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RESEARCH ARTICLE

ANTIBIOTIC RESISTANCE AND MORTALITY IN ICU PATIENTS: A RETROSPECTIVE ANALYSIS OF FIRST CULTURE GROWTH RESULTS IN RNT MEDICAL COLLEGE, UDAIPUR

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ABSTRACT

Background: Intensive care unit (ICU) patients are highly vulnerable to infections due to immunosuppression, invasive procedures, prolonged hospitalization, and widespread antibiotic exposure. Multidrug-resistant (MDR) organisms remain a major cause of hospital-acquired infections, limiting treatment options and increasing mortality. **Methods:** This retrospective observational study included 60 ICU patients aged ≥18 years with at least one positive microbiological culture. Only the first culture growth per patient was analyzed. Demographic data, clinical diagnoses, isolated organisms, and antibiotic susceptibility patterns were collected. Standard microbiological techniques and CLSI-based antimicrobial susceptibility testing were used. MDR organisms were defined as resistant to ≥1 agent in ≥3 antimicrobial classes. ICU mortality served as the primary outcome. **Results:** The mean patient age was 50.63 ± 18.82 years, with a female predominance (5:1). Respiratory involvement was most common (73.33%), with ventilator-associated pneumonia constituting 23.33% of diagnoses. Among 38 isolates, *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* were the most frequent (13.16% each). Other isolates included *Acinetobacter* species, *Acinetobacter baumannii*, *Enterococcus* species, and several less common pathogens. Antibiotic susceptibility testing revealed widespread resistance. Polymyxin B exhibited the highest activity across multiple Gram-negative organisms, while tigecycline, levofloxacin, and gentamycin showed moderate effectiveness. Carbapenems demonstrated variable sensitivity, and linezolid and vancomycin remained effective primarily against Gram-positive pathogens. **Conclusion:** MDR organisms are prevalent among ICU infections, with Gram-negative pathogens dominating the microbiological landscape. Significant resistance to multiple antibiotic classes underscores the urgent need for continuous surveillance, early targeted therapy, and strengthened antimicrobial stewardship to reduce ICU morbidity and mortality

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INTRODUCTION

Intensive care units (ICUs) provide advanced life-support for critically ill patients, yet these individuals face a markedly increased risk of infection due to factors such as immunosuppression, prolonged hospitalization, invasive procedures, and frequent exposure to broad-spectrum antibiotics.[1] As a result, ICU settings have become a major reservoir for multidrug-resistant (MDR) microorganisms, which significantly contribute to hospital-acquired infections and remain a leading cause of morbidity and mortality in critically ill patients.[2] The growing prevalence of antibiotic resistance further complicates empirical treatment selection and limits therapeutic options, particularly for Gram-negative organisms such as *Klebsiella pneumoniae*, *Escherichia coli*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii*, which frequently exhibit ESBL, AmpC, and carbapenemase production.[3] Similarly, Gram-positive pathogens including methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant *Enterococcus* (VRE) pose additional therapeutic challenges.[4] The clinical impact of these resistance mechanisms is profound, as MDR infections are strongly associated with prolonged ICU stays, increased risk of septic shock, and higher mortality rates.[5] Early and appropriate antimicrobial therapy is essential for improving outcomes; however, inappropriate or delayed treatment increases mortality and fosters further resistance development.[6] Because pathogen distribution and susceptibility patterns vary between hospitals and even among ICUs within the same institution, continuous local surveillance is critical to guide empirical therapy and optimize patient outcomes.[7] Given the rising resistance to carbapenems, cephalosporins, and other broad-spectrum agents[8], understanding local microbiological trends is essential. This retrospective analysis evaluates first culture growth results in ICU patients to assess antibiotic resistance patterns and their association with mortality.

MATERIAL AND METHODS

Study Design and Setting: This retrospective observational study was conducted in the Intensive Care Unit (ICU) of R.N.T. Medical College, Udaipur over a defined study period. The study aimed to evaluate the antibiotic resistance patterns of organisms isolated from the first positive culture of ICU patients and to assess their association with patient mortality.

Study Population: A total of 60 patients aged ≥18 years who were admitted to the ICU and had at least one positive microbiological culture (blood, urine, respiratory, or other sterile site samples) during their ICU stay were included.

Only the first culture growth for each patient was analyzed to avoid duplication and to reflect the initial infectious profile on ICU admission. Patients with incomplete medical records, negative cultures, or those transferred from other hospitals with ongoing antimicrobial therapy were excluded.

Data Collection: Data were retrieved from hospital electronic medical records and laboratory information systems. The following variables were recorded:

Demographic details (age, sex)
Duration of illness before ICU admission
Primary diagnosis and organ system involvement
Type of clinical specimen
Organisms isolated in the first positive culture
Antibiotic susceptibility patterns
ICU stay duration
Patient outcome (survivor/non-survivor)

Microbiological Analysis: Samples were processed according to standard microbiological techniques. Identification of bacterial and fungal isolates was performed using conventional biochemical tests or automated systems, depending on availability. Antimicrobial susceptibility testing (AST) was carried out using the Kirby–Bauer disk diffusion method or automated susceptibility analyzers, following CLSI guidelines. MDR organisms were defined as those resistant to at least one agent in three or more antimicrobial classes.

Outcome Measures: The primary outcome was ICU mortality. The secondary outcome was the distribution and resistance profile of organisms isolated from the first culture.

Statistical Analysis: Data were entered into Microsoft Excel and analyzed using appropriate statistical software. Categorical variables were expressed as frequencies and percentages, while continuous variables were described as mean ± standard deviation. Associations between antibiotic resistance patterns and mortality were evaluated using chi-square or Fisher's exact test, with $p < 0.05$ considered statistically significant.

RESULTS AND OBSERVATIONS

The study population had a mean age of 50.63 ± 18.82 years. There was a female predominance with a female-to-male ratio of 5:1 (50 females and 10 males). The mean duration of illness was 9.4 ± 4.87 days. Among the participants, 32 were alcohol users, while 28 were non-alcoholic. Diabetes mellitus was present in 24 patients, coronary artery disease in 12 patients, and hypertension in 28 patients.

Figure 1. Baseline Characteristics of the Study Participants

Parameter	Value
Age (years), Mean ± SD	50.63 ± 18.82
Gender, n (%)	
• Female	50 (83.3%)
• Male	10 (16.7%)
Duration of illness (days), Mean ± SD	9.4 ± 4.87
Alcohol use, n (%)	
• Alcoholic	32 (53.3%)
• Non-alcoholic	28 (46.7%)
Diabetes Mellitus, n (%)	24 (40.0%)
Hypertension, n (%)	28 (46.7%)
Coronary Artery Disease, n (%)	12 (20.0%)

In figure 2, The distribution of patients according to the system affected showed that the respiratory system was most commonly involved, accounting for 44 patients (73.33%), followed by the nervous system and urinary system, each affecting 6 patients (10.00%), while skin and soft tissue involvement was observed in 4 patients (6.67%). With respect to diagnosis, ventilator-associated pneumonia (VAP) was the most frequent condition, seen in 14 patients (23.33%), followed by VAP with Guillain–Barré syndrome (GBS) in 6 patients (10.00%). Community-acquired pneumonia was diagnosed in 8 patients (13.33%), while meningitis, UTI with sepsis, and CVA with aspiration pneumonitis were each observed in 4 patients (6.67%). Other less frequent diagnoses, each accounting for 2 patients (3.33%), included GBS, acute respiratory distress syndrome, COPD with secondary infection, ILD with secondary infection, pulmonary tuberculosis with ventilator-associated pneumonia (with or without UTI), pneumonia, renal cell carcinoma with right lower zone pneumonitis, and skin and soft tissue infection.

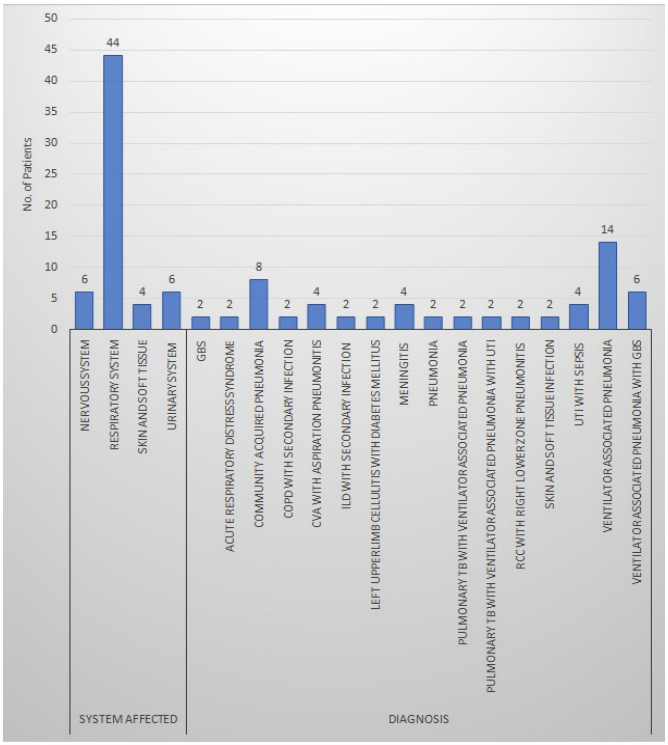

Figure 2. Distribution of Affected Systems and Clinical Diagnoses

In figure 3, The microbiological profile of the study population demonstrated a diverse range of organisms. Escherichia coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa were the most frequently isolated pathogens, each identified in 10

samples (13.16%). A similar proportion of samples were sterile, accounting for 10 cases (13.16%). Acinetobacter species were isolated in 6 cases (7.89%), while Acinetobacter baumannii was identified separately in 4 cases (5.26%). Pseudomonas species other than *P. aeruginosa* were also isolated in 6 samples (7.89%). Less commonly identified organisms, each constituting 2 samples (2.63%), included *Candida glabrata*, *Candida parapsilosis*, *Proteus vulgaris*, *Citrobacter freundii*, *Citrobacter koseri*, coagulase-positive *Staphylococcus aureus*, *Enterococcus*, *Klebsiella oxytoca*, and *Enterococcus species*. Overall, Gram-negative organisms predominated in the isolates, reflecting the significant burden of hospital-acquired and severe infections in the study population.

Figure 3. Microbiological Profile of Clinical Isolates

Organisms	No. of Patients	Percentage
Acinetobacter baumannii	4	5.26
Acinetobacter species	6	7.89
Candida glabrata	2	2.63
Proteus vulgaris	2	2.63
Candida parasilosis	2	2.63
Citrobacter freundi	2	2.63
Citrobacter koseri	2	2.63
Coagulase positive staph aureus	2	2.63
E Coli	10	13.16
Enterococcus	2	2.63
Enterococcus species	4	5.26
Klebsiella oxytoca	2	2.63
Klebsiella pneumoniae	10	13.16
Pseudomonas aeroginosa	10	13.16
Pseudomonas species	6	7.89
Sterile	10	13.16
Total	76	100.00

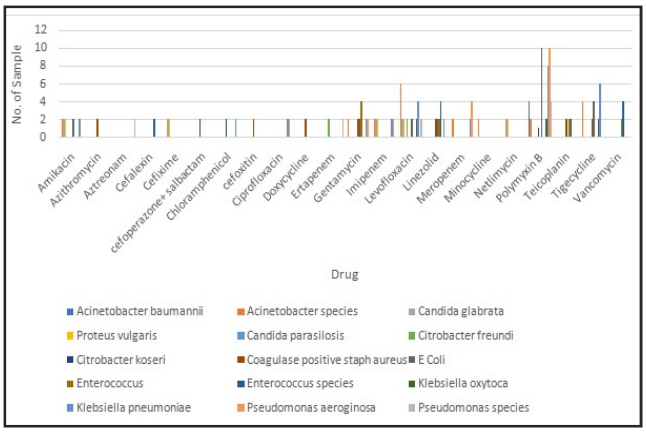

Figure 4: Antibiotic Sensitivity Pattern of Isolated Organisms

In figure 4, The antimicrobial susceptibility pattern revealed considerable variability across the isolated organisms. Gram-negative bacteria, particularly *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*, demonstrated sensitivity predominantly to higher-end antibiotics. Polymyxin B showed the widest activity, with notable sensitivity against *Acinetobacter baumannii*, *Acinetobacter species*, *E. coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and other *Pseudomonas* species, highlighting its role as a last-resort drug. Carbapenems such as imipenem and meropenem exhibited activity against selected isolates of *Acinetobacter species*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa*, though resistance was evident in several organisms. Aminoglycosides (amikacin, gentamicin) and fluoroquinolones (levofloxacin, ciprofloxacin) showed variable and organism-specific sensitivity, with better responses seen in *Acinetobacter species*, *E. coli*, and *Klebsiella pneumoniae*. Tigecycline demonstrated activity against *Acinetobacter species*, *E. coli*, and *Klebsiella pneumoniae*. Among Gram-positive organisms, coagulase-positive *Staphylococcus aureus* and *Enterococcus* species were mainly sensitive to linezolid, teicoplanin, and vancomycin. Overall, the antibiogram reflects a predominance of multidrug-resistant organisms, emphasizing the importance of culture-guided therapy and judicious use of broad-spectrum and reserve antibiotics.

DISCUSSION

In the present study, we evaluated the demographic characteristics, clinical spectrum, microbiological profile, and antimicrobial susceptibility patterns among patients admitted with severe infections. The study population had a mean age of 50.63 ± 18.82 years. There was a female predominance with a female-to-male ratio of 5:1 (50 females and 10 males). The mean duration of illness was 9.4 ± 4.87 days. Among the participants, 32 were alcohol users, while 28 were non-alcoholic. Diabetes mellitus was present in 24 patients, coronary artery disease in 12 patients, and hypertension in 28 patients. Analysis of system involvement demonstrated that the respiratory system was the most commonly affected, accounting for 73.33% of cases. This finding highlights the substantial burden of respiratory illnesses in critically ill patients, particularly those requiring intensive care and mechanical ventilation. Ventilator-associated pneumonia (VAP) emerged as the most frequent diagnosis, either alone (23.33%) or in combination with Guillain–Barré syndrome (GBS) (10.00%). Other significant diagnoses included community-acquired pneumonia, meningitis, urinary tract infection with sepsis, and cerebrovascular accident with aspiration pneumonitis. The predominance of respiratory involvement underscores the vulnerability of critically ill patients to secondary pulmonary infections, especially in the setting of prolonged ventilation and compromised host defenses.

The microbiological profile revealed a predominance of Gram-negative organisms, reflecting the pattern typically observed in hospital-acquired and ICU-related infections. Escherichia coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa were the most frequently isolated pathogens, each accounting for 13.16% of isolates. A notable proportion of samples (13.16%) were sterile, which may be attributable to prior antibiotic exposure before culture sampling. Acinetobacter species, including Acinetobacter baumannii, were also identified and remain clinically significant due to their well-known association with multidrug resistance. Other less frequently isolated organisms included Candida species, Enterococcus, Citrobacter species, Proteus vulgaris, and coagulase-positive Staphylococcus aureus. Overall, the microbiological findings reflect a spectrum of opportunistic and nosocomial pathogens commonly encountered in critically ill patients. In the present study antimicrobial susceptibility pattern demonstrated considerable variability, with a clear trend toward resistance to commonly used antibiotics. Polymyxin B exhibited the broadest activity across multiple Gram-negative organisms, including *Acinetobacter baumannii*, *E. coli*, *Klebsiella pneumoniae*, and *Pseudomonas* species, emphasizing its role as a last-resort agent in the management of multidrug-resistant infections. Carbapenems such as imipenem and meropenem showed activity against selected isolates; however, resistance

was evident in several organisms, reflecting the growing global concern of carbapenem resistance. Aminoglycosides and fluoroquinolones demonstrated organism-specific and variable sensitivity, while tigecycline showed useful activity against Acinetobacter and Enterobacterales. Among Gram-positive isolates, linezolid, teicoplanin, and vancomycin remained effective against *Staphylococcus aureus* and *Enterococcus* species.

A study by Kilinc M et al[9]found that mean age of the patients was 69.5±18.5 years, with the majority belonging to the elderly age group. In terms of gender distribution, 54.9% of the patients were male, while 45.1% were female. Golli et al. observed high rates of MDR in A. baumannii (97.77%), P. aeruginosa (65%), and K. pneumoniae (50%), underscoring the critical impact of these pathogens on patient outcomes.[10]
These findings align with previous studies highlighting the impact of MDR bacteria on poor patient outcomes in critical care settings.[10] The observed antibiogram highlights the high burden of multidrug-resistant organisms in the study population, necessitating reliance on reserve antibiotics. These findings reinforce the importance of culture-guided antimicrobial therapy, robust infection control practices, and strict antimicrobial stewardship to prevent further escalation of resistance. The predominance of respiratory infections further emphasizes the need for adherence to ventilator care bundles, early identification of infections, and timely de-escalation of antibiotics.

CONCLUSION

This study demonstrates that respiratory infections, particularly ventilator-associated pneumonia, are the leading cause of illness among ICU patients. Gram-negative organisms such as *E. coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* were the most frequently isolated pathogens, reflecting a high burden of multidrug-resistant infections. Antibiotic susceptibility patterns showed widespread resistance, with polymyxin B emerging as the most consistently effective drug, while other agents displayed variable activity. These findings highlight the growing challenge of antimicrobial resistance in the ICU and underscore the need for continuous microbiological surveillance, early targeted therapy, and robust antimicrobial stewardship strategies to improve patient outcomes and reduce mortality.

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