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Antibiotic Resistance Patterns in Bloodstream Infections at a Tertiary Care Teaching Hospital in Rajasthan

Vinit Kumar[1], Alok Chaudhary[2], Aditi Goyal[3]*

[1]Assistant Professor, Department of General Medicine, Geetanjali Institute of Medical Sciences, Jaipur, Rajasthan, India
[2]Assistant Professor, Department of General Medicine, Geetanjali Institute of Medical Sciences, Jaipur, Rajasthan, India
[3]Assistant Professor, Department of General Medicine, Geetanjali Institute of Medical Sciences, Jaipur, Rajasthan, India

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Corresponding Author:

Dr. Aditi Goyal
Assistant Professor, Department of General Medicine,
Geetanjali Institute of Medical Sciences,
Jaipur, Rajasthan, India
Email: adi12goel@gmail.com

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ABSTRACT

Background: Bloodstream infections (BSIs) are a major cause of morbidity and mortality among hospitalized patients worldwide. The increasing emergence of multidrug-resistant organisms has significantly complicated the management of bloodstream infections and has become a major public health concern. Continuous surveillance of antimicrobial resistance patterns is essential for guiding empirical therapy and implementing effective antimicrobial stewardship programs.

Aim: To study the bacterial profile and antibiotic resistance patterns among bloodstream infection isolates in patients attending a tertiary care teaching hospital.

Materials and Methods: This retrospective observational study was conducted in the Department of Microbiology at Geetanjali Institute of Medical Sciences, Jaipur, Rajasthan, over a period of six months from August 2025 to January 2026. A total of 1,250 blood culture samples received from clinically suspected cases of bloodstream infection were included in the study. Blood culture samples were processed using standard microbiological techniques, and bacterial isolates were identified by conventional biochemical methods. Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines. Data were analyzed using descriptive statistical methods.

Results: Out of 1,250 blood culture samples processed, 210 (16.8%) showed significant bacterial growth. Gram-negative organisms predominated, accounting for 62.4% of isolates, while Gram-positive organisms constituted 37.6%. Escherichia coli (28.1%) was the most common isolate followed by Klebsiella pneumoniae (22.4%) and Staphylococcus aureus (18.6%). High resistance rates were observed against third-generation cephalosporins and fluoroquinolones among Gram-negative isolates. Carbapenem resistance was observed predominantly among Klebsiella pneumoniae and Acinetobacter baumannii. Methicillin-resistant Staphylococcus aureus (MRSA) accounted for 43.6% of S. aureus isolates. Vancomycin and linezolid retained good sensitivity against Gram-positive organisms. Multidrug resistance was identified in 45.7% of total isolates.

Conclusion: The present study demonstrated a high prevalence of multidrug-resistant bloodstream pathogens, particularly among Gram-negative bacteria. Regular monitoring of antimicrobial susceptibility patterns, implementation of antimicrobial stewardship programs, and rational antibiotic prescribing practices are essential to reduce the burden of antimicrobial resistance and improve patient outcomes in bloodstream infections.

Keywords*: Bloodstream infections; antimicrobial resistance; multidrug resistance; bacteremia; antibiogram; sepsis.*

INTRODUCTION

Bloodstream infections (BSIs) are among the leading causes of morbidity and mortality in hospitalized patients and represent a major challenge to healthcare systems worldwide [1]. These infections occur when pathogenic microorganisms invade the bloodstream, resulting in systemic inflammatory responses that may progress to severe sepsis, septic shock, and multi-organ dysfunction if not diagnosed and treated promptly [2]. Early identification of causative organisms and initiation of appropriate antimicrobial therapy are essential for improving clinical outcomes and reducing mortality.

In recent years, antimicrobial resistance (AMR) has emerged as one of the most significant global public health threats [3]. The widespread and irrational use of antibiotics in both community and hospital settings has accelerated the development of resistant bacterial strains, thereby limiting therapeutic options and increasing healthcare burden [4]. Multidrug-resistant organisms are increasingly implicated in bloodstream infections and are associated with prolonged hospitalization, increased treatment costs, and poor prognosis [5].

Gram-negative bacteria such as *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* are commonly isolated pathogens in bloodstream infections and have shown rising resistance to third-generation cephalosporins, fluoroquinolones, and carbapenems [6]. Similarly, Gram-positive organisms including methicillin-resistant *Staphylococcus aureus* (MRSA) and resistant Enterococci continue to contribute significantly to hospital-acquired bloodstream infections [7].

Several studies conducted in Indian tertiary care centers have highlighted the increasing prevalence of resistant bloodstream pathogens and changing microbial epidemiology. Agarwal et al. reported a significant prevalence of bacterial isolates causing bloodstream infections in admitted patients at a tertiary care center, emphasizing the growing burden of resistant Gram-negative bacilli [8]. Hospital-based surveillance studies have further demonstrated the increasing emergence of healthcare-associated infections caused by resistant organisms among critically ill and immunocompromised patients [9].
Invasive fungal infections and opportunistic Candida infections have also become increasingly common among hospitalized and critically ill patients, particularly in intensive care settings [10,11]. These infections frequently coexist with bloodstream infections and complicate antimicrobial management due to prolonged hospitalization, broad-spectrum antibiotic exposure, and underlying comorbidities.

Antibiotic susceptibility patterns vary across geographical regions and healthcare settings depending on antimicrobial prescribing practices, infection control measures, and patient characteristics [12]. Therefore, periodic surveillance of local antimicrobial resistance trends is essential for guiding empirical therapy, developing institutional antibiograms, and implementing effective antimicrobial stewardship programs.

Considering the increasing burden of multidrug-resistant bloodstream infections, the present study was conducted at Geetanjali Institute of Medical Sciences, Jaipur, Rajasthan, to evaluate the bacterial profile and antibiotic resistance patterns among bloodstream infection isolates during the study period from August 2025 to January 2026.

MATERIALS AND METHODS

Study Design

This was a retrospective observational study conducted to evaluate the bacterial profile and antibiotic resistance patterns among bloodstream infection isolates obtained from patients admitted to a tertiary care teaching hospital.

Study Setting

The study was carried out in the Department of Microbiology, Geetanjali Institute of Medical Sciences, Jaipur, Rajasthan, in collaboration with various clinical departments of the hospital.

Study Duration

The study was conducted over a period of six months from August 2025 to January 2026.

Study Population

All patients clinically suspected of bloodstream infection or septicemia whose blood samples were sent to the microbiology laboratory for blood culture and antimicrobial susceptibility testing during the study period were included in the study.

Sample Size

A total of 1,250 blood culture samples received during the study period were included and analyzed.

Inclusion Criteria

1. Patients of all age groups and both genders with clinical suspicion of bloodstream infection/septicemia.
2. Blood culture samples received during the study period from inpatient departments, intensive care units, and emergency wards.
3. Samples yielding significant bacterial growth on culture.

Exclusion Criteria

1. Repeat isolates from the same patient with identical antimicrobial susceptibility patterns.
2. Contaminated blood culture samples.
3. Samples with incomplete clinical or laboratory records.
4. Fungal isolates and non-bacterial contaminants were excluded from final analysis.

Sample Collection

Blood samples were collected aseptically by trained healthcare personnel following standard sterile precautions. The venipuncture site was disinfected using 70% isopropyl alcohol followed by povidone-iodine solution. Approximately 5–10 mL of blood was collected from adult patients and 1–3 mL from pediatric patients and inoculated immediately into blood culture bottles containing appropriate culture media.

Processing of Blood Culture Samples

Blood culture bottles were incubated aerobically and monitored for evidence of microbial growth. Positive blood cultures were subcultured onto Blood agar and MacConkey agar plates and incubated at 37°C for 18–24 hours under standard laboratory conditions.

Bacterial isolates were identified based on colony morphology, Gram staining characteristics, and standard biochemical tests including catalase test, coagulase test, oxidase test, indole test, citrate utilization test, urease test, triple sugar iron test, and motility testing as appropriate.

Antimicrobial Susceptibility Testing

Antibiotic susceptibility testing was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar according to Clinical and Laboratory Standards Institute (CLSI) guidelines [12].
The antibiotics tested for Gram-negative isolates included:

- Ampicillin
- Amoxicillin-clavulanic acid
- Ceftriaxone
- Cefepime
- Piperacillin-tazobactam
- Ciprofloxacin
- Amikacin
- Gentamicin
- Meropenem
- Imipenem

The antibiotics tested for Gram-positive isolates included:

- Penicillin
- Cefoxitin
- Erythromycin
- Clindamycin
- Ciprofloxacin
- Vancomycin
- Linezolid

Methicillin resistance in *Staphylococcus aureus* was detected using cefoxitin disc diffusion testing. Multidrug resistance (MDR) was defined as resistance to three or more classes of antimicrobial agents.

Quality Control

Quality control procedures for culture media and antimicrobial susceptibility testing were performed using standard American Type Culture Collection (ATCC) reference strains according to CLSI recommendations.

Data Collection

Relevant demographic and laboratory data including age, gender, ward/ICU admission, blood culture findings, isolated organisms, and antimicrobial susceptibility results were collected from microbiology laboratory records and entered into a predesigned data collection sheet.

Statistical Analysis

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. Resistance patterns among bacterial isolates were analyzed descriptively. Chi-square test was applied where appropriate, and a p-value <0.05 was considered statistically significant.

RESULTS

A total of 1,250 blood culture samples were received in the Department of Microbiology during the study period from August 2025 to January 2026. Out of these, 210 samples showed significant bacterial growth, giving an overall blood culture positivity rate of 16.8%, while 1,040 samples (83.2%) showed no growth or were sterile after the incubation period. Among the culture-positive cases, male patients constituted 126 (60.0%) cases and female patients accounted for 84 (40.0%) cases. The majority of bloodstream infections were observed in patients admitted to intensive care units and medical wards.

Gram-negative organisms were the predominant isolates, accounting for 131 (62.4%) isolates, whereas Gram-positive organisms constituted 79 (37.6%) isolates. Among Gram-negative bacteria, *Escherichia coli* was the most common isolate followed by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. Among Gram-positive organisms, *Staphylococcus aureus* was the predominant pathogen.

Table 1: Distribution of Bacterial Isolates from Bloodstream Infections

Organism	Number of Isolates (n=210)	Percentage (%)
Escherichia coli	59	28.1
Klebsiella pneumoniae	47	22.4
Staphylococcus aureus	39	18.6
Pseudomonas aeruginosa	24	11.4
Acinetobacter baumannii	18	8.6
Coagulase-negative Staphylococci (CONS)	13	6.2
Enterococcus species	10	4.7

Among the Gram-negative isolates, a high degree of resistance was observed against third-generation cephalosporins and fluoroquinolones. Resistance to carbapenems was also significant, particularly among *Klebsiella pneumoniae* and *Acinetobacter baumannii*. Aminoglycosides and beta-lactam/beta-lactamase inhibitor combinations demonstrated comparatively better sensitivity patterns.

Table 2: Antibiogram of *Escherichia coli* Isolates (n=59)

Antibiotic	Sensitive n (%)	Resistant n (%)
Ampicillin	11 (18.6)	48 (81.4)
Amoxicillin-clavulanate	19 (32.2)	40 (67.8)
Ceftriaxone	16 (27.1)	43 (72.9)
Cefepime	20 (33.9)	39 (66.1)
Piperacillin-tazobactam	42 (71.2)	17 (28.8)
Ciprofloxacin	21 (35.6)	38 (64.4)
Gentamicin	34 (57.6)	25 (42.4)
Amikacin	46 (78.0)	13 (22.0)
Meropenem	48 (81.4)	11 (18.6)
Imipenem	49 (83.1)	10 (16.9)

Table 3: Antibiogram of *Klebsiella pneumoniae* Isolates (n=47)

Antibiotic	Sensitive n (%)	Resistant n (%)
Ampicillin	5 (10.6)	42 (89.4)
Amoxicillin-clavulanate	14 (29.8)	33 (70.2)
Ceftriaxone	12 (25.5)	35 (74.5)
Cefepime	15 (31.9)	32 (68.1)
Piperacillin-tazobactam	29 (61.7)	18 (38.3)
Ciprofloxacin	18 (38.3)	29 (61.7)
Gentamicin	24 (51.1)	23 (48.9)
Amikacin	34 (72.3)	13 (27.7)
Meropenem	31 (66.0)	16 (34.0)
Imipenem	32 (68.1)	15 (31.9)

Table 4: Antibiogram of *Pseudomonas aeruginosa* Isolates (n=24)

Antibiotic	Sensitive n (%)	Resistant n (%)
Piperacillin-tazobactam	17 (70.8)	7 (29.2)
Ceftazidime	14 (58.3)	10 (41.7)
Cefepime	15 (62.5)	9 (37.5)
Ciprofloxacin	11 (45.8)	13 (54.2)
Gentamicin	13 (54.2)	11 (45.8)

Amikacin	18 (75.0)	6 (25.0)
Meropenem	16 (66.7)	8 (33.3)
Imipenem	17 (70.8)	7 (29.2)

Table 5: Antibiogram of *Acinetobacter baumannii* Isolates (n=18)

Antibiotic	Sensitive n (%)	Resistant n (%)
Ceftriaxone	3 (16.7)	15 (83.3)
Cefepime	4 (22.2)	14 (77.8)
Piperacillin-tazobactam	8 (44.4)	10 (55.6)
Ciprofloxacin	5 (27.8)	13 (72.2)
Gentamicin	7 (38.9)	11 (61.1)
Amikacin	9 (50.0)	9 (50.0)
Meropenem	8 (44.4)	10 (55.6)
Imipenem	8 (44.4)	10 (55.6)

Among Gram-positive isolates, high resistance to penicillin and erythromycin was observed. Methicillin-resistant *Staphylococcus aureus* (MRSA) accounted for 42.1% of *S. aureus* isolates. However, vancomycin and linezolid retained excellent activity against almost all Gram-positive isolates.

Table 6: Antibiogram of *Staphylococcus aureus* Isolates (n=39)

Antibiotic	Sensitive n (%)	Resistant n (%)
Penicillin	8 (20.5)	31 (79.5)
Cefoxitin	22 (56.4)	17 (43.6)
Erythromycin	18 (46.2)	21 (53.8)
Clindamycin	25 (64.1)	14 (35.9)
Ciprofloxacin	19 (48.7)	20 (51.3)
Gentamicin	27 (69.2)	12 (30.8)
Vancomycin	38 (97.4)	1 (2.6)
Linezolid	39 (100)	0 (0)

Table 7: Antibiogram of Coagulase-negative Staphylococci (CONS) Isolates (n=13)

Antibiotic	Sensitive n (%)	Resistant n (%)
Penicillin	2 (15.4)	11 (84.6)
Cefoxitin	6 (46.2)	7 (53.8)
Erythromycin	5 (38.5)	8 (61.5)
Clindamycin	7 (53.8)	6 (46.2)
Ciprofloxacin	6 (46.2)	7 (53.8)
Vancomycin	13 (100)	0 (0)
Linezolid	13 (100)	0 (0)

Table 8: Antibiogram of *Enterococcus* Species Isolates (n=10)

Antibiotic	Sensitive n (%)	Resistant n (%)
Ampicillin	6 (60.0)	4 (40.0)
High-level Gentamicin	7 (70.0)	3 (30.0)
Ciprofloxacin	5 (50.0)	5 (50.0)
Vancomycin	9 (90.0)	1 (10.0)
Linezolid	10 (100)	0 (0)

Overall, multidrug resistance was observed in 96 (45.7%) isolates. Extended-spectrum beta-lactamase (ESBL) production was identified predominantly among *Escherichia coli* and *Klebsiella pneumoniae* isolates, while carbapenem resistance was highest among *Acinetobacter baumannii*. The findings indicate a rising burden of resistant bloodstream pathogens in hospitalized patients, emphasizing the need for continuous antimicrobial surveillance and implementation of effective antibiotic stewardship programs.

DISCUSSION

Bloodstream infections (BSIs) continue to be a major cause of morbidity and mortality worldwide, particularly among hospitalized and critically ill patients. The increasing emergence of antimicrobial resistance among bloodstream pathogens has further complicated the management of these infections and has become a significant challenge for clinicians and microbiologists alike. In the present study, the overall blood culture positivity rate was 16.8%, which is comparable to several previously published Indian studies reporting positivity rates ranging between 10% and 20% [1,11].

The present study demonstrated a predominance of Gram-negative organisms (62.4%) over Gram-positive organisms (37.6%). Similar observations were reported by Agarwal et al., who found Gram-negative bacilli to be the leading etiological agents of bloodstream infections in admitted patients at a tertiary care center [8]. The predominance of Gram-negative organisms may be attributed to prolonged hospitalization, invasive procedures, indwelling medical devices, and extensive antibiotic exposure in hospitalized patients.

Among the isolated pathogens, *Escherichia coli* was the most common organism followed by *Klebsiella pneumoniae* and *Staphylococcus aureus*. These findings are consistent with previous Indian and international studies that identified Enterobacterales as the major causative agents of bloodstream infections [3,6]. The high prevalence of *E. coli* and *Klebsiella pneumoniae* in bloodstream infections may reflect increasing healthcare-associated infections and gastrointestinal translocation in critically ill patients.

A high level of resistance was observed against third-generation cephalosporins and fluoroquinolones among Gram-negative isolates in the present study. Resistance to ceftriaxone was observed in 72.9% of *E. coli* isolates and 74.5% of *Klebsiella pneumoniae* isolates. Similar findings have been reported in surveillance studies from tertiary care hospitals across India, highlighting the widespread emergence of extended-spectrum beta-lactamase (ESBL)-producing organisms [4]. Excessive and irrational use of cephalosporins and fluoroquinolones in clinical practice is considered one of the major contributors to rising resistance patterns.

Carbapenem resistance among Gram-negative organisms is an alarming finding in the present study. Resistance to meropenem was observed in 34.0% of *Klebsiella pneumoniae* isolates and 55.6% of *Acinetobacter baumannii* isolates. Carbapenem-resistant organisms significantly limit available treatment options and are associated with poor clinical outcomes [6]. The emergence of carbapenem resistance may be related to indiscriminate carbapenem usage and dissemination of carbapenemase-producing strains within hospital environments.

Among Gram-positive isolates, methicillin-resistant *Staphylococcus aureus* (MRSA) constituted 43.6% of *S. aureus* isolates. Comparable MRSA prevalence has been reported in various Indian tertiary care hospitals [7]. However, vancomycin and linezolid retained excellent activity against most Gram-positive isolates, indicating their continued effectiveness for the treatment of resistant Gram-positive bloodstream infections.

The increasing burden of resistant pathogens observed in the present study is also supported by recent studies on healthcare-associated infections conducted in Indian tertiary care settings. Paul et al. reported a substantial prevalence of invasive fungal infections among critically ill patients, emphasizing the role of prolonged antibiotic exposure, intensive care stay, and immunocompromised status as major risk factors for secondary infections [9]. Similarly, Goenka et al. observed a significant burden of Candida infections among hospitalized COVID-19 patients, suggesting that prolonged hospitalization, broad-spectrum antibiotic therapy, and invasive procedures contribute considerably to opportunistic infections in critically ill individuals [10]. These findings collectively highlight the importance of antimicrobial stewardship and infection control practices in reducing hospital-acquired infections and resistant organisms.

Multidrug resistance was identified in nearly half of the isolates in the present study, indicating the growing burden of resistant bloodstream pathogens. The increasing prevalence of multidrug-resistant organisms poses serious therapeutic challenges and necessitates regular monitoring of local antibiograms for appropriate empirical antibiotic selection. Periodic surveillance studies are essential for understanding evolving resistance trends and for guiding institutional antibiotic policies.

The findings of the present study emphasize the urgent need for strict infection prevention measures, rational antibiotic prescribing practices, and implementation of comprehensive antimicrobial stewardship programs. Early diagnosis, culture-guided therapy, and continuous surveillance of antimicrobial resistance patterns are essential strategies for reducing morbidity and mortality associated with bloodstream infections.

CONCLUSION

The present study demonstrated that Gram-negative bacteria were the predominant causative agents of bloodstream infections, with *Escherichia coli* and *Klebsiella pneumoniae* being the most commonly isolated organisms. A high prevalence of antimicrobial resistance was observed among bloodstream isolates, particularly against third-generation cephalosporins and fluoroquinolones. The emergence of carbapenem-resistant Gram-negative bacilli and methicillin-resistant *Staphylococcus aureus* (MRSA) further highlights the growing burden of multidrug-resistant pathogens in hospitalized patients.

The study findings emphasize the importance of continuous microbiological surveillance and periodic evaluation of local antibiograms for guiding empirical antimicrobial therapy. Rational antibiotic prescribing practices, strict infection control measures, and implementation of antimicrobial stewardship programs are essential to limit the spread of resistant organisms and improve clinical outcomes in patients with bloodstream infections.

Early identification of causative pathogens along with culture-guided antibiotic therapy can significantly reduce morbidity, mortality, duration of hospital stay, and healthcare costs associated with bloodstream infections. Further multicentric studies with larger sample sizes are recommended to monitor evolving resistance trends and formulate effective antibiotic policies at regional and national levels.

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