Research Article

Antimicrobial Resistance Patterns of Bacterial Isolates from Patients Admitted to the Intensive Care Unit of A Tertiary Care Hospital

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ABSTRACT

Background: In intensive care units (ICUs), where critically sick patients are more vulnerable to healthcare-associated infections brought on by multidrug-resistant organisms, antimicrobial resistance (AMR) is a major problem.

Objective: To assess the trends of antibiotic resistance and ascertain the spread of bacterial infections isolated from intensive care unit patients.

Methods: Over the course of a year, a prospective observational study was carried out in the intensive care unit of a teaching hospital for tertiary care. Standard microbiological techniques were applied to the processing of clinical samples. Antimicrobial susceptibility tests and bacterial identification were carried out in accordance with Clinical and Laboratory Standards Institute (CLSI) recommendations

Results: After processing 420 clinical samples, 300 bacterial isolates were found. The majority were gram-negative organisms (76%). Pseudomonas aeruginosa (22%) and Klebsiella pneumoniae (18%) were the next most commonly isolated pathogens, after Acinetobacter baumannii (30%). Among Gram-negative isolates, cephalosporin, fluoroquinolone, and carbapenem resistance rates were found to be high. Of the isolates of S. aureus, 45% were methicillin-resistant (MRSA) strains. In 68% of the Gram-negative isolates, multidrug resistance was detected.

Conclusion: The high frequency of multidrug-resistant bacteria in intensive care unit patients emphasises the necessity of ongoing monitoring, stringent infection control procedures, and the execution of antimicrobial stewardship initiatives.

Keywords: Antimicrobial resistance, Intensive care units, Multidrug resistance, Bacterial isolates, Antibiogram.

INTRODUCTION

Particularly in intensive care units (ICUs), antimicrobial resistance (AMR) is a rapidly growing global public health issue. Because of their severe underlying conditions, extended hospital stays, frequent exposure to intrusive devices, and heavy use of broad-spectrum antibiotics, ICU patients are particularly vulnerable to infections. Multidrug-resistant organisms (MDROs) that cause healthcare-associated infections dramatically raise morbidity, mortality, and medical expenses[1]. With concerning resistance to several antibiotic classes, including carbapenems, gram-negative bacteria including Acinetobacter baumannii, Pseudomonas aeruginosa, and Klebsiella pneumoniae have become common ICU infections. Effective infection control and antimicrobial stewardship efforts, as well as the direction of empirical therapy, depend on an understanding of local antibiotic resistance patterns. The purpose of this study was to examine the antibiotic resistance trends and bacterial profile of isolates taken from tertiary care intensive care unit patients[2].

METHODS
Study Design and Setting

Over a 1-year period, a prospective observational study was carried out in the adult intensive care unit (ICU) of a tertiary care teaching hospital that treats critically sick surgical and medical patients in Telangana.

Study Population

During the study period, all ICU patients with microbiologically verified bacterial growth and clinical suspicion of infection were included. To reduce duplication and selection bias, only the initial isolate from each patient was examined.

Sample Collection and Microbiological Processing

Standard microbiological procedures were followed in the collection and processing of clinical specimens. Blood, urine, endotracheal aspirates, sputum, and wound swabs were among the sample types. The sample distribution was noted and examined as proportions with matching confidence intervals.

Bacterial Identification

Standard microbiological methods, such as Gramme staining, colony morphology, and biochemical tests, were used to identify the bacterial isolates.

Antimicrobial Susceptibility Testing

The Kirby-Bauer disc diffusion method was used to test for antimicrobial susceptibility, and the results were interpreted in compliance with CLSI recommendations. To show the accuracy of estimations, resistance rates were reported as proportions with 95% confidence intervals (95% CI).

Definition of Multidrug Resistance

According to widely recognised standards, multidrug resistance (MDR) is resistance to at least one antimicrobial agent in three or more antimicrobial classes.

Statistical Analysis

Descriptive statistical techniques were used to examine the data. Frequencies and percentages were used to sum up categorical variables. In order to assess the variability and dependability of resistance rates, 95% confidence intervals were computed for important proportions as needed.

RESULTS
Culture Positivity Rate

300 of the 420 clinical samples that were processed showed notable bacterial growth, resulting in a culture positive rate of 71.4% (95% CI: 67.0–75.7).

Distribution of Clinical Samples

The majority of samples (40.0%; 95% CI: 34.5–45.5) were endotracheal aspirates, followed by blood (26.0%; 95% CI: 21.1–30.9), urine (18.0%; 95% CI: 13.7–22.3), wound/pus samples (12.0%; 95% CI: 8.3–15.7), and sputum (4.0%; 95% CI: 1.8–6.2).

Distribution of Bacterial Isolates

Gram-negative bacteria accounted for 76.0% of isolates (95% CI: 71.2–80.8), while Gram-positive bacteria constituted 24.0% (95% CI: 19.2–28.8).

Acinetobacter baumannii was the most frequently isolated organism (30.0%; 95% CI: 24.8–35.2), followed by Pseudomonas aeruginosa (22.0%; 95% CI: 17.3–26.7) and Klebsiella pneumoniae (18.0%; 95% CI: 13.7–22.3).

Gram-positive bacteria made up 24.0% of isolates (95% CI: 19.2–28.8), whilst Gram-negative bacteria made up 76.0% (95% CI: 71.2–80.8).

The most often isolated bacterium was Acinetobacter baumannii (30.0%; 95% CI: 24.8–35.2), which was followed by Pseudomonas aeruginosa (22.0%; 95% CI: 17.3–26.7) and Klebsiella pneumoniae (18.0%; 95% CI: 13.7–22.3).

Antimicrobial Resistance Patterns
Gram-Negative Isolates

92% of isolates had ampicillin resistance (95% CI: 88.4–95.6). Third-generation cephalosporin resistance varied from 74% to 78% (95% CI roughly: 68.2–82.5). 69% of isolates had fluoroquinolone resistance (95% CI: 63.0–75.0).

For imipenem (95% CI: 41.5–54.5) and meropenem (95% CI: 38.6–51.4), carbapenem resistance was found in 48% and 45% of isolates, respectively. 6% of isolates had colistin resistance (95% CI: 3.0–9.0).

Gram-Positive Isolates: Methicillin resistance was seen in 45% of Staphylococcus aureus isolates (95% CI: 30.2–59.8). While all isolates remained sensitive to vancomycin and linezolid (100% susceptibility; 95% CI: 94.9–100), resistance to erythromycin and fluoroquinolones approached 50%.

Multidrug Resistance

A significantly greater MDR burden among Gram-negative organisms was seen in 68% of Gram-negative isolates (95% CI: 61.9–74.1) and 32% of Gram-positive isolates (95% CI: 21.2–42.8).

Sample type	Number (%)
Endotracheal aspirates	120 (40.0)
Blood	78 (26.0)
Urine	54 (18.0)
Pus/Wound swabs	36 (12.0)
Sputum	12 (4.0)

Bacterial Isolates

Gram-negative bacteria constituted 228 (76%) isolates, while Gram-positive bacteria accounted for 72 (24%).

Organism	Number (%)
Acinetobacter baumannii	90 (30.0)
Pseudomonas aeruginosa	66 (22.0)
Klebsiella pneumoniae	54 (18.0)
Escherichia coli	18 (6.0)
Staphylococcus aureus	44 (14.6)
Enterococcus spp	28 (9.4)

DISCUSSION

Gram-negative organisms accounted for more than three-quarters of the isolates (76%; 95% CI: 71.2–80.8), indicating a high incidence of antibiotic resistance among bacterial isolates from ICU patients. The results are highly precise and reliable, as evidenced by the small confidence intervals seen for large resistance estimations[5,6].

Acinetobacter baumannii was the most common pathogen, accounting for 30% of isolates (95% CI: 24.8–35.2). Treatment options are severely limited by high rates of resistance to cephalosporins and carbapenems, with carbapenem resistance approaching 50%. Despite being modest (6%; 95% CI: 3.0–9.0), colistin resistance is clinically significant due to the scarcity of treatment options. Gram-positive resistance in ICU settings is still relevant, as seen by the incidence of MRSA (45%; 95% CI: 30.2–59.8). Nonetheless, the continued susceptibility to linezolid and vancomycin indicates that these medications are still effective when used as directed. Gram-negative isolates have a greater percentage of MDR (68%; 95% CI: 61.9–74.1) than Gram-positive isolates, which highlights the critical need for focused antimicrobial stewardship and infection control measures in intensive care units[7,8].

CONCLUSION

More than two-thirds of the ICU bacterial isolates demonstrate multidrug resistance, reflecting a substantial burden of antibiotic resistance, especially among Gram-negative species. Consistent and clinically relevant resistance patterns are shown by the confidence intervals related to resistance estimate[9,10]. To stop the spread of multidrug-resistant organisms and enhance patient outcomes in critical care settings, routine antimicrobial resistance surveillance with periodic ICU-specific antibiogram generation, sensible antibiotic use, and improved infection control practices are crucial.

REFERENCES

1. World Health Organization. Global action plan on antimicrobial resistance. Geneva: WHO; 2015.
2. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing. CLSI supplement M100. Wayne, PA; 2023.
3. Vincent JL, Rello J, Marshall J, et al. International study of the prevalence and outcomes of infection in intensive care units. JAMA. 2009;302(21):2323–2329.
4. Magiorakos AP, Srinivasan A, Carey RB, et al. Multidrug-resistant, extensively drug-resistant and pandrug-resistant bacteria. Clin Microbiol Infect. 2012;18(3):268–281.
5. Tacconelli E, Carrara E, Savoldi A, Harbarth S, Mendelson M, Monnet DL, et al. Discovery, research, and development of new antibiotics: the WHO priority list of antibiotic-resistant bacteria. Lancet Infect Dis. 2018;18(3):318–327.

6. Sievert DM, Ricks P, Edwards JR, Schneider A, Patel J, Srinivasan A, et al. Antimicrobial-resistant pathogens associated with healthcare-associated infections. Infect Control Hosp Epidemiol. 2013;34(1):1–14.

7. Paterson DL, Bonomo RA. Extended-spectrum β-lactamases: a clinical update. Clin Microbiol Rev. 2005;18(4):657–686.

8. Rice LB. Federal funding for the study of antimicrobial resistance in nosocomial pathogens: no ESKAPE. J Infect Dis. 2008;197(8):1079–1081.

9. Kollef MH, Golan Y, Micek ST, Shorr AF, Restrepo MI. Appraising contemporary strategies to combat multidrug resistant Gram-negative bacterial infections. Proc Am Thorac Soc. 2011;8(6):546–551.

10. Tängdén T, Giske CG. Global dissemination of extensively drug-resistant carbapenemase-producing Enterobacteriaceae: clinical perspectives on detection, treatment and infection control. J Intern Med. 2015;277(5):501–512.