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Original Research Article

Antibiotic Resistance Pattern Among ICU Isolates: An Observational Study

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Abstract:

Background: Antimicrobial resistance among intensive care unit (ICU) pathogens has emerged as a major challenge in critical care settings due to increased morbidity, mortality, and limited therapeutic options. The present study evaluated the bacteriological profile and antibiotic resistance patterns among ICU isolates in a tertiary care hospital.

Material and Methods: This hospital-based observational study was conducted over a period of 12 months in the Department of Microbiology of a tertiary care teaching hospital. A total of 312 non-duplicate bacterial isolates obtained from ICU patients were included. Clinical specimens were processed using standard microbiological techniques, and antimicrobial susceptibility testing was performed by Kirby–Bauer disk diffusion method according to CLSI guidelines.

Results: Among 312 isolates, males constituted 60.3% of patients, and the majority belonged to the 46–60 years age group. Endotracheal aspirate was the most common specimen (31.4%). Klebsiella pneumoniae was the predominant isolate (26.3%), followed by Escherichia coli (18.6%) and Acinetobacter baumannii (17.3%). High resistance to ceftriaxone was observed among Gram-negative isolates, particularly Acinetobacter baumannii (88.9%) and Klebsiella pneumoniae (80.5%). Carbapenem resistance among Acinetobacter baumannii was 63.0%. Multidrug resistance was identified in 50.6% of isolates, with the highest prevalence seen in Acinetobacter baumannii (74.1%).

Conclusion: The study demonstrated a high burden of multidrug-resistant organisms in ICU settings, particularly among Gram-negative pathogens. Regular surveillance, rational antibiotic usage, and strict infection control measures are essential to combat rising antimicrobial resistance.

Keywords: Antibiotic Resistance, Intensive Care Unit, Multidrug Resistance, Gram-Negative Bacteria, Nosocomial Infections, Antimicrobial Susceptibility Testing.

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Introduction

Antimicrobial resistance (AMR) has emerged as one of the most significant threats to global public health, particularly in critically ill patients admitted to intensive care units (ICUs). The widespread and often empirical use of broad-spectrum antibiotics in ICUs has contributed substantially to the increasing prevalence of multidrug-resistant (MDR) organisms, leading to prolonged hospitalization, increased healthcare expenditure, and higher mortality rates [1]. ICU patients are especially vulnerable to healthcare-associated infections because of invasive procedures, mechanical ventilation, prolonged hospital stay, immunosuppression, and frequent exposure to antimicrobial agents [2].

Recent surveillance studies have demonstrated a progressive rise in resistance among both Gram-negative and Gram-positive pathogens isolated from ICU settings. Organisms such as Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa, and methicillin-resistant Staphylococcus aureus (MRSA) have become major causes of nosocomial infections worldwide [3]. Among these pathogens, carbapenem-resistant Enterobacterales and carbapenem-resistant Acinetobacter baumannii represent a major therapeutic challenge because of limited effective antimicrobial options and their association with poor clinical outcomes [4].

Several Indian studies have reported alarming rates of resistance to cephalosporins, fluoroquinolones, and carbapenems among ICU isolates, indicating a rapidly evolving resistance pattern across tertiary care centers [5]. Continuous monitoring of local antibiograms and resistance trends is therefore essential for guiding empirical therapy, optimizing antibiotic stewardship strategies, and preventing the dissemination of resistant strains within hospital environments [6].

In view of the increasing burden of antimicrobial resistance in critical care settings, the present study was undertaken to evaluate the bacteriological profile and antibiotic resistance patterns among bacterial isolates recovered from ICU patients in a tertiary care hospital.

Materials and Methods

This hospital-based observational study was conducted in the Department of Microbiology in collaboration with the Intensive Care Unit (ICU) of a tertiary care teaching hospital over a period of 12 months. The study was designed to evaluate the bacteriological profile and antibiotic resistance patterns among clinical isolates obtained from ICU patients.

All patients admitted to the ICU during the study period who showed clinical evidence suggestive of infection and from whom microbiological samples were sent for culture and sensitivity testing were considered eligible for inclusion. Non-duplicate bacterial isolates recovered from various clinical specimens including blood, urine, endotracheal aspirate, sputum, pus, wound swab, central venous catheter tip, and other body fluids were included in the study. Repeat isolates of the same organism with identical antibiograms obtained from the same patient were excluded to avoid duplication bias. Fungal isolates and contaminated samples were also excluded from analysis.

Based on previously published ICU antimicrobial resistance studies reporting culture positivity and multidrug resistance rates ranging between 20% and 50%, a minimum sample size of 250 isolates was considered adequate for reliable descriptive analysis and antimicrobial susceptibility assessment [7,8]. During the study period, a total of 312 culture-positive bacterial isolates fulfilling the inclusion criteria were analyzed.

Clinical specimens were collected under strict aseptic precautions and transported promptly to the microbiology laboratory for processing. Samples were inoculated onto standard culture media including blood agar, MacConkey agar, and chocolate agar wherever appropriate, followed by aerobic incubation at 37°C. Identification of bacterial isolates was performed using standard microbiological techniques based on colony morphology, Gram staining characteristics, and biochemical reactions. In selected cases, automated identification systems were utilized wherever available.

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. Antibiotics tested included beta-lactams, aminoglycosides, fluoroquinolones, carbapenems, glycopeptides, tetracyclines, polymyxins, and other routinely prescribed antimicrobial agents used in ICU practice. The isolates were categorized as sensitive, intermediate, or resistant based on CLSI interpretative criteria. Multidrug resistance was defined as acquired non-susceptibility to at least one agent in three or more antimicrobial classes.

Demographic and microbiological data including age, sex, type of specimen, isolated organism, and antibiotic susceptibility profile were recorded in a structured data collection form. Data were entered into Microsoft Excel and analyzed using Statistical Package for the Social Sciences (SPSS) software version 25.0. Categorical variables were expressed as frequencies and percentages. Continuous variables were represented as mean ± standard deviation wherever applicable.

Prior approval for the study was obtained from the Institutional Ethics Committee before commencement of the study. Patient confidentiality was maintained throughout the study, and no personal identifiers were disclosed at any stage of data analysis or publication.

Results

A total of 312 non-duplicate bacterial isolates obtained from ICU patients were included in the present study. The majority of patients belonged to the age group of 46–60 years (30.8%), followed by patients aged more than 60 years (27.5%). Male patients constituted 60.3% of the study population, while females accounted for 39.7% (Table 1).

Among the various clinical specimens processed, endotracheal aspirates represented the most common source of isolates, contributing 31.4% of the total samples. Blood cultures accounted for 20.5% of isolates, followed by urine specimens (18.6%), sputum samples (13.5%), and pus or wound swabs (10.3%). A smaller proportion of isolates were recovered from central venous catheter tips and other body fluids (Table 2).

Gram-negative organisms predominated among ICU isolates. Klebsiella pneumoniae was identified as the most frequently isolated pathogen, accounting for 26.3% of all isolates, followed by Escherichia coli (18.6%), Acinetobacter baumannii (17.3%), and Pseudomonas aeruginosa (14.7%). Among Gram-positive bacteria, Staphylococcus aureus constituted 12.2% of isolates, while Enterococcus species accounted for 5.8% (Table 3).

Analysis of antimicrobial susceptibility patterns among Gram-negative bacilli demonstrated high resistance rates to third-generation cephalosporins and fluoroquinolones. Resistance to ceftriaxone was observed in 80.5% of Klebsiella pneumoniae isolates, 72.4% of Escherichia coli, 88.9% of Acinetobacter baumannii, and 73.9% of Pseudomonas aeruginosa isolates. Carbapenem resistance was notably high among Acinetobacter baumannii isolates (63.0%). Colistin exhibited the lowest resistance rates across most Gram-negative isolates (Table 4).

Among Gram-positive organisms, resistance to penicillin and erythromycin was frequently observed. Penicillin resistance was detected in 84.2% of Staphylococcus aureus isolates and 77.8% of Enterococcus species. Vancomycin resistance remained low, being identified in only 5.3% of Staphylococcus aureus isolates and 5.6% of Enterococcus isolates. No resistance to linezolid was observed among the Gram-positive isolates included in the study (Table 5).

Multidrug resistance was identified in 50.6% of the total bacterial isolates. The highest prevalence of multidrug resistance was observed among Acinetobacter baumannii isolates (74.1%), followed by Klebsiella pneumoniae (58.5%) and Escherichia coli (48.3%). Comparatively lower multidrug resistance rates were observed among Gram-positive isolates (Table 6).

Table 1: Demographic Characteristics of ICU Patients Included in the Study (n = 312)

Variable	Number of Patients	Percentage (%)
Age Group (Years)		
18–30	52	16.7
31–45	78	25.0
46–60	96	30.8
>60	86	27.5
Gender		
Male	188	60.3
Female	124	39.7

Table 2: Distribution of Clinical Specimens Received from ICU Patients (n = 312)

Specimen Type	Number of Isolates	Percentage (%)
Endotracheal aspirate	98	31.4
Blood	64	20.5
Urine	58	18.6
Sputum	42	13.5
Pus/Wound swab	32	10.3
Central venous catheter tip	10	3.2
Other body fluids	8	2.5

Table 3: Bacteriological Profile of ICU Isolates (n = 312)

Bacterial Isolate	Number of Isolates	Percentage (%)
Klebsiella pneumoniae	82	26.3
Escherichia coli	58	18.6
Acinetobacter baumannii	54	17.3
Pseudomonas aeruginosa	46	14.7
Staphylococcus aureus	38	12.2
Enterococcus spp.	18	5.8
Proteus spp.	10	3.2
Other isolates	6	1.9

Table 4: Antibiotic Resistance Pattern Among Gram-Negative Isolates

Antibiotic	Klebsiella pneumoniae (n=82) Resistant n (%)	E. coli (n=58) Resistant n (%)	Acinetobacter baumannii (n=54) Resistant n (%)	Pseudomonas aeruginosa (n=46) Resistant n (%)
Ceftriaxone	66 (80.5)	42 (72.4)	48 (88.9)	34 (73.9)
Piperacillin–Tazobactam	38 (46.3)	24 (41.4)	36 (66.7)	22 (47.8)
Ciprofloxacin	54 (65.9)	38 (65.5)	40 (74.1)	28 (60.9)
Amikacin	30 (36.6)	18 (31.0)	28 (51.9)	16 (34.8)
Meropenem	26 (31.7)	12 (20.7)	34 (63.0)	14 (30.4)
Colistin	4 (4.9)	2 (3.4)	6 (11.1)	2 (4.3)

Table 5: Antibiotic Resistance Pattern Among Gram-Positive Isolates

Antibiotic	Staphylococcus aureus (n=38) Resistant n (%)	Enterococcus spp. (n=18) Resistant n (%)
Penicillin	32 (84.2)	14 (77.8)
Erythromycin	24 (63.2)	10 (55.6)
Ciprofloxacin	20 (52.6)	8 (44.4)
Gentamicin	14 (36.8)	6 (33.3)
Vancomycin	2 (5.3)	1 (5.6)
Linezolid	0 (0.0)	0 (0.0)

Table 6: Prevalence of Multidrug Resistance Among ICU Isolates

Organism	Total Isolates	MDR Isolates n (%)
Klebsiella pneumoniae	82	48 (58.5)
Escherichia coli	58	28 (48.3)
Acinetobacter baumannii	54	40 (74.1)
Pseudomonas aeruginosa	46	20 (43.5)
Staphylococcus aureus	38	16 (42.1)
Enterococcus spp.	18	6 (33.3)
Total	**312**	**158 (50.6)**

Discussion

The present study demonstrated a high burden of antimicrobial resistance among ICU isolates, with Gram-negative organisms predominating over Gram-positive bacteria. Klebsiella pneumoniae was the most frequently isolated pathogen, followed by Escherichia coli and Acinetobacter baumannii. Similar findings have been reported in recent ICU-based surveillance studies, where Gram-negative bacilli constituted the majority of healthcare-associated infections due to their ability to survive in hospital environments and rapidly acquire resistance determinants [9,10].

In the current study, endotracheal aspirates were the most common source of bacterial isolates. This observation may be attributed to the high frequency of mechanical ventilation and ventilator-associated respiratory infections in critically ill patients. Recent studies conducted in ICU settings have similarly identified respiratory specimens as the predominant source of multidrug-resistant organisms, particularly Acinetobacter baumannii and Pseudomonas aeruginosa [11].

A notable finding of the present study was the high resistance to third-generation cephalosporins and fluoroquinolones among Gram-negative isolates. Resistance to ceftriaxone exceeded 70% in most isolates, while carbapenem resistance was particularly high among Acinetobacter baumannii. Comparable resistance trends have been documented in recent international studies, indicating an alarming rise in carbapenem-resistant Acinetobacter baumannii (CRAB) in ICUs worldwide [12,13]. The increasing prevalence of CRAB poses a major therapeutic challenge because treatment options are often limited to older antibiotics such as colistin and tigecycline.

In our study, colistin retained relatively good activity against most Gram-negative isolates, with low resistance rates observed. Similar susceptibility patterns have been reported in recent molecular and phenotypic studies evaluating multidrug-resistant Acinetobacter baumannii isolates from ICU patients [14]. However, the emergence of colistin-resistant strains reported in some centers raises concern regarding the future effectiveness of last-resort antibiotics.

The prevalence of multidrug resistance in the present study was 50.6%, with the highest rate observed among Acinetobacter baumannii. This finding is consistent with recent genomic surveillance studies demonstrating that ICU-associated Acinetobacter baumannii isolates frequently exhibit extensive drug resistance and harbor multiple resistance genes [15]. Prolonged ICU stay, frequent invasive procedures, prior antibiotic exposure, and cross-transmission within intensive care settings contribute significantly to the spread of resistant pathogens [16].

The findings of the present study emphasize the urgent need for regular antimicrobial resistance surveillance, implementation of stringent infection control measures, and rational antibiotic prescribing practices in ICUs. Development of institution-specific antibiograms and strengthening antimicrobial stewardship programs may help reduce the emergence and dissemination of multidrug-resistant organisms in critical care units.

Conclusion

The present study demonstrated a high prevalence of antimicrobial resistance among bacterial isolates recovered from ICU patients, with Gram-negative organisms being the predominant pathogens. Klebsiella pneumoniae and Acinetobacter baumannii emerged as the most common and highly resistant isolates, showing substantial resistance to commonly prescribed antibiotics including cephalosporins, fluoroquinolones, and carbapenems. The considerable burden of multidrug-resistant organisms observed in the ICU highlights the growing challenge of healthcare-associated infections and limited therapeutic options. Continuous microbiological surveillance, judicious antibiotic utilization, strict infection control practices, and implementation of antimicrobial stewardship programs are essential to reduce the emergence and spread of resistant pathogens in critical care settings.

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