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Microbial Ecology of Bloodstream Infections: Pathogens and Resistance Dynamics

Bhavana Yadav[1]* and Maninder Kaur[1]

[1]*Department of Microbiology, Gian Sagar Medical College and Hospital, Ramnagar, Rajpura, Punjab, India.*

*dr.bhavanayadav@gmail.com (Corresponding Author)

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ABSTRACT

Background: Bloodstream infections (BSIs) remain a leading cause of morbidity and mortality worldwide, particularly in critically ill and hospitalized patients. The growing problem of antimicrobial resistance makes the management of these infections even more challenging and highlights the need for continuous surveillance of the distribution of pathogens and their patterns of susceptibility.

Purpose: The present study aimed to investigate the spectrum of bloodstream pathogens, antimicrobial susceptibility patterns, and resistance phenotypes among patients with culture-confirmed bloodstream infections.

Methods: All patients with culture-confirmed BSIs were included in this study. Demographic characteristics, microbiological profiles, and antimicrobial susceptibility data were retrieved from laboratory records. Bacterial isolates were identified and antimicrobial susceptibility testing was performed using standard microbiological methods.

Results: A total of 118 bloodstream isolates were examined. Gram-positive organisms predominated (70.3%) over Gram-negative organisms (29.7%). The most commonly isolated pathogen was Staphylococcus aureus (45.8%), followed by Coagulase-negative staphylococci (CoNS) (21.2%) and Escherichia coli (9.3%). Most infections were acquired in the ICU and NICU (59.3%). Of the Staphylococcus aureus isolates, 74.1% were methicillin resistant, and 68.0% of coagulase-negative staphylococci were methicillin resistant. Among the Gram-positive organisms, the highest susceptibility was observed to vancomycin (98.8%) and linezolid (100%). Among the Gram-negative isolates, the highest susceptibility was observed with carbapenems and β-lactam/β-lactamase inhibitor combinations, whereas high resistance was observed to third generation cephalosporins.

Conclusion: The high rates of methicillin resistance and the high level of resistance among Gram-negative pathogens highlight the importance of routine surveillance, institution-specific antibiograms, antimicrobial stewardship programs, and rigorous infection control practices.

1. Introduction

Bloodstream infections (BSIs) are among the most life-threatening infectious diseases encountered in clinical practice and are a major cause of morbidity, mortality, prolonged hospitalization, and increased health care expenditure worldwide. BSIs occur when pathogenic microorganisms enter the bloodstream and trigger a systemic inflammatory response that can progress to sepsis, septic shock, multiorgan failure, and death if diagnosis and treatment are delayed (Timsit *et al.*, 2014, 2020). Sepsis affects approximately 50 million people worldwide each year and is responsible for nearly 11 million deaths annually, accounting for roughly one-fifth of all deaths globally (Tatte *et al.*, 2026; Murray *et al.*, 2022). Thus, BSIs remain a significant public health problem, particularly in low- and middle-income countries with limited healthcare resources (Evans *et al.*, 2021).

Patients admitted to intensive care units (ICUs), neonatal intensive care units (NICUs), and other critical care settings are particularly vulnerable to bloodstream infections due to frequent use of invasive procedures, intravascular catheters, mechanical ventilation, prolonged hospitalization, immunosuppression, and exposure to broad-spectrum antimicrobial agents (Bassetti *et al.*, 2016; Russotto *et al.*,

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2015; Prowle *et al.*, 2011). Healthcare-associated BSIs impose a significant burden of patient morbidity and mortality and are linked to longer hospital stays and increased healthcare costs. Although critical care medicine and antimicrobial therapy have made significant progress, the mortality rates associated with severe bloodstream infections remain high, ranging from 25% to 50% in various studies (Bassetti *et al.*, 2016; Prowle *et al.*, 2011).

The epidemiology of bloodstream infections varies widely by geographical area, healthcare institution, and patient population. The spectrum of causative organisms has changed over the years with the evolution of healthcare practices, patterns of antimicrobial use, and infection control practices. Gram-positive and Gram-negative bacteria are important etiologic agents of BSI. The most frequently isolated pathogens include *Staphylococcus aureus, coagulase-negative staphylococci (CoNS)*, *Enterococcus species, Escherichia coli, Klebsiella pneumoniae, Acinetobacter species, and Pseudomonas aeruginosa* (Russotto *et al.*, 2015; Sonawane *et al.*, 2019). Knowledge of the local distribution of bloodstream pathogens is essential to guide empirical antimicrobial therapy and to improve patient outcomes.

A major challenge in the management of BSIs is the growing prevalence of antimicrobial resistance (AMR). The emergence and spread of multidrug-resistant organisms have reduced treatment options, increased the risk of treatment failure, and complicated the management of bloodstream infections (Tatte *et al.*, 2026; Murray *et al.*, 2022). During the last decade, resistance of Gram-negative organisms to third-generation cephalosporins, fluoroquinolones, and carbapenems has increased significantly. The emergence of methicillin-resistant *Staphylococcus aureus* (MRSA) and resistant *CoNS* also represents a significant challenge in health care settings (Ahsan *et al.*, 2016). It has been estimated that bacterial AMR is associated with approximately 4.95 million deaths per year, underscoring the urgent need for effective surveillance and antimicrobial stewardship strategies (Tatte *et al.*, 2026).

Rapid identification of the causative pathogen and knowledge of local antimicrobial susceptibility patterns are crucial for effective empirical therapy. Delayed or inappropriate antimicrobial treatment has been associated with increased mortality in patients with bloodstream infections (Timsit *et al.*, 2020). Thus, institution-specific antibiograms serve as useful tools for providing clinicians with updated information on the susceptibility profiles of commonly encountered pathogens. These data support evidence-based antimicrobial prescribing and antimicrobial stewardship programs and contribute to reducing the development and spread of resistant organisms (Iftikhar *et al.*, 2024; WHO, 2025).

Studies from India have demonstrated varied bacteriological profiles and antimicrobial resistance patterns among bloodstream isolates, reflecting regional differences in microbial epidemiology (Chaturvedi *et al.*, 2021; Sonawane *et al.*, 2019; Yousuf *et al.*, 2020). Therefore, continuous monitoring of the local distribution of pathogens and antimicrobial resistance trends is essential for optimizing empirical therapy, developing hospital antibiotic policies, and strengthening infection prevention and control practices.

In view of the increasing burden of bloodstream infections and the threat of antimicrobial resistance, the present study was carried out to evaluate the spectrum of bloodstream pathogens and their antimicrobial susceptibility patterns among patients with culture-confirmed bloodstream infections in a tertiary care center.

2. Material and Methods

2.1. Study Design and Objectives

The present retrospective observational study was conducted in the Department of Microbiology at a tertiary care hospital in North India. It included blood cultures collected from patients admitted to the inpatient department (IPD) between January 2024 and December 2025 that yielded clinically significant bacterial isolates. The objective of the study was to determine the spectrum of bloodstream pathogens and evaluate their antimicrobial susceptibility patterns.

2.2. Eligibility Criteria and Study Population

This study included all patients with positive blood cultures yielding clinically significant bacterial isolates during the study period. Patients of all age groups and both sexes were included. For *CoNS*, a single positive blood culture in the absence of compatible clinical findings was considered a contaminant and was excluded from the study. Isolates with incomplete microbiological records were also excluded. In contrast, repeated isolation of the same organism and/or compatible clinical findings supported the classification of *CoNS* as clinically significant bacteremia.

2.3. Microbiological Processing

Blood specimens were collected under aseptic precautions and processed according to standard microbiological procedures. Samples were processed using routine blood culture techniques. The isolates were identified using standard laboratory protocols based on colony morphology, Gram-staining characteristics, and conventional biochemical methods. Identified isolates were grouped as Gram-positive or Gram-negative organisms. Antimicrobial susceptibility testing (AST) was performed by the Kirby-Bauer disc diffusion method on Mueller Hinton agar (Bauer *et al.*, 1966). The zone diameters were interpreted, according to

the Clinical and Laboratory Standards Institute (CLSI) M100, 34th edition (2024). Cefoxitin disc diffusion was used as a phenotypic surrogate for detection of methicillin resistance in *Staphylococcus aureus* and *CoNS* in accordance with CLSI interpretive criteria. Multidrug resistance, extended-spectrum β-lactamase (ESBL) production, and carbapenemase production were not specifically assessed because dedicated phenotypic or molecular tests for these resistance mechanisms were not performed.

2.4. Data Collection

Data were collected retrospectively from microbiology laboratory records. Demographic characteristics (age and sex), blood culture results, isolated microorganisms, and antimicrobial susceptibility profiles were analyzed.

2.5. Statistical Analysis

Data were entered into Microsoft Excel and analyzed using IBM SPSS Statistics, version 26.0 (IBM Corp., Armonk, NY, USA). Descriptive statistics were used to summarize the data. Categorical variables were expressed as frequencies and percentages, with clearly specified denominators. The distributions of bacterial isolates, demographic characteristics, and ward-wise distribution were calculated using the 118 culture-positive samples as the denominator. Antibiotic susceptibility percentages were calculated using the number of isolates tested for each organism–antibiotic combination. Findings from small organism subgroups were interpreted cautiously.

3. Results

A total of 816 blood samples were received, of which 118 blood cultures were positive, giving a positivity rate of 14.5%. Among the 118 patients with bloodstream infections, females accounted for 50.8% and males for 49.2%. Neonates (33.9%) and elderly patients (33.1%) were the most affected, followed by the adults (28.0%), while pediatric patients accounted for only 5.1% of the study population. The highest proportion of bloodstream infections was observed among patients admitted to the ICU (36.4%), followed by the NICU (22.9%) and the medicine ward (17.8%) (Table 1).

Table 1: Demographic and Departmental Distribution of Culture Positive Cases (n = 118)

Characteristic	Category	n (%)
Gender	Male	58 (49.2)
	Female	60 (50.8)
Age	Neonate	40 (33.9)
	Paediatric	6 (5.1)
	Adult	33 (28.0)
	Elderly	39 (33.1)
Department/ Unit	ICU	43 (36.4)
	NICU	27 (22.9)
	Medicine	21 (17.8)
	Paediatrics	15 (12.7)
	Emergency	8 (6.8)
	Gynaecology	2 (1.7)
	Surgery	2 (1.7)

In total, 118 bloodstream isolates were obtained, with *Staphylococcus aureus* being the most common organism (45.8% of all isolates). *CoNS* were the second most common organisms, accounting for 21.2% of the isolates. Among Gram-positive organisms, *Enterococcus* spp. accounted for 3.4% of the isolates. The most common Gram-negative organism was *Escherichia coli* (9.3%), followed by *Pseudomonas aeruginosa* (4.2%). *Acinetobacter baumannii, Klebsiella pneumoniae,* and *Stenotrophomonas maltophilia* each accounted for 3.4% of the total isolates. Less frequently isolated organisms included *Citrobacter freundii* (2.5%), *Salmonella typhi* (1.7%), and *Proteus mirabilis* (1.7%) (Figure 1).

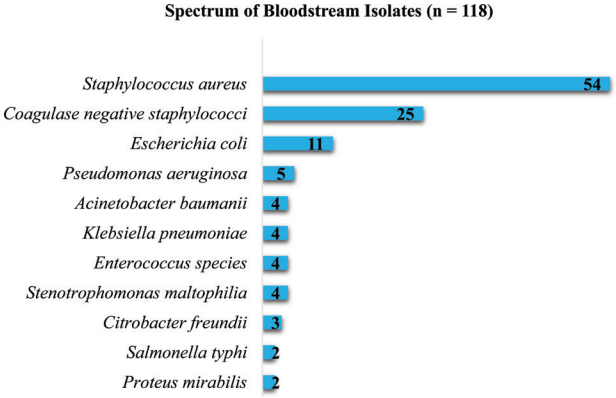

Figure 1: Spectrum of Organisms Isolated in Blood Culture Samples

Staphylococcus aureus was the most commonly isolated pathogen across the clinical departments, with the highest proportion of isolates coming from the ICU (40.7%), followed by the NICU (22.6%) and Medicine ward (13.2%). *CoNS* were distributed relatively uniformly across the Medicine ward (28.0%), ICU (24.0%), and NICU (24.0%). *Escherichia coli* was the most common Gram-negative isolate

in the ICU (45.5%) and Medicine ward (27.3%). The ICU accounted for 50.0% of the *Acinetobacter baumannii* and *Enterococcus* spp. isolates, while 75.0% of *Klebsiella pneumoniae* isolates were recovered from ICU patients. Among the *Pseudomonas aeruginosa* isolates, 40.0% were recovered from the NICU (Table 2).

Table 2: Distribution of Bloodstream Isolates across Clinical Departments

Organisms	**ICU n (%)**	**NICU n (%)**	**Medicine Ward n (%)**	**Paediatric Ward n (%)**	**Other Wards n (%)**
Staphylococcus aureus (n=54)	22 (40.7)	12 (22.2)	7 (13.0)	5 (9.3)	8 (14.8)
Coagulase negative Staphylococci (CoNS) (n=25)	6 (24.0)	6 (24.0)	7 (28.0)	5 (20.0)	1 (4.0)
Escherichia coli (n=11)	5 (45.5)	1 (9.1)	3 (27.3)	1 (9.1)	1 (9.1)
Acinetobacter baumannii (n=4)	2 (50.0)	1 (25.0)	0 (0.0)	1 (25.0)	0 (0.0)
Klebsiella pneumoniae (n=4)	3 (75.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (25.0)
Enterococcus spp. (n=4)	2 (50.0)	1 (25.0)	1 (25.0)	0 (0.0)	0 (0.0)
Pseudomonas aeruginosa (n=5)	1 (20.0)	2 (40.0)	1 (20.0)	1 (20.0)	0 (0.0)
Others (n=11)	3 (27.3)	4 (36.4)	2 (18.2)	2 (18.2)	1 (9.1)

Gram-positive organisms predominated in all age groups, accounting for 75.0% of isolates among neonates, 71.8% among elderly patients, and 66.7% among adults. Paediatric patients had a balanced distribution of Gram-positive and Gram-negative infections (50.0% each). The highest proportions of bloodstream infection cases were observed among neonates (33.9%) and elderly patients (33.1%), whereas the pediatric age group had the lowest proportion (5.1%). Bloodstream infections were distributed almost equally between females and males. Gram-positive isolates were more common than Gram-negative isolates in both females (68.3% vs 31.7%) and males (72.4% vs 27.6%) (Table 3).

Table 3: Demographic Distribution of Bloodstream Infections

Variable	**Domain**	**Gram-positive n (%)**	**Gram-negative n (%)**	**Total n (%)**
Age Group	Neonate	30 (75.0)	10 (25.0)	40 (33.9)
	Paediatric	3 (50.0)	3 (50.0)	6 (5.1)
	Adult	22 (66.7)	11 (33.3)	33 (28.0)
	Elderly	28 (71.8)	11 (28.2)	39 (33.1)
Gender	Female	41 (68.3)	19 (31.7)	60 (50.8)
	Male	42 (72.4)	16 (27.6)	58 (49.2)

Among the Gram-positive isolates, *Staphylococcus aureus* showed 100% susceptibility to linezolid (54/54), teicoplanin (54/54), and vancomycin (54/54), followed by doxycycline (38/54, 70.4%). Moderate susceptibility was observed to levofloxacin (27/54, 50.0%), clindamycin (26/54, 48.1%), and gentamicin (25/54, 46.3%). Lower susceptibility rates were observed for amoxicillin-clavulanate and cefoxitin (14/54, 25.9% each), tetracycline (14/54, 25.9%), penicillin (13/54, 24.1%), erythromycin (12/54, 22.2%), and azithromycin (8/54, 14.8%).

CoNS also showed 100% susceptibility to linezolid (25/25), teicoplanin (25/25), and vancomycin (25/25), with good susceptibility to doxycycline 17/25 (68.0%), gentamicin 16/25 (64.0%), tetracycline 15/25 (60.0%), and cotrimoxazole 15/25 (60.0%). However, low susceptibility was observed for levofloxacin (9/25, 36.0%), cefoxitin (8/25, 32.0%), erythromycin (6/25, 24.0%), penicillin (6/25, 24.0%), and azithromycin (5/25, 20.0%). Methicillin resistance was common among the *Staphylococcal* isolates. Of the 54 *Staphylococcus aureus* isolates, 40/54 (74.1%) were methicillin-resistant and 14/54 (25.9%) were methicillin-sensitive. Among the 25 *CoNS* isolates, 17/25 (68.0%) were methicillin-resistant and 8/25 (32.0%) were methicillin-sensitive.

Among the four isolates of *Enterococcus* species, susceptibility was 4/4 (100%) to linezolid and teicoplanin, while vancomycin and ampicillin showed susceptibility in 3/4 (75.0%) isolates each. Most other antibiotics, such as ciprofloxacin, levofloxacin, gentamicin, tetracycline, penicillin, and erythromycin, showed poor activity, with susceptibility rates of 25% (1/4) each. High-level gentamicin resistance was observed in 50% (2/4) of the isolates (Table 4).

Table 4: Percentage Susceptibility of Gram-positive Bloodstream Isolates to Different Antibiotics (n=83)

Antibiotic	Staphylococcus Aureus **(n = 54)**	CoNS **(n = 25)**	Enterococcus **Species (n = 4)**
Ciprofloxacin	11/54 (20.4%)	8/25 32%	1/4 25%
Levofloxacin	27/54 (50.0%)	9/25 (36%)	1/4 (25%)
Gentamicin	25/54 (46.3%)	16/25 (64%)	1/4 (25%)
Tetracycline	14/54 (25.9%)	15/25 (60%)	1/4 (25%)
Doxycycline	38/54 (70.4%)	17/25 (68%)	NT
Cefoxitin	14/54 (25.9%)	8/25 (32%)	NT
Cotrimoxazole	23/54 (42.6%)	15/25 (60%)	NT
Penicillin	13/54 (24.1%)	6/25 (24%)	1/4 (25%)
Ampicillin	NT	NT	3/4 (75%)
Amoxicillin-clavulanate	14/54 (25.9%)	8/25 (32%)	NT
Linezolid	54/54 (100%)	25/25 (100%)	4/4 (100%)
Erythromycin	12/54 (22.2%)	6/25 (24%)	0/4 (0%)
Azithromycin	8/54 (14.8%)	5/25 (20%)	NT
Clindamycin	26/54 (48.1%)	12/25 (48%)	NT
Teicoplanin	54/54 (100%)	25/25 (100%)	4/4 (100%)
High-level gentamicin resistance	NT	NT	2/4 (50%)
Vancomycin	54/54 (100%)	25/25 (100%)	3/4 (75%)

Note: NT = not tested

Among lactose-fermenting GNB, *Escherichia coli* (n = 11) showed the highest susceptibility to meropenem (90.9%) and imipenem (90.9%), followed by amikacin (81.8%) and piperacillin-tazobactam (81.8%), while gentamicin showed susceptibility in 72.7% of isolates. Susceptibility to cephalosporins, monobactams, and fluoroquinolones was low, ranging from 25% to 36%. Among the *Klebsiella pneumoniae* isolates (n = 4) and *Citrobacter freundii* isolates (n = 3), the highest susceptibility was observed with carbapenems (*K. pneumoniae*, 50%; *C. freundii*, 66.7%), piperacillin-tazobactam (*K. pneumoniae*, 50% and *C. freundii*, 66.7%). Both *K. pneumoniae* and *C. freundii* showed poor susceptibility to cephalosporins and fluoroquinolones. *Proteus mirabilis* and *Salmonella typhi* were completely susceptible to piperacillin-tazobactam, imipenem, and meropenem (100%).

Among non-fermenters, *Pseudomonas aeruginosa* showed good susceptibility to amikacin, ceftazidime, cefepime, piperacillin-tazobactam, imipenem, and meropenem (80% each). Fluroquinolones, aminoglycosides, and monobactams each showed a susceptibility of 60%. *Acinetobacter baumannii* showed the highest susceptibility to piperacillin-tazobactam (75%), while susceptibility to most other antibiotics was low to moderate. *Stenotrophomonas maltophilia* showed complete susceptibility to cotrimoxazole (100%) and good susceptibility to levofloxacin and minocycline (75% each). Low susceptibility to several

cephalosporins, including ceftriaxone, cefuroxime, cefotaxime, ceftazidime, and cefepime, was observed among the Gram-negative isolates, suggesting reduced in-vitro activity against several of the organisms studied. However, meropenem showed the highest susceptibility rate, followed by imipenem and piperacillin-tazobactam, demonstrating good activity of carbapenems and beta-lactam/beta-lactamase inhibitor combinations against Gram-negative bloodstream pathogens (Table 5).

Table 5: Percentage Susceptibility of Gram-negative Bloodstream Isolates to Different Antibiotics (n = 35)

Antibiotics	E. coli **(n=11)**	K. pneumoniae **(n=4)**	C. freundii **(n=3)**	P. mirabilis **(n=2)**	S. typhi **(n=2)**	Ps. aeruginosa **(n=5)**	S. maltophilia **(n=4)**	A. baumannii **(n=4)**
Ciprofloxacin	2/11 (18.2%)	1/4 (25%)	1/3 (33.3%)	1/2 (50%)	1/2 (50%)	3/5 (60%)	3/4 (75%)	1/4 (25%)
Levofloxacin	4/11 (36.4%)	1/4 (25%)	1/3 (33.3%)	1/2 (50%)	1/2 (50%)	3/5 (60%)	NT	1/4 (25%)
Gentamicin	8/11 (72.7%)	1/4 (25%)	2/3 (66.7%)	1/2 (50%)	NT	3/5 (60%)	3/4 (75%)	1/4 (25%)
Amikacin	9/11 (81.8%)	1/4 (25%)	2/3 (66.7%)	1/2 (50%)	NT	4/5 (80%)	NT	2/4 (50%)
Tobramycin	8/11 (72.7%)	2/4 (50%)	2/3 (66.7%)	NT	NT	3/5 (60%)	NT	2/4 (50%)
Cefuroxime	2/11 (18.2%)	1/4 (25%)	1/3 (33.3%)	NT	NT	NT	NT	NT
Cefotaxime	2/11 (18.2%)	1/4 (25%)	1/3 (33.3%)	1/2 (50%)	2/2 (100%)	NT	NT	NT
Ceftriaxone	2/11 (18.2%)	1/4 (25%)	1/3 (33.3%)	1/2 (50%)	2/2 (100%)	NT	NT	NT
Ceftazidime	4/11 (36.4%)	1/4 (25%)	1/3 (33.3%)	1/2 (50%)	NT	4/5 (80%)	NT	2/4 (50%)
Cefepime	5/11 (45.5%)	1/4 (25%)	1/3 (33.3%)	1/2 (50%)	NT	4/5 (80%)	NT	1/4 (25%)
Piperacillin-tazobactam	9/11 (81.8%)	2/4 (50%)	2/3 (66.7%)	2/2 (100%)	NT	4/5 (80%)	NT	3/4 (75%)
Imipenem	10/11 (90.9%)	2/4 (50%)	2/3 (66.7%)	2/2 (100%)	2/2 (100%)	4/5 (80%)	NT	2/4 (50%)
Meropenem	10/11 (90.9%)	2/4 (50%)	2/3 (66.7%)	2/2 (100%)	2/2 (100%)	4/5 (80%)	NT	2/4 (50%)
Cotrimoxazole	4/11 (36.4%)	2/4 (50%)	1/3 (33.3%)	1/2 (50%)	2/2 (100%)	NT	4/4 (100%)	1/4 (25%)
Tetracycline	2/11 (18.2%)	1/4 (25%)	1/3 (33.3%)	NT	1/2 (50%)	NT	3/4 (75%)	1/4 (25%)
Aztreonam	4/11 (36.4%)	1/4 (25%)	1/3 (33.3%)	NT	1/2 (50%)	3/5 (60%)	2/4 (50%)	NT
Chloramphenicol	NT	NT	NT	NT	2/2 (100%)	NT	NT	NT
Ampicillin	NT	NT	NT	NT	2/2 (100%)	NT	NT	NT

Note: NT = not tested

The majority of pathogens causing bloodstream infections were isolated from patients admitted to critical care units. The most common pathogen was *Staphylococcus aureus,* isolated predominantly from ICU settings (62.9% isolates) compared with 37.7% from non-ICU settings. A strong association with critical care units was observed, with 75.0% of the *Acinetobacter baumannii* and *Klebsiella pneumoniae* isolates recovered from patients admitted to the ICU. *Pseudomonas aeruginosa* was also more frequently isolated in ICU settings (60.0%) than in non-ICU areas (40.0%).

Escherichia coli showed a relatively balanced distribution, although slightly more than half of the isolates (54.5%) were recovered from ICU patients. In contrast, *CoNS* were almost equally distributed between ICU (48.0%) and non-ICU sites (52.0%) (Table 6).

Table 6: Distribution of Major Pathogens in ICU Versus Non-ICU Settings

Organism	**ICU n (%)**	**Non-ICU n (%)**
Staphylococcus aureus (n=54)	34 (63)	20 (37)
Coagulase negative Staphylococci (n=25)	12 (48.0)	13 (52.0)
Escherichia coli (n=11)	6 (54.5)	5 (45.5)
Acinetobacter baumannii (n=4)	3 (75.0)	1 (25.0)
Pseudomonas aeruginosa (n=5)	3 (60.0)	2 (40.0)
Klebsiella pneumoniae (n=4)	3 (75.0)	1 (25.0)

4. Discussion

Bloodstream infections remain a major cause of morbidity and mortality worldwide, especially among hospitalized and critically ill patients. The growing emergence of antimicrobial resistance has further complicated the management of these infections, emphasizing the need for continuous surveillance of the distribution of pathogens and their susceptibility patterns to guide empirical therapy and infection control policies**.** The present study was undertaken to evaluate the microbiological profile and antimicrobial susceptibility patterns of blood stream infections in a tertiary care hospital.

In the present study, Gram-positive organisms predominated, accounting for 83/118 (70.3%) isolates, while Gram-negative organisms accounted for 35/118 (29.7%). The most common pathogen in the present study was *Staphylococcus aureus* (45.8% of all isolates), followed by *CoNS* (21.2%) and *Escherichia coli* (9.3%). The predominance of Gram-positive organisms in our study is consistent with findings from previous studies, in which Gram-positive pathogens accounted for 69.5% and 58.7% of bloodstream infections, respectively (Yadav *et al.*, 2024; Gamit *et al.*, 2025; Tatte *et al.*, 2026). These findings highlight the important role of Gram-positive organisms in bloodstream infections. Comparison with national surveillance data further demonstrates the variability of bloodstream infection epidemiology. According to the Indian Council of Medical Research (2025), Gram-negative bacteria accounted for 72.1% of healthcare-associated bloodstream infections, while Gram-positive bacteria accounted for 17.7% (AMRSN, 2024 report). This finding is not in accordance with the findings of the present study. The comparison shows that the distribution of BSI pathogens varies considerably according to the healthcare setting, geographical region, and patient population.

Most infections were acquired in critical care areas. ICU and NICU patients contributed to 59.3% of all the bloodstream infections. The high burden of bloodstream infections in critically ill patients has been repeatedly reported and is often linked to invasive procedures, prolonged hospitalization, and extensive exposure to antimicrobials (Bassetti *et al.*, 2016; Russotto *et al.*, 2015). *S. aureus* was the predominant organism in the ICU, NICU, and medicine wards. Gram-negative organisms such as *E. coli, Acinetobacter baumannii, Klebsiella pneumoniae, and Pseudomonas aeruginosa* were concentrated in critical care settings. Importantly, 75.0% of *Acinetobacter spp*. and *Klebsiella spp.* isolates were isolated from ICU patients. Similar observations have been reported in ICU-based studies in which multidrug-resistant Gram-negative bacilli were predominantly isolated from critically ill patients (Gamit *et al.*, 2025; Sonawane *et al.*, 2019).

Staphylococcal isolates showed a notably high rate of methicillin resistance. Methicillin-resistant *S. aureus* constituted 74.1% (40/54) of *S. aureus* isolates, and methicillin-resistant *CoNS* constituted 68.0% (17/25) of *CoNS* isolates. Previous studies have reported comparably high rates of MRSA, with methicillin resistance observed in nearly 77% of *S. aureus* bloodstream isolates, highlighting the persistent challenge of MRSA in healthcare settings (Tatte *et al.*, 2026; Murray *et al.*, 2022).

The antimicrobial susceptibility profile of Gram-positive isolates showed high resistance to penicillin (75.9%), ciprofloxacin (75.9%), and levofloxacin (55.4%). Similar resistance patterns have been reported in other studies, particularly for beta-lactams and fluoroquinolones (Tatte *et al.*, 2026; Yousuf *et al.*, 2020). Organism-specific analysis further showed 100% susceptibility of both *S. aureus* and *CoNS* to linezolid, teicoplanin, and vancomycin, while *Enterococcus* remained 100% susceptible to linezolid and teicoplanin, with 75% susceptibility to vancomycin. The findings for Enterococcus spp. should be interpreted cautiously, as only four isolates were identified in the study. Therefore, these findings may not reflect the overall pattern of enterococcal resistance in the study population. Antimicrobial selection should be guided by the susceptibility results, clinical indications, and antimicrobial stewardship principles. The susceptibility to fluoroquinolones, penicillin, and macrolides remained low across most Gram-positive pathogens. The high prevalence of methicillin resistance among *S. aureus* and *CoNS* highlights the importance of appropriate antimicrobial susceptibility testing and careful

selection of treatment for serious Gram-positive bloodstream infections. Similar findings have been reported by other investigators (Sonawane *et al.*, 2019; Tatte *et al.*, 2026).

Substantial antimicrobial resistance to third-generation cephalosporins was observed among Gram-negative isolates. Similar resistance rates to cephalosporins have also been reported among ICU bloodstream isolates (Gamit *et al.*, 2025). Other Indian studies have also reported high resistance to cephalosporins and fluoroquinolones (Chaturvedi *et al.*, 2021; Yousuf *et al.*, 2020). However, in the current study, carbapenems and piperacillin–tazobactam were relatively effective. Organism-specific analysis demonstrated that *E. coli* showed the highest susceptibility to meropenem and imipenem (90.9%), while *Pseudomonas aeruginosa* was most susceptible to amikacin, ceftazidime, cefepime, piperacillin-tazobactam, and carbapenems (80% each). *Proteus mirabilis* and *Salmonella typhi* were completely susceptible to piperacillin-tazobactam and carbapenems, whereas *Stenotrophomonas maltophilia* showed complete susceptibility to cotrimoxazole. In contrast, *Acinetobacter baumannii, Klebsiella pneumoniae,* and *Citrobacter freundii* demonstrated lower susceptibility to cephalosporins and fluoroquinolones, highlighting the variable susceptibility profiles among Gram-negative pathogens. Previous studies have also reported high susceptibility to carbapenems, with rates exceeding 70% (Sonawane *et al.*, 2019; Tatte *et al.*, 2026).

The changing epidemiology of bloodstream infections in tertiary care settings is reflected by the predominance of Gram-positive pathogens, particularly *S. aureus*, the high prevalence of methicillin resistance, and considerable antimicrobial resistance among Gram-negative organisms. These findings highlight the need for continuous microbiological surveillance, institution-specific antibiograms, judicious antimicrobial prescribing, and robust infection prevention strategies to guide empirical therapy and limit the emergence and spread of multidrug-resistant organisms (Bassetti *et al.*, 2016; Timsit *et al.*, 2020; Yousuf *et al.*, 2020).

One of the major strengths of the present study is the extensive assessment of bloodstream pathogens and their antimicrobial susceptibility patterns across different age groups and hospital departments in a tertiary care setting. This study provides important local epidemiological data to inform empirical antibiotic treatment and antimicrobial stewardship programs. However, the study has some limitations, including its single-center design, relatively small sample size, retrospective nature, and lack of clinical outcome data, which may affect the generalizability of the findings. Since this study included only culture-positive cases identified from laboratory records, some degree of selection bias cannot be ruled out. Moreover, details such as the likely source of infection, previous antibiotic use, and patient outcomes were not available in the records reviewed. The absence of these clinical details limited our ability to assess their possible influence on the distribution of organisms and the antimicrobial susceptibility patterns observed in the study. The study did not specifically assess individual isolates for multidrug resistance, ESBL production, or carbapenem-resistant Enterobacterales (CRE). Therefore, the prevalence of these resistance patterns could not be accurately estimated. We recommend future multicenter studies with larger sample sizes and molecular characterization of resistance mechanisms to better understand evolving resistance trends and optimize infection control strategies.

5. Conclusion

The present study revealed that Gram-positive bacteria were the predominant cause of bloodstream infections, with Staphylococcus *aureus* being the most commonly isolated pathogen. Methicillin resistance was highly prevalent among staphylococcal isolates, and resistance to several commonly used antibiotics was substantial. Vancomycin and linezolid retained high in vitro activity against the tested Gram-positive isolates, while carbapenems showed relatively higher susceptibility among several Gram-negative organisms. Most culture-positive cases were identified in critical care settings, particularly the ICU and NICU. These findings highlight the importance of continuous microbiological surveillance, institution-specific antibiograms, antimicrobial stewardship programs, and effective infection prevention and control practices to support appropriate empirical therapy and limit the emergence and spread of antimicrobial resistance.

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Author Contributions

Bhavana Yadav: Conceptualization, Methodology, Data Curation, Formal Analysis, Writing – Original Draft, and Writing – Review & Editing.
Maninder Kaur: Writing – Review & Editing.
All authors reviewed and approved the final version of the manuscript.

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Conflict of Interest

The authors declare that they have no conflicts of interest.

Human and Animal Rights

No animals were used in this research. All procedures performed in studies involving human participants were in accordance with the ethical standards of the institutional and/or research committee.

Data Availability Statement

The authors declare that the data supporting the conclusions of this study are available upon reasonable request from the corresponding author, Yadav, B.

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