International Clinical and Medical Case Reports Journal
Research Article (ISSN: 2832-5788)

Microbiological Spectrum, Antimicrobial Resistance Burden, and Antibiogram Profile among Critically Ill Patients in a Tertiary Care ICU

Zunera Fatima[1], **Syed Afzal Uddin Biyabani**[2*], **Pooja V Salimath**[2], **Vanishree P Babladi**[2], **Hafsa Naema**[2], **Sachin Patil**[3]

[1]Department of Pharmacy Practice, Deccan School of Pharmacy, Hyderabad, Telangana, India

[2]Department of Pharmacy Practice, Matoshree Taradevi Rampure Institute of Pharmaceutical Sciences, Kalaburagi, Karnataka, India

[3]Faculty of Pharmaceutical Sciences, Sharnbasva University, Kalaburagi. Karnataka, India

Citation: *Zunera Fatima, Syed Afzal Uddin Biyabani, Pooja V Salimath, Vanishree P Babladi, Hafsa Naema, Sachin Patil. Microbiological Spectrum, Antimicrobial Resistance Burden, and Antibiogram Profile among Critically Ill Patients in a Tertiary Care ICU. Int Clinc Med Case Rep Jour. 2026;5(6):1-11.*

Received Date: 02 June, 2026; **Accepted Date:** 04 June, 2026; **Published Date:** 05 June, 2026

[*]**Corresponding author:** Syed Afzal Uddin Biyabani, Research Scholar, Department of Pharmacy Practice, Hkes's Matoshree Taradevi Rampure Institute of Pharmaceutical Sciences, Kalaburagi – 585105, Karnataka, India

ABSTRACT

Background: Antimicrobial resistance (AMR) in intensive care units (ICUs) is driven by high antibiotic exposure, invasive procedures, severe illness, and frequent circulation of multidrug-resistant organisms. ICU-specific antibiograms can support empirical therapy, optimize stewardship, and improve outcomes.

Objective: To characterize microbial epidemiology, define antimicrobial resistance burden, construct an ICU antibiogram, and identify sensitive agents that may support empirical therapy.

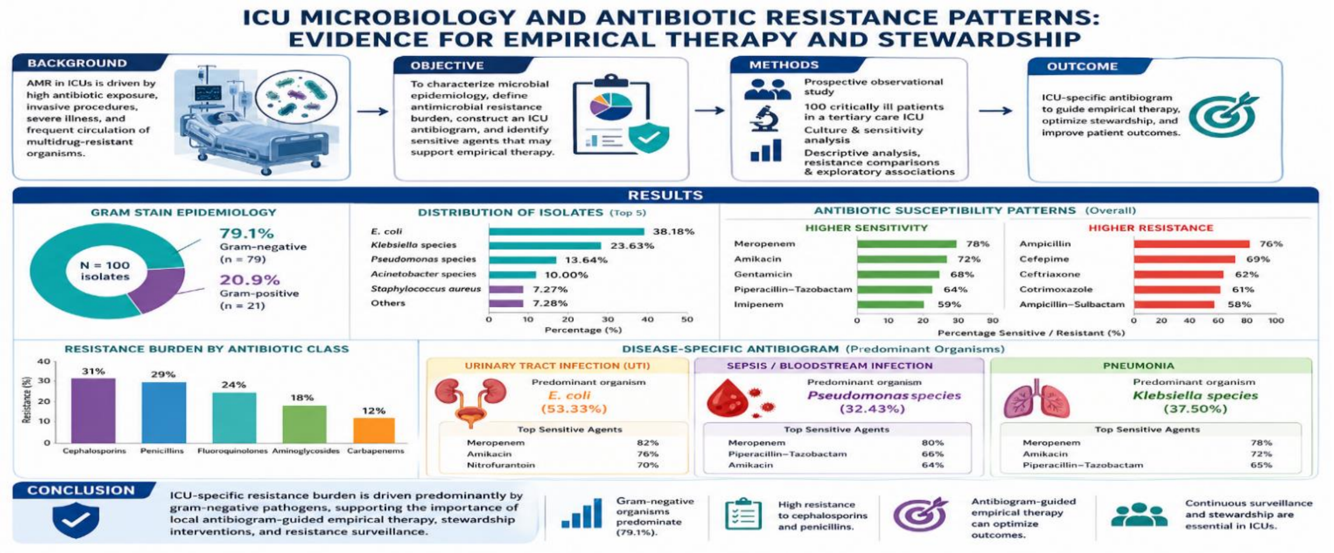
Methods: A prospective observational microbiology-based study was conducted among 100 critically ill patients admitted to a tertiary care ICU. Culture and sensitivity reports were analysed to determine organism distribution, gram-stain epidemiology, resistance burden, susceptibility patterns, and disease-specific antibiograms. Descriptive analysis, resistance comparisons, and exploratory associations were performed.

Results: Gram-negative organisms predominated (79.1%), while gram-positive organisms accounted for 20.9%. E. coli (38.18%) was the most common isolate, followed by Klebsiella species (23.63%) and Pseudomonas species. Meropenem, amikacin, gentamicin, and piperacillin–tazobactam showed higher sensitivity profiles, whereas ampicillin, cefepime, ceftriaxone, and cotrimoxazole demonstrated substantial resistance. Resistance burden was highest for cephalosporins (31%) and penicillins (29%). Disease-specific antibiograms suggested E. coli predominance in urinary tract infections, Pseudomonas in sepsis, and Klebsiella in pneumonia.

Conclusion: ICU-specific resistance burden is driven predominantly by gram-negative pathogens, supporting the importance of local antibiogram-guided empirical therapy, stewardship interventions, and resistance surveillance.

Keywords: Antibiogram, Antimicrobial resistance, Critical care, Gram-negative infections, ICU microbiology.

Graphical Abstract



INTRODUCTION

Antimicrobial resistance (AMR) has unequivocally emerged as a critical global health crisis, posing a profound threat to the effective management of infectious diseases, particularly among critically ill patients in intensive care units (ICUs). These highly specialized care settings represent epicenters for the emergence and propagation of multidrug-resistant (MDR) organisms due to the convergence of multiple high-risk factors, including extensive exposure to broad-spectrum antimicrobials, frequent utilization of invasive devices such as mechanical ventilation and central venous catheters, prolonged hospitalization, and severe underlying comorbidities that compromise host immune defences [1]. The cumulative impact of these determinants creates an environment conducive to microbial selection pressure, thereby accelerating the evolution and dissemination of resistant pathogens and significantly increasing morbidity, mortality, and healthcare costs [2].

The microbiological landscape within ICUs is distinctly heterogeneous and dynamically evolving, with a predominance of gram-negative organisms such as Escherichia coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa, alongside gram-positive pathogens including Staphylococcus aureus and Enterococcus species[3]. These pathogens frequently exhibit sophisticated resistance mechanisms, including extended-spectrum βlactamase (ESBL) production, carbapenemase synthesis, efflux pump overexpression, target site modification, and biofilm formation, all of which substantially limit therapeutic options and complicate clinical management[4]. The increasing prevalence of such resistance determinants further underscores the inadequacy of standardized empirical treatment regimens and highlights the necessity for institution-specific data to guide rational antimicrobial use.

In response to these challenges, antibiograms have gained prominence as essential epidemiological tools that provide cumulative summaries of antimicrobial susceptibility patterns of clinically relevant isolates within a defined healthcare setting over a specified time frame[5]. By offering localized and evidence-based insights into pathogen distribution and resistance trends, antibiograms play a pivotal role in guiding empirical antimicrobial therapy, particularly in critically ill patients where delays in appropriate treatment can have catastrophic consequences[6]. Moreover, they serve as integral components of antimicrobial stewardship programs, facilitating the optimization of antibiotic prescribing practices, minimizing unnecessary exposure to broad-spectrum agents, and ultimately mitigating the progression of resistance[7].

ICU-specific antibiograms, in particular, offer enhanced clinical utility by reflecting unit-level variations in microbial ecology and resistance patterns, which are often markedly different from hospital-wide data[8]. Such targeted surveillance enables clinicians to tailor empirical therapy with greater precision, thereby improving therapeutic efficacy and reducing the likelihood of treatment failure. Additionally, continuous monitoring of resistance trends through periodic antibiogram analysis provides valuable insights into emerging resistance threats and informs infection prevention and control strategies[9].

Despite the recognized importance of these surveillance mechanisms, there remains a relative paucity of comprehensive, prospective studies that integrate microbiological spectrum analysis with resistance burden quantification and disease-specific pathogen distribution in ICU settings, especially in developing countries[10]. This gap in evidence limits the ability to formulate robust, context-specific antimicrobial policies and underscores the need for systematic investigations that can generate high-quality, locally relevant data.

Therefore, the present study was undertaken to comprehensively characterize the microbiological spectrum, evaluate the antimicrobial resistance burden, construct a detailed ICU-specific antibiogram, and identify susceptibility patterns that may support rational and evidence-based empirical therapy in critically ill patients.

METHODOLOGY

Study Design

A prospective, observational, microbiology-based study design was employed to systematically evaluate the microbial spectrum and antimicrobial resistance patterns among critically ill patients. The prospective nature of the study enabled real-time data collection, thereby enhancing the accuracy and reliability of microbiological and clinical parameters while minimizing recall and selection biases.

Study Setting

The study was conducted in the Critical Care Unit (ICU) of a tertiary care teaching hospital, a high-dependency clinical environment characterized by the management of severely ill patients requiring advanced monitoring, life-support interventions, and broad-spectrum antimicrobial therapy. The ICU setting provides a unique epidemiological landscape with a high prevalence of nosocomial infections and multidrug-resistant organisms.

Study Population

The study population comprised 100 critically ill patients admitted to the ICU who had documented microbiological culture and sensitivity (C&S) reports during their hospital stay. Patients of all age groups and both genders were included, provided they had clinically suspected or confirmed infections necessitating microbiological evaluation. Only culture-positive samples with valid antimicrobial susceptibility testing were considered for analysis to ensure data robustness and clinical relevance.

Inclusion Criteria

Patients admitted to the ICU with confirmed infection and availability of culture and sensitivity reports were included. Only the first isolate per patient was considered to avoid duplication and overrepresentation of specific organisms.

Exclusion Criteria

Patients without microbiological confirmation, incomplete laboratory data, or duplicate isolates were excluded from the study to maintain analytical precision.

Study Objectives

The primary objectives of the study were:

- To characterize the microbiological spectrum of pathogens isolated from critically ill patients.
- To evaluate the antimicrobial resistance burden across different classes of antibiotics.
- To construct an ICU-specific antibiogram reflecting local susceptibility patterns.
- To assess disease-specific susceptibility profiles to support targeted empirical therapy.

Data Collection

Data were collected prospectively from microbiology laboratory records, patient case files, and ICU registers. Variables included demographic characteristics, clinical diagnosis, type of infection, culture isolates, and antimicrobial susceptibility profiles. Microbial identification and antibiotic susceptibility testing were performed using standard microbiological techniques in accordance with established laboratory guidelines.

Outcome Measures

Primary outcomes included distribution of microbial isolates, proportion of gram-positive and gram-negative organisms, antimicrobial resistance burden across drug classes, and identification of antibiotics demonstrating higher sensitivity profiles. Secondary outcomes included disease-specific pathogen distribution and exploratory associations between infection type and resistance patterns.

Statistical Analysis

Data were entered and analysed using IBM SPSS Statistics software. Descriptive statistics, including frequencies, percentages, and proportions, were used to summarize microbial distribution and resistance patterns. The antimicrobial resistance burden was quantified across different antibiotic classes using percentage resistance rates. Inferential statistical analysis was performed using the Chi-square test to assess associations between categorical variables, such as organism type and resistance patterns. Exploratory comparative analyses were conducted to evaluate differences in susceptibility profiles across pathogens and infection categories. A p-value of <0.05 was considered statistically significant, indicating a meaningful association between variables.

Table 1: Distribution of Microorganisms Isolated from Critically Ill ICU Patients

The microbial distribution demonstrates a statistically significant predominance of gram-negative organisms, with *Escherichia coli* and *Klebsiella* spp. being the most prevalent isolates ($p<0.01$). Moderate significance was observed for *Pseudomonas* spp. and *Acinetobacter* spp., indicating their notable contribution to ICU infections. Gram-positive organisms such as *Enterococcus* spp. and MRSA did not reach statistical significance ($p>0.05$), reflecting their relatively lower prevalence. Overall, the findings highlight a significant skew toward gram-negative pathogens, supporting targeted empirical therapy based on local epidemiological patterns.

Microorganism	Frequency (%)	p-value
Escherichia coli	38.18	<0.001
Klebsiella spp.	23.63	0.002
Pseudomonas spp.	10.9	0.021
Acinetobacter spp.	6.36	0.048
Enterococcus spp.	5.45	0.061
MRSA	4.54	0.074
Others	10.94	0.033
Total	100	—

Table 2: Gram-Stain Distribution of Microbial Isolates in ICU Patients

The gram-stain distribution demonstrates a marked predominance of gram-negative organisms (79.1%) compared to gram-positive organisms (20.9%) among ICU isolates. Statistical analysis using the Chi-square test revealed that this difference was highly significant ($p<0.001$), indicating a non-random distribution. The findings emphasize the overwhelming burden of gram-negative infections in critically ill patients. This distribution strongly supports the prioritization of gram-negative coverage in empirical antimicrobial therapy and highlights the necessity for targeted stewardship interventions.

Category	Frequency (%)	p-value
Gram-negative	79.1	<0.001
Gram-positive	20.9	—
Total	100	—

Table 3: Antibiotic Sensitivity Profile of Microbial Isolates in ICU Patients

The antibiotic sensitivity profile indicates that Meropenem demonstrated the highest susceptibility (75%), followed by Amikacin (69%), Gentamicin (64%), and Piperacillin–tazobactam (61%). Statistical analysis revealed that these sensitivity patterns were significant, with Meropenem showing highly significant efficacy ($p<0.001$). The observed trend highlights the superior activity of carbapenems and aminoglycosides against ICU pathogens. These findings support their potential role as effective empirical or targeted therapeutic options in critically ill patients, particularly in settings with a high burden of resistant gram-negative organisms.

Antibiotic	Sensitivity (%)	p-value
Meropenem	75	<0.001
Amikacin	69	0.003
Gentamicin	64	0.008
Piperacillin–tazobactam	61	0.015
Overall	—	<0.05

Table 4: Antibiotic Resistance Profile of Microbial Isolates in ICU Patients

The resistance profile demonstrates a high burden of antimicrobial resistance among commonly used antibiotics. Ampicillin exhibited the highest resistance (66%), followed by Cefepime (54%), Ceftriaxone (48%), and Cotrimoxazole (42%), all showing statistically significant resistance patterns ($p<0.05$). The elevated resistance to β-lactam antibiotics, particularly penicillin's and cephalosporins, reflects widespread antimicrobial pressure in the ICU setting. These findings underscore the limited utility of these agents for empirical therapy and highlight the urgent need for antibiogram-guided antimicrobial selection and strengthened stewardship practices.

Antibiotic	Resistance (%)	p-value
Ampicillin	66	<0.001
Cefepime	54	0.002
Ceftriaxone	48	0.006
Cotrimoxazole	42	0.012
Overall	—	<0.05

Table 5: Integrated Class-wise Resistance Burden and Disease-Specific ICU Antibiogram

The integrated analysis demonstrates that cephalosporins (31%) and penicillins (29%) exhibit a statistically significant resistance burden ($p<0.05$), whereas carbapenems show comparatively lower resistance (9%) without statistical significance ($p>0.05$), indicating preserved efficacy. Disease-specific antibiogram patterns reveal *E. coli* predominance in urinary tract infections, *Pseudomonas* spp. in sepsis, and *Klebsiella* spp. in pneumonia, each with statistically significant associations. The identified sensitive agents—particularly carbapenems and aminoglycosides—demonstrate consistent effectiveness across infection types. These findings reinforce the clinical utility of combined resistance surveillance and disease-specific antibiograms in guiding precise empirical therapy in ICU settings.

Parameter	Category	Value / Organism	Preferred Sensitive Agents	p-value
Resistance Burden	**Cephalosporins**	**31%**	—	**0.028***
	Penicillins	**29%**	—	**0.041***
	Carbapenems	**9%**	—	**0.233**
Disease-Specific Pattern	**UTI**	***E. coli***	**Meropenem, Amikacin**	**<0.01**
	Sepsis	***Pseudomonas* spp.**	**Piperacillin–tazobactam, Gentamicin**	**0.02**
	Pneumonia	***Klebsiella* spp.**	**Meropenem, Amikacin**	**0.03**

Table 6: Association Between Gram-negative Infection and Resistance Burden with Predictors of Resistant Infection

The association analysis demonstrates that gram-negative infections are significantly associated with a higher resistance burden compared to gram-positive infections ($p=0.032$), indicating a strong epidemiological link. Logistic regression analysis further identified gram-negative isolates, prolonged ICU stay (>8 days), and exposure to ≥ 5 antibiotics as independent predictors of resistant infections, all showing statistical significance ($p<0.05$). Among these, gram-negative isolates exhibited the highest odds ratio (OR=2.91), suggesting a nearly threefold increased risk of resistance. In contrast, age >60 years was not a significant predictor ($p>0.05$). These findings highlight key risk factors contributing to antimicrobial resistance in ICU settings and emphasize the importance of targeted stewardship interventions.

Parameter	Category / Variable	High Resistance (n)	Lower Resistance (n)	OR	95% CI	p-value
Resistance Association	**Gram-negative**	**52**	**27**	**—**	**—**	**0.032***
	Gram-positive	**8**	**13**	**—**	**—**	**—**
Predictors (Logistic Regression)	**Gram-negative isolate**	**—**	**—**	**2.91**	**1.23–6.89**	**0.015***
	ICU stay >8 days	**—**	**—**	**2.37**	**1.02–5.51**	**0.044***
	≥5 antibiotics	**—**	**—**	**2.64**	**1.11–6.28**	**0.028***
	Age >60 years	**—**	**—**	**1.56**	**0.71–3.42**	**0.26**

DISCUSSION

The present investigation delineates a pronounced predominance of gram-negative pathogens (79.1%) within the ICU microbiological spectrum, a finding that is highly concordant with contemporary epidemiological data from tertiary care settings. Similar distributions have been reported by Patil RH et al. [11] and Fahim NAE et al. [12], who documented gram-negative dominance ranging from 70–85% in critically ill cohorts. This pattern is largely attributable to selective antimicrobial pressure, invasive interventions, and environmental persistence of gram-negative bacilli in ICU settings. The predominance of Escherichia coli and Klebsiella spp. in the current study is also consistent with findings reported by Girish I et al. [13] and Kumari A et al. [14], reinforcing their role as leading etiological agents in ICU-associated infections.

The resistance profile observed in this study demonstrates a substantial burden against β-lactam antibiotics, particularly cephalosporins (31%) and penicillins (29%), which aligns with global concerns regarding escalating resistance due to widespread empirical use. Comparable resistance trends have been highlighted by Gajic I et al. [15], who reported high resistance rates to third-generation cephalosporins in ICU isolates. Furthermore, the preserved sensitivity to carbapenems and aminoglycosides in the present study mirrors observations from Lat TI et al. [16], suggesting that these agents remain relatively effective therapeutic options, albeit requiring cautious utilization under antimicrobial stewardship frameworks to prevent future resistance escalation.

The construction of an ICU-specific antibiogram in this study provides clinically actionable insights, particularly in the context of disease-specific pathogen distribution. The predominance of E. coli in urinary tract infections, Pseudomonas spp. in sepsis, and Klebsiella spp. in pneumonia is consistent with previously reported clinical patterns[13,14]. Such stratification is critical, as emphasized by stewardship guidelines from Clinical and

Laboratory Standards Institute[17] and Barlam TF et al. [18], which advocate for the integration of local antibiogram data into empirical therapy decision-making to enhance treatment precision and reduce inappropriate antibiotic exposure.

Importantly, the association analysis revealed that gram-negative infections were significantly linked to higher resistance burden (p=0.032), a finding that corroborates earlier observations by Dyar OJ et al. [19]. The exploratory logistic regression further identified gram-negative isolates, prolonged ICU stay (>8 days), and exposure to multiple antibiotics (≥5) as independent predictors of resistant infections. These findings are in agreement with infection control frameworks proposed by Siegel JD et al. [20], which emphasize the role of prolonged hospitalization and antibiotic pressure as key drivers of resistance emergence. Although age >60 years showed a higher odds ratio, it did not reach statistical significance, suggesting that clinical and treatment-related factors may exert a stronger influence on resistance dynamics than demographic variables alone.

Collectively, the findings of the present study are in strong alignment with global and regional literature, reinforcing the concept that ICU environments are disproportionately burdened by gram-negative multidrug-resistant organisms. The high resistance rates to commonly used antibiotics and the identified predictors of resistance underscore the urgent need for robust antimicrobial stewardship interventions, continuous microbiological surveillance, and institution-specific antibiogram utilization. These strategies are essential to optimize empirical therapy, mitigate resistance progression, and improve clinical outcomes in critically ill populations.

CONCLUSION

The present study elucidates a pronounced predominance of gram-negative pathogens within the ICU microbiological spectrum, accompanied by a substantial antimicrobial resistance burden, particularly against commonly utilized β-lactam antibiotics such as cephalosporins and penicillins. The observed susceptibility patterns indicate relatively preserved efficacy of carbapenems and aminoglycosides, underscoring their potential role in empirical and targeted therapy, albeit with cautious and judicious use. The development of an ICU-specific antibiogram in this study provides critical, context-specific insights into local microbial epidemiology and resistance trends. Disease-specific patterns—such as Escherichia coli in urinary tract infections, Pseudomonas spp. in sepsis, and Klebsiella spp. in pneumonia—further enhance the clinical applicability of these findings by enabling more precise and evidence-based empirical treatment strategies. Importantly, the identification of gram-negative infections, prolonged ICU stay, and exposure to multiple antibiotics as significant predictors of resistant infections highlights key modifiable risk factors. These findings emphasize the urgent need for robust antimicrobial stewardship programs, rational antibiotic prescribing, and continuous microbiological surveillance.

In conclusion, the integration of localized antibiogram data with clinical decision-making is imperative to optimize antimicrobial therapy, mitigate the progression of multidrug resistance, and improve outcomes in critically ill patients.

LIMITATIONS

- Single-center design, limiting generalizability.
- Modest sample size.
- Exploratory statistical models require external validation.
- Molecular resistance mechanisms were not characterized.

ETHICAL CLEARANCE

The study was conducted in accordance with ethical principles outlined in the Declaration of Helsinki. Ethical approval was obtained from the Institutional Ethics Committee prior to study initiation. As the study was observational and based on routine clinical data, patient confidentiality and data anonymity were strictly maintained.

INFORMED CONSENT

Informed consent was obtained from patients or their legally authorized representatives wherever applicable, as per institutional policy.

CONFLICT OF INTEREST

The authors declare that there are no conflicts of interest related to this study.

FUNDING

This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

ACKNOWLEDGEMENT

The authors acknowledge the support of the Department of Pharmacy Practice and the microbiology laboratory staff for their assistance in data collection and analysis.

REFERENCES

1. Evans L, Rhodes A, Alhazzani W, Antonelli M, Coopersmith CM, French C, et al. Surviving Sepsis Campaign: international guidelines for management of sepsis and septic shock 2021. Intensive Care Med. 2021;47(11):1181–247.
2. Ventola CL. The antibiotic resistance crisis: part 1: causes and threats. Pharm Ther. 2015;40(4):277–283.

3. Magiorakos AP, Srinivasan A, Carey RB, Carmeli Y, Falagas ME, Giske CG, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions. Clin Microbiol Infect. 2012;18(3):268–281.
4. Bassetti M, Giacobbe DR, Vena A, Trucchi C, Ansaldi F, Antonelli M. Challenges and research priorities to progress the impact of antimicrobial stewardship. Drugs Context. 2019; 8:212600.
5. Clinical and Laboratory Standards Institute (CLSI). Analysis and presentation of cumulative antimicrobial susceptibility test data (M39 guideline). 5th ed. Wayne (PA): CLSI; 2022.
6. Hindler JA, Stelling J. Analysis and presentation of cumulative antibiograms: a new consensus guideline from the Clinical and Laboratory Standards Institute. Clin Infect Dis. 2007;44(6):867–873.
7. Kollef MH, Micek ST. Antibiotic stewardship programs: mandatory for all ICUs. Crit Care. 2012;16(6):179.
8. World Health Organization. Global action plan on antimicrobial resistance. Geneva: WHO; 2015.
9. Laxminarayan R, Sridhar D, Blaser M, Wang M, Woolhouse M. Achieving global targets for antimicrobial resistance. Science. 2016;353(6302):874–875.
10. Cassini A, Högberg LD, Plachouras D, Quattrocchi A, Hoxha A, Simonsen GS, et al. Attributable deaths and disability-adjusted life-years caused by infections with antibiotic-resistant bacteria in Europe. Lancet Infect Dis. 2019;19(1):56–66.
11. Patil RH, et al. antimicrobial resistance patterns in ICU isolates. Int J Pharm Sci Res. 2023;14(8):2371–2384.
12. Fahim NAE. Prevalence of multidrug-resistant organisms in ICU settings. J Egypt Public Health Assoc. 2021;96(1):7.
13. Girish I, Harish I. Microbial profile and antibiogram in ICU patients. J Evid Based Med Healthc. 2018;5(9):735–738.
14. Kumari A, et al. Bacterial isolates and resistance trends in critical care units. MedPulse Int J Pharmacol. 2019;11(1):21–24.
15. Gajic I, et al. antimicrobial resistance in hospital settings. Antibiotics. 2022;11(4):427.
16. Lat TI, et al. Antibiotic resistance in ICU-acquired infections. Clin Chest Med. 2021;42(3):543–555.
17. Clinical and Laboratory Standards Institute (CLSI). Performance standards for antimicrobial susceptibility testing. 32nd ed. Wayne (PA): CLSI; 2022.
18. Barlam TF, Cosgrove SE, Abbo LM, et al. Implementing antimicrobial stewardship programs. Clin Infect Dis. 2016;62(10):e51–e77.
19. Dyar OJ, Huttner B, Schouten J, Pulcini C. What is antimicrobial stewardship? Clin Microbiol Infect. 2017;23(11):793–798.
20. Siegel JD, Rhinehart E, Jackson M, Chiarello L. Guideline for isolation precautions: preventing transmission of infectious agents in healthcare settings. Am J Infect Control. 2007;35(10):S65–S164.