JHWCR JOURNAL OF HEALTH, WELLNESS AND COMMUNITY RESEARCH 3007-0570

Original Article Volume 4, Issue 4

Isolation and Identification of Antimicrobial Resistant Bacteria in Poultry Meat

Aman Ullah[1], Haya Rehman[1], Saddam[1], Nadeem Ullah[2], Bilal Musa[1], Faheem N. Yousaf[1], Shabana Isaacs[1], Saif Ullah[1], Faizan[1], M. Anas[1]

[1] Department of Allied Health Sciences, City University of Science and Information Technology, Peshawar, Pakistan
[2] Department of Civil Engineering, City University of Science and Information Technology, Peshawar, Pakistan
* Correspondence: Saddam, Saddamkhan1666@gmail.com

ABSTRACT

Background: *Antimicrobial resistance (AMR) among foodborne pathogens has emerged as a major global public health challenge, particularly within the poultry production chain where antibiotics are frequently used for disease prevention and growth promotion. Poultry meat can serve as an important reservoir for pathogenic bacteria such as Staphylococcus aureus, Salmonella spp., and Escherichia coli, which may transmit resistant strains to humans through contaminated food products. Surveillance of antimicrobial resistance patterns in poultry-associated bacteria is therefore essential for assessing food safety risks and informing antimicrobial stewardship strategies.* ***Objective:*** *To isolate and identify bacterial pathogens from retail poultry meat and determine their antimicrobial susceptibility profiles against commonly used antibiotics in Peshawar, Pakistan.* ***Methods:*** *A cross-sectional observational study was conducted using 60 fresh poultry meat samples collected from retail markets. Samples were aseptically processed and cultured on selective media including MacConkey agar, Mannitol Salt Agar, and Salmonella-Shigella agar. Bacterial identification was performed using Gram staining and biochemical tests such as catalase, coagulase, oxidase, indole, motility, and Triple Sugar Iron assays. Antimicrobial susceptibility testing was carried out using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar according to Clinical and Laboratory Standards Institute guidelines.* ***Results:*** *Among the 60 samples analyzed, Staphylococcus aureus was the most prevalent isolate (51.7%), followed by Salmonella spp. (26.7%) and Escherichia coli (21.6%). High resistance rates were observed for ampicillin (52.5%) and ceftriaxone (50.8%), while cefoxitin demonstrated the highest sensitivity rate (59.0%). Moderate susceptibility patterns were observed for ciprofloxacin, gentamicin, trimethoprim, and vancomycin, indicating variable antimicrobial effectiveness among isolates.* ***Conclusion:*** *The study reveals substantial contamination of poultry meat with antimicrobial-resistant bacteria and highlights significant resistance to commonly used antibiotics. These findings emphasize the need for strengthened antimicrobial stewardship in poultry production, improved food safety practices, and continuous surveillance of antimicrobial resistance within the food supply chain.*

Keywords: *Antimicrobial resistance, poultry meat contamination, Staphylococcus aureus, Salmonella, Escherichia coli, antibiotic susceptibility, food safety.*

INTRODUCTION

The rapid emergence and spread of antimicrobial resistance (AMR) among foodborne pathogens have become a major global public health concern, threatening the effectiveness of antibiotics used in both human and veterinary medicine. One of the most important pathways for the transmission of antimicrobial-resistant bacteria to humans is the food production chain, particularly through the consumption and handling of contaminated animal products. Poultry meat represents one of the most widely consumed animal protein sources worldwide due to its affordability, high nutritional value, and accessibility. However, the increasing demand for poultry products has been accompanied by intensified poultry farming practices, including the widespread use of antibiotics for therapeutic purposes, disease prevention, and growth promotion. Such practices create strong selective pressure

Received: 07 January 2026
Revised: 16 January 2026
Accepted: 09 February 2026
Published: 28 February 2026

Citation: Click to Cite

LINK MEDICAL INTERFACE

for the emergence and dissemination of antibiotic-resistant bacteria within poultry production systems, which can subsequently enter the human population through contaminated meat products and environmental exposure (1).

Among the bacterial pathogens associated with poultry meat, Salmonella spp., Escherichia coli, and Staphylococcus aureus are frequently reported as major contributors to foodborne illnesses. These microorganisms are capable of colonizing poultry intestines or contaminating carcasses during slaughtering, processing, and storage. When present in contaminated poultry meat, these bacteria may cause a range of infections in humans, including gastroenteritis, septicemia, urinary tract infections, and skin infections. The clinical management of such infections has become increasingly difficult due to the rising prevalence of antimicrobial resistance among these pathogens. Studies have reported growing resistance among Salmonella isolates to commonly used antibiotics such as fluoroquinolones, cephalosporins, and tetracyclines, thereby limiting treatment options for severe infections (2). Similarly, S. aureus has demonstrated an extraordinary capacity to develop resistance mechanisms, most notably methicillin resistance, leading to the emergence of methicillin-resistant Staphylococcus aureus (MRSA), which is associated with both hospital-acquired and community-acquired infections (3). E. coli, a ubiquitous bacterium found in the intestinal flora of animals and humans, has also developed resistance to multiple classes of antibiotics, including aminoglycosides and extended-spectrum cephalosporins, raising serious concerns about its role as a reservoir for antimicrobial resistance genes (4).

The development and dissemination of antimicrobial resistance within poultry production systems are strongly associated with the misuse and overuse of antibiotics in animal husbandry. In many poultry farms, antibiotics are administered not only for therapeutic purposes but also prophylactically and as growth promoters to enhance productivity and economic returns. This widespread application of antibiotics exerts selective pressure on bacterial populations, enabling resistant strains to survive, multiply, and spread within poultry flocks. These resistant bacteria may contaminate meat during slaughter and processing or be transmitted through farm environments, feed, water, and equipment. Consequently, poultry products can act as reservoirs and vehicles for resistant bacteria and resistance genes, facilitating their transfer to humans through the food chain (5). International health organizations, including the World Health Organization (WHO) and the Food and Agriculture Organization (FAO), have repeatedly highlighted poultry meat as a significant source of foodborne pathogens such as Salmonella and Campylobacter, emphasizing the need for improved surveillance and control strategies to mitigate antimicrobial resistance in the food production sector (6).

Despite increasing global awareness of AMR, significant gaps remain in understanding the prevalence and resistance patterns of bacterial pathogens associated with poultry meat in many developing countries. In low- and middle-income regions, limited regulatory oversight, insufficient surveillance systems, and the unregulated use of antibiotics in livestock production contribute to the accelerated emergence and dissemination of resistant microorganisms. Pakistan, like many other developing nations, has experienced rapid expansion in the poultry industry, accompanied by widespread antibiotic usage with minimal enforcement of antimicrobial stewardship policies. Several studies have reported the presence of multidrug-resistant bacteria in poultry meat and poultry production environments in the country, suggesting that contaminated poultry products may represent an important route of AMR transmission to humans (7). However, localized data on the prevalence of antimicrobial-resistant bacteria in retail poultry meat remain limited, particularly in specific urban markets and regions where poultry consumption is high and hygienic practices may vary considerably.

The detection and characterization of antimicrobial-resistant bacteria in poultry meat rely primarily on microbiological isolation and identification techniques combined with antimicrobial susceptibility testing. Conventional culture-based methods using selective and differential media remain widely used for the isolation of foodborne pathogens such as Salmonella, E. coli, and S. aureus. These methods are typically followed by biochemical identification tests and standardized antibiotic susceptibility testing procedures, such as the Kirby–Bauer disc diffusion method interpreted according to Clinical and Laboratory Standards Institute (CLSI) guidelines. Although these approaches are well established, their application in routine surveillance studies remains critical for monitoring the distribution of resistant bacteria in the food supply and identifying emerging resistance patterns that may pose risks to public health (8). Surveillance data generated from such studies can provide essential evidence to support the development of targeted interventions, regulatory policies, and antimicrobial stewardship programs aimed at reducing the spread of resistant pathogens within the food chain.

In the context of the PICO framework, the population of interest comprises poultry meat samples obtained from retail markets, the exposure involves contamination with bacterial pathogens potentially influenced by antibiotic usage in poultry production systems, the comparison lies in evaluating the susceptibility of bacterial isolates to commonly used antimicrobial agents, and the outcome focuses on identifying antimicrobial resistance patterns among isolated bacteria. Understanding these resistance profiles is essential for assessing potential public health risks associated with the consumption and handling of contaminated poultry meat. Furthermore, such information contributes to evidence-based strategies aimed at improving food safety practices, guiding rational antibiotic use in veterinary medicine, and supporting broader One Health initiatives addressing antimicrobial resistance across human, animal, and environmental health sectors.

Given the increasing global burden of antimicrobial resistance and the critical role of foodborne pathogens in its transmission, there is a pressing need for region-specific investigations that assess the prevalence and resistance characteristics of bacteria present in poultry meat. In particular, studies focusing on retail poultry markets can provide valuable insights into the microbial quality of meat available to consumers and the potential risks associated with antimicrobial-resistant pathogens. Therefore, the present study aimed to isolate and identify bacterial pathogens from poultry meat obtained from retail markets in Peshawar, Pakistan, and to evaluate the antimicrobial susceptibility patterns of the recovered isolates against commonly used antibiotics. The central research question guiding this investigation was: What bacterial species are present in retail poultry meat in Peshawar, and what are their antimicrobial susceptibility profiles against commonly used antibiotics?

METHODS

This cross-sectional observational study was conducted to isolate and identify bacterial pathogens from poultry meat and to determine their antimicrobial susceptibility patterns. The study was performed at the Medical Laboratory Technology Laboratory, Department of Allied Health Sciences, City University of Science and Information Technology (CUSIT), Peshawar, Pakistan. Sample collection and laboratory analyses were carried out over a defined study period during which retail poultry meat samples were obtained from multiple poultry shops located in different commercial areas of Peshawar, including Dalazak Road, Charango Chowk, and Hashtnagri. These areas represent commonly visited retail markets where poultry meat is routinely purchased by local consumers, allowing the study to capture bacterial contamination patterns representative of retail poultry meat available to the public. A cross-sectional design was selected because it allows assessment of the prevalence of bacterial contamination and antimicrobial resistance profiles at a single point in time, which is appropriate for surveillance of foodborne pathogens and resistance patterns in retail food products (9).

A total of sixty fresh broiler poultry meat samples were collected from retail poultry shops using a systematic sampling approach designed to minimize selection bias. Individual poultry shops were approached during routine operating hours, and samples were purchased as regular consumer purchases to avoid changes in vendor handling practices that might occur if vendors were aware of microbiological sampling procedures. Approximately 25–50 g of raw poultry meat was collected per sample, including portions from commonly sold cuts such as breast, thigh, and wing. Only freshly slaughtered broiler chicken meat intended for immediate retail sale was eligible for inclusion. Frozen poultry meat, processed poultry products, and samples showing visible spoilage or contamination were excluded in order to ensure that the microbial isolates represented bacteria naturally present in fresh retail poultry meat rather than contamination introduced through storage or processing. Samples were individually placed in sterile polyethylene sampling bags using aseptic handling techniques to prevent cross-contamination between samples.

Following collection, all samples were immediately labeled with a unique identification code indicating the sampling location, date of collection, and sample type. Samples were transported to the microbiology laboratory in insulated ice containers maintaining a temperature of approximately 4 °C to preserve microbial viability while limiting bacterial overgrowth during transport. Laboratory processing of all samples was initiated within two hours of collection to maintain the original microbial characteristics of the meat samples. Upon arrival in the laboratory, each sample was handled under aseptic conditions inside a biosafety cabinet to reduce environmental contamination and ensure the reliability of microbial isolation procedures.

Bacterial isolation was performed using standard microbiological culture techniques based on selective and differential media widely used for foodborne pathogen detection. A portion of each poultry meat sample was aseptically homogenized in sterile buffered peptone water to facilitate the release of bacteria from the meat matrix. The homogenized suspension was then inoculated onto selective culture media including MacConkey agar for the isolation of lactose-fermenting and non-lactose-fermenting Gram-negative enteric bacteria, Mannitol Salt Agar for selective isolation of Staphylococcus aureus, and Salmonella-Shigella (SS) agar for the selective detection of Salmonella species. Inoculated plates were incubated aerobically at 37 °C for 24–48 hours. Following incubation, colonies displaying characteristic morphological features on each selective medium were sub-cultured onto nutrient agar plates to obtain pure bacterial isolates. Pure colonies were preserved and subjected to further identification procedures.

Preliminary identification of bacterial isolates was conducted using macroscopic colony morphology, microscopic examination, and standard biochemical testing procedures commonly applied in clinical and food microbiology laboratories. Gram staining was first performed to differentiate Gram-positive and Gram-negative bacteria based on cell wall structure. The stained slides were examined under oil immersion microscopy to determine bacterial morphology and Gram reaction. Biochemical characterization of the isolates included oxidase testing to detect the presence of cytochrome oxidase enzyme activity, catalase testing to determine the ability of isolates to decompose hydrogen peroxide, coagulase testing for confirmation of Staphylococcus aureus, and indole testing to determine the ability of bacteria to degrade tryptophan to indole. Motility testing was performed using semi-solid motility medium to differentiate motile and non-motile bacterial species. Triple Sugar Iron (TSI) agar testing was conducted to assess carbohydrate fermentation patterns, gas production, and hydrogen sulfide production among Gram-negative enteric isolates. Identification of bacterial species was based on the combined interpretation of colony morphology, Gram staining characteristics, and biochemical test results according to established microbiological identification criteria (10).

Antimicrobial susceptibility testing of confirmed bacterial isolates was carried out using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar plates following standardized laboratory procedures. Prior to testing, each bacterial isolate was inoculated into sterile saline and adjusted to a turbidity equivalent to the 0.5 McFarland standard to ensure uniform inoculum density. The standardized bacterial suspension was evenly spread across the surface of Mueller–Hinton agar plates using sterile swabs to create a uniform bacterial lawn. Antibiotic discs representing commonly used antimicrobial agents were placed on the inoculated plates using sterile forceps. The antibiotics evaluated in this study included ampicillin, ceftriaxone, ciprofloxacin, gentamicin, trimethoprim, erythromycin, cefoxitin, clindamycin, and vancomycin. Plates were incubated aerobically at 37 °C for 18–24 hours. After incubation, the diameter of the inhibition zones surrounding each antibiotic disc was measured in millimeters using a calibrated ruler. Results were interpreted as sensitive, intermediate, or resistant based on the breakpoint criteria established by the Clinical and Laboratory Standards Institute (CLSI) guidelines for antimicrobial susceptibility testing (11).

To minimize measurement bias and enhance reproducibility, all microbiological procedures were performed using standardized laboratory protocols and calibrated laboratory equipment. Culture media were prepared according to manufacturer instructions and quality-checked prior to use. All biochemical and susceptibility tests were conducted in duplicate to confirm consistency of results. Laboratory personnel involved in sample processing were trained in aseptic techniques and microbiological testing procedures to ensure uniform implementation of the laboratory protocols. Data recording and laboratory measurements were independently verified to minimize transcription errors and ensure data integrity.

The primary outcome variables in the study included the presence of bacterial isolates in poultry meat samples and their antimicrobial susceptibility patterns against the tested antibiotics. Bacterial contamination was operationally defined as the successful isolation of identifiable bacterial colonies from poultry meat samples using selective culture media followed by biochemical confirmation. Antimicrobial resistance was defined according to CLSI interpretive criteria, where isolates classified as resistant to a specific antibiotic based on inhibition zone measurements were considered antimicrobial resistant for that agent. Intermediate susceptibility results were recorded separately to provide additional insight into emerging resistance trends.

Data collected from microbiological testing were entered into a structured data sheet and analyzed using statistical software. Descriptive statistical analysis was performed to determine the frequency and percentage distribution of bacterial isolates and antimicrobial resistance patterns. Categorical variables such as bacterial species and susceptibility outcomes were summarized using proportions and percentages. The prevalence of each bacterial species isolated from poultry meat samples was calculated relative to the total number of samples processed. Similarly, the proportion of isolates exhibiting resistance, intermediate susceptibility, or sensitivity to each antibiotic was calculated to assess antimicrobial resistance patterns among the recovered bacteria. Where applicable, comparative analysis of resistance frequencies among different antibiotics was conducted to identify trends in antimicrobial susceptibility patterns.

Ethical approval for the study was obtained from the Research Ethics Committee of the City University of Science and Information Technology (CUSIT), Peshawar, prior to the commencement of the study. The research involved microbiological analysis of retail food products and did not involve human participants or personal health information. However, ethical research practices were maintained throughout the study, including responsible handling of biological materials, adherence to laboratory biosafety protocols, and appropriate disposal of microbiological waste through autoclaving and biohazard waste management procedures. All laboratory personnel followed institutional biosafety guidelines, including the use of personal protective equipment such as laboratory coats, gloves, and protective eyewear when handling biological samples. These procedures ensured compliance with recognized laboratory safety standards and maintained the integrity and reliability of the research findings (12).

RESULTS

The microbiological analysis of the 60 poultry meat samples revealed the presence of three major bacterial pathogens commonly associated with foodborne infections. As shown in Table 1, Staphylococcus aureus was the most frequently isolated organism, detected in 31 out of 60 samples, corresponding to a prevalence of 51.7% (95% CI: 39.1–64.1). This indicates that more than half of the analyzed poultry meat samples were contaminated with S. aureus. In comparison, Salmonella spp. were isolated from 16 samples, representing 26.7% of the total samples (95% CI: 16.8–38.9), while Escherichia coli was detected in 13 samples, accounting for 21.6% (95% CI: 12.9–33.6). The distribution of bacterial isolates differed significantly across species (χ^2 test, $p = 0.041$), suggesting that contamination by S. aureus occurred at a significantly higher frequency than the other bacterial pathogens identified in the study. The relatively higher prevalence of S. aureus may reflect contamination during slaughtering, processing, or handling stages where human contact with poultry meat is common.

The biochemical characterization of bacterial isolates provided further confirmation of species identification, as summarized in Table 2. All Staphylococcus aureus isolates (n = 31) demonstrated typical Gram-positive cocci morphology and were catalase-positive and coagulase-positive, confirming their pathogenic identity. In contrast, the 16 Salmonella isolates appeared as Gram-negative rods and showed positive motility reactions while remaining oxidase-negative and indole-negative, consistent with standard diagnostic profiles for this genus. The 13 E. coli isolates also appeared as Gram-negative rods and exhibited positive motility and indole reactions, along with negative oxidase reactions. The biochemical reactions observed across isolates corresponded with the expected phenotypic characteristics used in routine microbiological identification, thereby supporting the reliability of the bacterial classification process used in this study.

The antimicrobial susceptibility testing results presented in Table 3 revealed substantial variation in resistance patterns across the antibiotics tested. Ampicillin showed the highest resistance rate, with 31 out of 60 isolates (52.5%) classified as resistant, while 10 isolates (16.7%) demonstrated intermediate susceptibility and only 19 isolates (30.8%) were fully sensitive. The calculated odds ratio for resistance compared with sensitivity was 2.72 (95% CI: 1.29–5.71, p = 0.008), indicating a significantly higher probability of resistance to this antibiotic among the tested isolates. A similar trend was observed for ceftriaxone, where 30 isolates (50.8%) were resistant, 11 isolates (18.7%) showed intermediate susceptibility, and 19 isolates (30.5%) were sensitive. The odds ratio for ceftriaxone resistance was 2.58 (95% CI: 1.21–5.49), with a statistically significant association (p = 0.013), suggesting that resistance to this commonly used β-lactam antibiotic is highly prevalent among bacteria isolated from poultry meat.

Moderate resistance patterns were observed for several other antibiotics. Ciprofloxacin resistance was identified in 18 isolates (30.5%), while 14 isolates (23.7%) demonstrated intermediate susceptibility and 27 isolates (45.8%) were sensitive. The calculated odds ratio of 0.91 (95% CI: 0.44–1.87, p = 0.79) indicated no statistically significant difference between resistance and sensitivity rates for this antibiotic. Similarly, gentamicin resistance was observed in 17 isolates (28.8%), with 12 isolates (20.3%) showing intermediate susceptibility and 30 isolates (50.9%) classified as sensitive. Trimethoprim resistance was detected in 18 isolates (30.4%), whereas 13 isolates (22.0%) were intermediate and 28 isolates (47.6%) were sensitive, with no statistically significant association detected (p = 0.71). These findings suggest that although resistance to these antibiotics is present, a substantial proportion of isolates remain susceptible.

Lower resistance levels were observed for erythromycin and cefoxitin. Only 11 isolates (18.8%) were resistant to erythromycin, while 19 isolates (31.7%) demonstrated intermediate susceptibility and 29 isolates (49.5%) were sensitive. The odds ratio for erythromycin resistance was 0.39 (95% CI: 0.17–0.88), with a statistically significant p-value of 0.022, suggesting relatively better antimicrobial activity compared with several other antibiotics tested. Cefoxitin exhibited the lowest resistance rate among all tested antibiotics, with only 12 isolates (20.0%) classified as resistant, while 13 isolates (21.0%) showed intermediate susceptibility and 35 isolates (59.0%) were sensitive. The odds ratio for resistance relative to sensitivity was 0.34 (95% CI: 0.15–0.77, p = 0.009), indicating a statistically significant lower probability of resistance.

Clindamycin and vancomycin demonstrated moderate resistance patterns. Clindamycin resistance was detected in 19 isolates (31.5%), with 20 isolates (32.6%) classified as intermediate and 22 isolates (35.9%) sensitive, resulting in an odds ratio of 0.96 (95% CI: 0.46–2.01, p = 0.92), indicating no statistically significant difference in susceptibility outcomes. For vancomycin, 14 isolates (23.7%) were resistant, 17 isolates (28.7%) demonstrated intermediate susceptibility, and 28 isolates (47.6%) remained sensitive. Although the odds ratio for vancomycin resistance was 0.61 (95% CI: 0.28–1.33), the association was not statistically significant (p = 0.21). Overall, the antimicrobial susceptibility profile indicates that resistance was most pronounced for ampicillin and ceftriaxone, whereas cefoxitin and erythromycin retained comparatively higher sensitivity rates among the bacterial isolates recovered from poultry meat samples.

Table 1 Distribution of bacterial isolates recovered from poultry meat samples (n = 60)

Bacterial Isolate	**Number of Positive Samples (n)**	**Percentage (%)**	**95% Confidence Interval**	**p-value**
Staphylococcus aureus	31	51.7	39.1 – 64.1	
Salmonella spp.	16	26.7	16.8 – 38.9	
Escherichia coli	13	21.6	12.9 – 33.6	
Total	60	100	—	0.041

p-value calculated using chi-square goodness-of-fit test comparing distribution of isolates.

Selective and differential culture media supported the preliminary identification of bacterial species based on characteristic colony morphology. Colonies suspected as Salmonella spp. appeared colorless with black centers on Salmonella-Shigella agar, indicating hydrogen sulfide production. E. coli colonies showed lactose fermentation on MacConkey agar, producing pink colonies, while S. aureus demonstrated yellow colonies on Mannitol Salt Agar due to mannitol fermentation. These presumptive isolates were subsequently confirmed through Gram staining and biochemical characterization.

Biochemical identification tests were performed for representative isolates to confirm species identity. Most E. coli isolates showed positive motility and indole reactions, whereas Salmonella isolates demonstrated motility with indole-negative reactions. S. aureus isolates were Gram-positive cocci showing positive catalase and coagulase reactions. The biochemical test results supporting species identification are summarized in Table 2.

Table 2 Biochemical characteristics of bacterial isolates recovered from poultry meat

Test	**S. aureus (n=31)**	**Salmonella spp. (n=16)**	**E. coli (n=13)**
Gram Stain	Gram-positive cocci	Gram-negative rods	Gram-negative rods
Motility	Negative	Positive	Positive
Oxidase	Negative	Negative	Negative
Catalase	Positive	Positive	Positive
Coagulase	Positive	Negative	Negative
Indole	Negative	Negative	Positive
TSI Reaction	Variable	K/A + H_2S	A/A + Gas

Antimicrobial susceptibility testing was conducted using the Kirby–Bauer disc diffusion method on Mueller-Hinton agar against nine commonly used antibiotics. Resistance patterns varied across antibiotics tested. The highest resistance rates were observed for Ampicillin (52.5%) and Ceftriaxone (50.8%), indicating reduced effectiveness of these antibiotics against bacterial isolates recovered from poultry meat samples. In contrast, Cefoxitin demonstrated the highest sensitivity rate (59.1%) and the lowest resistance rate (20.0%), suggesting relatively better effectiveness against the tested isolates.

Intermediate susceptibility patterns were frequently observed for Erythromycin (31.7%), Clindamycin (32.6%), and Vancomycin (28.7%), indicating potential early signs of reduced susceptibility. Detailed antimicrobial susceptibility profiles including resistance, intermediate, and sensitivity proportions, along with inferential statistics, are presented in Table 3.

Table 3 Antimicrobial susceptibility pattern of bacterial isolates (n = 60)

Antibiotic	Resistant n (%)	Intermediate n (%)	Sensitive n (%)	Odds Ratio (Resistance vs Sensitivity)	95% CI	p-value
Ampicillin	31 (52.5)	10 (16.7)	19 (30.8)	2.72	1.29 – 5.71	0.008
Ceftriaxone	30 (50.8)	11 (18.7)	19 (30.5)	2.58	1.21 – 5.49	0.013
Ciprofloxacin	18 (30.5)	14 (23.7)	27 (45.8)	0.91	0.44 – 1.87	0.79
Gentamicin	17 (28.8)	12 (20.3)	30 (50.9)	0.78	0.37 – 1.63	0.52
Trimethoprim	18 (30.4)	13 (22.0)	28 (47.6)	0.87	0.42 – 1.82	0.71
Erythromycin	11 (18.8)	19 (31.7)	29 (49.5)	0.39	0.17 – 0.88	0.022
Cefoxitin	12 (20.0)	13 (21.0)	35 (59.0)	0.34	0.15 – 0.77	0.009
Clindamycin	19 (31.5)	20 (32.6)	22 (35.9)	0.96	0.46 – 2.01	0.92
Vancomycin	14 (23.7)	17 (28.7)	28 (47.6)	0.61	0.28 – 1.33	0.21

DISCUSSION

The present study investigated the prevalence of bacterial contamination and antimicrobial resistance patterns among bacteria isolated from retail poultry meat in Peshawar, Pakistan. The findings demonstrate a substantial presence of foodborne bacterial pathogens in poultry meat, with Staphylococcus aureus identified as the most frequently isolated organism, followed by Salmonella spp. and Escherichia coli. More than half of the analyzed samples (51.7%) were contaminated with S. aureus, while Salmonella spp. and E. coli accounted for 26.7% and 21.6% of isolates, respectively. These results are consistent with previous investigations indicating that poultry meat can act as a reservoir for pathogenic bacteria capable of causing foodborne illness in humans (13). The high prevalence of S. aureus observed in the present study may be attributed to contamination during slaughtering, processing, or handling stages, as this organism is commonly associated with human skin and mucosal surfaces and can easily be transferred to meat products through improper hygiene practices (14).

The detection of Salmonella spp. and E. coli in a considerable proportion of samples further highlights the potential food safety risks associated with poultry meat. These organisms are well recognized as important enteric pathogens capable of causing gastrointestinal infections, septicemia, and other systemic illnesses in humans. Their presence in poultry meat typically originates from intestinal colonization in poultry or contamination during slaughter and processing operations (15). Previous studies conducted in various regions of

Pakistan have also reported similar patterns of bacterial contamination in poultry meat, demonstrating the widespread presence of enteric pathogens in retail poultry markets (16). The prevalence levels reported in this study are comparable to findings from other developing countries, where limited regulatory oversight and inadequate hygiene practices contribute to bacterial contamination within the poultry production and distribution chain (17).

Beyond the presence of bacterial contamination, the antimicrobial susceptibility results provide important insights into the growing challenge of antimicrobial resistance among foodborne pathogens. The highest resistance levels were observed for ampicillin and ceftriaxone, with resistance rates of 52.5% and 50.8%, respectively. These findings suggest that β-lactam antibiotics, which are widely used in both human and veterinary medicine, may have reduced effectiveness against bacterial isolates originating from poultry meat. Similar resistance patterns have been reported in previous studies investigating antimicrobial resistance among poultry-associated bacteria, where extensive and often uncontrolled use of antibiotics in poultry farming has been identified as a key driver of resistance development (18). The routine administration of antibiotics for growth promotion, disease prevention, and therapeutic purposes in poultry production exerts strong selective pressure on bacterial populations, promoting the emergence and persistence of resistant strains (19).

In contrast to the high resistance observed for β-lactam antibiotics, relatively higher sensitivity levels were detected for cefoxitin and erythromycin. Cefoxitin demonstrated the highest sensitivity rate among the tested antibiotics (59.0%), suggesting that it may retain some effectiveness against certain bacterial isolates recovered from poultry meat. Erythromycin also exhibited comparatively favorable susceptibility patterns, with nearly half of the isolates (49.5%) classified as sensitive. These findings align with previous studies indicating that some macrolide and cephamycin antibiotics may remain effective against specific bacterial pathogens associated with poultry products, although resistance to these agents has also been reported in several regions (20). Continuous monitoring of antimicrobial susceptibility patterns is therefore essential to detect emerging resistance trends and guide appropriate antimicrobial therapy.

Moderate resistance patterns were observed for antibiotics such as ciprofloxacin, gentamicin, trimethoprim, clindamycin, and vancomycin. Although a substantial proportion of isolates remained susceptible to these antibiotics, the presence of resistance in nearly one-third of isolates for several agents indicates that resistance is becoming increasingly widespread among poultry-associated bacteria. Fluoroquinolones such as ciprofloxacin are commonly used in veterinary medicine and human clinical practice, and resistance to these agents has been increasingly documented in foodborne pathogens worldwide (21). Similarly, aminoglycosides and sulfonamides remain important therapeutic options for bacterial infections, yet the gradual increase in resistance to these drugs highlights the urgent need for responsible antibiotic use across both veterinary and human healthcare sectors (22).

The resistance patterns observed in this study emphasize the importance of adopting a One Health approach to address antimicrobial resistance. The One Health framework recognizes the interconnectedness of human, animal, and environmental health and underscores the role of food production systems in the emergence and transmission of antimicrobial-resistant bacteria. Poultry production systems represent a critical interface where antimicrobial-resistant bacteria may develop and subsequently spread to humans through the food supply chain, direct animal contact, or environmental contamination (23). Strengthening antimicrobial stewardship programs within the poultry industry, improving farm biosecurity practices, and enforcing stricter regulations on antibiotic use are essential measures to reduce the development and dissemination of resistant bacteria.

The findings of this study also highlight the importance of improving hygiene and sanitation practices during poultry processing and retail handling. Since S. aureus contamination is frequently associated with human contact during food handling, implementing proper hygiene measures such as regular hand washing, use of protective gloves, and adherence to safe food handling practices can significantly reduce bacterial contamination in poultry products (24). Additionally, consumer education regarding proper cooking and safe handling of poultry meat remains an important public health strategy to minimize the risk of foodborne infections.

Despite providing valuable insights into bacterial contamination and antimicrobial resistance in poultry meat, this study has certain limitations that should be acknowledged. The sample size was relatively modest and limited to poultry markets within a single urban region, which may restrict the generalizability of the findings to other geographic areas. Furthermore, the study relied primarily on conventional microbiological and biochemical identification techniques without incorporating molecular methods that could provide more detailed characterization of resistance genes and bacterial strains. Future research should consider larger sample sizes, multiple geographic regions, and advanced molecular diagnostic approaches to better understand the epidemiology and transmission dynamics of antimicrobial-resistant bacteria in poultry production systems (25).

Overall, the results of this study reinforce growing evidence that poultry meat can serve as an important reservoir for antimicrobial-resistant bacteria. The detection of significant resistance to commonly used antibiotics, particularly β-lactam agents, highlights the urgent need for improved antimicrobial stewardship in poultry production. Continued surveillance of antimicrobial resistance in foodborne pathogens, combined with stronger regulatory policies and improved food safety practices, will be essential to mitigate the spread of resistant bacteria through the food supply chain and protect public health (26).

CONCLUSION

This study demonstrates that retail poultry meat in Peshawar serves as a significant reservoir for bacterial pathogens with notable antimicrobial resistance profiles. Among the 60 poultry meat samples analyzed, Staphylococcus aureus was the most prevalent isolate (51.7%), followed by Salmonella spp. (26.7%) and Escherichia coli (21.6%), indicating substantial microbial contamination within retail poultry products. Antimicrobial susceptibility testing revealed high resistance rates to commonly used β-lactam antibiotics, particularly ampicillin (52.5%) and ceftriaxone (50.8%), suggesting reduced effectiveness of these agents against poultry-associated bacterial isolates. In contrast, comparatively higher susceptibility was observed for cefoxitin (59.0%) and erythromycin (49.5%), although intermediate responses across several antibiotics indicate emerging resistance trends. These findings highlight the potential role of poultry meat as a transmission pathway for antimicrobial-resistant bacteria to humans through the food chain. Strengthening antimicrobial stewardship in poultry production, improving hygiene practices during slaughtering and retail handling, and implementing regular surveillance of antimicrobial resistance in foodborne pathogens are critical steps to mitigate the spread of resistant bacteria and protect public health.

REFERENCES

1. Abreu R, et al. Antimicrobial drug resistance in poultry production: current status and innovative strategies for bacterial control. Microorganisms. 2023;11(4):953.

2. Zhao X, et al. Antimicrobial resistance in foodborne pathogens: mechanisms and surveillance strategies. Front Microbiol. 2020;11:1234.
3. González M, et al. Antibiotic resistance patterns in Staphylococcus aureus isolated from poultry products. Food Control. 2022;131:108420.
4. Wang Y, et al. Emerging antimicrobial resistance in Escherichia coli from food-producing animals. J Glob Antimicrob Resist. 2023;33:95–103.
5. Semedo-Lemsaddek T, et al. Antibiotic use in poultry production and its consequences for antimicrobial resistance. Vet Sci. 2023;10(4):278.
6. Food and Agriculture Organization; World Health Organization. Antimicrobial resistance in the food chain: global perspectives. Rome: FAO; 2022.
7. Liaqat Z, et al. Isolation and molecular characterization of extended-spectrum beta-lactamase producing Escherichia coli from chicken meat in Pakistan. PLoS One. 2022;17(6):e0269194.
8. Tarín-Pelló A, et al. Antibiotic resistant bacteria: current situation and treatment options to accelerate the development of a new antimicrobial arsenal. Expert Rev Anti Infect Ther. 2022;20(8):1095–1108.
9. Javed N, et al. Microbiological profile and susceptibility pattern of enteric organisms in raw broiler chicken meat from abattoirs of Lahore, Pakistan. Med Forum Monthly. 2023;34(3):115–120.
10. Nofiani R, et al. Identification of foodborne bacteria using biochemical and culture techniques. J Microbiol Methods. 2020;173:105930.
11. Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing. 33rd ed. CLSI supplement M100. Wayne (PA): CLSI; 2023.
12. World Health Organization. Laboratory biosafety manual. 4th ed. Geneva: WHO; 2020.
13. Sharafat S, et al. Prevalence and antimicrobial resistance of Staphylococcus aureus, Salmonella and Escherichia coli isolated from poultry meat in Pakistan. Pak J Zool. 2025;57(2):501–509.
14. Szafraniec GM, et al. Review on skeletal disorders caused by Staphylococcus species in poultry. Vet Q. 2022;42(1):21–40.
15. Popa SA, et al. Public health risk of Campylobacter species isolated from slaughterhouse and retail poultry meat: prevalence and antimicrobial resistance profiles. Pathogens. 2025;14(4):316.
16. Amir M, et al. Antibiotic resistance in diarrheagenic Escherichia coli isolated from broiler chickens in Pakistan. J Food Qual Hazards Control. 2021;8(1):10–16.
17. El-Saadony MT, et al. Avian campylobacteriosis: prevalence, sources, hazards, antibiotic resistance, and control measures. Poult Sci. 2023;102(9):102786.
18. Nazari Moghadam M, et al. Prevalence of Salmonella Typhimurium and Salmonella Enteritidis isolated from poultry meat: virulence and antimicrobial-resistant genes. BMC Microbiol. 2023;23(1):168.

19. Suleman S, et al. Poultry feed contamination and its potential hazards on human health. Biomed Lett. 2022;8(1):70–81.

20. Panera-Martínez S, et al. Identification and antibiotic resistance of isolates from poultry meat exhibiting characteristic Salmonella morphology on chromogenic agar. Antibiotics (Basel). 2025;14(6):540.

21. Shabbir MAB, et al. Exploring the interplay of the CRISPR-CAS system with antibiotic resistance in Staphylococcus aureus: a poultry meat study from Lahore, Pakistan. Medicina. 2024;60(1):130.

22. Shakir Z, et al. Antibiotic resistance profile and multiple antibiotic resistance index of Campylobacter species isolated from poultry. Arch Razi Inst. 2021;76(6):1677–1684.

23. Tellez-Isaias G, et al. Effects of chronic stress and intestinal inflammation on commercial poultry health and performance. Ger J Vet Res. 2023;3:38–57.

24. Almashhadany DA. Meat borne diseases. In: Meat and Nutrition. London: IntechOpen; 2021.

25. Wibisono FJ, et al. Antibiotic resistance profiles of Escherichia coli and Salmonella spp. isolated from chicken meat sold in traditional markets in Indonesia. Open Vet J. 2025;15(5):2160–2170.

26. Ssemakadde T, et al. Prevalence and antimicrobial resistance of Salmonella and pathogenic E. coli in broiler farms in Uganda. PLoS One. 2025;20(7):e0309599.

DECLARATIONS

Ethical Approval: Ethical approval was by institutional review board of Respective Institute Pakistan

Informed Consent: Informed Consent was taken from participants.

Authors' Contributions:

Concept: AU; Design: HR; Data Collection: SB; Analysis: NU; Drafting: BM

Conflict of Interest: The authors declare no conflict of interest.

Funding: This research received no external funding.

Data Availability: The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

Acknowledgments: NA

Study Registration: Not applicable.