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Emergence of multidrug-resistant bacterial pathogens in clinical isolates: a hospital-based study

Abstract

The emergence of multidrug-resistant (MDR) bacterial pathogens has become a major global public health concern, posing significant challenges to the effective management of infectious diseases and increasing the burden on healthcare systems. This hospital-based study aimed to investigate the prevalence and antimicrobial resistance patterns of multidrug-resistant bacterial pathogens isolated from clinical specimens collected from patients with suspected bacterial infections. Clinical samples, including urine, blood, sputum, wound swabs, pus, and other body fluids, were processed using standard microbiological techniques for bacterial isolation and identification. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines, and isolates resistant to three or more classes of antimicrobial agents were classified as multidrug resistant. The study demonstrated the widespread occurrence of MDR pathogens among both Gram-positive and Gram-negative bacteria, with higher resistance observed against commonly prescribed antibiotics, while comparatively better susceptibility was noted for selected reserve antimicrobial agents. The increasing prevalence of MDR organisms highlights the growing challenge of therapeutic failure, prolonged hospital stays, increased healthcare costs, and elevated risks of morbidity and mortality. These findings emphasize the urgent need for continuous antimicrobial resistance surveillance, implementation of robust infection prevention and control measures, rational antibiotic prescribing practices, and effective antimicrobial stewardship programs to limit the spread of resistant pathogens. Furthermore, regular monitoring of local resistance trends is essential for guiding empirical therapy and improving patient outcomes. The present study contributes valuable epidemiological data on multidrug resistance in clinical isolates and underscores the importance of coordinated efforts to combat the escalating threat of antimicrobial resistance in hospital settings.

Keywords: antibiotic resistance, mdr, clinical isolates, hospital acquired infections (hais)

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Introduction

The emergence and rapid dissemination of multidrug-resistant (MDR) bacterial pathogens represent one of the most pressing challenges confronting modern healthcare systems worldwide. Antimicrobial resistance (AMR) has evolved into a global public health crisis, compromising the effectiveness of antibiotics that have long been regarded as the cornerstone of infectious disease treatment. The increasing prevalence of MDR bacteria has resulted in prolonged hospital stays, increased healthcare expenditures, therapeutic failures, and higher rates of morbidity and mortality.[1] According to international health agencies, antimicrobial resistance threatens decades of medical progress by limiting treatment options for common bacterial infections and reducing the success of routine surgical procedures, organ transplantation, cancer chemotherapy, and intensive care interventions. Multidrug resistance is generally defined as the ability of a bacterial isolate to resist the activity of at least one antimicrobial agent in three or more different classes of antibiotics.[2] The emergence of MDR organisms is driven by several interconnected factors, including the indiscriminate use of antibiotics in human medicine, self-medication, inappropriate prescription practices, incomplete treatment regimens, and the extensive application of antimicrobial agents in agriculture and animal husbandry. These practices exert selective pressure on bacterial populations, facilitating the evolution, survival, and dissemination of resistant strains. Furthermore, globalization, increased international travel, and inadequate infection prevention measures have accelerated the spread of resistant pathogens across healthcare facilities and communities.[3]

Hospitals serve as important reservoirs for antimicrobial-resistant microorganisms because they provide an environment where susceptible patients, frequent antibiotic exposure, and invasive medical procedures coexist. Intensive care units, surgical wards, and long-term care facilities are particularly vulnerable to the emergence and transmission of MDR pathogens. Patients with prolonged hospitalization, chronic illnesses, immunosuppression, indwelling medical devices, and repeated exposure to broad-spectrum antibiotics are at significantly greater risk of acquiring healthcare-associated infections caused by resistant bacteria.[4] Consequently, hospital-acquired infections remain a substantial contributor to patient morbidity and mortality worldwide. A wide range of bacterial species have developed multidrug resistance, with Gram-negative organisms presenting particular concern due to their complex resistance mechanisms and limited treatment options. Members of the family Enterobacterales, including *Escherichia coli* and *Klebsiella pneumoniae*, have demonstrated increasing resistance to β-lactam antibiotics through the production of extended-spectrum β-lactamases (ESBLs) and carbapenemases.[5] Similarly, *Pseudomonas aeruginosa* and *Acinetobacter baumannii* exhibit intrinsic and acquired resistance mechanisms that make them among the most difficult pathogens to treat in hospital settings. Among Gram-positive bacteria, methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant *Enterococcus* species (VRE), and resistant strains of *Streptococcus pneumoniae* continue to pose serious therapeutic challenges. The widespread occurrence of these organisms has significantly complicated empirical antibiotic therapy and necessitated the use of expensive reserve antibiotics. [6]The development of antimicrobial resistance involves multiple molecular and biochemical mechanisms. These include enzymatic degradation or modification of antibiotics, alterations in antibiotic target sites, reduced membrane permeability, activation of efflux pumps, and the formation of biofilms that protect bacterial communities from antimicrobial action.[7]

Horizontal gene transfer through plasmids, transposons, and integrons further facilitates the rapid dissemination of resistance genes among bacterial populations, allowing resistance traits to spread across different species and genera. The continuous evolution of these mechanisms has contributed to the emergence of pathogens resistant to multiple classes of antibiotics, thereby limiting available therapeutic options. Clinical microbiology laboratories play a critical role in detecting multidrug-resistant organisms through routine culture, bacterial identification, and antimicrobial susceptibility testing.[8] The Kirby–Bauer disk diffusion method, performed according to Clinical and Laboratory Standards Institute (CLSI) guidelines, remains one of the most widely used methods for evaluating bacterial susceptibility to antimicrobial agents. Regular surveillance of antimicrobial resistance patterns provides valuable epidemiological information that assists clinicians in selecting appropriate empirical therapy and supports infection prevention and control strategies within healthcare facilities. Local resistance data are particularly important because antimicrobial susceptibility patterns often vary across geographic regions and individual hospitals depending on prescribing practices, patient populations, and infection control measures.[9] The increasing prevalence of MDR pathogens has also highlighted the importance of antimicrobial stewardship programs, which promote the judicious use of antibiotics to preserve their effectiveness and minimize the emergence of resistance. Effective stewardship involves appropriate antibiotic selection, optimal dosing, de-escalation of therapy based on culture results, and education of healthcare professionals regarding rational antimicrobial use. Alongside stewardship, comprehensive infection prevention strategies—including hand hygiene, environmental cleaning, surveillance cultures, patient isolation when indicated, and adherence to standard precautions—are essential for reducing the transmission of resistant organisms within healthcare settings.[10]

Continuous surveillance of multidrug-resistant bacterial pathogens in clinical specimens is essential for understanding local epidemiological trends and guiding evidence-based treatment strategies. Clinical isolates obtained from urine, blood, sputum, wound swabs, pus, and other body fluids provide valuable information regarding the bacterial species responsible for infections and their antimicrobial susceptibility profiles. Monitoring resistance patterns over time enables healthcare institutions to identify emerging resistance trends, update antibiotic policies, improve patient management, and implement targeted infection control interventions.[11] The present hospital-based study was undertaken to investigate the emergence of multidrug-resistant bacterial pathogens isolated from clinical specimens obtained from patients with suspected bacterial infections. The study aims to identify the predominant bacterial pathogens, evaluate their antimicrobial susceptibility profiles, determine the prevalence of multidrug resistance, and generate local epidemiological data that may contribute to improved clinical decision-making and antimicrobial stewardship. The findings are expected to support clinicians in selecting appropriate empirical therapy, strengthen infection prevention and control measures, and contribute to ongoing efforts aimed at combating the growing global challenge of antimicrobial resistance.[12]

Predominant pathogens in the study

Among the bacterial pathogens isolated from clinical specimens, *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* are recognized as two of the most clinically significant opportunistic pathogens associated with healthcare-associated infections and multidrug resistance. These Gram-negative bacteria are frequently isolated from specimens such as urine, sputum, blood, wound swabs, pus, and respiratory secretions, particularly from hospitalized patients with prolonged hospital stays, invasive medical devices, immunocompromised conditions, or prior exposure to broad-spectrum antibiotics.[13] Their remarkable ability to survive in diverse hospital environments, coupled with the acquisition of multiple antimicrobial resistance mechanisms, has made them major contributors to nosocomial infections worldwide. The increasing prevalence of multidrug-resistant strains of these organisms has significantly reduced therapeutic options and complicated the management of severe bacterial infections. *Pseudomonas aeruginosa* is a non-fermentative, aerobic Gram-negative bacillus that possesses exceptional metabolic versatility and environmental adaptability.[14] It is widely distributed in soil, water, hospital equipment, disinfectants, and moist clinical environments, allowing it to persist in healthcare settings for extended periods. Clinically, *P. aeruginosa* is an important cause of ventilator-associated pneumonia, bloodstream infections, urinary tract infections, burn wound infections, surgical site infections, and chronic respiratory infections in patients with cystic fibrosis and chronic obstructive pulmonary disease.[15] The organism exhibits intrinsic resistance to several classes of antibiotics because of its low outer membrane permeability, expression of multidrug efflux pumps, production of chromosomal AmpC β-lactamase, and ability to form biofilms on medical devices and host tissues. In addition to intrinsic resistance, *P. aeruginosa* readily acquires resistance through chromosomal mutations and horizontal gene transfer, leading to the production of extended-spectrum β-lactamases, carbapenemases, and aminoglycoside-modifying enzymes.[16]

The emergence of carbapenem-resistant *P. aeruginosa* has become a serious therapeutic challenge because carbapenems have traditionally been reserved as last-line agents for treating severe Gram-negative infections. Biofilm formation further enhances bacterial survival by protecting the organism from host immune responses and limiting antibiotic penetration, thereby contributing to persistent and recurrent infections. *Klebsiella pneumoniae* is another prominent Gram-negative member of the family Enterobacterales and is one of the leading causes of both community-acquired and hospital-acquired infections.[17] It commonly causes pneumonia, urinary tract infections, septicemia, liver abscesses, and wound infections, particularly among elderly, critically ill, diabetic, or immunocompromised patients. The organism possesses several important virulence factors, including a thick polysaccharide capsule that protects against phagocytosis, lipopolysaccharides that stimulate inflammatory responses, fimbriae that facilitate adherence to host tissues, and siderophores that promote iron acquisition during infection.[18] The clinical significance of *K. pneumoniae* has increased substantially due to the widespread emergence of multidrug-resistant strains producing extended-spectrum β-lactamases (ESBLs) and carbapenemases such as KPC, NDM, VIM, OXA-48, and IMP enzymes. These resistance mechanisms hydrolyze a broad range of β-lactam antibiotics, including third-generation cephalosporins and carbapenems, leaving limited treatment options such as polymyxins, tigecycline, or newer β-lactam/β-lactamase inhibitor combinations.[19]

The rapid dissemination of resistance genes through plasmids and other mobile genetic elements has accelerated the spread of multidrug-resistant *K. pneumoniae* within hospitals and across geographic regions. The predominance of *P. aeruginosa* and *K. pneumoniae* among multidrug-resistant clinical isolates underscores the urgent need for continuous microbiological surveillance, routine antimicrobial susceptibility testing, and effective infection prevention strategies.[20] Monitoring their resistance profiles provides valuable epidemiological information for guiding empirical antibiotic therapy, supporting antimicrobial stewardship programs, and reducing the transmission of resistant pathogens within healthcare facilities. Early detection of multidrug-resistant isolates, combined with strict infection control practices and rational antibiotic use, is essential to minimize treatment failures, improve patient outcomes, and combat the growing burden of antimicrobial resistance in hospital settings.[21]

Methodology

Study design

i. Hospital-based study
ii. Study period (e.g., April 2026 to May 2026).
iii. Conducted in the Department of clinical Microbiology Omega Hospital and Department of Microbiology at Aurora's Degree & PG College.

Urine sample collection

Urine specimens should be collected using aseptic techniques according to standard microbiological procedures.

Types of specimens

i. Midstream clean-catch urine (MSU)
ii. Catheter urine

Collection procedure

i. Patients were instructed to clean the periurethral area before specimen collection.
ii. Approximately 10–20 mL of urine was collected in a sterile, wide-mouthed, leak-proof container.
iii. Samples were transported to the microbiology laboratory within 2 hours of collection. If a delay is anticipated, specimens were stored at 2–8°C and were processed within 24 hours.

Sample processing

Urine specimens were cultured using a calibrated inoculating loop (0.001 mL or 0.01 mL) on:

i. Blood agar
ii. MacConkey agar

Plates were incubated aerobically at **35–37°C for 18–24 hours**.

Significant bacteriuria was interpreted according to accepted microbiological criteria, such as colony counts of $\geq 10^5$ CFU/mL for clean-catch specimens, while lower counts were considered significant in symptomatic patients or catheterized specimens.

Identification of isolates

Isolates were identified based on:

i. Colony morphology
ii. Gram staining
iii. Standard biochemical tests

For *Klebsiella* spp the following tests were performed

i. Lactose fermentation
ii. Indole
iii. Citrate utilization
iv. Urease
v. Triple Sugar Iron (TSI)
vi. Motility

For *Pseudomonas* spp the following tests were performed

i. Oxidase test
ii. Pigment production
iii. Growth at 42°C
iv. Oxidative-fermentative glucose test
v. Nitrate reduction

Antimicrobial susceptibility testing (AST)

Antimicrobial susceptibility testing was performed using the **Kirby–Bauer disc diffusion method** on Mueller–Hinton agar according to the latest Clinical and Laboratory Standards Institute (CLSI) or European Committee on Antimicrobial Susceptibility Testing (EUCAST) guidelines.

Definition of multidrug resistance

Multidrug resistance was defined as **non-susceptibility to at least one antimicrobial agent in three or more antimicrobial classes**, following the internationally accepted criteria proposed by Magiorakos AP and colleagues.

Data collection

The following variables were recorded:

i. Patient age
ii. Sex
iii. Inpatient or outpatient status
iv. Ward or ICU
v. Urine specimen type
vi. Organism isolated
vii. Colony count
viii. Antibiotic susceptibility profile
ix. MDR status
x. ESBL and carbapenemase status (if tested)

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Results

Figure 1 Pseudomonas on Kings B agar medium.

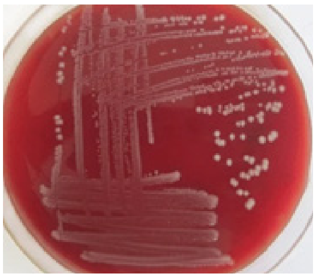

Figure 2 Klebsiella on EMB agar medium.

Figure 3 MDR exhibited by Klebsiella on Mueller Hinton agar.

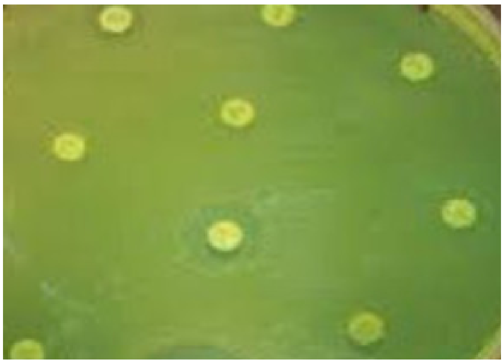

Figure 4 MDR exhibited by Pseudomonas on Kings B medium.

Table 1 Depiction of *Klebsiella pneumonia* susceptibility pattern to different antibiotics

S.No	Antimicrobial agent	MIC (micrograms)	Interpretation
1	Amoxicillin	>=32	Resistant
2	Piperacillin	>=128	Resistant
3	Cefuroxime	>=64	Resistant
4	Ceftriaxone	>=64	Resistant
5	Cefoperazone	>=64	Resistant
6	Cefepime	>=32	Resistant
7	Ertapenem	>=8	Resistant
8	Imipenem	>=16	Resistant
9	Meropenem	>=16	Resistant
10	Amikacin	>=32	Resistant
11	Gentamicin	>=16	Resistant
12	Ciprofloxacin	>=4	Resistant
13	Colistin	>=1	Intermediate
14	Trimethoprim	>=320	Resistant

Table 1 Continued.....

Table 2 Depiction of *Pseudomonas aureginosa* susceptibility pattern to different antibiotics

S.No	Antimicrobial agent	MIC (micrograms)	Interpretation
1	Cefoperazone	>=64	Intermediate
2	Cefepime	>=32	Resistant
3	Imipenem	>=16	Resistant
4	Meropenem	>=16	Resistant
5	Amikacin	>=32	Resistant
6	Ciprofloxacin	>=4	Resistant
7	Colistin	>=1	Resistant
8	Trimethoprim	>=320	Resistant
9	Cefepime	>=32	Resistant
10	Ertapenem	>=8	Resistant
11	Cefuroxime	>=64	Resistant

Table 3 Biochemical tests confirming the identity of the organisms

S.No	Biochemical test	Klebsiella pneumonia	*Pseudomonas aureginosad*
1	Gram Stain	-Ve	-Ve
2	Indole	-Ve	-Ve
3	Methyl red	-Ve	-Ve
4	Vogus Proskauer	+Ve	-Ve
5	Citrate test	+Ve	+Ve
6	Catalase test	+Ve	+Ve
7	Urease test	+Ve	-Ve
8	Oxidase	-Ve	+Ve

Discussion

The present study evaluated the antimicrobial resistance patterns and multidrug resistance (MDR) among urinary isolates of *Klebsiella* spp. and *Pseudomonas* spp. recovered from patients attending a tertiary care hospital. Both organisms are recognized as important healthcare-associated pathogens because of their ability to acquire multiple resistance mechanisms, including extended-spectrum β-lactamase (ESBL) and carbapenemase production. The findings of the present study demonstrate that both pathogens continue to exhibit high levels of resistance to commonly prescribed antibiotics, emphasizing the growing challenge of managing urinary tract infections caused by Gram-negative bacteria. Similar kind of research demonstrations have been carried out by Murray *et al*., in 2019. The emergence and rapid dissemination of multidrug-resistant (MDR) bacterial pathogens have become one of the most significant challenges confronting modern healthcare systems worldwide. The present hospital-based study highlights the increasing prevalence of MDR bacteria among clinical isolates, emphasizing the growing threat posed by antimicrobial resistance (AMR) to patient management and infection control practices. The observed resistance patterns in this study are consistent with the global trend of escalating antimicrobial

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resistance reported by several investigators over the past decade.[22] The widespread occurrence of MDR pathogens in clinical settings reflects the combined effects of inappropriate antibiotic usage, prolonged hospitalization, indiscriminate prescription practices, inadequate infection prevention measures, and the horizontal transfer of resistance genes among bacterial populations. In the present investigation, Gram-negative bacteria constituted the majority of MDR isolates, with species such as *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* exhibiting high levels of resistance to multiple antibiotic classes. Similar findings have been reported by Magiorakos *et al.,*[10] who established standardized definitions for MDR, extensively drug-resistant (XDR), and pandrug-resistant (PDR) bacteria and emphasized the predominance of Gram-negative organisms in hospital-acquired infections.[23] Likewise, the multicenter surveillance conducted by the Centers for Disease Control and Prevention (CDC) identified *K. pneumoniae*, *A. baumannii*, and *P. aeruginosa* as among the most problematic MDR pathogens associated with increased morbidity and mortality in hospitalized patients.

The antimicrobial resistance profile observed among *Pseudomonas* isolates in the present study is also consistent with global trends. *Pseudomonas aeruginosa* possesses intrinsic resistance mechanisms, including reduced membrane permeability, multidrug efflux pumps, and biofilm formation, which contribute to limited therapeutic options. Recent studies have reported increasing resistance to carbapenems, cephalosporins, and fluoroquinolones among hospital-acquired *Pseudomonas* isolates, particularly in intensive care units. These findings support the observation that empirical therapy for infections caused by *Pseudomonas* is becoming increasingly difficult and should be guided by local antimicrobial susceptibility data. This is very similar to the work of Suay-García *et al*.,[36] that has illustrated the significance of MDR among clinical isolates.

The predominance of *Escherichia coli* among clinical isolates observed in this study agrees with previous investigations by Gupta et al.[4], Tamma et al.[31] and many regional surveillance studies, which consistently reported *E. coli* as the leading cause of urinary tract infections, bloodstream infections, and wound infections. The increasing resistance of *E. coli* to third-generation cephalosporins and fluoroquinolones is largely attributed to the dissemination of extended-spectrum β-lactamase (ESBL)-producing strains. Similar observations have been documented by Paterson and Bonomo[31],who highlighted the rapid global expansion of ESBL-producing Enterobacteriaceae and their significant impact on therapeutic outcomes.[24] The high prevalence of MDR *Klebsiella pneumoniae* observed in the present study also corroborates findings reported by Pitout and Laupland,[25] who described the emergence of carbapenem-resistant and ESBL-producing *Klebsiella* species as a major public health concern. Recent studies from Asia, Europe, and Africa have similarly demonstrated increasing resistance among *K. pneumoniae* isolates to carbapenems, aminoglycosides, and fluoroquinolones.[25] The acquisition of carbapenemase genes such as *bla*KPC, *bla*NDM, and *bla*OXA-48 has significantly reduced the effectiveness of last-resort antibiotics, thereby limiting treatment options for severe infections. The present findings also revealed considerable multidrug resistance among *Pseudomonas aeruginosa* and *Acinetobacter baumannii*, organisms that are well recognized for their intrinsic resistance mechanisms and remarkable ability to acquire additional resistance determinants.[26]

Comparable resistance trends have been reported by Peleg et al.,[31] who emphasized the adaptability of these opportunistic pathogens in intensive care units. The production of carbapenemases, overexpression of efflux pumps, biofilm formation, and reduced membrane permeability collectively contribute to the multidrug-resistant phenotype observed in these bacteria. The increasing isolation of MDR *Acinetobacter* species from critically ill patients has become a persistent concern due to their association with ventilator-associated pneumonia, bloodstream infections, and prolonged hospital stays.[27] Among Gram-positive organisms, the occurrence of methicillin-resistant *Staphylococcus aureus* (MRSA) observed in this study is comparable to previous reports from hospital surveillance programs worldwide. Chambers and DeLeo (2009) demonstrated that MRSA remains one of the most prevalent healthcare-associated pathogens despite improvements in infection control measures. Although several countries have reported declining MRSA prevalence following the implementation of antibiotic stewardship programs, many developing nations continue to experience persistently high MRSA rates because of limited antimicrobial surveillance and inconsistent infection prevention practices.[28] The antibiotic susceptibility profile obtained in the present study demonstrated widespread resistance to commonly prescribed antibiotics such as ampicillin, amoxicillin-clavulanate, ceftriaxone, cefotaxime, ciprofloxacin, and cotrimoxazole. Similar resistance patterns have been documented by the World Health Organization (WHO) Global Antimicrobial Resistance Surveillance System (GLASS), which consistently reports increasing resistance among bacterial pathogens against first-line empirical therapies. The reduced effectiveness of these antibiotics may be attributed to their frequent empirical use, inappropriate self-medication, incomplete treatment courses, and unrestricted availability in several healthcare settings.[29]

A comparative analysis of both organisms suggests that although *Klebsiella* spp. are more frequently isolated from urinary tract infections, *Pseudomonas* spp. generally exhibit broader intrinsic resistance and a greater capacity to survive in the hospital environment. Recent comparative studies conducted by Malik *et al*.,[26] have similarly demonstrated that infections caused by multidrug-resistant *Pseudomonas* are associated with greater therapeutic challenges, more frequent inappropriate empirical therapy, and prolonged hospitalization compared with infections caused by ESBL-producing *Klebsiella pneumoniae*. Nevertheless, both pathogens remain significant contributors to healthcare-associated urinary tract infections and require continuous microbiological surveillance. Conversely, comparatively higher susceptibility was observed toward reserve antibiotics such as colistin, tigecycline, linezolid, and vancomycin depending on the bacterial species involved. Similar observations have been reported in several tertiary-care hospital studies where these antibiotics retained activity against MDR isolates. However, increasing reports of colistin-resistant Enterobacteriaceae and vancomycin-resistant enterococci indicate that even these last-line therapeutic options are becoming progressively compromised.[30] Therefore, reliance on reserve antibiotics should be carefully regulated through antimicrobial stewardship programs to delay the emergence of additional resistance. The prevalence of MDR isolates observed in the present study appears comparable to reports from several tertiary care hospitals in developing countries, although variations exist among different geographic regions. Such differences may be explained by disparities in antibiotic prescription practices, infection control policies, hospital infrastructure, patient demographics, and local antimicrobial stewardship initiative.[31] Studies conducted in India, China, Nigeria, and other low- and middle-income countries have consistently demonstrated MDR prevalence ranging between 40% and 80%, indicating that antimicrobial resistance continues to represent a substantial burden in resource-limited healthcare settings. In contrast, hospitals implementing comprehensive antimicrobial stewardship programs and active surveillance systems have reported comparatively lower MDR rates, highlighting the effectiveness of coordinated infection prevention strategies.[32]

One of the major contributors to the increasing burden of MDR bacteria is the inappropriate and excessive use of broad-spectrum antibiotics. Numerous studies have demonstrated that indiscriminate antimicrobial exposure creates selective pressure favoring resistant bacterial populations. Livermore (2003) and subsequent investigators emphasized that resistance genes spread rapidly through plasmids, transposons, and integrons, facilitating the dissemination of MDR organisms both within hospitals and in the community.[33] The increasing mobility of patients, international travel, and global healthcare networks further accelerate the transmission of resistant strains across geographic boundaries. The present study further supports the importance of continuous microbiological surveillance in identifying local resistance trends and guiding empirical antibiotic therapy. Regular monitoring of antimicrobial susceptibility profiles allows clinicians to optimize treatment decisions while minimizing unnecessary exposure to broad-spectrum antibiotics.[34] Similar recommendations have been proposed by the WHO Global Action Plan on Antimicrobial Resistance, which emphasizes integrated surveillance, antimicrobial stewardship, infection prevention, and public awareness as key strategies for combating AMR. Despite providing valuable epidemiological information, the present study has certain limitations. Being hospital-based, the findings may not fully represent resistance patterns within the general community.[35] Additionally, molecular characterization of resistance genes, including ESBLs, carbapenemases, and methicillin resistance determinants, was not performed, limiting the ability to identify the underlying genetic mechanisms responsible for multidrug resistance.

Future investigations incorporating whole-genome sequencing, molecular epidemiology, and multicenter surveillance would provide deeper insights into the transmission dynamics and evolution of MDR pathogens.[36] Overall, the findings of this study reinforce previous reports indicating that multidrug-resistant bacterial pathogens continue to emerge at an alarming rate in healthcare facilities. The similarity of resistance patterns with those reported in national and international studies suggests that antimicrobial resistance is a widespread and evolving problem requiring coordinated global action. Strengthening antimicrobial stewardship, implementing evidence-based infection control practices, promoting rational antibiotic prescribing, improving diagnostic microbiology services, and conducting continuous surveillance remain essential strategies for reducing the burden of MDR infections and preserving the efficacy of currently available antimicrobial agents.[37]

Conclusion

The present study highlights the growing emergence of multidrug-resistant (MDR) bacterial pathogens among clinical isolates, with *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* identified as two of the most significant contributors to healthcare-associated infections. Their widespread occurrence and increasing resistance to multiple classes of antimicrobial agents underscore the serious challenges faced in the management of bacterial infections in hospital settings. The ability of these organisms to acquire and disseminate resistance determinants through diverse mechanisms, including biofilm formation, production of β-lactamases, activation of efflux pumps, and horizontal gene transfer, has substantially reduced the effectiveness of commonly prescribed antibiotics and limited available therapeutic options.

The findings reinforce the importance of routine microbiological surveillance and antimicrobial susceptibility testing for the early detection of resistant pathogens and the development of hospital-specific antibiograms. Such information is essential for guiding appropriate empirical therapy, minimizing inappropriate antibiotic use, and improving clinical outcomes. Equally important is the implementation of comprehensive antimicrobial stewardship programs that promote the rational use of antibiotics, optimize treatment strategies, and reduce the selective pressure responsible for the emergence of resistant bacterial strains. Strengthening infection prevention and control practices, including strict adherence to hand hygiene, environmental sanitation, appropriate patient isolation when indicated, and continuous monitoring of healthcare-associated infections, is essential to prevent the transmission of MDR organisms within healthcare facilities. Although the present study provides valuable information on the prevalence and resistance patterns of MDR bacterial pathogens, further investigations involving larger sample sizes, multicenter surveillance, and molecular characterization of antimicrobial resistance genes are warranted to better understand the epidemiology and transmission dynamics of these organisms. Continuous monitoring of resistance trends, combined with advances in rapid diagnostic methods and evidence-based infection control strategies, will play a crucial role in combating antimicrobial resistance. A coordinated approach involving clinicians, microbiologists, infection control teams, policymakers, and public health authorities is essential to preserve the effectiveness of existing antimicrobial agents and improve patient care in the face of the escalating global threat posed by multidrug-resistant bacterial pathogens.

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Conflicts of interest

The authors declare that there are no conflicts of interest.

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