

Assessment of Antibiotic Use and Resistance Patterns in ICU Patient

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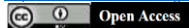
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ABSTRACT

Intensive care units (ICUs), deliver advanced medical interventions to severely ill patients. These patients face heightened vulnerability to nosocomial infections stemming from multiple contributing elements, including underlying immunosuppression, extended hospitalizations, frequent exposure to invasive procedures, and the routine empirical administration of broad-spectrum antibiotics.

To assess antibiotic use and characterize the antimicrobial resistance patterns of bacterial and fungal isolates among patients admitted to the intensive care unit.

The study included 100 patients admitted in intensive care unit during the study period. At the time of sample collection, all patients were receiving prescribed antibiotic therapy, including cephalosporin's, imipenem, meropenem, and vancomycin. Clinical specimens including tracheal aspirates, blood and urine samples were collected from these patients and submitted to the microbiology laboratory for culture and antimicrobial susceptibility testing. The antimicrobial susceptibility test and the identification of the isolated microorganisms were done using the VITEK® 2 Compact System (bioMérieux, France).

Pseudomonas aeruginosa was the most common isolates 37.5% followed by *Acinetobacter baumannii* 31.3%, *Klebsiella pneumoniae* and *Staphylococcus aureus* each were 8.3% of the isolates, *Escherichia coli* and *Candida albicans* were each detected in 6.3% of isolates, whereas *Proteus mirabilis* was the least frequently isolated organism, representing 2%. The high level of antimicrobial resistance observed in *A. baumannii*. Among the 41 Gram-negative bacterial isolates, 8 (19.5%) were identified as MDR, whereas 24 (58.5%) were classified as XDR.

The high proportion of MDR and XDR isolates observed in this study highlights the therapeutic challenges associated with bacterial infections in the ICU.

Introduction

Intensive care units (ICUs), deliver advanced medical interventions to severely ill patients. These patients face heightened vulnerability to nosocomial infections stemming from multiple contributing elements, including underlying immunosuppression, extended hospitalizations, frequent exposure to invasive procedures, and the routine empirical administration of broad-spectrum antibiotics [1]. Although the therapeutic efficacy of antibiotics is universally acknowledged when administered under appropriate clinical indications, their misuse remains widespread. This persistent inappropriate administration occurs despite the crucial role of antibiotic stewardship in contemporary evidence-based medicine [2]. Intensive care units constitute a high-risk setting for antimicrobial resistance [3]. Healthcare-associated infections acquired within ICUs account for 20% to 25% of the total global burden of nosocomial infections in acute care settings. This substantial epidemiological footprint is driven by a combination of key clinical determinants, notably the escalating reliance on invasive medical devices, the expanded administration of immunosuppressive pharmacotherapy, and the widespread, irrational prescribing of antimicrobial therapy among critically ill cohorts [4]. A substantial majority of ICU patients receive broad-spectrum antimicrobial agents. While these regimens represent critical, life-

sustaining interventions for severe infections, their application in unconfirmed cases may be clinically unwarranted, thereby exposing individuals to secondary antibiotic-associated harms [5]. Antimicrobial resistance represents a formidable global public health crisis, projected to become a predominant cause of mortality worldwide in the near future. Consequently, an essential countermeasure against this threat is the strict minimization of indiscriminate antibiotic usage. Within healthcare systems, ICUs serve as primary epicenters for both extensive, high-density prescribing and the heightened prevalence of multidrug-resistant pathogens. [6]. The incidence of infections caused by bacteria that are resistant to antibiotics is constantly increasing. Infections with resistant bacteria are associated with higher morbidity, mortality and costs [7].

The global proliferation of pathogenic multidrug-resistant (MDR) bacterial strains represents an escalating and critical peril to human health. Historically, these resistant phenotypes were infrequent and largely confined to healthcare-associated settings; however, in contemporary epidemiological landscapes, their dissemination has become remarkably pervasive across both clinical and community environments[8]. This issue is prevalent among both Gram-positive and Gram-negative bacterial species, which include mainly *A. baumannii*, *E. coli*, *P. aeruginosa*, and *K. Pneumonia* Gram-negative, along with *S. aureus*, *S. pneumoniae*, *E. faecium*, and *E. faecalis* Gram-positive. Evidence indicates that antibiotic resistance within these bacterial species primarily arises from plasmid-mediated horizontal gene transfer carrying resistance determinants. This accelerated development of resistance is driven by several critical factors, including the overexploitation and excessive administration of broad-spectrum drugs, as well as a pronounced scarcity of target-oriented antimicrobial agents [9].

Materials and methods

A cross-sectional descriptive study was conducted in Kirkuk City at Azadi Teaching Hospital from March to August 2026. The study included 100 patients admitted in (ICU) during the study period. At the time of sample collection, all patients were receiving prescribed antibiotic therapy, including cephalosporin's, imipenem, meropenem, and vancomycin. Clinical specimens including tracheal aspirates, blood and urine samples were collected from these patients and submitted to the microbiology laboratory for culture and antimicrobial susceptibility testing. The samples were cultured on Blood agar, MacConkey agar, Chocolate agar and Sabouraud Dextrose agar, as appropriate for the type of specimen. The antimicrobial susceptibility test and the identification of the isolated microorganisms were done using the VITEK® 2 Compact System (bioMérieux, France).

Statistical Analysis

Data are presented as frequencies and percentages. Statistical analyses were performed using IBM SPSS Statistics (Version 27.0 for Windows)

Ethical Approval

The study was conducted in accordance with the ethical principles outlined in the Declaration of Helsinki. The study protocol, subject information and consent form were evaluated and approved by a local ethics committee.

Results and Discussions

The study population comprised of predominantly males (63%) while females was (37%). The mean age of study population was 39.3 years. The mean patient days of admission during study period were 6 days. Pathogenic microorganisms were isolated from 48 (48%) of the samples. Table 1 shows that 41 of bacterial isolates were Gram-negative bacteria, while 4 of them was Gram-positive bacteria and 3 of them was Fungi.

Table 1: Distribution of microorganism isolated from ICU patient

Microorganism	Number	Percentage
<i>Pseudomonas aeruginosa</i>	18	37.6 %
<i>Acinetobacter baumannii</i>	15	31.2 %
<i>Klebsiella pneumoniae</i>	4	8.3 %
<i>E. coli</i>	3	6.3 %
<i>Proteus mirabilis</i>	1	2 %
<i>Staphylococcus aureus</i>	4	8.3 %
<i>Candida albicans</i>	3	6.3 %
Total	48	100 %

According to Table 1, a total of 48 microorganisms were isolated, with *Pseudomonas aeruginosa* being the most common (18 isolates, 37.5%), followed by *Acinetobacter baumannii* (15 isolates, 31.3%). These two organisms together represented approximately two-thirds of the recovered isolates, indicating their predominance among microorganisms isolated from ICU patients. This finding is consistent with a study conducted in Erbil, which also reported a high prevalence of these organisms among ICU isolates [10].

The predominance of *P. aeruginosa* in the present study is of clinical significance, given its established role as an opportunistic pathogen and its frequent association with healthcare-associated infections, especially in critically ill patients. Individuals admitted to ICUs are commonly exposed to invasive procedures, mechanical ventilation, prolonged hospital stays, and broad-spectrum antimicrobial treatment, which can increase their risk of infection with opportunistic Gram-negative organisms. In addition, the capacity of *P. aeruginosa* to persist in healthcare environments and acquire antimicrobial resistance may facilitate its continued occurrence in ICU settings [11].

Similarly, the relatively high prevalence of *A. baumannii* is of particular clinical relevance in ICU settings due to its ability to survive for extended periods in hospital environments and its strong association with multidrug-resistant infections. Its considerable proportion among the isolates identified in the present study may reflect both the increased susceptibility of critically ill patients to infection and the organism's capacity to persist, disseminate, and survive within healthcare settings. [12].

Other microorganisms were identified at lower frequencies with *Escherichia coli* and *Candida albicans* were each detected in 6.3% of isolates, whereas *Proteus mirabilis* was the least frequently isolated organism, representing 2%. Despite their lower prevalence, the presence of these microorganisms among ICU patients is clinically significant, as they may cause serious infections, particularly in individuals with underlying medical conditions or impaired host defenses. Overall, the predominance of *P. aeruginosa* and *A. baumannii* in the present ICU population emphasizes the importance of regular microbiological surveillance and antimicrobial susceptibility testing. [13].

The antimicrobial resistance patterns of Gram _ negative bacterial isolates recovered from ICU patients are presented in Table 2. *Pseudomonas aeruginosa* showed a high level of resistance to several tested antibiotics, with the highest resistance observed to ciprofloxacin (100%), followed by tobramycin (94%), levofloxacin (83%), cefepime (77%), piperacillin (72%) and meropenem (66%). Resistance to imipenem was comparatively lower at 22% while 50% of isolates were resistant to ceftazidime. No resistance result was reported for ceftriaxone and gentamicin.

A. baumannii exhibited a notably high level of antimicrobial resistance, with 100% of isolates resistant to piperacillin, piperacillin–tazobactam, ceftazidime, ceftriaxone, imipenem, ciprofloxacin,

levofloxacin and tobramycin. Resistance to cefepime and meropenem was also very high, reaching 93%, while amikacin and gentamicin showed the same resistance rate of 93%. Among the *K. pneumoniae* isolates, complete resistance (100%) was observed to piperacillin and ceftazidime. Resistance to ceftriaxone was 75%, whereas piperacillin–tazobactam, cefepime, and meropenem each showed resistance rates of 50%. Lower resistance rates of 25% were recorded for imipenem, amikacin, ciprofloxacin, levofloxacin and tobramycin, while gentamicin resistance was observed in 50% of isolates.

E. coli exhibited complete resistance (100%) to piperacillin, piperacillin–tazobactam, ceftazidime, cefepime, and ciprofloxacin. Resistance rates of 33% were observed for ceftriaxone, imipenem and amikacin, while levofloxacin resistance reached 66%. Similarly, *P. mirabilis* demonstrated 100% resistance to piperacillin, piperacillin–tazobactam, ceftazidime, ceftriaxone, cefepime, ciprofloxacin, levofloxacin and tobramycin. In contrast, no resistance to imipenem, meropenem, amikacin, or gentamicin was detected among the *P. mirabilis* isolates. The findings of the present study indicate a substantial burden of antimicrobial resistance among the principal Gram-negative organisms recovered from ICU patients, with particularly high resistance observed in *A. baumannii* and *P. aeruginosa*. Of particular concern was the resistance profile of *A. baumannii*, which showed complete resistance (100%) to imipenem and a very high resistance rate (93%) to meropenem.

This finding is clinically significant because carbapenem antibiotics have traditionally played an important role in the treatment of severe infections caused by *A. baumannii* [14].

Table 2: Antibiotic resistance pattern in percentage of Gram_ negative bacteria

Antibiotic	<i>P. aeruginosa</i> (n = 18)	<i>A. baumannii</i> (n = 15)	<i>K. pneumonia</i> (n = 4)	<i>E. coli</i> (n = 3)	<i>P. mirabilis</i> (n = 1)
Piperacillin	72 %	100 %	100 %	100 %	100 %
Piperacillin_ Tazobactam	66 %	100 %	50 %	100 %	100 %
Ceftazidime	50 %	100 %	100 %	100 %	100 %
Cefepime	77 %	93 %	50 %	100 %	100 %
Ceftriaxone	-	100 %	75 %	33 %	100 %
Imipenem	22 %	100 %	25 %	33 %	0 %
Meropenem	66 %	93 %	50 %	66 %	0 %
Amikacin	55 %	93 %	25 %	33 %	0 %
Ciprofloxacin	100 %	100 %	25 %	100 %	100 %
Levofloxacin	83 %	100 %	25 %	66 %	100 %
Tobramycin	94 %	100 %	25 %	100 %	100 %
Gentamicin	-	93 %	50 %	100 %	0 %

This study findings are consistent with previous an ICU based study in Ahvaz, Iran [15], which reported high resistance among *A. baumannii*, including 88.5% resistance to meropenem, 84.8% to amikacin, 96.9% to ciprofloxacin and 84.7% to ceftazidime. *P. aeruginosa* also showed substantial resistance, including 64.3% to meropenem, 73.5% to amikacin, 77.6% to ceftazidime and 68.2% to ciprofloxacin. These results are broadly comparable with the high resistance observed in the present ICU population, although the exact rates differed between the studies.

The high level of antimicrobial resistance observed in *A. baumannii* may be associated with the extensive use of broad-spectrum antibiotics among critically ill patients, prolonged stays in the ICU and the organism's ability to survive and persist within the hospital environment [16]. Importantly, evidence from a systematic review and meta-analysis indicates that prior exposure to several antimicrobial classes, including carbapenems, aminoglycosides, fluoroquinolones, penicillins and third-generation cephalosporins, is associated with the isolation of resistant *A. baumannii* among ICU patients [17]. Overall, the elevated antimicrobial resistance rates identified in the present study emphasize the importance of ongoing antimicrobial susceptibility monitoring, responsible antibiotic use, and effective infection prevention and control practices within ICU settings.

Table 3: Antibiotic resistance pattern in percentage for *Staphylococcus aureus* (No. = 4)

Antibiotic	Resistance %
Cefoxitin	50%
Gentamicin	25%
Ciprofloxacin	50%
Trimethoprem/sulfamethoxazole	25%
Clindamycin	25%
Erythromycin	50%
Tetracycline	0%
Chloramphenicol	0%
Vancomycin	0%

The antimicrobial susceptibility profile of *Staphylococcus aureus* showed in table 3, the highest resistance to cefoxitin, ciprofloxacin and erythromycin (50% each), followed by gentamicin, trimethoprim/sulfamethoxazole and clindamycin (25% each). No resistance was detected to tetracycline, chloramphenicol, or vancomycin. The 50% cefoxitin resistance suggests a considerable proportion of methicillin-resistant isolates. These finding is consistence with a study conducted in Nepal [18].

The three isolates of *Candida albicans* showed resistance to itraconazole in rate 66%, voriconazole 66%, fluconazole 33% while all of them were sensitive to flucytosin and caspofungin.

Table 4: The distribution of multidrug-resistant (MDR) and extensively drug-resistant (XDR) bacterial isolates recovered from ICU patients

Microorganism	MDR No. (%)	XDR No. (%)
<i>P. aeruginosa</i> (No. = 18)	7 (38.8 %)	6 (33.3 %)
<i>A. baumannii</i> (No.= 15)	0	15 (100 %)
<i>K. pneumonia</i> (No. = 4)	1(25 %)	1(25%)
<i>E. coli</i> (No. = 3)	0	1 (33.3%)
<i>P. mirabilis</i> (No. = 1)	0	1
Total	8 (19.5%)	24 (58.5%)

Table 4 presents the distribution of multidrug-resistant (MDR) and extensively drug-resistant (XDR) bacterial isolates recovered from ICU patients. Among the 41 Gram-negative bacterial isolates, 8 (19.5%) were identified as MDR, whereas 24 (58.5%) were classified as XDR. *Pseudomonas aeruginosa* demonstrated a substantial degree of resistance, with 7 (38.8%) isolates categorized as MDR and 6 (33.3%) as XDR. The highest resistance burden was observed among *Acinetobacter baumannii*,

with all 15 isolates (100%) meeting the criteria for XDR. Of the *Klebsiella pneumoniae* isolates, 1 (25.0%) was classified as MDR and another 1 (25.0%) as XDR. Among the three *Escherichia coli* isolates, 1 (33.3%) was categorized as XDR, while the single *Proteus mirabilis* isolate was also classified as XDR.

One of the most notable findings of the present study was the complete predominance of the XDR phenotype among *A. baumannii* isolates. All 15 isolates (100%) were classified as XDR, reflecting a very high level of antimicrobial resistance in this organism. This finding is comparable with a study conducted in three major hospitals in Jordan, which analyzed 148 *A. baumannii* isolates obtained from ICU patients and reported that 90% were XDR, while 96.7% showed resistance to carbapenems. The authors considered the high prevalence of XDR *A. baumannii* to be a significant concern for infection management in ICU settings [19].

The XDR rate of 100% observed in the present study was slightly higher than the 90% reported in the Jordanian study. This variation may be explained by the small number of *A. baumannii* isolates included in the current study ($n = 15$), in addition to differences in antimicrobial exposure, infection-control practices, patient characteristics, and the antibiotic panels used for susceptibility testing. Despite these differences, the comparable findings between the two studies further indicate that *A. baumannii* can serve as an important reservoir of extensively drug-resistant organisms in ICU environments. In the present study, *P. aeruginosa* also demonstrated a considerable burden of drug resistance, with 33.3% of isolates classified as XDR and 38.8% as MDR. These results are in agreement with findings from an ICU-based study in India by Gill et al., which reported substantial MDR and XDR phenotypes among *P. aeruginosa* isolates and highlighted the clinical significance of these resistant strains in intensive-care settings [20].

The high prevalence of XDR organisms observed in the present study may be attributed to several factors, including extensive use of broad-spectrum antibiotics, prolonged hospital stays, invasive medical procedures, mechanical ventilation, and the selective pressure exerted by repeated or prolonged antimicrobial exposure [21]. This finding is particularly relevant given that all patients enrolled in the present study were receiving prescribed antibiotics at the time of specimen collection. The high prevalence of XDR *A. baumannii* is therefore of considerable clinical concern, as infections caused by these highly resistant organisms can be challenging to manage because of the limited therapeutic options available.

Overall, the findings of the present study indicate a considerable burden of antimicrobial resistance among bacterial isolates recovered from ICU patients, with XDR organisms representing 58.5% of all isolates. The most notable finding was the complete predominance of the XDR phenotype among *A. baumannii*, as all isolates (100%) were classified as XDR. *P. aeruginosa* also showed substantial proportions of both MDR and XDR isolates. Collectively, these findings underscore the significant challenge posed by antimicrobial resistance in the ICU and emphasize the importance of continuous microbiological surveillance and prudent antibiotic use.

Conclusion

The present study demonstrates a considerable burden of bacterial infections and antimicrobial resistance among patients admitted to the ICU. The high proportion of MDR and XDR isolates observed in this study highlights the therapeutic challenges associated with bacterial infections in the ICU, where critically ill patients are particularly vulnerable to healthcare-associated infections and frequently require antimicrobial therapy. These findings emphasize the importance of continuous local surveillance of antimicrobial resistance patterns to support evidence-based selection of empirical and targeted antimicrobial treatment. In addition, strengthening antimicrobial stewardship, routine antimicrobial susceptibility testing and strict infection prevention and control measures is essential to reduce the selection and transmission of resistant microorganisms. Continued monitoring of resistance trends and implementation of appropriate infection-control strategies may contribute to improving antimicrobial management and patient care in ICU settings.

References:

1. Kilinc, M., *Antibiotic resistance and mortality in ICU patients: A retrospective analysis of first culture growth results*. Antibiotics, 2025. 14(3): p. 290.
2. *Ten golden rules for optimal antibiotic use in hospital settings: the WARNING call to action*. World Journal of Emergency Surgery, 2023. 18(1): p. 50.
3. Barnsteiner, S., et al., *Antimicrobial resistance and antibiotic consumption in intensive care units, Switzerland, 2009 to 2018*. Eurosurveillance, 2021. 26(46): p. 2001537.
4. Saxena, S., et al., *Antimicrobial consumption and bacterial resistance pattern in patients admitted in ICU at a tertiary care center*. Journal of infection and public health, 2019. 12(5): p. 695-699.
5. Denny, K.J., et al., *When not to start antibiotics: avoiding antibiotic overuse in the intensive care unit*. Clinical Microbiology and Infection, 2020. 26(1): p. 35-40.
6. Mokrani, D., et al., *Antibiotic stewardship in the ICU: time to shift into overdrive*. Annals of intensive care, 2023. 13(1): p. 39.
7. Bassetti, S., et al., *Optimizing antibiotic therapies to reduce the risk of bacterial resistance*. European journal of internal medicine, 2022. 99: p. 7-12.
8. Mancuso, G., et al., *Bacterial antibiotic resistance: the most critical pathogens*. Pathogens, 2021. 10(10): p. 1310.
9. Bharadwaj, A., et al., *Multidrug-resistant bacteria: their mechanism of action and prophylaxis*. BioMed research international, 2022. 2022(1): p. 5419874.
10. Baban, S.T., *Molecular detection of carbapenemase-producing Pseudomonas aeruginosa isolated from intensive care units of surgical specialty hospital in Erbil city*. Medical Journal of Babylon, 2020. 17(2): p. 185-193.
11. Parit, S.D., et al., *Pseudomonas aeruginosa in Ventilator-Associated Pneumonia: A Comprehensive Review of Resistance and Clinical Outcomes*. Cureus, 2026. 18(5).
12. Puttegowda, D., et al., *Prevalence and antimicrobial resistance of Acinetobacter baumannii isolated from endotracheal aspirates in a tertiary-care intensive care unit from South India*. Frontiers in Microbiology, 2026. 17: p. 1784001.
13. Rawson, T.M., et al., *Management of bacterial and fungal infections in the ICU: diagnosis, treatment, and prevention recommendations*. Infection and drug resistance, 2023: p. 2709-2726.
14. Nguyen, M. and S. Joshi, *Carbapenem resistance in Acinetobacter baumannii, and their importance in hospital-acquired infections: a scientific review*. Journal of applied microbiology, 2021. 131(6): p. 2715-2738.
15. Izadpour, F., et al., *An Investigation of Antibacterial Resistance Patterns Among Acinetobacter baumannii and Pseudomonas aeruginosa Isolates Collected from Intensive Care Units of a University-Affiliated Hospital in Ahvaz, Iran*. Jundishapur J Microbiol, 2016. 9(8): p. e35624.
16. Cavallo, I., et al., *Acinetobacter baumannii in the critically ill: complex infections get complicated*. Frontiers in Microbiology, 2023. Volume 14 - 2023.
17. De Blasiis, M., et al., *Impact of antibiotic exposure on antibiotic-resistant Acinetobacter baumannii isolation in intensive care unit patients: a systematic review and meta-analysis*. Journal of Hospital Infection, 2024. 143: p. 123-139.
18. Khanal, S., et al., *β -Lactamase-Producing Multidrug-Resistant Bacterial Pathogens from Tracheal Aspirates of Intensive Care Unit Patients at National Institute of Neurological and Allied Sciences, Nepal*. International scholarly research notices, 2013. 2013(1): p. 847569.
19. Ababneh, Q., et al., *Predominance of extensively-drug resistant Acinetobacter baumannii carrying bla OXA-23 in Jordanian patients admitted to the intensive care units*. PLoS One, 2025. 20(2): p. e0317798.
20. Gill, J., et al., *Prevalence of multidrug-resistant, extensively drug-resistant, and pandrug-resistant Pseudomonas aeruginosa from a tertiary level intensive care unit*. Journal of global infectious diseases, 2016. 8(4): p. 155.
21. Golli, A.-L., et al., *Trends in the antimicrobial resistance pattern of bacterial gram-negative pathogens in elderly patients admitted to the intensive care unit*. Microorganisms, 2025. 13(10): p. 2330.