Journal of Biological Research

Bollettino della Società Italiana di Biologia Sperimentale

eISSN 2284-0230 - pISSN 1826-883

https://www.pagepressjournals.org/index.php/jbr/index

J Biol Res 2025 [Online ahead of print]

To cite this Article:

Anwar KA, Homar SQ, Mustafa AM, et al. **Growing patterns of multi-drug resistance in wound infections: a retrospective cross-sectional study from northern Iraq.** *J Biol Res* doi: 10.4081/jbr.2025.13807

Growing patterns of multi-drug resistance in wound infections: a retrospective cross-sectional study from northern Iraq

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Key words: multidrug resistance, wound culture, pathogenic bacteria, risk factor.

Conflicts of interest: the author(s) have no conflicts of interest to disclose.

Funding: None.

Contributions: KAA, SQH and FHK were significant contributors to the conception of the study and the literature search for related studies. HSA, WAH, BAA, RQS, HAY and SMA were involved in the literature review, study's design, critical revision of the manuscript, and participation in data collection. AMM, FHK, and DAH were involved in the literature review,

study design, and manuscript writing. SHA, DMH, and AKR were involved in Literature review, final approval of the manuscript, and processing of the tables. FHK and AMM confirm the authenticity of all the raw data. All authors approved the final version of the manuscript.

Ethics approval: the study's ethical approval was obtained from the ethical committee of Kscien organization (No. 28, approved on 01/12/2022).

Patient consent: written informed consent for both participation in the study and publication of the results was obtained from the patients or their guardians.

Availability of data and materials: the datasets generated and analyzed during the current study are available from the corresponding author upon reasonable request.

Abstract

Despite growing concerns over wound infections, there are limited nationwide studies exploring the distribution of pathogens and their resistance patterns. Considering regional variations in resistance, this single-center study conducted in Iraq aims to investigate the distribution of pathogenic bacteria and their antimicrobial resistance in wound infections. This retrospective cross-sectional study analyzed wound culture data from inpatients in a single center located in Iraq between January and December 2023. Wound specimens were tested for microbial identification and antimicrobial susceptibility. Patient data, including clinical and laboratory information, were obtained from electronic medical records. Patients were classified into Multidrug Resistance (MDR) and non-MDR groups based on susceptibility results. A p-value of

<0.05 was considered statistically significant. A total of 195 samples were collected from 145 patients, with 178 (91.2%) showing microbial growth. Among these, 97 (54.5%) were single infections, and 81 (45.5%) were mixed infections. Among Gram-positive isolates, *Staphylococcus aureus* was the most common isolate present in 29 (16.3%) samples. For Gram-negative isolates, *Escherichia coli* was identified in 35 (19.7%) samples, and *Pseudomonas aeruginosa* in 21 (11.8%) samples. Gram-positive isolates showed high resistance rates, particularly to cefixime 12 (92.3%). Among Gram-negative isolates, resistance was highest to rifampin and clindamycin, with 100% resistance noted. A total of 149 (83.7%) isolates were MDR. This study highlights the growing issue of antibiotic resistance, especially in *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae*. The increasing prevalence of MDR necessitates stronger infection control, enhanced antibiotic stewardship, and personalized treatment strategies to improve patient outcomes in healthcare settings across Iraq.

Introduction

Wound infections represent a multifaceted pathological condition that can present as either a rapidly developing acute issue or a long-standing chronic problem. These infections pose significant health risks and, if left untreated, can lead to extended treatment periods.[1] Wounds are categorized in various ways, including by their origin, appearance, and healing stages. Common types include diabetic foot ulcers, pressure ulcers, surgical site infections, and burn injuries.[2,3] Trauma, whether accidental or intentional, is the primary cause of most wounds, while hospital-acquired wounds, such as those resulting from surgical procedures or medical devices, represent a distinct group. Furthermore, pressure ulcers, often resulting from prolonged immobility, present additional concerns.[4]

Common bacterial species associated with wound infections include *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Acinetobacter baumannii*. The distribution

of pathogens is determined by various factors, including geographic location and the underlying causes of wounds.[5,6] Various antibiotics, such as carbapenems, aminoglycosides, colistin, and β-lactams, are used to treat these infections. However, prolonged use of antibiotics can lead to complications ranging from mild issues like diarrhea to more severe consequences, including antibiotic resistance and potentially fatal leukopenia.[7] Antimicrobial resistance is a significant global health challenge, leading to higher rates of morbidity, mortality, and healthcare expenses. In 2019, these infections were directly linked to 1.27 million deaths worldwide, with nearly 5 million deaths associated with resistance overall. By 2050, this number could escalate to 10 million annually, surpassing cancer-related mortality. If not addressed promptly and appropriately, these infections can progress to life-threatening conditions, particularly in developing countries.[8] The rise of Multidrug-Resistant (MDR) bacteria poses an additional challenge to wound management.[1] The 2024 update of the World Health Organization's bacterial priority pathogens list underscores the growing global health threat posed by MDR organisms, especially carbapenem-resistant Enterobacterales, which are frequently responsible for wound infections.[9]

Despite the growing concern over cutaneous wound infections, nationwide studies investigating the distribution and antimicrobial susceptibility of associated pathogens remain limited.[10] The local pathogen spectrum and antimicrobial resistance patterns play a critical role in optimizing antibiotic use and infection control, given the regional variations in resistance. Although previous studies conducted in Iraq have examined aspects of wound infections and antimicrobial resistance, data on the distribution of pathogenic bacteria and their resistance patterns remain limited, particularly within the context of the current healthcare setting. Therefore, this single-center study aims to contribute additional, up-to-date data on the microbial spectrum and MDR patterns in wound infections in Iraq, thereby complementing and expanding the existing regional literature.[11]

Materials and Methods

Sample collection and data recording

This retrospective cross-sectional study utilized routine data from wound cultures collected from inpatients at Smart Health Tower, Sulaymaniyah, Iraq, between January and December 2023. Wound specimens were collected from various types of wounds for microbiological analysis. Each specimen underwent bacterial culture, followed by microbial identification and antimicrobial susceptibility testing to determine the infecting microorganisms and their resistance patterns. Patient data were systematically recorded, including both clinical and laboratory information, which was accessed from the Smart Health Tower electronic medical record system. The system is continuously updated in real time by healthcare professionals following standardized protocols to ensure the accuracy of patient records. Clinical data included anonymized patient identifiers, gender, age, department of care, comorbidities, medical history, and primary diagnosis. Laboratory data consisted of the bacterial culture results and antibiotic resistance patterns. Ethical approval for this study was granted by the Kscien Organization, in accordance with their established ethical guidelines for research involving human subjects. The research was conducted in compliance with all relevant ethical standards, ensuring the protection of patient confidentiality and adherence to protocols for handling sensitive clinical and laboratory data.

Inclusion and exclusion criteria

The inclusion criteria were: i) patients diagnosed with all types of wound infections; ii) positive microbial cultures from wound specimens; and iii) availability of complete clinical records, defined as documentation of demographic data (age and gender), wound type and location, culture and antibiotic susceptibility results, and classification of infection origin (community-acquired or hospital-acquired).

The exclusion criteria included: i) duplicate bacterial strains isolated from the same patient within the study period; ii) culture results deemed contaminated or inconclusive; and iii) patients with incomplete documentation in any of the above-mentioned data elements. This strict data requirement was applied to ensure consistency and minimize selection bias in the analysis.

Patient classification

Patients were categorized based on the results of microbial cultures and antimicrobial susceptibility testing into two groups: the MDR group, which included patients with infections caused by MDR microorganisms, and non-MDR group, which included patients without MDR infections. If both resistant and susceptible bacteria were isolated from the same patient, the patient was classified in the MDR group.

Bacterial culture

Samples were cultured following standard microbiological protocols. Wounds were cleansed using sterile saline before gently swabbing the wound secretions with a sterile cotton swab, which was then transferred to a sterile container. The specimens were promptly transported to the microbiology laboratory. In the laboratory, the samples were inoculated onto blood agar plates, MacConkey agar plates, and nalidixic acid cetrimide agar plates. All plates were incubated aerobically and anaerobically at 36°C for 18-24 hours, after which colonies were examined for size and morphology. Single colonies were selected based on their appearance and transferred onto new agar plates for isolation and purification.

Bacterial identification and antimicrobial susceptibility testing

The isolated bacterial strains were identified and tested for antimicrobial susceptibility using both conventional microbiological techniques and standardized protocols. Identification was performed using the conventional method and the BD Phoenix™ 50 system.[12] Antimicrobial susceptibility testing was carried out using the Kirby-Bauer disk diffusion method and BD Phoenix™ 50 system. The antibiotics tested include amikacin, gentamicin, ticarcillin/clavulanate, ampicillin-sulbactam, ampicillin, amoxicillin-clavulanate, piperacillin-tazobactam, cefuroxime, ceftriaxone, cefepime, cefpodoxime, cefixime, cefotaxime, azithromycin, erythromycin, ciprofloxacin, levofloxacin, trimethoprim-sulfamethoxazole,

clindamycin, tetracycline, doxycycline, tigecycline, imipenem, meropenem, nitrofurantoin, and rifampin. The results of antimicrobial susceptibility tests were interpreted in accordance with the guidelines from the Clinical and Laboratory Standards Institute.[13] Antibiotic susceptibility was categorized as susceptible, intermediate, or resistant.

Statistical analysis

The MDR was defined as resistance to at least one antimicrobial agent from three or more different classes.[14] Statistical analyses were performed using IBM Statistical Package for the Social Sciences (SPSS) statistics 26.0. Patient demographic and clinical data were extracted from the system, and potential risk factors were identified. Normality of continuous data was tested using the Shapiro-Wilk test. For normally distributed data, means and standard deviations were calculated, and intergroup comparisons were made using independent t-tests. Non-normally distributed data were expressed as medians with quartile ranges and analyzed using the Mann-Whitney U test. Categorical variables were compared using chi-square tests, Fisher's exact test. Statistical significance was considered at a p-value of <0.05.

Results

Sample collection and microbial growth

A total of 195 wound culture samples were collected from 145 patients. Of these, microbial growth was detected in 178 (91.3%) samples, while 17 (8.7%) samples showed no growth. Among the positive cultures, 97 (54.5%) cases were caused by a single bacterial strain, whereas 81 (45.5%) cases involved mixed bacterial infections. Furthermore, 66 (51.6%) isolates were Gram-negative and 62 (48.4%) isolates were Gram-positive.

Distribution of single and mixed infections

Gender distribution differed significantly between single and mixed infections, with single infections observed in 40 (49.4%) women, and mixed infections in 21 (44.7%) women ($p < 0.001$). Hypertension was reported in 18 (22.2%) cases of single infection and 8 (17.0%) cases of mixed infection ($p < 0.001$). The median length of hospital stay was 4 days (Quartile range - QR: 1-13) for single infections, 3 days (QR: 1-7) for mixed infections, with no significant difference between groups ($p = 0.644$) (Table 1). Among the single infections, surgical site wounds accounted for the highest proportion 35 (43.2%), followed by other wound types 33 (40.7%). In cases of mixed infections, surgical site wounds accounted for 18 (38.3%) cases (Figure 1).

Prevalence of specific bacterial isolates

Among the 178 identified isolates, *Staphylococcus aureus* was the most common Gram-positive bacterium, detected in 29 (16.3%) samples, followed by *Staphylococcus epidermidis* in 16 (9.0%) samples, and *Enterococcus faecalis* in 15 (8.4%) samples. Among Gram-negative bacteria, *Escherichia coli* was the predominant isolate, identified in 35 (19.7%) samples, followed by *Pseudomonas aeruginosa*, found in 21 (11.8%) samples (Table 2).

Antibiotic sensitivity and resistance in gram-positive bacteria

Among the tested Gram-positive isolates, 54 (98.2%) were sensitive to tigecycline, 49 (94.2%) to nitrofurantoin, 48 (85.7%) to rifampin, and 17 (81.0%) to imipenem. However, high resistance rates were noted, with 12 (92.3%) resistant to cefixime, 19 (79.2%) to amoxicillin-clavulanate, 7 (77.8%) to azithromycin, and 51 (75.0%) to erythromycin. Among these isolates, *Enterococcus faecalis* demonstrated the highest resistance rate (62.0%), followed by *Staphylococcus haemolyticus* (54.4%). In wound-specific patterns, *Enterococcus faecalis* showed the highest resistance at surgical sites (78%) and diabetic foot wounds (66.6%), while *Staphylococcus aureus* resistance peaked at 49.5% in diabetic foot wounds (Figure 2). Overall, Gram-positive bacterial isolates exhibited a total resistance rate of 47.9% (Table 3).

Antibiotic sensitivity and resistance in gram-negative bacteria

Among the Gram-negative isolates, the highest sensitivities were observed to meropenem (59, 79.7%), amikacin (56, 76.7%), piperacillin-tazobactam (55, 75.3%), and imipenem (54, 73.0%). In contrast, all isolates (100%) were resistant to rifampin, clindamycin, erythromycin, azithromycin, and cefpodoxime. Among the Gram-negative bacteria, *Klebsiella pneumoniae* exhibited the highest resistance frequency, accounting for 122 (67.0%) isolates, followed by *Pseudomonas aeruginosa* with 212 (65.4%) isolates. In wound-specific patterns, *Pseudomonas aeruginosa* showed the highest resistance of 82.4% in ear swabs and 69.6% in surgical site infections, while *Klebsiella pneumoniae* resistance peaked at 75.6% in other wound types (Figure 3). The overall resistance rate among Gram-negative isolates was 58.8% (Table 4).

Multidrug-resistant isolates

A total of 149 (83.7%) isolates were identified as MDR. Among the 92 Gram-positive isolates, 72 (78.3%) were MDR, while 77 (89.5%) of the 86 Gram-negative isolates were MDR. Within the Gram-positive group, 13 (86.7%) of *Enterococcus faecalis* and 5 (83.3%) of *Staphylococcus haemolyticus* were MDR. Among the Gram-negative isolates, all *Morganella morganii* isolates (7, 100.0%) and 32 (91.4%) of *Escherichia coli* were classified as MDR (Table 5).

Risk factor for MDR infections

In this study, MDR was more common among men (59, 88.1%) compared to women (51, 83.6%), though the difference was not statistically significant (p=0.455). Patients with MDR infections had a significantly higher mean age (52.15±20.07 years) than those with non-MDR infections (37.89±23.03 years), p=0.007. Hospital-acquired infections were more frequently associated with MDR 54 (93.1%) compared to community-acquired infections 56 (80.0%), p=0.049 (Table 6).

Discussion

Wound infections represent a significant global health challenge, particularly in developing countries, where an aging population and complex surgeries have increased their prevalence. These infections lead to prolonged recovery, higher healthcare costs, and severe complications.[15] This study evaluated the prevalence of bacterial species isolated from various wound infections. Of the 145 patients included, 128 demonstrated positive bacterial growth, resulting in an isolation rate of 88.3%. This rate is higher than the 75% isolation rate reported in a cross-sectional study conducted in Ethiopia.[16] However, it closely aligns with the findings of Ahmed et al. in Upper Egypt and Mohammed et al. in Northwest Ethiopia, who reported isolation rates of 82.9% and 83.9%, respectively.[17,18] The observed difference may be attributed to variations in the etiology of bacterial infections and the sources of wound infections from which the samples were collected. Additionally, differences in infection control protocols and antibiotic prophylaxis practices could significantly influence bacterial growth. The fastidious nature of certain bacteria may also account for their inability to grow in some cases.[19] Furthermore, the prevalence of monobacterial infections (54.5%) in the current study was higher than that of polybacterial infections (45.5%). This observation is consistent with the findings of Hassan *et al.* in North Egypt, who reported a higher proportion of monobacterial isolates (60%) compared to mixed bacterial species (40%).[20] Similarly, Bessa *et al.* in Italy observed a predominance of monomicrobial infections, with a reported isolation rate of 72.8%.[21] In contrast, Ahmed *et al.* in Upper Egypt documented a higher prevalence of polybacterial infections (55%) relative to monobacterial infections (45%).[17] The presence of monotypic or polymicrobial bacterial communities is influenced by several factors, including the wound condition, microbial density, previous wound treatments, dermal moisture, and nutrient availability,[22] which may help explain the variations observed between the studies.

Regarding the distribution of Gram-negative and Gram-positive bacteria in wound infections, this study observed a nearly equal distribution of Gram-negative (51.6%) and Gram-positive (48.4%) bacterial isolates, consistent with the findings of Bessa *et al.*[21] However, other studies examining bacterial prevalence in wound infections reported a higher prevalence of Gram-negative bacteria compared to Gram-positive strains.[20,22] These discrepancies may be attributed to differences in the demographic profiles of study participants. The current study identified *Escherichia coli*, *Staphylococcus aureus* and *Pseudomonas aeruginosa* as the most prevalent

pathogens, which aligns with the findings of Puca *et al.*[23] who found these three bacteria as the most common pathogens in a study involving 239 patients with wound infections. Similarly, the findings of Wang *et al.*[1] corroborate this, as they identified *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Enterobacter cloacae*, and *Enterococcus faecalis* as the most commonly isolated bacterial species in cases of wound infections.

The high susceptibility of wounded skin to *Staphylococcus aureus* infections can be attributed to its extensive colonization on the skin's surface.[24] In this study, *Staphylococcus aureus, Staphylococcus epidermidis* and *Enterococcus faecalis* emerged as the predominant Gram-positive isolates responsible for wound infections. Among these, *Staphylococcus aureus* exhibited the highest prevalence, accounting for 16.3% of cases. This finding aligns with previous studies conducted by Hobbs et al. in New Zealand and Wang et al. in the Jiaxing Region of Eastern China, both of which reported *Staphylococcus aureus* as one of the most frequently isolated pathogens in wound infections.[1,25]

Escherichia coli, a natural inhabitant of the gastrointestinal tract, is frequently associated with skin infections, particularly in perirectal areas among individuals with incontinence. Furthermore, individuals undergoing gastrointestinal or lower spinal surgical procedures face an elevated risk of developing *Escherichia coli* related infections. Alongside *Escherichia coli*, *Pseudomonas* species are significant pathogens contributing to nosocomial infections, including pneumonia, urinary tract infections, and wound infections. These infections are notably prevalent in healthcare settings, especially among immunocompromised patients, such as those undergoing surgical interventions or receiving antibiotic therapy.[26] In this study, *Escherichia coli* and *Pseudomonas aeruginosa* were the most frequently isolated Gram-negative pathogens. This observation aligns with findings by Ahmed *et al.* who reported *Pseudomonas aeruginosa* as the second most common pathogen in wound infections among patients in Upper Egypt.[17] Similarly, a study in Nigeria documented a high prevalence of wound infections caused by bacterial pathogens, including *Staphylococcus aureus*, *Escherichia coli* , and *Pseudomonas aeruginosa*.[26] Consistent with these findings, Mama et al. found that *Escherichia coli* was the most prevalent Gram-negative species in their study, followed by *Proteus species*, with *Pseudomonas aeruginosa* showing the lowest prevalence.[27] The discrepancies observed among these studies

can likely be attributed to variations in sample size, environmental conditions, healthcare practices, and the health status of the studied populations.

Infection control following surgery remains a significant concern for healthcare professionals worldwide, particularly due to the growing issue of antimicrobial resistance. The inappropriate use of antibiotics in treating bacterial infections has significantly contributed to the rising prevalence of bacterial resistance.[28] In this study, among Gram-positive strains, β-lactam antibiotics exhibited notably high resistance rates. Specifically, cefixime demonstrated the highest resistance rate at 92.3% against Gram-positive isolates, followed by amoxicillin-clavulanate, with a resistance rate of 79.2%. These findings are in agreement with a study conducted in Upper Egypt, which reported similar high resistance rates to β-lactam antibiotics in Gram-positive isolates, ranging from 84.6% to 98.7%.[17] In contrast, the most effective antibiotics for Gram-positive isolates in the current study were tigecycline and nitrofurantoin, with resistance rates of only 1.8% and 5.8%, respectively. Tigecycline showed complete sensitivity against all isolates of *Staphylococcus aureus*, *Staphylococcus epidermidis*, *Streptococcus agalactiae*, and *Enterococcus faecalis*, with no resistant strains identified. These results are consistent with the findings of a study, which also found no resistance to tigecycline in *Staphylococcus aureus* and *Enterococcus faecalis* isolates.[1] In contrast, a cross-sectional study conducted in Bangladesh identified meropenem, gentamicin, and amikacin as the most effective antimicrobials against Gram-positive bacteria. The study also reported no resistance to meropenem in *Staphylococcus* spp. and *Staphylococcus aureus* isolates.[29] However, in the current study, the resistance rates for meropenem, gentamicin, and amikacin among Gram-positive isolates were 28.0%, 40.3%, and 66.7%, respectively.

In the current study, *Klebsiella pneumoniae* exhibited the highest resistance rate among Gram-negative bacteria, with a resistance of 67.0%, followed closely by *Pseudomonas aeruginosa* at 65.4%. β-lactam antibiotics showed significantly high resistance rates. All *Pseudomonas aeruginosa* isolates were resistant to a wide range of antibiotics, including ampicillin, amoxicillin-clavulanate, ceftriaxone, cefixime, cefotaxime, azithromycin, erythromycin, trimethoprim-sulfamethoxazole, clindamycin, tetracycline, doxycycline, tigecycline, nitrofurantoin, and rifampin. These findings are consistent with those by Ahmed *et al.*, who also observed high resistance rates among *Pseudomonas aeruginosa* isolates, ranging from 62.5% to

100% against β-lactam antibiotics.[17] In contrast, a study conducted in China by Wang *et al.* found that *Pseudomonas aeruginosa* exhibited relatively low resistance rates to several commonly used antibiotics, including levofloxacin (7.2%), ciprofloxacin (9.0%), cefepime (3.6%), imipenem (5.4%), and meropenem (3.6%), with none of the resistance rates exceeding 10%.[1] In the present study, however *Pseudomonas aeruginosa* showed moderate resistance to levofloxacin (47.6%), ciprofloxacin (42.9%), and cefepime (38.1%).

In the present study, *Klebsiella pneumoniae* demonstrated complete (100%) resistance to a broad range of β-lactam antibiotics, including ticarcillin/clavulanate, ampicillin-sulbactam, ampicillin, cefuroxime, ceftriaxone, cefepime, cefpodoxime, cefixime, and cefotaxime. These findings align with previous studies that have reported alarmingly high levels of β-lactam resistance among *Klebsiella* species.[30] Similarly, a regional review from Asia underscored the growing threat of multidrug-resistant *Klebsiella* spp., particularly in relation to β-lactam antibiotics.[31] Supporting this trend, a recent study conducted in Iraq involving 150 stool isolates from both healthy individuals and patients also demonstrated that *Klebsiella* spp. exhibited consistently higher resistance to β-lactam antibiotics, most notably to ampicillin-sulbactam and ceftriaxone, further emphasizing the widespread and escalating resistance burden in this genus.[32]

The high prevalence of MDR organisms observed in this study, with 83.7% of wound culture isolates identified as MDR, represents a critical finding that reflects the broader antimicrobial resistance crisis affecting healthcare facilities across Iraq. This result is consistent with findings from a single-center cross-sectional study conducted in Iraq, which examined both community-acquired and hospital-acquired infections and reported a MDR prevalence of 79.3% among hospital-acquired cases.[33] Although the current rate is higher than that reported in another study conducted at Smart Health Tower, Iraq, which analyzed 1,185 urine cultures and found an overall MDR rate of 57.3%, the same study observed higher MDR rates among Gram-positive bacteria (67.7%) compared to Gram-negative bacteria (49.9%).[34]

Several factors may explain the high MDR prevalence observed in the current study. These include the empirical and often unregulated use of broad-spectrum antibiotics without prior culture testing, limited implementation of antibiotic stewardship programs, and the high burden of hospital-acquired infections. In addition, delayed wound care, prolonged hospital stays, inadequate wound hygiene, and frequent use of invasive medical devices contribute to chronic

colonization and selection pressure for resistant organisms. These factors collectively underscore the urgent need for coordinated antimicrobial resistance surveillance and evidence-based prescribing policies across the country.[32]

The prevalence of MDR was notably higher among Gram-negative isolates compared to Gram-positive species. Specifically, the MDR rate for Gram-negative bacteria was 89.5%, which surpasses the 59.3% MDR rate reported in a study conducted in Ethiopia.[32] In contrast, the overall MDR rate for Gram-positive isolates was 78.3%, exceeding the 50% MDR prevalence observed in a previous study.[17] Additionally, Melake *et al.* documented a MDR prevalence of 73.5% in *Staphylococcus aureus* isolated from burn wounds in Egypt.[35] The prolonged use of broad-spectrum antibiotics, while common in clinical practice, contributes significantly to bacterial gene mutations, thereby accelerating the development of antimicrobial resistance.[32] Opportunistic pathogens acquired in hospital settings are pervasive in the healthcare environment, colonizing patients' skin, mucosal surfaces, and commonly touched hospital surfaces. Under conditions of critically compromised immunity, whether due to exacerbated comorbidities, hypoproteinemia, or severe trauma, these pathogens can progress from colonization to infection. This translocation delays wound healing and heightens the risk of MDR infections, underscoring the need for targeted strategies to mitigate these risks.[36] In this study, various risk factors for MDR infections were evaluated. Among them, patient age and the source of infection, whether community-acquired or hospital-acquired, were found to be significant. Additionally, while the type of wound specimen did not reach statistical significance, it approached near significance as a potential risk factor for MDR infections. Contrasting these findings, other studies have identified different key risk factors. For instance, surgical interventions, prolonged hospital stays, and the use of three or more antibiotics have been strongly associated with MDR infections both in the hospital and the community.[1,33] Similarly, a study conducted in Shandong, China, reported that hospital length of stay, hypoproteinemia, and open injuries were independent risk factors for MDR-infected wound complications in orthopedic trauma patients.[37]

This study acknowledges several limitations that should be considered. The retrospective design restricted the research to a single hospital with a relatively small sample size, which may limit the broader applicability of the findings to other regions or healthcare settings. Furthermore, the

data collection process was hindered by the absence of key clinical parameters, such as wound depth, which could provide additional insights into the nature of the infections. Importantly, molecular testing for resistance genes was not performed due to the retrospective nature of the study and limited availability of molecular diagnostic resources during the study period. This limits the ability to precisely identify specific resistance mechanisms, such as extended-spectrum beta-lactamases or carbapenemases. Additionally, the study did not develop a predictive model for MDR infections in wounds due to the insufficient number of suitable subjects required for rigorous validation of such a model's predictive validity. Therefore, further research involving a multi-center prospective study design is necessary. This would provide a more comprehensive understanding of the factors contributing to wound infections and their management.

Conclusions

This study underscores the critical challenge posed by antibiotic-resistant pathogens, particularly *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Klebsiella pneumoniae*, within the healthcare setting in Iraq. The rising prevalence of MDR, especially among Gram-negative isolates in this regional context, underscores the urgent need for enhanced infection control measures, robust antibiotic stewardship, and effective patient management strategies. The findings highlight the necessity of ongoing surveillance and the implementation of individualized treatment regimens to address these resistant pathogens and improve patient outcomes.

References

1. Wang C, Niu X, Bao S, et al. Distribution patterns and antibiotic resistance profiles of bacterial pathogens among patients with wound infections in the Jiaxing Region from 2021 to 2023. Infect Drug Resist 2024;17:2883-96.

2. Lo ZJ, Mak MH, Liang S, et al. Development of an explainable artificial intelligence model for Asian vascular wound images. Int Wound J 2024;21:e14565.

3. Frykberg RG, Banks J. Challenges in the treatment of chronic wounds. Adv Wound Care 2015;4:560-82.

4. Khalid F, Poulose C, Farah DF, et al. Prevalence and antimicrobial susceptibility patterns of wound and pus bacterial pathogens at a Tertiary Care Hospital in Central Riyadh, Saudi Arabia. Microbiol Res 2024;15:2015-34.

5. Fijan S, Frauwallner A, Langerholc T, et al. Efficacy of using probiotics with antagonistic activity against pathogens of wound infections: an integrative review of literature. Biomed Res Int 2019;2019:7585486.

6. Ghafoor MA, Othman KA, Mahmood LJ, et al. Phenotypic and molecular characterization of the blaTEM gene in extended-spectrum beta-lactamase-producing *Klebsiella pneumoniae*. Barw Med J 2024;3:139.

7. Taati Moghadam M, Khoshbayan A, Chegini Z, et al. Bacteriophages, a new therapeutic solution for inhibiting multidrug-resistant bacteria causing wound infection: lesson from animal models and clinical trials. Drug Des Dev Ther 2020;14:1867-83.

8. Salih RQ, Abdalla BA, Mustafa AM, et al. Changing face of antimicrobial resistance: A cross-section study. Barw Med J 2024;2:14-28

9. World Health Organization. WHO Bacterial Priority Pathogens List, 2024: Bacterial Pathogens of Public Health Importance, to Guide Research, Development and Strategies to Prevent and Control Antimicrobial Resistance. World Health Organization; 2024.

10. Guan H, Dong W, Lu Y, et al. Distribution and antibiotic resistance patterns of pathogenic bacteria in patients with chronic cutaneous wounds in China. Front Med 2021;8:609584.

11. Abdullah HO, Abdalla BA, Kakamad FH, et al. Predatory publishing lists: a review on the ongoing battle against fraudulent actions. Barw Med J 2024;2:26-30.

12. Hong JS, Kim D, Kang DY, et al. Evaluation of the BD Phoenix M50 automated microbiology system for antimicrobial susceptibility testing with clinical isolates in Korea. Microb Drug Resist 2019;25:1142-8.

13. Weinstein MP, Lewis JS. The clinical and laboratory standards institute subcommittee on antimicrobial susceptibility testing: background, organization, functions, and processes. J Clin Microbiol 2020;58:10-128.

14. Magiorakos AP, Srinivasan A, Carey RB, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin Microbiol Infect 2012;18:268-81.

15. Freedman BR, Hwang C, Talbot S, et al. Breakthrough treatments for accelerated wound healing. Sci Adv 2023;9:eade7007.

16. Mengesha RE, Kasa BG, Saravanan M, et al. Aerobic bacteria in post-surgical wound infections and pattern of their antimicrobial susceptibility in Ayder Teaching and Referral Hospital, Mekelle, Ethiopia. BMC Res Notes 2014;7:1-6.

17. Ahmed EF, Rasmi AH, Darwish AM, et al. Prevalence and resistance profile of bacteria isolated from wound infections among a group of patients in upper Egypt: a descriptive cross-sectional study. BMC Res Notes 2023;16:106.

18. Mohammed A, Seid ME, Gebrecherkos T, et al. Bacterial isolates and their antimicrobial susceptibility patterns of wound infections among inpatients and outpatients attending the University of Gondar Referral Hospital, Northwest Ethiopia. Int J Microbiol 2017;2017:8953829.

19. Mulu W, Kibru G, Beyene G, et al. Postoperative nosocomial infections and antimicrobial resistance pattern of bacteria isolates among patients admitted at Felege Hiwot Referral Hospital, Bahirdar, Ethiopia. Ethiop J Health Sci 2012;22:7-18.

20. Hassan MA, Abd El-Aziz S, Elbadry HM, et al. Prevalence, antimicrobial resistance profile, and characterization of multi-drug-resistant bacteria from various infected wounds in North Egypt. Saudi J Biol Sci 2022;29:2978-88.

21. Bessa LJ, Fazii P, Di Giulio M, et al. Bacterial isolates from infected wounds and their antibiotic susceptibility pattern: some remarks about wound infection. Int Wound J 2015;12:47-52.

22. Upreti N, Rayamajhee B, Sherchan SP, et al. Prevalence of methicillin resistant *Staphylococcus aureus*, multidrug resistant and extended spectrum β-lactamase producing gram negative bacilli causing wound infections at a tertiary care hospital of Nepal. Antimicrob Resist Infect Control 2018;7:1-0.

23. Puca V, Marulli RZ, Grande R, et al. Microbial species isolated from infected wounds and antimicrobial resistance analysis: Data emerging from a three-years retrospective study. Antibiotics 2021;10:1162.

24. Sharara SL, Maragakis LL, Cosgrove SE. Decolonization of *Staphylococcus aureus*. Infect Dis Clin North Am 2021;35:107-33.

25. Hobbs MR, Grant CC, Thomas MG, et al. *Staphylococcus aureus* colonisation and its relationship with skin and soft tissue infection in New Zealand children. Eur J Clin Microbiol Infect Dis 2018;37:2001-10.

26. Tom IM, Ibrahim MM, Umoru AM, et al. Infection of wounds by potential bacterial pathogens and their resistogram. Open Access Lib J 2019;6:1-3.

27. Mama M, Abdissa A, Sewunet T. Antimicrobial susceptibility pattern of bacterial isolates from wound infection and their sensitivity to alternative topical agents at Jimma University Specialized Hospital, South-West Ethiopia. Ann Clin Microbiol Antimicrob 2014;13:14.

28. Hollis A, Maybarduk P. Antibiotic resistance is a tragedy of the commons that necessitates global cooperation. J Law Med Ethics 2015;43:33-7.

29. Nobel FA, Islam S, Babu G, et al. Isolation of multidrug resistance bacteria from the patients with wound infection and their antibiotics susceptibility patterns: A cross-sectional study. Ann Med Surg 2022;84:104895.

30. Alam MM, Islam MN, Hawlader MD, et al. Prevalence of multidrug resistance bacterial isolates from infected wound patients in Dhaka, Bangladesh: a cross-sectional study. Int J Surg Open 2021;28:56-62.

31. Effah CY, Sun T, Liu S, et al. *Klebsiella pneumoniae*: an increasing threat to public health. Ann Clin Microbiol Antimicrob 2020;19:1.

32. Mustafa AM, Soor TA. Antibiotic resistance patterns of co-isolated *Escherichia coli* and *Klebsiella* spp.: a cross-sectional study on their association with antibiotic usage intensity. J Biol Res Bollett Soc Ital Biol Sper 2025; https://doi.org/10.4081/jbr.2025.13803.

33. Mustafa AM, Salih RQ, Yaseen HA, et al. Evolution of antimicrobial resistance in community vs. hospital-acquired infections. Barw Med J 2024;3:138.

34. Abdalla BA, Anwar KA, Fakhreddin SS, et al. Decoding urinary tract infections: pathogen profiles and antimicrobial resistance in a cross-sectional study. Afr J Urol 2025;31:37.

35. Sleem AS, Melake NA, Eissa NA, et al. Prevalence of multidrug-resistant bacteria isolated from patients with burn infection. Menoufia Med J 2015;28:677-84.

36. Xia W, He W, Luo T, et al. Risk factors for multidrug-resistant bacterial infections in patients with diabetic foot ulcers: a systematic review and meta-analysis. Ann Palliat Med 2021;10:126182630-12630.

37. Liang M, Liu Q. Distribution and risk factors of multidrug-resistant Bacteria infection in orthopedic patients. J Healthc Eng 2022;2022:2114661.

Table 1. Comparison of clinical and demographic variables between single and mixed bacterial infections.

Variables	Bacterial Infection		Total	p-Value
	Single Infection	Mixed Infection		
Gender, n (%)				
Female	40(49.4)	21(44.7)	61(47.6)	<0.001
Male	41(50.6)	26(55.3)	67(52.3)	
Age (Mean, SD)	52.17(22.2)	46.64(18.5)	50.1(20.7)	0.152
Asthma, n (%)				
Yes	1(1.3)	2(4.2)	3(2.3)	
No	56(69.1)	32(68.1)	88(68.8)	<0.001
Not mentioned	24(29.6)	13(27.7)	37(28.9)	
Heart Failure, n (%)				
Yes	10(12.4)	4(8.5)	14(10.9)	
No	47(58.0)	30(63.8)	77(60.2)	<0.001
Not mentioned	24(29.6)	13(27.7)	37(28.9)	
Renal insufficiency, n (%)				
Yes	8(9.9)	5(10.6)	13(10.2)	
No	49(60.5)	29(61.7)	78(60.9)	<0.001
Not mentioned	24(29.6)	13(27.7)	37(28.9)	
Hypertension, n (%)				
Yes	18(22.2)	8(17.0)	26(20.3)	
No	39(48.2)	26(55.3)	65(50.8)	<0.001
Not mentioned	24(29.6)	13(27.7)	37(28.9)	
Diabetes, n (%)				
Yes	18(22.2)	14(29.8)	32(25.0)	
No	39(48.2)	20(42.5)	59(46.1)	<0.001
Not mentioned	24(29.6)	13(27.7)	37(28.9)	
Cancer, n (%)				
Yes	6(7.4)	6(12.8)	12(9.4)	
No	51(63.0)	28(59.5)	79(61.7)	<0.001
Not mentioned	24(29.6)	13(27.7)	37(28.9)	
Obesity, n (%)				
Yes	10(12.3)	10(65.4)	20(15.6)	
No	47(58.0)	24(51.1)	71(55.5)	<0.001
Not mentioned	24(29.6)	13(27.7)	37(28.9)	
Length of Hospital stays in days (Median, QR)	4(1-13)	3(1-7)	4(1-10)	0.644
Types of wound specimens, n (%)				
Diabetic foot	4(4.9)	11(23.4)	15(11.7)	
Ear swab	6(7.4)	1(2.1)	7(5.5)	
Surgical site	35(43.2)	18(38.3)	53(41.4)	0.012
Vaginal site	3(3.7)	1(2.1)	4(3.1)	
Others	33(40.7)	16(34.0)	49(38.3)	

SD, Standard deviation, QR, Quartile range.

Table 2. Distribution of bacterial isolates identified in wound culture samples.

Variables	Isolates Number	Percentage
Gram-positive bacteria		
Staphylococcus aureus	29	16.3
Staphylococcus epidermidis	16	9.0
Enterococcus faecalis	15	8.4
Staphylococcus haemolyticus	6	3.4
Streptococcus species	6	3.4
Staphylococcus species	6	3.4
Corynebacterium species	5	2.8
Streptococcus agalactiae	3	1.7
Enterococcus species	2	1.1
Others	4	2.2
Gram-negative bacteria		
Escherichia coli	35	19.7
Pseudomonas aeruginosa	21	11.8
Klebsiella pneumoniae	11	6.2
Morganella morganii	7	3.9
Citrobacter species	2	1.1
Proteus species	2	1.1
Others	8	4.5
Total	178	100%

Table 3. Antimicrobial susceptibility pattern of Gram-positive Bacteria isolated from wound cultures.

Antibiotics, Number of cases (%)	*Staphylococcus aureus*		*Staphylococcus epidermidis*		*Enterococcus faecalis*		*Staphylococcus haemolyticus*		*Streptococcus agalactiae*		Total
	T	R	T	R	T	R	T	R	T	R	R (N, %)
Amikacin	5	4(80.0)	6	2(33.3)	3	3(100.0)	1	1(100.0)	3	2(66.7)	12(66.7)
Gentamicin	28	5(17.6)	16	6(37.5)	15	11(73.3)	5	3(60.0)	3	2(66.7)	27(40.3)
Ampicillin-sulbactam	0	0(0.0)	2	2(100.0)	1	0(0.0)	0	0(0.0)	0	0(0.0)	2(66.7)
Ampicillin	21	21(100.0)	13	12(92.3)	13	2(15.4)	3	3(100.0)	0	0(0.0)	38(76.0)
Amoxicillin-Clavulanate	8	8(100.0)	7	7(100.0)	5	2(40.0)	2	2(100.0)	2	0(0.0)	19(79.2)
Piperacillin-Tazobactam	6	5(83.3)	1	0(0.0)	2	1(50.0)	0	0(0.0)	2	0(0.0)	6(54.5)
Cefuroxime	7	2(28.6)	3	0(0.0)	3	3(100.0)	3	0(0.0)	1	0(0.0)	5(29.4)
Ceftriaxone	10	4(40.0)	7	5(71.4)	3	3(100.0)	5	2(40.0)	2	0(0.0)	14(51.9)
Cefepime	5	3(60.0)	3	1(33.3)	3	3(100.0)	2	2(100.0)	1	0(0.0)	9(64.3)
Cefpodoxime	3	2(66.7)	2	1(50.0)	3	3(100.0)	2	2(100.0)	1	0(0.0)	8(72.7)
Cefixime	3	2(66.7)	2	2(100.0)	4	4(100.0)	2	2(100.0)	2	2(100.0)	12(92.3)
Cefotaxime	25	11(44.0)	15	10(66.7)	12	11(91.7)	3	2(66.7)	2	0(0.0)	34(59.6)
Azithromycin	4	4(100)	1	0(0.0)	1	1(100)	3	2(66.7)	0	0(0.0)	7(77.8)
Erythromycin	29	21(72.4)	16	12(75.0)	14	10(71.4)	6	5(83.3)	3	3(100.0)	51(75.0)
Ciprofloxacin	29	15(51.7)	16	7(43.8)	14	8(57.1)	5	5(100.0)	3	1(33.3)	36(53.7)
Levofloxacin	29	13(44.8)	16	5(31.3)	13	8(61.5)	6	4(66.7)	1	0(0.0)	30(46.1)
Trimethoprim-Sulfamethoxazole	28	10(35.7)	15	7(46.7)	11	10(90.9)	6	4(66.7)	3	2(66.7)	33(52.4)
Clindamycin	27	17(63.0)	16	4(25.0)	11	11(100.0)	4	1(25.0)	2	1(50.0)	34(56.7)
Tetracycline	27	17(63.0)	16	8(50.0)	15	12(80.0)	5	2(40.0)	2	1(50.0)	40(61.5)
Doxycycline	7	4(57.1)	2	2(100.0)	5	2(40.0)	4	0(0.0)	1	1(100.0)	9(47.4)
Tigecycline	27	0(0.0)	13	0(0.0)	10	0(0.0)	5	1(20.0)	0	0(0.0)	1(1.8)
Imipenem	6	1(16.7)	4	0(0.0)	8	2(25.0)	1	1(100.0)	2	0(0.0)	4(19.0)
Meropenem	11	2(18.2)	6	1(16.7)	3	2(66.7)	2	2(100.0)	3	0(0.0)	7(28.0)
Nitrofurantoin	23	1(4.3)	15	0(0.0)	11	2(18.2)	3	0(0.0)	0	0(0.0)	3(5.8)
Rifampin	29	6(20.7)	16	0(0.0)	4	2(50.0)	5	0(0.0)	2	0(0.0)	8(14.3)
Total	397	178(44.8)	229	94(41.0)	187	116(62.0)	83	46(55.4)	41	15(36.6)	449 (47.9)

T, Total, R, Resistant.

Table 4. Antimicrobial susceptibility profile of Gram-negative Bacteria isolated from wound samples.

Antibiotics, number of cases (%)	*Escherichia coli*		*Pseudomonas aeruginosa*		*Klebsiella pneumoniae*		*Morganella morganii*		Total
	T	R	T	R	T	R	T	R	R (N, %)
Amikacin	34	5(14.7)	21	8(38.1)	11	4(36.4)	7	0(0.0)	17(23.3)
Gentamicin	33	14(42.4)	21	7(33.3)	11	6(54.5)	7	2(28.6)	29(40.3)
Ticarcillin/clavulanate	7	5(71.4)	3	2(66.7)	1	1(100.0)	0	0(0.0)	8(72.7)
Ampicillin-sulbactam	7	4(57.1)	0	0(0.0)	1	1(100.0)	0	0(0.0)	5(62.5)
Ampicillin	26	25(96.1)	16	16(100.0)	10	10(100.0)	7	7(100.0)	58(98.3)
Amoxicillin-Clavulanate	34	14(41.2)	16	16(100.0)	11	5(45.5)	7	7(100.0)	42(61.8)
Piperacillin-Tazobactam	34	7(20.6)	21	4(19.0)	11	6(54.5)	7	1(14.3)	18(24.7)
Cefuroxime	34	30(88.2)	17	16(94.1)	11	11(100.0)	6	6(100.0)	63(92.6)
Ceftriaxone	35	28(80.0)	17	17(100.0)	10	10(100.0)	7	2(28.6)	57(82.6)
Cefepime	35	26(74.3)	21	8(38.1)	11	10(90.9)	7	1(14.3)	45(60.8)
Cefpodoxime	7	7(100.0)	0	0(0.0)	1	1(100.0)	0	0(0.0)	8(100.0)
Cefixime	9	6(66.7)	2	2(100.0)	3	3(100.0)	0	0(0.0)	11(78.6)
Cefotaxime	16	14(87.5)	4	4(100.0)	4	4(100.0)	1	0(0.0)	22(88.0)
Azithromycin	0	0(0.0)	1	1(100.0)	2	2(100)	0	0(0.0)	3(100.0)
Erythromycin	8	8(100.0)	6	6(100.0)	3	3(100.0)	2	2(100.0)	19(100.0)
Ciprofloxacin	35	26(74.3)	21	9(42.9)	11	7(63.6)	7	1(14.3)	43(58.1)
Levofloxacin	34	24(70.6)	21	10(47.6)	11	6(54.5)	6	1(16.7)	41(56.9)
Trimethoprim-Sulfamethoxazole	35	23(65.7)	16	16(100.0)	11	10(90.9)	7	5(71.4)	54(78.3)
Clindamycin	13	13(100.0)	8	8(100.0)	2	2(100.0)	3	3(100.0)	26(100.0)
Tetracycline	12	11(91.7)	9	9(100.0)	1	1(100.0)	3	1(33.3)	22(88.0)
Doxycycline	4	3(75.0)	4	4(100.0)	1	1(100.0)	0	0(0.0)	8(88.9)
Tigecycline	32	2(62.5)	16	16(100.0)	11	1(9.1)	6	6(100.0)	25(38.5)

Imipenem	35	5(14.3)	21	6(28.6)	11	4(36.4)	7	5(71.4)	20(27.0)
Meropenem	35	5(14.3)	21	6(28.6)	11	4(36.4)	7	0(0.0)	15(20.3)
Nitrofurantoin	25	4(16.0)	16	16(100.0)	10	8(80.0)	6	6(100.0)	34(59.6)
Rifampin	7	7(100.0)	5	5(100.0)	1	1(100.0)	2	2(100.0)	15(100.0)
Total	586	316(53.9)	324	212(65.4)	182	122(67.0)	112	58(51.8)	708(58.8%)

T, Total, R, Resistant.

Table 5. Distribution of resistance levels and multidrug resistance in various bacterial species causing wound infections.

Isolated bacteria, number of cases (%)	Total (R0-R6)	R0	R1	R2	R3	R4	R5	R6	MDR
Escherichia coli	35(100)	1(2.9)	1(2.9)	1(2.9)	7(20.0)	4(11.4)	4(11.4)	17(48.5)	32(91.4)
Staphylococcus aureus	29(100)	0(0.0)	4(13.8)	3(10.3)	3(10.3)	4(13.8)	4(13.8)	11(37.9)	22(75.9)
Pseudomonas aeruginosa	21(100)	0(2.2)	0(13.5)	2(13.5)	1(24.7)	3(27)	4(13.5)	11(5.6)	19(90.5)
Staphylococcus epidermidis	16(100)	0(3.2)	1(6.3)	2(12.5)	2(12.5)	4(25.0)	2(12.5)	5(31.3)	13(81.3)

Enterococcus faecalis	15(100)	0(0.0)	2(13.3)	0(0.0)	1(6.7)	2(13.3)	0(0.0)	10(66.7)	13(86.7)
Klebsiella pneumoniae	11(100)	0(0.0)	0(0.0)	1(9.1)	3(27.3)	0(0.0)	0(0.0)	7(63.6)	10(90.9)
Morganella morganii	7(100)	0(0)	0(0.0)	0(0.0)	0(0.0)	1(14.3)	1(14.3)	5(71.4)	7(100.0)
Staphylococcus haemolyticus	6(100)	0(0.0)	0(0.0)	1(16.7)	1(16.7)	1(16.7)	1(16.7)	2(33.3)	5(83.3)

R0, Sensitive to all classes of antibiotics, R1, Resistance to one class of antibiotic, R2, Resistance to two classes of antibiotics, R3, Resistance to three classes of antibiotics, R4, Resistance to four classes of antibiotics, R5, Resistance to five classes of antibiotics, R6, Resistance to six classes of antibiotics, MDR, Multidrug resistance.

Table 6. Association of demographic and clinical factors with multidrug resistance (MDR) in bacterial isolates.

Variables, n (%)	MDR	Non-MDR	Total	p-Value
Gender Female Male	 51(83.6) 59(88.1)	 10(16.4) 8(11.9)	 61(100.0) 67(100.0)	0.455
Age (Mean, SD)	52.15(20.07)	37.89(23.03)	50.1(20.7)	0.007
Type of Infection Single Mixed	 70(86.4) 40(85.1)	 11(13.6) 7(14.9)	 81(100.0) 47(100.0)	0.428

Length of Hospital stays in days (Median, QR)	4(1-10)	3(1-5-9.5)	4(1-10)	0.767
Types of Clinical specimens				
Diabetic foot	13(86.7)	2(13.3)	15(100.0)	
Ear swab	7(100.0)	0(0.0)	7(100.0)	
Surgical site	48(90.6)	5(9.4)	53(100.0)	0.06
Vaginal site	2(50.0)	2(50.0)	4(100.0)	
Others	40(81.6)	9(18.4)	49(100.0)	
Setting				
Community-acquired	56(80.0)	14(20)	70(100.0)	0.049
Hospital-acquired	54(93.1)	4(6.9)	58(100.0)	

MDR, Multi drug resistance, SD, Standard deviation, QR, Quartile range.

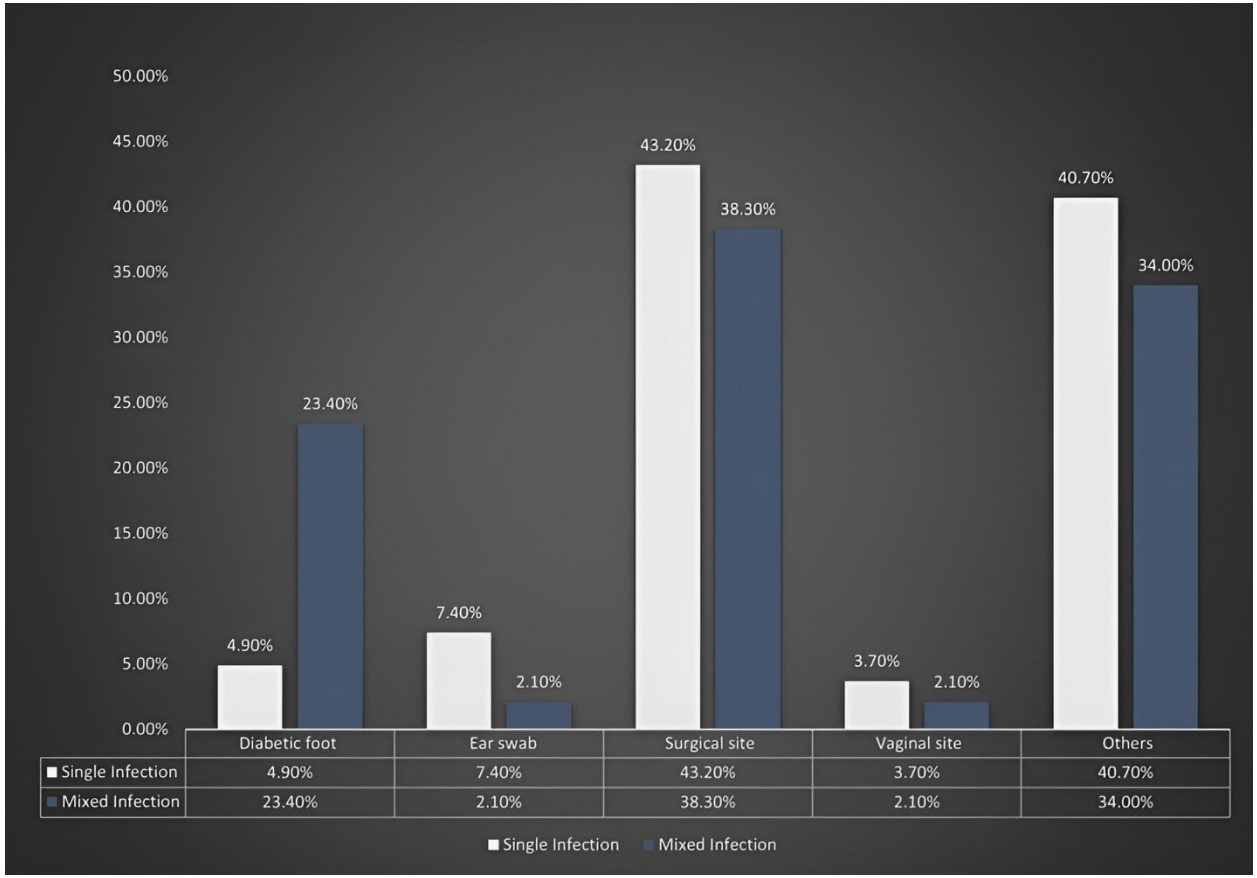

Figure 1. Distribution of single and mixed infections across different wound types.

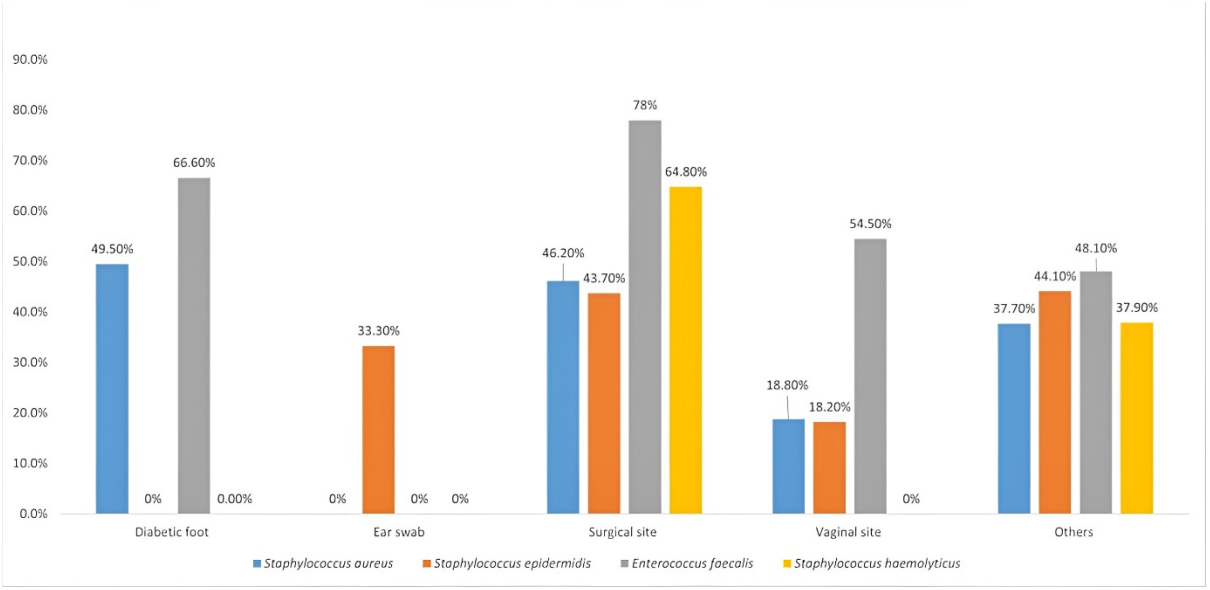

Figure 2. Antibiotic resistance rates of Gram-positive isolates in different wound types.

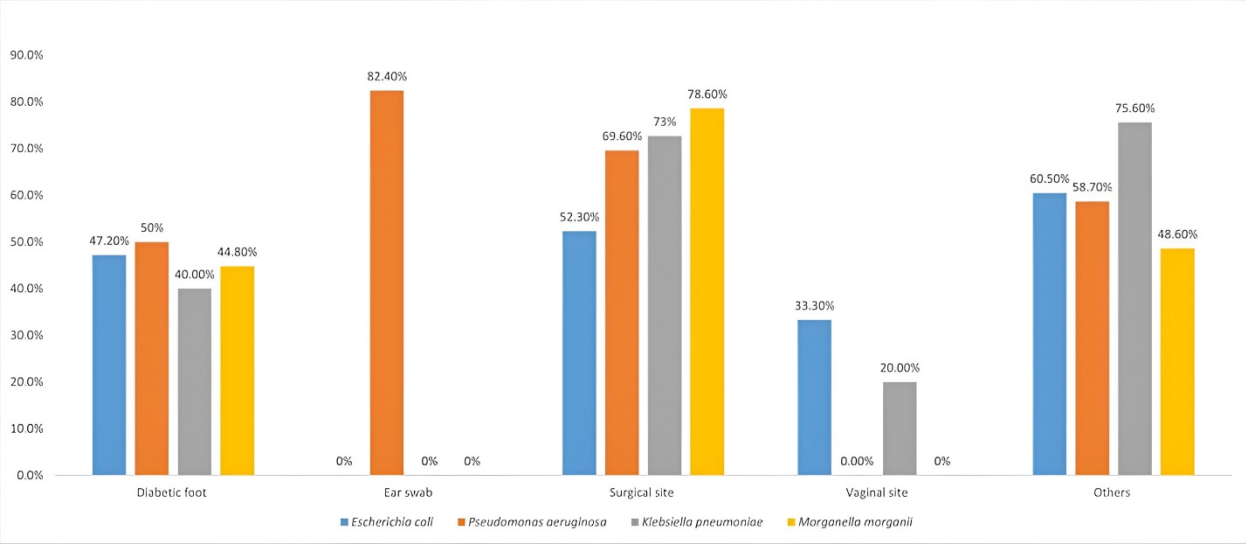

Figure 3. Antibiotic resistance rates of Gram-negative isolates in different wound types.