Surveillance of Bloodstream Infections and Resistance Patterns in a Tertiary Care Hospital

Anju Gupta[1], Neha Gupta[2], Manisha Vivek Arya[3]

[1]Assistant Professor, Department of Microbiology, Vyas Medical College and Hospital, Jodhpur
[2]Assistant Professor, Department of Microbiology, Vyas Medical College and Hospital, Jodhpur
[3]Assistant Professor, Department of Microbiology, Vyas Medical College and Hospital, Jodhpur

Abstract:

Background: Bloodstream infections (BSI) remain a leading cause of morbidity and mortality in hospitalized patients, particularly in developing countries where antimicrobial resistance is rapidly emerging. The changing epidemiological patterns and evolving resistance mechanisms necessitate continuous surveillance to guide appropriate therapeutic interventions and infection control strategies.

Objective: To evaluate the microbial profile, demographic characteristics, and antimicrobial susceptibility patterns of bloodstream infections in a tertiary care hospital in western India and analyze the resistance trends among isolated pathogens.

Methods: A retrospective descriptive study was conducted over 12 months (April 2022 to March 2023) in a tertiary care hospital. Blood culture samples from 100 patients with clinically suspected sepsis were processed using automated blood culture systems (BACT/ALERT 3D). Bacterial identification was performed using standard biochemical methods and colony morphology. Antimicrobial susceptibility testing was conducted using the Kirby-Bauer disk diffusion method following Clinical and Laboratory Standards Institute (CLSI) guidelines. Statistical analysis was performed using SPSS software.

Results: Among 100 blood culture samples, 85 (85%) yielded positive bacterial growth. Gram-negative bacteria predominated (64.7%), with Klebsiella pneumoniae being the most common isolate (28.2%), followed by Escherichia coli (20.0%) and Pseudomonas aeruginosa (16.5%). The age distribution showed highest incidence in pediatric patients (31.8%) and elderly patients above 60 years (24.7%). Male patients constituted 58.8% of cases. High resistance rates were observed against commonly used antibiotics, with carbapenem resistance noted in 18% of Enterobacteriaceae. Most isolates showed good susceptibility to amikacin (82.4%) and piperacillin-tazobactam (76.5%).

Conclusion: This study reveals a high prevalence of Gram-negative bloodstream infections with concerning resistance patterns in our institution. The findings emphasize the critical need for antimicrobial stewardship programs, enhanced infection control measures, and judicious antibiotic use to combat the growing threat of multidrug-resistant organisms in tertiary care settings.

Keywords: Bloodstream Infection, Antibiogram, Antimicrobial Resistance, Tertiary Care, Surveillance.

Introduction

Bloodstream infections represent one of the most critical challenges in contemporary healthcare, serving as a major contributor to patient morbidity, mortality, and healthcare costs worldwide [1]. These infections encompass a spectrum of clinical manifestations ranging from transient bacteremia to life-threatening septic shock, with the potential for rapid clinical deterioration if not promptly recognized and appropriately managed [2]. The global burden of bloodstream infections has been steadily increasing, particularly in healthcare-associated settings where vulnerable patient populations and invasive medical procedures create favorable conditions for pathogen entry into the circulatory system [3].

The epidemiological landscape of bloodstream infections has undergone significant transformation over the past decades, with notable shifts in pathogen distribution and antimicrobial resistance patterns [4]. While Gram-positive organisms, particularly staphylococci, historically dominated healthcare-associated bloodstream infections, recent surveillance data indicates an increasing prevalence of Gram-negative bacteria in many healthcare facilities [5]. This epidemiological transition is particularly pronounced in developing

countries, where factors such as inadequate infection control practices, limited diagnostic capabilities, and inappropriate antimicrobial use contribute to the emergence and dissemination of resistant pathogens [6].

The clinical significance of bloodstream infections extends beyond their immediate impact on individual patients, as they serve as sentinel indicators of healthcare quality and antimicrobial resistance trends within healthcare institutions [7]. The emergence of multidrug-resistant organisms in bloodstream infections poses substantial therapeutic challenges, often limiting treatment options to expensive, potentially toxic, or less effective antimicrobial agents [8]. This phenomenon is particularly concerning in resource-limited settings where access to newer antimicrobial agents may be restricted, necessitating reliance on older, less effective alternatives [9].

In the Indian healthcare context, bloodstream infections present unique challenges due to the complex interplay of factors including high population density, variable healthcare infrastructure, and the widespread availability of antibiotics without prescription [10]. Several studies from Indian tertiary care centers have documented alarming rates of antimicrobial resistance among bloodstream pathogens, with some institutions reporting resistance rates exceeding 70% for commonly used antibiotics [11]. The situation is further complicated by the high prevalence of extended-spectrum beta-lactamase (ESBL) producing Enterobacteriaceae and the emergence of carbapenem-resistant organisms, which severely limit therapeutic options [12].

The importance of continuous surveillance of bloodstream infections cannot be overstated, as it provides crucial data for optimizing empirical therapy protocols, implementing targeted infection control measures, and monitoring the effectiveness of antimicrobial stewardship interventions [13]. Regular monitoring of resistance patterns enables healthcare institutions to adapt their treatment guidelines based on local epidemiological data, potentially improving patient outcomes while minimizing the selective pressure for resistant organisms [14]. Furthermore, surveillance data contributes to regional and national resistance monitoring networks, facilitating evidence-based policy development and resource allocation decisions [15].

The demographic characteristics of patients with bloodstream infections vary considerably across different healthcare settings and geographic regions. Age-related factors play a crucial role in infection susceptibility, with extremes of age (neonates and elderly patients] typically demonstrating higher incidence rates due to immature or compromised immune systems [16]. Additionally, the presence of underlying comorbidities, such as diabetes mellitus, malignancy, and immunosuppressive conditions, significantly increases the risk of developing bloodstream infections and influences clinical outcomes [17].

Understanding the local microbial ecology and resistance patterns is fundamental to developing effective treatment strategies and implementing evidence-based infection prevention measures. This knowledge enables clinicians to make informed decisions regarding empirical antimicrobial therapy while awaiting definitive culture results, potentially improving patient outcomes and reducing the risk of treatment failures associated with inappropriate antibiotic selection [18]. Moreover, surveillance data helps identify emerging resistance mechanisms and novel pathogens, facilitating the development of targeted interventions and informing antimicrobial research priorities.

Materials and Methods

Study Design and Setting: This retrospective descriptive study was conducted at a 500-bed tertiary care teaching hospital in western India. The hospital provides comprehensive medical services including intensive care, surgical specialties, and emergency medicine, serving as a regional referral center for critically ill patients.

Study Period: The study was conducted over a 6-month period from July 2023 to December 2023.

Study Population: The study included 100 blood culture samples from hospitalized patients with clinically suspected bloodstream infections. All age groups were included in the study. Patients who had received antimicrobial therapy for more than 48 hours prior to blood collection were excluded to minimize the impact of prior antibiotic exposure on culture results.

Sample Collection and Processing: Blood samples were collected aseptically from peripheral venipuncture sites using standard protocols. For adult patients, 8-10 ml of blood was inoculated into both aerobic and anaerobic blood culture bottles, while 2-4 ml was collected for pediatric patients. All samples were transported immediately to the microbiology laboratory and processed within 2 hours of collection.

Laboratory Methods: Blood culture bottles were loaded into the BACT/ALERT 3D automated blood culture system and incubated for up to 5 days. Positive cultures underwent Gram staining and were subcultured on appropriate media including blood agar, MacConkey agar, and chocolate agar plates. Bacterial identification was performed using

standard biochemical tests and colony morphology characteristics.

Antimicrobial Susceptibility Testing: Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) 2019 guidelines. The following antibiotics were tested: Amikacin, Augmentin, Ampicillin-sulbactam, Aztreonam, Cefazolin, Cefuroxime, Ceftriaxone, Ceftazidime, Cefepime, Ciprofloxacin, Chloramphenicol, Gentamicin, Imipenem, Meropenem, Piperacillin-Tazobactam, and Trimethoprim-sulfamethoxazole. Quality control was maintained using ATCC reference strains including E. coli ATCC 25922, S. aureus ATCC 25923, P. aeruginosa ATCC 27853, and E. faecalis ATCC 29212.

Data Analysis: Data were entered and analyzed using SPSS version 25.0 software. Descriptive statistics were used for categorical and continuous variables. Chi-square tests were applied for comparing categorical variables where appropriate.

Ethical Considerations: This retrospective study was conducted using bacterial isolates and their susceptibility patterns without patient intervention. Institutional ethical approval was obtained prior to study commencement.

Results

Overall Culture Positivity and Demographics: Out of 100 blood culture samples processed, 85 (85%) yielded positive bacterial growth. The age distribution of patients with positive blood cultures ranged from 2 days to 82 years, with a mean age of 42.3 ± 19.8 years. Male patients comprised 58.8% of cases, while female patients accounted for 41.2%, resulting in a male-to-female ratio of 1.43:1.
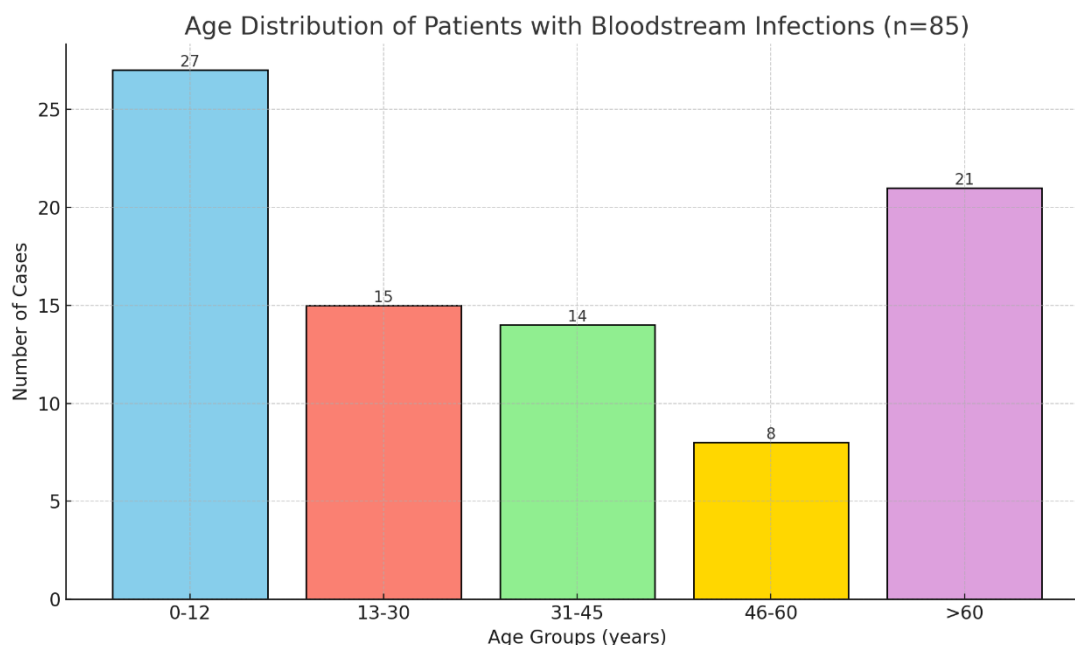

Figure 1: Age Distribution of Patients with Bloodstream Infections (n=85)

The age distribution demonstrates a bimodal pattern with the highest incidence in the pediatric age group (0-12 years) representing 31.8% of cases, followed by elderly patients above 60 years constituting 24.7% of infections. This pattern reflects the vulnerability of patients at the extremes of age to bloodstream infections. The pediatric predominance may be attributed to immature immune systems and higher rates of healthcare-associated procedures in this population. The significant representation of elderly patients aligns with their increased susceptibility due to age-related immune dysfunction and higher prevalence of comorbid conditions.

Microbial Profile: The study revealed a predominance of Gram-negative bacteria (55 isolates, 64.7%) over Gram-positive bacteria (30 isolates, 35.3%). The detailed distribution of bacterial isolates is presented in Table 1.

Table 1: Distribution of Bacterial Isolates from Bloodstream Infections (n=85)

Organism	Number	Percentage
Klebsiella pneumoniae	24	28.2%
Escherichia coli	17	20.0%
Pseudomonas aeruginosa	14	16.5%
Staphylococcus aureus	12	14.1%
Acinetobacter baumannii	8	9.4%
Enterococcus species	6	7.1%
Enterobacter aerogenes	2	2.4%
Salmonella species	2	2.4%

The microbial profile reveals Klebsiella pneumoniae as the predominant pathogen, accounting for more than one-quarter of all isolates. This finding is consistent with the increasing recognition of K. pneumoniae as a major healthcare-associated pathogen worldwide. Escherichia coli, traditionally the most common cause of community-acquired bloodstream infections, ranked second in our study. The significant presence of non-fermenting Gram-negative bacteria, particularly Pseudomonas aeruginosa and Acinetobacter baumannii, highlights the challenge posed by these opportunistic pathogens in hospital settings. Among Gram-positive bacteria, Staphylococcus aureus remained an important pathogen, while Enterococcus species contributed a smaller proportion of infections.

Antimicrobial Susceptibility Patterns: The antimicrobial susceptibility testing revealed varying resistance patterns across different bacterial species. Table 2 presents the resistance rates for major Gram-negative pathogens.

Table 2: Antimicrobial Resistance Patterns in Gram-negative Bacteria

Antibiotic	K. pneumoniae (n=24)	E. coli (n=17)	P. aeruginosa (n=14)	A. baumannii (n=8)
Ampicillin-sulbactam	75.0%	70.6%	-	87.5%
Ceftriaxone	66.7%	58.8%	-	75.0%
Ceftazidime	62.5%	52.9%	42.9%	87.5%
Ciprofloxacin	70.8%	64.7%	50.0%	75.0%
Gentamicin	58.3%	47.1%	35.7%	62.5%
Amikacin	20.8%	11.8%	14.3%	25.0%
Imipenem	16.7%	5.9%	35.7%	62.5%
Meropenem	12.5%	5.9%	28.6%	50.0%
Piperacillin-Tazobactam	25.0%	17.6%	21.4%	37.5%

The resistance patterns among Gram-negative bacteria demonstrate concerning levels of resistance to commonly used antibiotics. High resistance rates were observed against beta-lactam antibiotics, with third-generation cephalosporin resistance exceeding 50% in most species. Carbapenem resistance, while lower in Enterobacteriaceae, reached significant levels in non-fermenting bacteria. Amikacin showed the best overall activity against Gram-negative pathogens, followed by piperacillin-tazobactam. These findings suggest extensive beta-lactamase production among clinical isolates and highlight the need for carbapenem-sparing strategies to preserve these critical antimicrobial agents.

Gram-positive Resistance Profile: Table 3 summarizes the antimicrobial resistance patterns observed in Gram-positive bacterial isolates.

Table 3: Antimicrobial Resistance Patterns in Gram-positive Bacteria

Antibiotic	S. aureus (n=12)	Enterococcus spp. (n=6)
Penicillin	91.7%	83.3%
Ampicillin	-	66.7%
Erythromycin	66.7%	83.3%
Clindamycin	50.0%	-
Ciprofloxacin	58.3%	50.0%
Gentamicin	41.7%	66.7%
Chloramphenicol	25.0%	16.7%
Vancomycin	0%	16.7%
Linezolid	0%	0%
Teicoplanin	0%	16.7%

Gram-positive bacteria demonstrated high resistance rates to penicillin, with over 90% of S. aureus isolates showing resistance. Methicillin resistance was detected in 58.3% of S. aureus isolates based on cefoxitin disk testing. Enterococcus species showed high resistance to multiple antibiotics, with vancomycin resistance detected in one isolate (16.7%). All isolates remained susceptible to linezolid, making it a reliable therapeutic option for resistant Gram-positive infections. The resistance patterns emphasize the importance of appropriate empirical therapy selection and the value of rapid diagnostic methods in guiding treatment decisions.

Discussion

Our study provides valuable insights into the current epidemiological trends and antimicrobial resistance patterns of bloodstream infections in a tertiary care hospital in western India. The high culture positivity rate of 85% is notably higher than many previously reported studies, which typically range from 10-30% [19]. This elevated positivity rate may reflect the stringent clinical criteria used for blood culture ordering in our institution, ensuring that cultures are obtained from patients with high clinical suspicion of bloodstream infections.

The predominance of Gram-negative bacteria in our study aligns with global trends showing an epidemiological shift toward these pathogens in healthcare-associated bloodstream infections [20]. The high prevalence of Klebsiella pneumoniae as the leading cause of bloodstream infections is particularly noteworthy and consistent with reports from other Indian healthcare facilities [21]. This organism has emerged as a major healthcare-associated pathogen due to its ability to rapidly acquire and disseminate resistance mechanisms, coupled with its capacity to survive in hospital environments and spread through cross-transmission [22].

The age distribution pattern observed in our study, with peak incidence in pediatric and elderly populations, reflects the well-established epidemiological characteristics of bloodstream infections [23]. The high incidence in pediatric patients may be attributed to several factors including immature immune systems, higher rates of invasive procedures, and prolonged hospital stays associated with complex medical conditions. The significant burden in elderly patients reflects age-related immune senescence, increased prevalence of comorbidities, and frequent exposure to healthcare interventions that increase infection risk [24].

The antimicrobial resistance patterns documented in our study are deeply concerning and reflect the global crisis of antimicrobial resistance. The high rates of resistance to third-generation cephalosporins among Enterobacteriaceae suggest widespread extended-spectrum beta-lactamase (ESBL) production, which is consistent with previous reports from Indian healthcare settings [25]. ESBL production not only confers resistance to penicillins and cephalosporins but also often co-occurs with resistance to other antibiotic classes, significantly limiting therapeutic options [26].

Perhaps most alarming is the detection of carbapenem resistance in 18% of Enterobacteriaceae isolates, representing a critical threat to patient care. Carbapenem-resistant Enterobacteriaceae (CRE) infections are associated with high mortality rates and limited treatment options, often requiring combination therapy with potentially toxic agents [27]. The emergence of CRE in our institution necessitates immediate implementation of enhanced infection control measures and antimicrobial stewardship interventions to prevent further dissemination.

The resistance patterns among non-fermenting Gram-negative bacteria, particularly Pseudomonas aeruginosa and Acinetobacter baumannii, highlight the therapeutic challenges posed by these opportunistic pathogens [28]. These organisms possess intrinsic resistance mechanisms and readily acquire additional resistance determinants, making them formidable healthcare-associated pathogens. The high resistance rates observed against multiple antibiotic classes underscore the need for combination therapy and the development of novel therapeutic strategies.

Among Gram-positive bacteria, the detection of methicillin resistance in over half of S. aureus isolates is concerning, though comparable to rates reported from other Indian institutions (29). The presence of vancomycin-resistant Enterococcus, though limited to a single isolate, represents an emerging threat that requires vigilant surveillance and containment measures. The universal susceptibility to linezolid provides a reliable therapeutic option, though judicious use is essential to preserve its effectiveness [30].

The therapeutic implications of our findings are substantial and necessitate a comprehensive approach to antimicrobial therapy in our institution. The high resistance rates to commonly used empirical antibiotics suggest that current treatment protocols may require revision to incorporate broader-spectrum agents or combination therapy for serious infections. However, this approach must be balanced against the need to minimize antimicrobial pressure and preserve the effectiveness of critical antibiotics.

This study has several important limitations that should be acknowledged. The single-center design limits the generalizability of findings to other healthcare institutions with different patient populations, antimicrobial usage patterns, or infection control practices. The retrospective nature of the study restricted access to detailed clinical information that could have provided insights into risk factors, treatment outcomes, and mortality rates associated with different pathogens. The relatively small sample size of 100 isolates may not capture the full spectrum of resistance patterns present in our institution, and seasonal variations in pathogen distribution may not be adequately represented. Additionally, the lack of molecular characterization of resistance mechanisms limits our understanding of the genetic basis of resistance and potential for horizontal transmission between bacterial species.

Conclusion

This study demonstrates a high prevalence of Gram-negative bloodstream infections with alarming rates of antimicrobial resistance in our tertiary care facility. The predominance of Klebsiella pneumoniae and the significant emergence of carbapenem resistance represent critical challenges requiring immediate intervention. These findings underscore the urgent need for comprehensive antimicrobial stewardship programs, enhanced infection control measures, and continuous surveillance of resistance patterns. Implementation of rapid diagnostic methods, rational antibiotic prescribing practices, and robust infection prevention strategies are essential to combat the growing threat of multidrug-resistant bloodstream infections and preserve the effectiveness of available antimicrobial agents for optimal patient care.

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