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A STUDY ON BACTERIOLOGICAL PROFILE AND ANTIBIOGRAM OF BLOOD CULTURE ISOLATES FROM CRITICAL CARE UNITS IN A TERTIARY CARE CENTRE OF WESTERN UTTAR PRADESH

Clinical Microbiology

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ABSTRACT

Bloodstream infections (BSIs) are a major cause of morbidity and mortality in critically ill patients, especially in intensive care units where invasive procedures and prolonged hospitalization increase infection risk. The emergence of multidrug-resistant (MDR) organisms further complicates treatment.This cross-sectional study was conducted in critical care units of a tertiary care centre in Western Uttar Pradesh. Blood samples from suspected sepsis cases were processed using standard microbiological methods. Identification of isolates was done by conventional and automated techniques. Antimicrobial susceptibility testing was performed by the Kirby–Bauer disc diffusion method as per Clinical and Laboratory Standards Institute (CLSI) guidelines. Of the total blood cultures processed, 31.5% were positive. Gram-negative bacilli predominated, with Klebsiella pneumoniae (28.6%), Escherichia coli (13.4%), and Pseudomonas aeruginosa (7.3%) being the most common isolates. Among Gram-positive organisms, Staphylococcus aureus (30%) was predominant, including methicillin-resistant strains. High resistance was noted to cephalosporins and fluoroquinolones, while carbapenems, colistin, vancomycin, and linezolid remained effective. MDR Gram-negative organisms predominate in ICU-related BSIs. Continuous antibiogram surveillance and strict antimicrobial stewardship are essential for effective management.

KEYWORDS

Bloodstream infection, antibiogram, critical care, multidrug resistance, tertiary care centre.

INTRODUCTION

Bloodstream infections (BSIs) represent a significant clinical challenge worldwide and are associated with considerable morbidity and mortality, particularly among critically ill patients [1]. These infections may be classified as primary when no identifiable source is detected, or secondary when a definite focus of infection is established [2]. The presence of viable microorganisms in the bloodstream, irrespective of clinical manifestations, is defined as bacteremia.

The spectrum of pathogens responsible for BSIs varies across geographical regions and healthcare settings. Gram-positive organisms such as *Staphylococcus spp.*, *Enterococcus spp.*, and coagulase-negative staphylococci (CoNS) are frequently encountered, while Gram-negative bacteria including *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* have increasingly emerged as predominant pathogens in hospital settings [3].

In intensive care units (ICUs), BSIs constitute a serious but potentially preventable complication. Critically ill patients are particularly vulnerable due to factors such as prolonged hospitalization, invasive procedures, mechanical ventilation, and immunocompromised status. These infections significantly contribute to increased healthcare costs, extended hospital stays, and higher mortality rates. Inappropriate empirical antimicrobial therapy, which occurs in a substantial proportion of cases, has been shown to adversely affect patient outcomes [4–7].

Device-associated infections, especially catheter-related bloodstream infections, represent a major proportion of ICU-acquired BSIs [8,9]. Additionally, infections such as ventilator-associated pneumonia frequently act as sources of secondary bacteremia [10,11]. Blood culture remains the gold standard for diagnosis, and timely identification of the causative organism along with its antimicrobial susceptibility pattern is essential for appropriate management.

In view of the rising burden of multidrug-resistant organisms, periodic surveillance of bacteriological profiles and antibiogram patterns is crucial. Therefore, the present study was undertaken to evaluate the distribution of blood culture isolates and their antimicrobial susceptibility patterns among patients admitted to critical care units in a tertiary care centre of Western Uttar Pradesh.

MATERIALS AND METHODS

This prospective study was conducted in the Department of Microbiology at K.D. Medical College Hospital & Research Centre, Mathura, after obtaining approval from the Institutional Ethics Committee. The study was carried out over a period of one year, from July 2024 to June 2025.

All blood culture samples obtained from hospitalized patients admitted to various intensive care units (ICUs) during the study period were included. Samples showing mixed bacterial growth, repeat samples from the same patient, and those yielding probable contaminants such as diphtheroids, *Micrococcus*, and aerobic spore-forming *Bacillus* species were excluded from the study. All isolates obtained from culture-positive blood samples during the study period were analyzed.

Blood samples were collected under strict aseptic precautions and inoculated into blood culture bottles. An automated blood culture system (BACTEC) was used for incubation and detection of microbial growth. Bottles flagged positive by the system were removed aseptically, and samples were subcultured onto 5% sheep blood agar and MacConkey agar plates. The inoculated plates were incubated aerobically at 37°C for 18–24 hours.

Identification of bacterial isolates was performed based on colony morphology, Gram staining, and standard biochemical tests. Antimicrobial susceptibility testing (AST) of all isolates was carried out on Mueller–Hinton agar using the Kirby–Bauer disc diffusion method. The results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) 2022 guidelines [12]. Commercially available antibiotic discs (HiMedia Laboratories Pvt. Ltd., India) were used for susceptibility testing.

RESULTS

A total of 520 blood culture samples were received from patients admitted to various critical care units (Medical ICU, Surgical ICU, Neonatal ICU, and Pediatric ICU) during the study period. Of these, 164 samples (31.5%) yielded significant bacterial growth, while 356 samples (68.5%) showed no growth after 5 days of incubation.

1. Distribution of Blood Culture Positivity Across Critical Care Units

Among the positive cultures, the highest yield was from the Medical ICU (42.7%), followed by the Surgical ICU (28.7%), Neonatal ICU (18.3%), and Pediatric ICU (10.3%).

Table-1: Distribution of blood culture positivity across critical care units

ICU Type	Samples Received (n)	Culture Positive (n)	Culture Positivity (%)
Medical ICU	210	70	33.3
Surgical ICU	150	47	31.3
Neonatal ICU	90	30	33.3
Pediatric ICU	70	17	24.3
Total	520	164	31.5

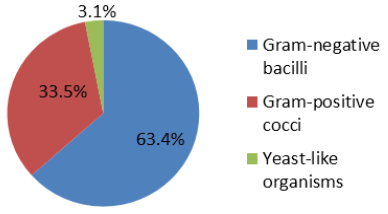
2. Gram Stain Distribution of Isolates

Out of the 164 isolates, Gram-negative bacteria predominated (63.4%), followed by Gram-positive cocci (33.5%), and yeast-like organisms (3.1%).

Table 2- Gram Stain Distribution Of Blood Culture Isolates

Type of Organism	Number of Isolates (n=164)	Percentage (%)
Gram-negative bacilli	104	63.4
Gram-positive cocci	55	33.5
Yeast-like organisms	5	3.1
Total	164	100

Fig.-1: Gram stain distribution of Blood Culture Isolates



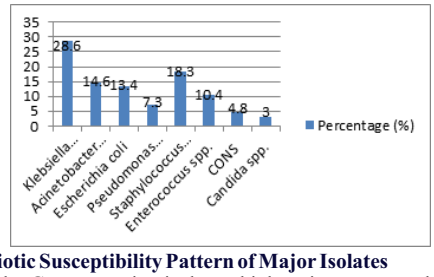
3. Bacteriological Profile of Blood Culture Isolates

The most common isolate was Klebsiella pneumoniae (28.6%), followed by Acinetobacter baumannii (14.6%), Escherichia coli (13.4%), and Pseudomonas aeruginosa (7.3%) among Gram-negative bacteria. Among Gram-positive cocci, Staphylococcus aureus (18.3%) (of which 64.7% were MRSA) was predominant, followed by Enterococcus spp. (10.4%) and Coagulase-Negative Staphylococci (CONS) (4.8%).

Table 3- Bacteriological Profile of Blood Culture Isolates

Organism Isolated	No. of Isolates (n=164)	Percentage (%)
Klebsiella pneumoniae	47	28.6
Acinetobacter baumannii	24	14.6
Escherichia coli	22	13.4
Pseudomonas aeruginosa	12	7.3
Staphylococcus aureus	30	18.3
Enterococcus spp.	17	10.4
CONS (Staph. epidermidis)	8	4.8
Candida spp.	5	3.0
Total	164	100

Fig. 2- Distribution of bacterial isolates from blood cultures



4. Antibiotic Susceptibility Pattern of Major Isolates

Among the Gram-negative isolates, high resistance was observed to third-generation cephalosporins. Carbapenems (meropenem, imipenem) and colistin showed the highest sensitivity, followed by piperacillin-tazobactam and amikacin.

Table 4 - Antibiotic Susceptibility Pattern of Gram negative Isolates

Antibiotic	K. pneumoniae (%)	A. baumannii (%)	E. coli (%)	P. aeruginosa (%)
Amikacin	52	38	68	58
Cefotaxime	20	10	25	15
Ceftazidime	25	15	30	20
Piperacillin Tazobactam	48	40	65	60
Meropenem	72	55	78	70
Imipenem	74	50	80	68
Colistin	98	96	100	100

Among Gram-positive cocci, vancomycin (100%) and linezolid (98%) retained excellent activity. High resistance to penicillin (86%) and erythromycin (70%) was observed among S. aureus isolates.

5. Multidrug Resistance (MDR) Profile

Out of 164 isolates, 68 (41.5%) were identified as multidrug-resistant (MDR) based on standard criteria (resistance to ≥1 agent in ≥3 antimicrobial classes). MDR was most frequent in A. baumannii (62.5%) and K. pneumoniae (55.3%), followed by S. aureus (40.0%). Among Staphylococcus aureus isolates, 30% were found to be methicillin-resistant (MRSA) based on cefoxitin resistance.

Table 5 - Antibiotic Susceptibility Pattern of Gram positive Isolates

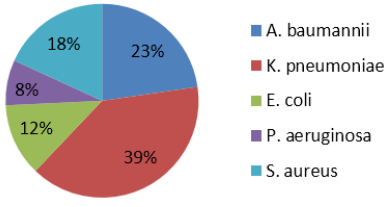
Antibiotic	S. aureus (%)	Enterococcus spp. (%)	CONS (%)
Cefoxitin*	70	_	75
Penicillin	14	20	10
Erythromycin	30	40	25
Clindamycin	55	60	50
Ciprofloxacin	48	45	40
Gentamicin	60	55	58
Vancomycin	100	100	100
Linezolid	98	96	100
Teicoplanin	95	94	100

*Cefoxitin resistance was used as a surrogate marker for detection of methicillin-resistant Staphylococcus aureus (MRSA) as per CLSI guidelines.

Table 6 - Multidrug Resistance (MDR) Profile

Organism	MDR Isolates (n)	MDR (%)
A. baumannii	15	62.5
K. pneumoniae	26	55.3
E. coli	8	36.3
P. aeruginosa	5	41.6
S. aureus	12	40.0
Total MDR	68	41.5

Fig. 3- Distribution of MDR isolates (%)



Summary of Findings:

- Blood culture positivity rate: 31.5%
- Predominance of Gram-negative bacilli (63.4%)
- Most frequent isolate: K. pneumoniae (28.6%)
- Carbapenems and colistin were the most effective agents for Gram-negatives.
- Vancomycin and linezolid retained activity against Gram-positive cocci.
- MDR prevalence among total isolates: 41.5%, with highest rates in *A. baumannii* and *K. pneumoniae.* - 30% of *S. aureus* isolates were MRSA based on cefoxitin resistance.

DISCUSSION

Bloodstream infections in critically ill patients continue to pose a major therapeutic and epidemiological challenge due to their rapid progression and association with high mortality. The findings of the present study demonstrate a clear predominance of Gram-negative organisms, along with a substantial burden of multidrug resistance, which is consistent with recent trends observed in tertiary care settings [13–15].

The predominance of Gram-negative bacilli, particularly *Klebsiella pneumoniae* and *Acinetobacter baumannii*, reflects the evolving epidemiology of ICU infections. This shift may be attributed to increased use of invasive devices, prolonged ICU stays, and selective antibiotic pressure. These organisms are well known for their ability to acquire multiple resistance mechanisms, including production of extended-spectrum β-lactamases and carbapenemases, which significantly limit therapeutic options [16–19].

The isolation of *Staphylococcus aureus*, including a considerable proportion of methicillin-resistant strains, highlights the continued relevance of Gram-positive pathogens in bloodstream infections. Coagulase-negative staphylococci (CoNS) also remain important, particularly in the context of device-related infections. The preserved susceptibility of Gram-positive isolates to vancomycin and linezolid is encouraging; however, continuous monitoring is necessary to detect any emerging resistance [20,21,22]. These patterns reinforce the need for accurate species identification and susceptibility testing to distinguish contaminants from true pathogens (particularly for CoNS) and to steer therapy [23].

The antimicrobial susceptibility patterns observed in this study indicate high resistance to commonly used antibiotics such as third-generation cephalosporins and fluoroquinolones. This finding underscores the limited utility of these agents as empirical therapy in ICU settings. Carbapenems and colistin demonstrated comparatively higher efficacy against Gram-negative isolates, although increasing reliance on these last-resort drugs raises concerns regarding the emergence of pan-resistant strains and associated toxicity [14,16,18]. The high prevalence of multidrug-resistant organisms observed in the present study further emphasizes the need for rational antibiotic use. Empirical therapy in ICU patients should be guided by local antibiogram data rather than generalized treatment protocols. Early initiation of appropriate therapy, followed by de-escalation based on culture results, is essential to improve clinical outcomes and reduce selective pressure [13,17,20].

Infection prevention and control measures play a pivotal role in reducing the incidence of bloodstream infections. Strict adherence to hand hygiene, aseptic techniques during invasive procedures, and implementation of device-care bundles are critical components of infection control strategies. Regular surveillance and feedback mechanisms can further help in identifying lapses and improving compliance [24].

From a diagnostic perspective, timely processing of blood cultures and accurate identification of pathogens are crucial for guiding therapy. Strengthening laboratory capacity and ensuring rapid reporting can significantly enhance patient management and antimicrobial stewardship efforts [15,19].

This study has certain limitations, including its single-centre design and lack of molecular characterization of resistance mechanisms. Additionally, correlation with clinical outcomes was not assessed. Despite these limitations, the study provides valuable insight into the local epidemiology and resistance patterns of bloodstream infections in critical care settings. Future studies incorporating multicentre data and molecular analysis of resistance determinants would further enhance understanding and help in developing region-specific guidelines. Implementation of robust antimicrobial stewardship programs, along with continuous surveillance, is essential to combat the growing threat of antimicrobial resistance [13,14,16].

CONCLUSION

In conclusion, our study reinforces that bloodstream infections in ICU settings of tertiary care centres in India are frequently caused by Gram-negative pathogens with high levels of antimicrobial resistance. Localized empiric therapy guided by unit antibiograms, robust antimicrobial stewardship, strict infection control, and improved diagnostic capacity are critical to optimize care for critically ill patients and to contain the threat of multidrug resistance in the region. Continued surveillance, combined with interventional studies linking stewardship and IPC measures to clinical outcomes, is urgently needed to inform evidence-based policy at institutional and state levels.

CONFLICT OF INTEREST- There are no conflicts of interest.

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