritis cases in Burkina Faso. BMC Infectious Diseases, 24: 808. https://doi.org/10.1186/s12879-024-09709-y

Barata R, Saavedra MJ and Almeida G (2024). A decade of antimicrobial resistance in human and animal *Campylobacter* spp. isolates. Antibiotics, 13(9): 904. https://doi.org/10.3390/antibiotics13090904

Bukari Z, Emmanuel T, Woodward J, Ferguson R, Ezughara M, Darga N and Lopes BS (2025). The global challenge of *Campylobacter*: antimicrobial resistance and emerging intervention strategies. Tropical Medicine and Infectious Disease, 10(1): 25. https://doi.org/10.3390/tropicalmed10010025

Chala G, Eguale T, Abunna F, Asrat D and Stringer A (2021). Identification and characterization of *Campylobacter* species in livestock, humans, and water in livestock owning households of peri-urban Addis Ababa, Ethiopia: A One Health approach. Frontiers in Public Health, 9: 750551.

https://doi.org/10.3389/fpubh.2021.750551

Demiroğlu EG, Şahin M and Büyük F (2022). Isolation and characterization of thermophilic *Campylobacter* species from geese raised in Kars region (Turkey) using cultural, molecular and mass spectrometry methods. Iranian Journal of Veterinary Research, 23(1): 24–31. https://doi.org/10.22099/IJVR.2021.41103.5962

El-Saadony MT, Saad AM, Yang T, Salem HM, Korma SA, Ahmed AE, Mosa WFA, Abd El-Mageed TA, Selim S, Al Jaouni SK, Zaghloul RA, Abd El-Hack ME, El-Tarabily KA and Ibrahim SA (2023). Avian campylobacteriosis: prevalence, sources, hazards, antibiotic resistance, poultry meat contamination, and control measures. Poultry Science, 102(9): 102786. https://doi.org/10.1016/j.psj.2023.102786

Fani F, Aminshahidi M, Firoozian N and Rafaatpour N (2019). Prevalence, antimicrobial resistance, and virulence-associated genes of *Campylobacter* isolates from raw chicken meat in Shiraz, Iran. Iranian Journal of Veterinary Research, 20(4): 283–288.

Gahamanyi N, Song DG, Yoon KY, Mboera LEG, Matee MI, Mutangana D, Amachawadi RG, Komba EVG and Pan CH (2021). Antimicrobial resistance profiles, virulence genes, and genetic diversity of thermophilic *Campylobacter* species isolated from a layer poultry farm in Korea. Frontiers in Microbiology, 12: 622275. https://doi.org/10.3389/fmicb.2021.622275

Grace D, Knight-Jones TJD, Melaku A, Alders R and Jemberu WT (2024). The public health importance and management of infectious poultry diseases in smallholder systems in Africa. *Foods*, 13(3):411. https://doi.org/10.3390/foods13030411.

Hasan M, Talukder S, Mandal AK, Tasmim ST, Parvin S, Ali Y, Sikder MH, Callaghan TJ, Soares Magalhães RJ and Islam T (2025). Antimicrobial resistance profiles of *Campylobacter* spp. recovered from chicken farms in two districts of Bangladesh. Foodborne Pathogens and Disease, 22(2): 118–130. https://doi.org/10.1089/fpd.2023.0079

Hassen KA, Fafetine J, Augusto L, Mandomando I, Garrine M and Sileshi GW (2026). Antimicrobial resistance in selected foodborne pathogens in sub-Saharan Africa: a systematic review and meta-analysis. Antibiotics (Basel), 15(1): 87. https://doi.org/10.3390/antibiotics15010087

Kholeif M, Sayed MG, Fotouh A, Abd-Allah DA, Ewida RM, Elbestawy AR, Alm Eldin NK and Diab MS (2025). Prevalence and molecular characterization of multidrug resistant *Campylobacter* isolated from animals and humans as a One Health approach. Scientific Reports, 15: 30262. https://doi.org/10.1038/s41598-025-13120-1

Kostoglou D, Simoni M, Vafeiadis G, Kaftantzis NM and Giaouris E (2023). Prevalence of *Campylobacter* spp., *Salmonella* spp., and *Listeria monocytogenes* in retail raw chicken meat and ready-to-eat leafy salads in Greece. Foods, 12(24): 4502. https://doi.org/10.3390/foods12244502

Kuang S, Wang Z, Hu X, Dong Z, Wang C, Xiao Y, Li Z, Shi D, Li S and Zhou Z (2025). Prevalence and genetic characteristics of *Campylobacter jejuni* from laying hens in Hubei Province, China. BMC Veterinary Research, 21: 84. https://doi.org/10.1186/s12917-025-04600-7

Mayyas A, Al-Qadiri HM, Al-Holy MA, Olaimat AN, Alsmairat TN, Al-Slaihat AH, Al-Alami N, Amr RA, Alaseili R, Bakri FG, Rasco BA and Mahasneh ZMH (2025). Antimicrobial resistance patterns of *Campylobacter jejuni* isolated from retail raw chicken meat in Jordan. Poultry Science, 104(11): 105657. https://doi.org/10.1016/j.psj.2025.105657

Mbai J, Njoroge S, Obonyo M, Otieno C, Owiny M and Fèvre EM (2022). *Campylobacter* positivity and public health risks in live bird markets in Busia, Kenya: a value chain analysis. Transboundary and Emerging Diseases, 69(5): e1839–e1853. https://doi.org/10.1111/tbed.14518

Melaku A, Admasu T and Ambelu A (2025). Determinants of hand hygiene compliance among healthcare workers in public and private hospitals of Addis Ababa, Ethiopia. Infection Prevention in Practice, 8(1): 100488. https://doi.org/10.1016/j.infpip.2025.100488

Mohan V, Strepis N, Mitsakakis K, Becker K, Chindelevitch L, Shivaperumal N, Swe-Han

KS and Hays J (2025). Antimicrobial resistance in *Campylobacter* spp. focusing on *C. jejuni* and *C. coli* – a narrative review. Journal of Global Antimicrobial Resistance, 43: 372–389. https://doi.org/10.1016/j.jgar.2025.05.008

Nepal A, Bhandari N, Subedi R and Hendrie D (2026). Antibiotics use patterns in low- and middle-income countries: a systematic review analysis. Inquiry, 63: 469580261420724. https://doi.org/10.1177/00469580261420724

Neyaz LA, Arafa SH, Alsulami FS, Ashi H, Elbanna K and Abulreesh HH (2024). Culture-based standard methods for the isolation of *Campylobacter* spp. in food and water. *Polish* Journal of Microbiology, 73(4): 433–454. https://doi.org/10.33073/pjm-2024-046

Njoga EO, Chah KF and Oguttu JW (2026). Drivers of zoonotic *Campylobacter* species transmission in slaughterhouse settings: insights from Nigeria for global One Health improvement. One Health, 22: 101371. https://doi.org/10.1016/j.onehlt.2026.101371

Njoga EO, Mshelbwala PP, Ogugua AJ, Enemuo-Edo EC, Onwumere-Idolor OS, Ogunniran TM, Bernard SN, Ugwunwarua JC, Anidobe EC, Okoli CE, Godwin E, Enem SI and Oguttu JW (2025). *Campylobacter* colonisation of poultry slaughtered at Nigerian slaughterhouses: prevalence, antimicrobial resistance, and risk of zoonotic transmission. Tropical Medicine and Infectious Disease, 10(9): 265. https://doi.org/10.3390/tropicalmed10090265

Njoga EO, Nwankwo IO and Ugwunwarua JC (2019). Epidemiology of thermotolerant *Campylobacter* infection in poultry in Nsukka agricultural zone, Nigeria. International Journal of One Health, 5: 92–98.

Nwankwo IO, Faleke OO, Salihu MD, Magaji AA, Musa U, Garba J and Ibitoye EB (2016). Detection and viability of *Campylobacter* species isolate from different species of poultry and humans in Sokoto State, Nigeria. International Journal of One Health, 2: 19–23.

Nyokabi S, Birner R, Bett B, Isuyi L, Grace D, Güttler D and Lindahl J (2018). Informal value chain actors' knowledge and perceptions about zoonotic diseases and biosecurity in Kenya and the importance for food safety and public health. Tropical Animal Health and Production, 50(3): 509–518. https://doi.org/10.1007/s11250-017-1460-z

Okello P, Bjöersdorff OG, Hansson I, Boqvist S and Erume J (2025). Prevalence and antimicrobial resistant *Campylobacter* spp. in broiler chicken carcasses and hygiene practices in informal urban markets in a low-income setting. PLoS ONE, 20(1): e0318516. https://doi.org/10.1371/journal.pone.0318516

Orisile AG, Lim RHM, Naqvi AA and Amlogu A (2026). A systematic review of antimicrobial stewardship practices and challenges in sub-Sahara Africa regulated retail medicine settings. JAC-Antimicrobial Resistance, 8(1): dlaf235. https://doi.org/10.1093/jacamr/dlaf235

Ovuru KF, Izah SC, Ogidi OI, Imarhiagbe O and Ogwu MC (2023). Slaughterhouse facilities in developing nations: sanitation and hygiene practices, microbial contaminants and sustainable management system. Food Science and Biotechnology, 33(3): 519–537. https://doi.org/10.1007/s10068-023-01406-x

Popa SA, Herman V, Sallam KI, Tîrziu E, Andor C, Morar A, Imre M, Ban-Cucerzan A, Pătrînjan RT, Pocinoc A and Imre K (2025). Genotypic and phenotypic characterization of antimicrobial resistance and virulence in *Campylobacter* spp. isolated from turkeys: uncovering a neglected reservoir in the One Health context. Antibiotics, 14(9): 935. https://doi.org/10.3390/antibiotics14090935

Severino N, Reyes C, Fernandez Y, Azevedo V, Francisco LED, Ramos RT, Maroto-Martín LO and Franco EF (2025). Bacterial foodborne diseases in Central America and the Caribbean: a systematic review. Microbiology Research, 16(4): 78. https://doi.org/10.3390/microbiolres16040078

Shariati A, Arshadi M, Khosrojerdi MA, Abedinzadeh M, Ganjalishahi M, Maleki A, Heidary M and Khoshnood S (2022). The resistance mechanisms of bacteria against ciprofloxacin and new approaches for enhancing the efficacy of this antibiotic.

Frontiers in Public Health, 10: 1025633. https://doi.org/10.3389/fpubh.2022.1025633

Sparaciari FE, Firth C, Karlsson EA and Horwood PF (2025). Zoonotic disease risk at traditional food markets. Journal of Virology, 99(8): e0071825. https://doi.org/10.1128/jvi.00718-25

Taha-Abdelaziz K, Singh M, Sharif S, Sharma S, Kulkarni RR, Alizadeh M, Yitbarek A and Helmy YA (2023). Intervention strategies to control *Campylobacter* at different stages of the food chain. Microorganisms, 11(1): 113. https://doi.org/10.3390/microorganisms11010113

Tramuta C, Garcia-Vozmediano A, CeRTiS Clinical Laboratories Group, Maurella C, Bianchi DM, Decastelli L and Pitti M (2024). Phenotypic antimicrobial resistance profiles of human *Campylobacter* species isolated in Northwest Italy, 2020–2023. Microorganisms, 12(3): 426. https://doi.org/10.3390/microorganisms12030426

Vaz CSL, Voss-Rech D, Pozza JS, Coldebella A and Silva VS (2014). Isolation of *Campylobacter* from Brazilian broiler flocks using different culturing procedures. Poultry Science, 93(11): 2887–2892.

Veronese P and Dodi I (2024). *Campylobacter jejuni/coli* infection: is it still a concern? Microorganisms, 12(12): 2669. https://doi.org/10.3390/microorganisms12122669

Wang CA, Love WJ, Jara M, van Vliet AHM, Thakur S and Lanzas C (2025). Risk factors for fluoroquinolone- and macrolide-resistance among swine *Campylobacter coli* using multi-layered chain graphs. PLoS Computational Biology, 21(8): e1012797. https://doi.org/10.1371/journal.pcbi.1012797

Whiley H, van den Akker B, Giglio S and Bentham R (2013). The role of environmental reservoirs in human campylobacteriosis. International Journal of Environmental Research and Public Health, 10(11): 5886–5907. https://doi.org/10.3390/ijerph10115886

Worku M, Tessema B, Ferede G, Ochieng L, Leliso SA, Mutua F, Moodley A, Grace D and Gelaw B (2024). *Campylobacter jejuni* and *Campylobacter coli* infection, determinants and antimicrobial resistance patterns among under-five children with diarrhea in Amhara National Regional State, Northwest Ethiopia. PLoS ONE, 19(7): e0304409. https://doi.org/10.1371/journal.pone.0304409

World Health Organization (2020). *Campylobacter:* the global view of campylobacteriosis. World Health Organization.

Woźniak-Biel A, Bugla-Płoskońska G, Kielsznia A, Korzekwa K, Tobiasz A, Korzeniowska-Kowal A and Wieliczko A (2018). High prevalence of resistance to fluoroquinolones and tetracycline *Campylobacter* spp. isolated from poultry in Poland. Microbial Drug Resistance, 24(3): 314–322.

Wu S, Jia R, Wang Y, Li J, Li Y, Wang L, Wang Y, Liu C, Jia EM, Wang Y, Zhang G and Liu J (2024). Prevalence, diversity, and virulence of *Campylobacter* carried by migratory birds at four major habitats in China. Pathogens, 13(3): 230.

Wysok B, Sołtysiuk M and Stenzel T (2022). Wildlife waterfowl as a source of pathogenic *Campylobacter* strains. Pathogens, 11(2): 113.

Zainol MFA, Safiyanu MB, Aziz SA, Omar AR, Chuang KP and Mariatulqabtiah AR (2024). Campylobacteriosis and control strategies against *Campylobacter* in poultry farms. Journal of Microbiology and Biotechnology, 34(5): 987–993.

Zenebe T, Zegeye N and Eguale T (2020). Prevalence of *Campylobacter* species in human, animal, and food of animal origin and their antimicrobial susceptibility in Ethiopia: a systematic review and meta-analysis. Annals of Clinical Microbiology and Antimicrobials, 19: 61.

Zhang X, Tang M, Zhou Q, Zhang J, Yang X and Gao Y (2018). Prevalence and characteristics of *Campylobacter* throughout the slaughter process of different broiler batches. Frontiers in Microbiology, 9: 2092. https://doi.org/10.3389/fmicb.2018.02092

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