



Isolation and Characterization of Bacterial Isolates from Poultry Shop Wastewater and Their Antimicrobial Susceptibility Patterns in Samawah City, Iraq

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Abstract

Poultry shop wastewater represents a significant source of environmental pollution because it contains high organic loads and may harbor bacterial isolates capable of contaminating surrounding soil and water resources. This study investigated the occurrence of bacterial isolates in wastewater discharged from poultry shops in Samawah City, Iraq, and evaluated the antimicrobial susceptibility profiles of the recovered isolates. Wastewater samples were collected from 10 poultry shops; bacterial isolates were recovered and characterized using standard microbiological, microscopic, morphological, and biochemical methods. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. A total of 46 bacterial isolates were recovered from 6 bacterial groups, with *Enterobacter spp.* and *Escherichia coli* being the most frequently isolated, each accounting for 21.74% (10/46) of the isolates, followed by *Micrococcus spp.* 19.57%, *Staphylococcus epidermidis* 17.37%, *Staphylococcus aureus* 15.22%, and *Streptococcus spp.* 4.35%. The isolates exhibited variable antimicrobial resistance patterns across the tested antibiotics, with resistance observed among several bacterial groups. These findings suggest that poultry shop wastewater may represent a potential environmental reservoir of antimicrobial-resistant bacteria and highlight the importance of appropriate wastewater management, microbiological surveillance, and prudent antimicrobial use in poultry-related activities.

Keywords: Poultry wastewater; Bacterial contamination; Antimicrobial resistance; Multidrug resistance; Environmental health.

1.0 Introduction

The rapid expansion of the poultry industry has substantially increased the generation of wastewater containing organic matter, suspended solids, nutrients, blood residues, feathers, fecal materials, and diverse microbial communities (Aruwa et al. 2021). When discharged without adequate treatment, poultry wastewater can contaminate surrounding soil and surface water, deteriorate environmental quality, and may facilitate the persistence and dissemination of potentially pathogenic microorganisms. In addition to its high pollutant load, poultry wastewater may serve as a reservoir of bacteria with significant public health importance, particularly in areas where waste management practices and environmental regulations are inadequate. Consequently, effective monitoring and management of poultry wastewater have become essential components of environmental protection and disease prevention strategies worldwide (Gržinić et al. 2023; Manyi-Loh et al. 2018). The microbiological composition of poultry wastewater is of particular concern because it frequently contains pathogenic and opportunistic bacteria originating from poultry feces, intestinal contents, processing activities, and contaminated equipment (Gu et al. 2019). Among the microorganisms commonly detected are *Escherichia coli*, *Staphylococcus aureus*, *Salmonella spp.*, *Enterobacter spp.*, *Streptococcus spp.*, and other bacteria capable of causing gastrointestinal, respiratory, skin, and systemic infections in humans. These pathogens can be disseminated through wastewater into surrounding environments, increasing the risk of exposure for poultry workers, nearby residents, animals, and aquatic ecosystems (Gržinić et al. 2023). Consequently, untreated poultry wastewater has been recognized as an important environmental source of microbial contamination and may represent a potential for the transmission of infectious diseases, particularly in regions where wastewater treatment and biosecurity measures are insufficient (Aruwa et al. 2021; Lutful Kabir 2010). The widespread use of antimicrobial agents in poultry production has contributed to the emergence and dissemination of antimicrobial-resistant bacteria in poultry-associated environments (Manyi-Loh et al. 2018). Wastewater generated from poultry shops may contain antibiotic-resistant bacteria and may contribute to the environmental dissemination of antimicrobial resistance. These microorganisms can persist in the environment and facilitate the spread of antimicrobial resistance through water systems, posing a growing challenge to both environmental and public health (Larsson et al. 2022). The World Health Organization has identified antimicrobial resistance as one of the most significant global health threats, emphasizing the need for continuous surveillance of resistant bacteria in animal production systems and their associated waste streams. Therefore, investigating the antimicrobial susceptibility profiles of bacterial isolates recovered from poultry wastewater is essential for understanding potential health risks and supporting evidence-based strategies to mitigate the environmental dissemination of antimicrobial resistance (Larsson et al. 2022; Mancuso et al. 2021). Despite the growing body of research on microbial contamination associated with poultry production, most studies have focused on commercial poultry farms, poultry litter, or slaughterhouse effluents, whereas limited attention has been given to wastewater generated from retail poultry shops, particularly in developing countries (Gržinić et al. 2023; Hedman et al. 2020). However, information on the bacterial contamination and antimicrobial susceptibility profiles of wastewater generated by retail poultry shops in Iraq, particularly in Samawah City, remains limited. The absence of such data limits the assessment of environmental contamination and public health risks associated with the improper disposal of untreated poultry wastewater (Al-Mohammed et al. 2021; Al-Obaidi et al. 2022). Therefore, generating baseline data on the bacterial diversity and antimicrobial susceptibility of isolates recovered from poultry shop wastewater is essential to support environmental

monitoring, improve wastewater management practices, and provide scientific evidence for public health protection and policy development (Gržinić et al. 2023; Larsson et al. 2022). The present study aimed to isolate and characterize bacterial isolates from wastewater discharged by poultry shops in Samawah City, Iraq, and to evaluate their antimicrobial susceptibility patterns.

2.0 Material and Methods

2.1 Study Area

This study was conducted in Samawah City, Al-Muthanna Governorate, southern Iraq, where numerous poultry shops operate to meet the increasing demand for fresh poultry products. Wastewater generated from these shops is commonly discharged into municipal drainage systems or surrounding environments with limited or no prior treatment, raising concerns regarding environmental contamination and the dissemination of pathogenic microorganisms. The study area was selected because of the high density of poultry shops and the lack of published information on the microbiological quality of poultry shop wastewater in the region. Wastewater samples were collected from selected poultry shops distributed across different locations in Samawah City to provide baseline information on bacterial contamination and antimicrobial susceptibility patterns in poultry shop wastewater.

2.2 Wastewater Sample Collection

Wastewater samples were collected from 10 selected poultry shops located in different areas of Samawah City, Al-Muthanna Governorate, Iraq, during April 2026. One wastewater sample was collected from the discharge point of each poultry shop immediately after poultry processing activities, using sterile 100-mL polypropylene bottles. The samples were labeled, placed in insulated ice boxes at 4 ± 2 °C, and transported to the Microbiology Laboratory within 2–4 h of collection. Upon arrival, samples were processed immediately for bacteriological analysis to minimize changes in their microbial composition and prevent external contamination.

2.3 Isolation and Identification of Bacterial Isolates

Wastewater samples were thoroughly mixed before bacteriological analysis and serially diluted in sterile physiological saline to facilitate the recovery of well-isolated colonies. Appropriate aliquots of 0.1 mL were inoculated onto Blood agar, MacConkey agar, Mannitol Salt Agar, UTI Chromogenic Agar (UTIC) to facilitate the recovery and presumptive differentiation of different bacterial groups. All culture media were prepared according to the manufacturers' instructions and sterilized by autoclaving at 121 °C for 15 min before use. The inoculated plates were incubated aerobically at 37 ± 1 °C for 24–48 h. Following incubation, colonies were examined for their morphology, including size, shape, color, margin, elevation, and hemolytic activity where applicable (Lin et al. 2023; Whitman et al. 2015). Representative bacterial growth on the different culture media is shown in Figure 1. Each morphologically distinct colony type recovered from the culture media was purified and considered a separate bacterial isolate for identification and subsequent antimicrobial susceptibility testing. Preliminary identification was performed using Gram staining and microscopic examination, followed by biochemical tests, including catalase, oxidase, coagulase, indole, methyl red, Voges–Proskauer, citrate utilization, urease, triple sugar iron, and motility tests. Bacterial identification was performed presumptively based on the combined cultural, microscopic,

and biochemical characteristics according to standard microbiological procedures and Bergey's Manual of Systematic Bacteriology. Bergey's Manual of Systematic Bacteriology (Brenner et al. 2005).

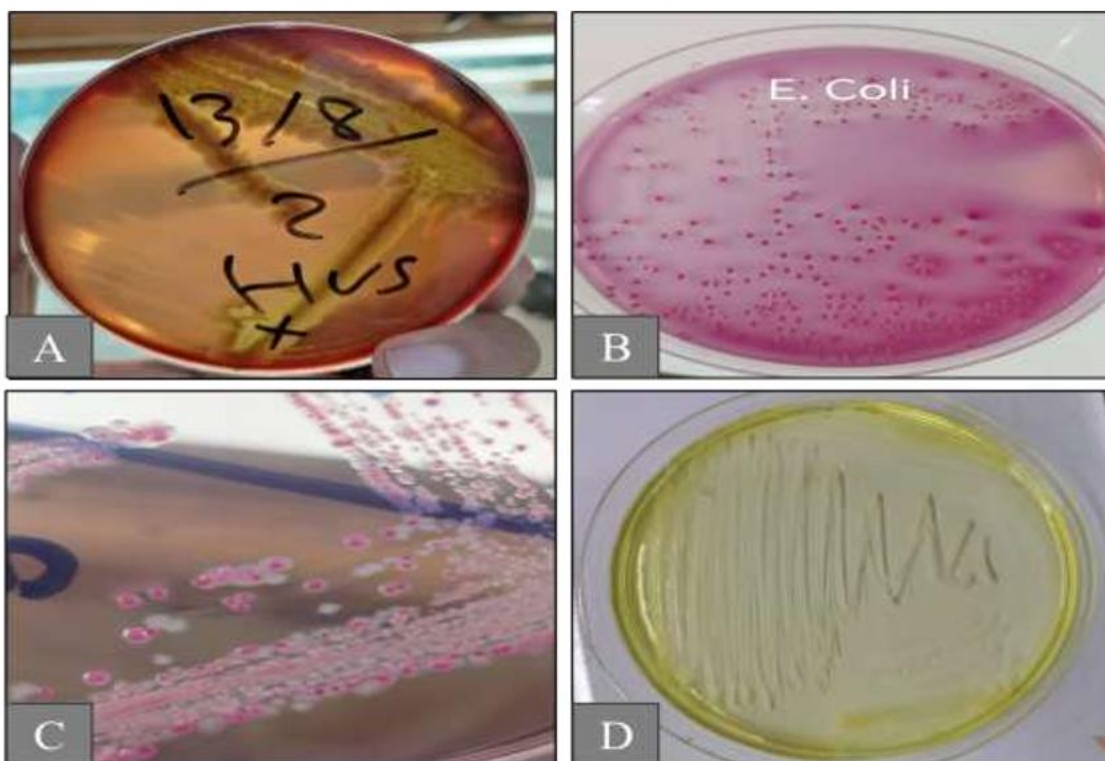


Figure 1. Representative bacterial growth on different culture media; **A).** *Streptococcus* on blood agar **B).** *E. coli* in the middle of the MacConkey; **C).** *Enterobacter spp.* on MacConkey agar; **D).** *Staphylococcus aureus* on Mannitol Salt Agar.

2.4 Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar according to the Clinical and Laboratory Standards Institute (CLSI. 2024) guidelines. Fresh bacterial colonies were suspended in sterile normal saline, and the turbidity of each suspension was adjusted to a 0.5 McFarland standard (approximately 1.5×10^8 CFU/mL). The standardized bacterial suspension was evenly inoculated onto the surface of Mueller–Hinton agar using a sterile cotton swab. Antimicrobial disks were aseptically placed on the inoculated agar, and the disk potencies and manufacturers were recorded for each antimicrobial agent. The plates were incubated aerobically at 37 ± 1 °C for 18–24 h. 37 ± 1 °C for 18–24 h. The diameters of the inhibition zones were measured in millimeters, and the isolates were categorized as susceptible, intermediate, or resistant according to the CLSI (2024) interpretive criteria **Figure 2**. The antimicrobial agents tested included Netilmicin, Ofloxacin, Meropenem, Chloramphenicol, Ciprofloxacin, Levofloxacin, Tobramycin, Norfloxacin, Amikacin, Cefoxitin, Nalidixic acid, Gentamicin, Cefuroxime, Tetracycline, Azithromycin, Clindamycin, Trimethoprim, Erythromycin, Ceftriaxone, Ampicillin, Amoxicillin/Clavulanic acid, Aztreonam, and Linezolid. For each bacterial group, resistance percentages were calculated based on the number of resistant isolates relative to the number of isolates tested for the corresponding antimicrobial agent (CLSI. 2024; Lin et al. 2023).

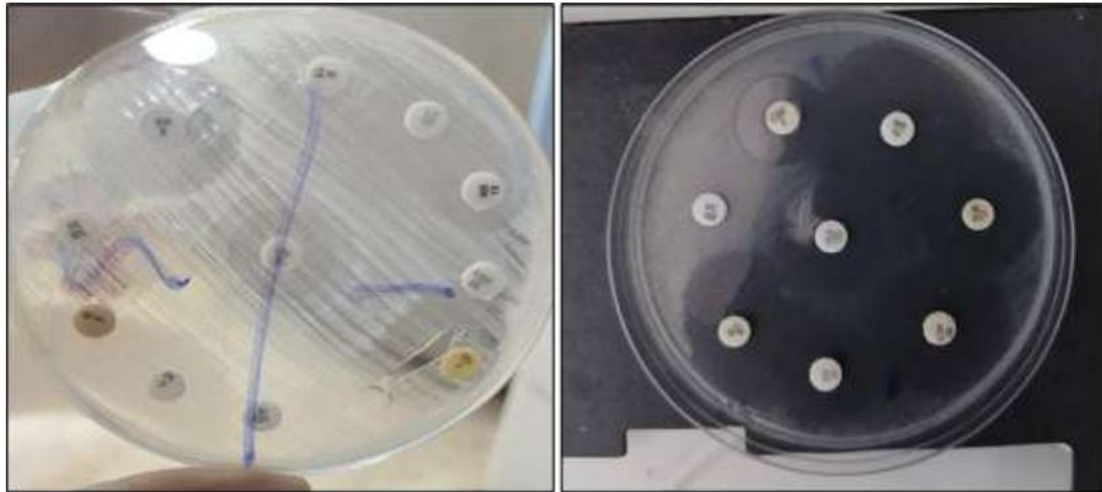


Figure 2. Representative antimicrobial susceptibility testing by the Kirby–Bauer disk diffusion method.

3.1 Results

3.1.1 Distribution of Bacterial Isolates in Poultry Shop Wastewater

Microbiological analysis of the collected wastewater samples revealed the presence of several bacterial groups, including potentially pathogenic and opportunistic organisms. A total of 46 bacterial isolates representing six bacterial groups were recovered from the 10 poultry wastewater samples. *Escherichia coli* and *Enterobacter* spp. were the most frequently recovered bacterial groups, each accounting for 21.74% (10/46; 95% CI: 12.26–35.57%) of the total isolates. This was followed by *Micrococcus* spp. (19.57%; 9/46; 95% CI: 10.65–33.17%), *Staphylococcus epidermidis* (17.39%; 8/46; 95% CI: 9.09–30.72%), and *Staphylococcus aureus* (15.22%; 7/46; 95% CI: 7.57–28.22%). *Streptococcus* spp. showed the lowest frequency, accounting for 4.35% (2/46; 95% CI: 1.20–14.53%) of the recovered isolates (**Table 1**). The distribution of bacterial species indicates that poultry shop wastewater harbors a diverse bacterial community with potential environmental and public health significance.

Table 1. Distribution and percentage of bacterial isolates recovered from poultry shop wastewater.

Bacteria species	Isolation number	percentage %	95% Confidence Interval (%)
<i>Escherichia coli</i>	10	21.74	12.26–35.57
<i>Micrococcus</i> spp.	9	19.57	10.65–33.17
<i>Staphylococcus aureus</i>	7	15.22	7.57–28.22
<i>Staphylococcus epidermidis</i>	8	17.37	9.09–30.72
<i>Streptococcus</i> spp.	2	4.35	1.20–14.53
<i>Enterobacter</i> spp.	10	21.74	12.26–35.57
Total	46	100	

Note: Values are presented as number (n) and percentage (%). The 95% confidence intervals for proportions were calculated using the **Wilson score method**.

3.1.2 Morphological and Biochemical Characteristics of the Isolated Bacteria

The bacterial isolates recovered from poultry shop wastewater were identified based on their colony morphology, Gram-staining reaction, microscopic characteristics, and biochemical profiles. The isolates exhibited distinct morphological and biochemical characteristics that supported their presumptive differentiation and identification according to standard microbiological procedures. The combined use of conventional culture techniques and biochemical assays supported the presumptive identification of Gram-positive and Gram-negative bacterial groups recovered from the wastewater samples.

3.1.3 Antimicrobial Susceptibility Profiles of the Bacterial Isolates

The antimicrobial resistance profiles varied considerably among the bacterial groups and antimicrobial agents tested (Table 2). *Enterobacter* spp. exhibited resistance to several antimicrobial agents, with 100% resistance observed to amikacin, amoxicillin/clavulanic acid, ampicillin, aztreonam, chloramphenicol, ciprofloxacin, ceftiofur, nalidixic acid, norfloxacin, and the antimicrobial designated as F in the dataset. In contrast, no resistance was observed to gentamicin, levofloxacin, meropenem, netilmicin, ofloxacin, tetracycline, or tobramycin.

Escherichia coli showed 100% resistance to amoxicillin/clavulanic acid, ampicillin, aztreonam, ceftiofur, and tetracycline, while no resistance was observed to several other tested agents. Among the Gram-positive bacterial groups, *S. aureus* showed 100% resistance to tetracycline, azithromycin, and clindamycin, whereas resistance to ciprofloxacin and erythromycin was 42%. *S. epidermidis* showed 100% resistance to tetracycline, azithromycin, and clindamycin and 50% resistance to ciprofloxacin and erythromycin. *Micrococcus* spp. showed complete resistance to azithromycin, clindamycin, and trimethoprim, whereas *Streptococcus* spp. showed complete resistance to azithromycin, clindamycin, and erythromycin. Overall, the findings demonstrate heterogeneous antimicrobial resistance patterns among the recovered bacterial groups.

Table 2. Antimicrobial resistance profile of bacterial isolates recovered from poultry shop wastewater.

Antibiotic	<i>E. coli</i>	<i>Micrococcus spp.</i>	<i>S. aureus</i>	<i>S. epidermidis</i>	<i>Streptococcus spp.</i>	<i>Enterobacter spp.</i>
AK	0%	—	—	—	—	100%
AMC	100%	—	—	—	—	100%
AMP	100%	—	—	—	—	100%
ATM	100%	—	—	—	—	100%
C	0%	0%	0%	0%	0%	100%
CIP	0%	0%	42%	50%	0%	100%
CN	0%	0%	0%	0%	0%	0%
CRO	0%	—	—	—	—	—
F	0%	0%	0%	0%	0%	100%
FOX	100%	—	—	—	—	100%
LE	0%	0%	0%	0%	0%	0%
MEM	0%	—	—	—	—	0%
NA	0%	—	—	—	—	100%

NET	0%	—	—	—	—	0%
NOR	0%	—	—	—	—	100%
OF	0%	0%	0%	0%	0%	0%
TE	100%	0%	100%	100%	—	0%
TOB	0%	—	—	—	—	0%
AZM	—	100%	100%	100%	100%	—
DA	—	100%	100%	100%	100%	—
E	—	0%	42%	50%	100%	—
IPM	—	0%	0%	0%	0%	—
LZ	—	0%	0%	0%	0%	—
TR	—	100%	0%	0%	0%	—
VA	—	0%	0%	0%	0%	—
P	—	—	—	—	0%	—

Note: Values represent the percentage of resistant isolates. — = antimicrobial agent not tested for the corresponding bacterial group.

3.1.4. Breadth of Antimicrobial Resistance among Bacterial Groups

The breadth of antimicrobial resistance varied among the bacterial groups recovered from poultry shop wastewater (**Table 3**). Enterobacter spp. showed the broadest resistance pattern, with resistance detected against 10 of the 17 antimicrobial agents tested (58.82%). Staphylococcus aureus and Staphylococcus epidermidis each showed resistance to 5 of 14 tested antimicrobial agents (35.71%). Escherichia coli exhibited resistance to 5 of 18 tested antimicrobial agents (27.78%), while Streptococcus spp. showed resistance to 3 of 13 tested agents (23.08%). Micrococcus spp. showed resistance to 3 of 14 tested antimicrobial agents (21.43%). Overall, these findings demonstrate variation in the breadth of phenotypic antimicrobial resistance among the bacterial groups. The proportions presented in Table 3 represent the percentage of tested antimicrobial agents for which resistance was detected and should not be interpreted as the prevalence of resistant isolates.

Table 3. Breadth of antimicrobial resistance among bacterial groups isolated from poultry shop wastewater.

Bacterial group	No. of antimicrobials tested	Antimicrobials showing resistance, n	Proportion of tested antimicrobials showing resistance (%)
<i>Escherichia coli</i>	18	5	27.78
<i>Micrococcus spp.</i>	14	3	21.43
<i>Staphylococcus aureus</i>	14	5	35.71
<i>Staphylococcus epidermidis</i>	14	5	35.71
<i>Streptococcus spp.</i>	13	3	23.08
<i>Enterobacter spp.</i>	17	10	58.82

3.1.5 Multidrug Resistance Patterns

Multidrug resistance (MDR), defined in this study as resistance to three or more antimicrobial classes, was detected in 44 of the 46 bacterial isolates, corresponding to an overall MDR prevalence of **95.65%**

(95% CI: 85.47–98.80%). Only two isolates (4.35%) did not meet the MDR criterion. As illustrated in **Figure 3**, MDR was therefore highly prevalent among the bacterial isolates recovered from poultry shop wastewater.

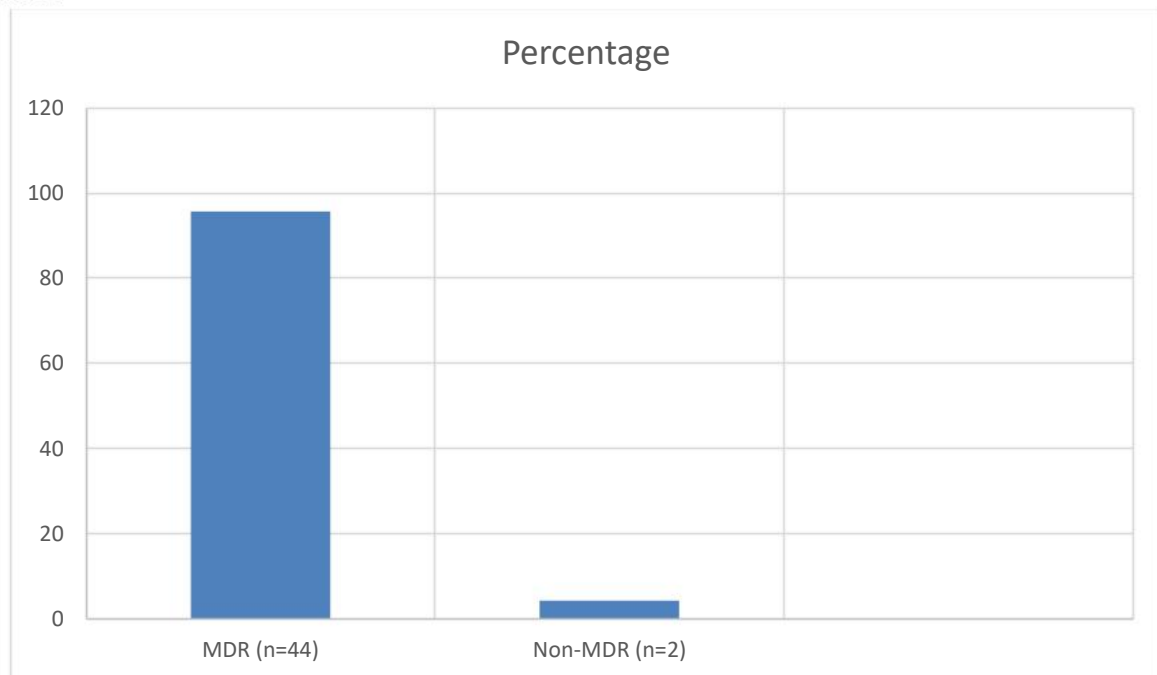


Figure 3. Prevalence of multidrug-resistant (MDR) bacterial isolates recovered from poultry shop wastewater.

3.2. Discussion

3.2.1 Occurrence of Potentially Pathogenic and Opportunistic Bacteria in Poultry Shop Wastewater

The microbiological analysis of poultry shop wastewater revealed the presence of several pathogenic and opportunistic bacterial species, including *Escherichia coli*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus spp.*, *Enterobacter spp.*, and *Micrococcus spp.* The occurrence of these microorganisms reflects the microbiological complexity of poultry wastewater and indicates contamination originating from poultry feces, intestinal contents, blood, feathers, processing equipment, and handling practices during slaughtering and processing operations (Gržinić et al. 2023; Hedman et al. 2020). Among the recovered isolates, *E. coli* is widely recognized as an indicator of fecal contamination, suggesting that poultry wastewater may contain untreated biological waste capable of introducing enteric pathogens into the environment (Ugbo et al. 2023). Similarly, the isolation of *S. aureus* highlights potential contamination from poultry carcasses, processing equipment, and workers, whereas *S. epidermidis* likely reflects contamination associated with skin microbiota and environmental surfaces (Machado Da Silva et al. 2026; Tong et al. 2015). Although *Micrococcus spp.* are generally considered environmental microorganisms, their detection demonstrates the diverse bacterial composition of poultry wastewater and may also indicate inadequate hygienic conditions during processing (Kumar et al. 2020; Saha et al. 2020). The recovery of *Enterobacter spp.* and *Streptococcus spp.* further supports the view that poultry wastewater can harbor bacteria originating from both animal and environmental sources. These genera have been frequently reported in poultry production systems and wastewater environments and are recognized for their ability to survive under favorable environmental conditions, thereby contributing to

the persistence and dissemination of microbial contaminants (Krzemiński et al. 2020; Larsson et al. 2022). Overall, the diversity of bacterial species identified in the present study demonstrates that poultry shop wastewater represents a potential source of environmental microbial contamination. Without appropriate collection, treatment, and disposal practices, these microorganisms may be released into surrounding drainage systems and water bodies, increasing opportunities for environmental dissemination and potential human exposure.

3.2.2. Antimicrobial Resistance Patterns of the Isolated Bacteria

The antimicrobial susceptibility profiles of the bacterial isolates recovered from poultry shop wastewater revealed varying levels of resistance to the antibiotics tested, indicating the presence of antimicrobial-resistant bacteria within the wastewater environment. The occurrence of resistant isolates is of considerable concern because poultry wastewater can act as an environmental reservoir that facilitates the persistence and dissemination of antimicrobial-resistant bacteria and potentially contributes to the environmental dissemination of antimicrobial resistance. The discharge of untreated wastewater into drainage channels or surface waters may therefore contribute to the environmental spread of antimicrobial resistance, increasing the likelihood of human and animal exposure (Krzemiński et al. 2020; Larsson et al. 2022; Ugbo et al. 2023). The emergence of antimicrobial resistance in poultry-associated bacteria has been closely linked to the extensive and, in some cases, inappropriate use of antibiotics for disease treatment, prevention, and growth promotion in poultry production. Such practices create selective pressure that favors the survival and proliferation of resistant bacterial populations (Fu et al. 2022). However, the present study assessed phenotypic antimicrobial resistance and did not investigate the specific resistance genes or genetic mechanisms responsible for the observed resistance patterns. These bacteria may subsequently transfer resistance determinants to other microorganisms through horizontal gene transfer, thereby accelerating the spread of antimicrobial resistance within environmental microbial communities (Lin et al. 2021). The findings of the present study are consistent with reports from different regions of the world demonstrating that poultry production systems and their associated wastewater represent important reservoirs of antimicrobial-resistant bacteria. Environmental contamination with resistant microorganisms has become a major public health concern because it reduces the effectiveness of antimicrobial therapy and increases the risk of difficult-to-treat infections (Gržinić et al. 2023; Hedman et al. 2020). The World Health Organization has identified antimicrobial resistance as one of the leading global health threats, emphasizing the urgent need for integrated surveillance and responsible antimicrobial stewardship across the human, animal, and environmental sectors (WHO. 2023). From a One Health perspective, poultry shop wastewater represents a critical interface linking animal production, environmental contamination, and human health. Inadequate treatment and disposal of wastewater may facilitate the dissemination of resistant bacteria into water resources, agricultural soils, and food production systems, thereby increasing opportunities for exposure and transmission. Consequently, strengthening wastewater management practices, implementing routine microbiological surveillance, and promoting the prudent use of antimicrobials in poultry production are essential measures for limiting the environmental spread of antimicrobial resistance and protecting public health.

3.2.3 Environmental and Public Health Implications

The findings of the present study demonstrate that poultry shop wastewater constitutes a potential environmental reservoir of potentially pathogenic and antimicrobial-resistant. When discharged without appropriate treatment, contaminated wastewater may introduce these microorganisms into municipal drainage systems, surface water bodies, and surrounding soils, thereby increasing the likelihood of environmental dissemination. Such contamination may alter the microbial quality of receiving environments and facilitate the persistence of bacterial contaminants beyond the original source (Gržinić et al. 2023). From a public health perspective, untreated poultry wastewater may increase the risk of human exposure through direct contact with contaminated wastewater, occupational activities, or indirect exposure to contaminated water resources (Alam et al. 2019). Poultry workers, waste handlers, and nearby residents may therefore be at greater risk of encountering potentially pathogenic bacteria, particularly in areas where wastewater management and sanitation infrastructure are inadequate. In addition, the environmental dissemination of antimicrobial-resistant bacteria may complicate the treatment of bacterial infections and contribute to the global burden of antimicrobial resistance (Himu et al. 2023). These findings support the implementation of effective wastewater treatment systems, routine microbiological surveillance, and antimicrobial stewardship programs within the poultry production sector (Alhassan et al. 2025). Furthermore, strengthening collaboration among environmental, veterinary, and public health authorities within a One Health framework is essential for reducing the environmental dissemination of bacterial contamination and antimicrobial resistance. Such integrated approaches will contribute to improved environmental sustainability, enhanced public health protection, and evidence-based policy development for poultry waste management in Iraq and other developing countries (Larsson et al. 2022; WHO. 2023).

4.0 Conclusion

This study demonstrated that wastewater generated by poultry shops in Samawah City, Iraq, harbors a diverse community of potentially pathogenic and opportunistic bacteria, including *Escherichia coli*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus spp.*, *Enterobacter spp.*, and *Micrococcus spp.* The occurrence of these microorganisms indicates that poultry shop wastewater may serve as a significant source of microbial contamination and poses potential environmental and public health risks when discharged without appropriate treatment. The antimicrobial susceptibility results further revealed isolates resistant to commonly used antibiotics, with 44 of the 46 isolates (95.65%) meeting the study definition of multidrug resistance. This finding highlights the substantial burden of phenotypic antimicrobial resistance among the recovered bacterial isolates and emphasizes the potential role of poultry wastewater as a reservoir for antimicrobial-resistant bacteria. These findings reinforce the importance of adopting a One Health approach that recognizes the interconnectedness of environmental, animal, and human health in addressing the spread of potentially pathogenic and antimicrobial-resistant microorganisms. The findings of this study underscore the need to strengthen wastewater management practices in poultry shops through effective collection, treatment, and disposal systems. Routine microbiological monitoring and responsible antimicrobial stewardship should also be integrated into poultry production to minimize environmental contamination and reduce the dissemination of antimicrobial resistance. Future studies should employ molecular techniques to characterize bacterial virulence factors and antimicrobial resistance genes, investigate seasonal variations in wastewater microbiota, and evaluate the effectiveness of wastewater treatment strategies in reducing microbial

contamination. Such investigations will provide valuable evidence to support sustainable poultry waste management and protect environmental and public health.

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