

Current Scenario of Prevalence of Blood Stream Infection in a Tertiary Care Centre in Eastern India

Shehnaz Firdaus^{1*}, Kananbala Sahu², Preetam Kumar Kar³, SA Idrees⁴

¹Assistant Professor, Dept. of Microbiology, Hitech Medical College and Hospital, Bhubaneswar, Odisha, India

²Assistant Professor, Department of Dermatology, IMS & SUM Hospital Campus 2, Bhubaneswar, Odisha, India

³Assistant Professor, Dept. of Community Medicine, SCB Medical College, Cuttack, Odisha, India

⁴Assistant Professor, Dept. of Psychiatry, Hitech Medical College and Hospital, Bhubaneswar, Odisha, India

***Address for Correspondence:** Dr. Shehnaz Firdaus, Assistant Professor, Dept. of Microbiology, Hitech Medical College and Hospital, Bhubaneswar, Odisha, India

E-mail: shehnazz86@yahoo.com

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ABSTRACT

Background: Bloodstream infection (BSI) is one of the most important causes of morbidity and mortality globally, specifically among ICU and high-risk patients. The causes of BSI can be bacterial, viral, fungal and protozoal. Management of BSI cases is difficult due to an increase in microbial resistance. Hence a selection of proper antimicrobial agents empirically and a blood culture report before starting antibiotics are two major steps in treating BSIs. Moreover, as BSI are major cause of healthcare-associated infections, timely identification and appropriate treatment are of utmost importance.

Methods: A prospective cross-sectional study was conducted from May 2024 to October 2024 among BSI-suspected adult patients of age ≥ 18 years admitted to ICU and wards at a tertiary care hospital in Odisha. A systematic random sampling method was used to select patients. A blood culture was done. Bacterial isolation, identification and antimicrobial susceptibility tests of the isolates were performed. Prevalence percentages were determined.

Results: 1,210 blood culture samples were collected, with a bacteriological positivity rate of 15.7% (190/1,210). Gram-negative bacteria accounted for 65.7% of cases, while Gram-positive cocci made up 34.2%. *Klebsiella* sp. was the most prevalent Gram-negative isolate (68%), followed by *Pseudomonas aeruginosa*, *Acinetobacter* sp., and *Escherichia coli*. Among Gram-positive isolates, *Staphylococcus aureus* was most common (44.6%), followed by *Enterococcus* sp. Gram-negative isolates showed the highest sensitivity to Imipenem, while Gram-positive isolates were most sensitive to Vancomycin.

Conclusion: Blood culture is the mainstay of diagnosis of BSI. The AST pattern of the causative pathogenic bacteria can guide the judicious use of antibiotics for the treatment of BSI.

Key-words: Bloodstream infection, Healthcare-associated infection, MDR, ESBL

INTRODUCTION

Worldwide, bloodstream infections (BSIs) continue to rank among the leading causes of morbidity and mortality [1]. Bacterial, viral, fungal, and protozoal factors can all contribute to BSI. The presence of live bacteria in blood without any multiplication is known as bacteremia

and it can manifest as temporary, ongoing, or sporadic. A condition known as septicemia occurs when bacteria proliferate, move through the bloodstream, and may create toxins that damage the host's organs. Both Gram-negative bacteria like *E. coli*, *Klebsiella* sp., and *Proteus* sp. and Gram-positive bacteria like *Staphylococcus*, Coagulase-negative *Staphylococcus*, and *Enterococcus* are responsible for BSI. [2]

The presence of live bacterial or fungal germs in the bloodstream that cause or have caused an inflammatory response characterized by changes in clinical, biochemical, and haemodynamic parameters is what defines bloodstream infections (BSIs), which are infectious disorders. Despite significant advancements in

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supportive care and the availability of broad-spectrum, effective antibiotics, bloodstream infections continue to be a leading cause of morbidity and mortality. About 3–8% of bloodstream infections are caused by bacterial endocarditis. [3] Patients with BSI are susceptible to sepsis, which is brought on by a dysregulated host immunological response. They are to blame for significant mortality, expensive medical care, and extended hospital stays [4]. Treatment optimisation depends on the early identification of infections and the assessment of their susceptibility. Worldwide, blood culture has long been acknowledged as the gold standard for conclusive identification of bacterial and fungal diseases. Even within the same hospital, the pattern of antibiotic susceptibility and the distribution of bacteria appear to change over time [5]

In order to help in routinely updating the antibiogram and assisting doctors in initiating a presumed prophylactic and empirical treatment to reduce morbidity and mortality, it is crucial to continuously monitor the aetiology of bloodstream infections [6]. In the age of rapidly rising multi-drug resistance worldwide, rigorous surveillance also prevents the emergence of multi-drug-resistant organisms in the hospital setting because the antibiotic pipeline is essentially dry.[7] Understanding the bacteriological flora in BSI cases and the pattern of antibiotic susceptibility of the identified strains in a tertiary care hospital was the goal of the current investigation.

MATERIALS AND METHODS

Place of study- A prospective cross-sectional study was conducted among 1210 BSI suspected patients from ICU and wards for a period of 6 months (May 2024 to October 2024) in a Tertiary care Hospital in Odisha.

Inclusion Criteria- The inclusion criteria for the study subjects were (1) all patients ≥ 18 years admitted to ICU and wards and (2) patients who are suspected to have BSI. The following variables were included: age, gender, admitting department, name of the organism, antibiotics used for susceptibility testing and susceptibility results of each antibiotic tested.

Exclusion Criteria- The exclusion criteria were: (1) patients below the age of 18 years and (2) OPD patients.

Research Design- Before antimicrobial therapy, 5–10 ml blood samples were obtained aseptically, stored in BacT/ALERT FA and PF plus-aerobic bottles, respectively, and processed in an automated BACTEC system.[11] The BACTEC technology immediately indicated adequate bacteria growth. Even after seven days of incubation, no signal was produced in the absence of microbe development, and the sample was deemed sterile for aerobic organisms.

Using standard biochemical techniques, positive blood culture bottles were detected after being subcultured onto Mac Conkey and Blood agar media. Kirby Bauer's disc diffusion method was used to screen for antibiotic susceptibility under CLSI recommendations.

Statistical Analysis- Data collected from institutional databases, including patient information, were compiled, and statistically analyzed using appropriate statistical methods. The frequency and percentage of positive blood cultures, as well as the antibiotic susceptibility testing (AST) patterns of the causative pathogens, were analyzed to determine trends in the distribution of bacteria and their resistance profiles. The significance level for analysis was set at $p < 0.05$. Statistical tests such as chi-square or Fisher's exact test may have been applied where appropriate for categorical variables, and descriptive statistics were used to summarize the results.

Ethics committee approval- Information on patients was gathered from institutional databases. Informed consent was not necessary, although institutional ethics committee approval was acquired.

RESULTS

In this study out of 1210 samples, 190 were found to be bacteriologically positive 15.7% (190/1210 samples). The distribution of bacteriologically positive cases across different age groups is shown in Table 1. Most cases were observed in the elderly age group of 41–60 and >60 years of age.

Table 1: Age Group Distribution of Bacteriologically Positive Cases

Age Group (yrs)	No. of Positive Cases	Percentage
18–40	55	28.9%

41–60	67	35.2%
>60	68	35.7%
Total	190	100%

The gender-wise distribution of bacteriologically positive cases is summarized in Table 2. A slightly higher percentage of cases was observed in males compared to females.

Table 2: Bacteriological Profile by Gender

Gender	No. of Positive Cases	Percentage
Male	116	61.1%
Female	74	38.9%
Total	190	100%

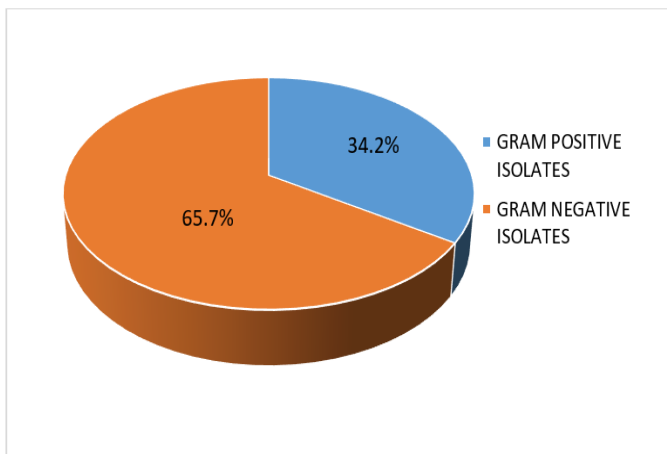


Fig. 1: Percentages of Gram-Positive and Gram-Negative Bacteria Isolated from Blood Cultures

Table 3 summarizes the distribution of Gram-negative isolates. The majority of BSI were caused by Gram-negative bacilli. A total of 125 Gram-negative isolates were identified, accounting for 65.7% of the bacteriologically positive samples. *Klebsiella sp.* was the most frequently isolated Gram-negative bacterium with a total of 68 (54.4%), followed by *P. aeruginosa* 37 (29.6%), *Acinetobacter sp.* 12 (9.6%), *E. coli* 8 (6.4%).

Table 3: Distribution of gram-negative Isolates

Gram Negative Isolates	No. of Positive Isolates	Percentage
<i>Klebsiella species</i>	68	54.4%
<i>P. aeruginosa</i>	37	29.6%
<i>Acinetobacter sp.</i>	12	9.6%
<i>E. coli</i>	8	6.4%
Total	125	100%

Table 4 summarizes the distribution of Gram-positive isolates. The majority of the Gram-positive isolates were *S. aureus* 29 (44.6%) followed by CoNS 22 (33.8%) and *Enterococcus sp.* 14 (21.5%) The antibiotic susceptibility testing of isolates was done. The sensitivity percentage of all the Gram-negative isolates and all the Gram-positive isolates were determined and tabulated as shown below.

Table 4: Distribution of gram-positive Isolates

Gram Positive Isolates	No. of Positive Isolates	Percentage
<i>S. aureus</i>	29	44.6%
Coagulase-negative <i>Staphylococcus</i>	22	33.8%
<i>Enterococcus sp.</i>	14	21.5%
Total	65	100%

As summarized in Table 5 Gram-negative isolates showed sensitivity to Imipenem (82.6%), Meropenem (79.8%) followed by Piperacillin- Tazobactam (62.3%), Ampicillin Sulbactam (49%), Gentamycin (40.3%), Amikacin (39.5%), Cotrimoxazole (37.2%), Cefepime (27.1%) and Ampicillin (16.5%).

Table 5: Sensitivity patterns with different antibiotics in Gram-negative bacteria

Antibiotic	Sensitivity (%)
Imipenem	82.6%
Meropenem	79.8%
Colistin	65.4%
Piperacillin Tazobactam	62.3%
Gentamicin	40.3%
Ampicillin Sulbactam	49%
Amikacin	39.5%
Co-trimoxazole	37.2%
Cefipime	27.1%
Ceftriaxone	22.5%
Ampicillin	16.5%

As summarized in Table 6 Gram-positive isolates showed sensitivity to Vancomycin (98.2%), Teicoplanin (92.4%), Linezolid (90.5%), Doxycycline (72.5%), Gentamycin (49.5%), Cotrimoxazole (42%) and Ofloxacin (32.6%).

Table 6: Sensitivity patterns with different antibiotics in Gram-positive bacteria

Antibiotic	Sensitivity (%)
Vancomycin	98.2%
Teicoplanin	92.4%
Linezolid	90.5%
Doxycycline	72.5%
Gentamycin	49.5%
Cotrimoxazole	42%
Ofloxacin	32.6%
Levofloxacin	25.3%
Erythromycin	10.3%
Penicillin	9.4%
Chloramphenicol	6.3%

DISCUSSION

In this study, all blood samples were collected from patients suspected to have septicemia; however, the blood culture showed positive results in 15.7% of patients, hence these were confirmed cases of septicemia. The blood cultures of the remaining suspected patients showed no growth of any bacteria. This may be due to prior antibiotic administration in such patients.

We also observed that the majority of isolates were predominantly Gram-negative, accounting for 65.7% and Gram-positive were found to be 34.2%. Similarly, Kumar *et al.* in their study demonstrated the high prevalence of Gram-negative organisms isolated from bloodstream infections. This may be due to the rise of antimicrobial resistance in gram-negative organisms.^[1] Few of the recently evolving mechanisms of resistance are due to multi-drug-resistant genes.

In another study conducted by Gill MK and Sharma S. in North India, researchers found 53% were Gram-positive bacteria (GPB) 39.3% were Gram-negative bacteria (GNB) and 11(7.9%) were non-albicans *Candida*.^[2]

In a recent study conducted in Manipur by Ningthoujam *et al.* It was found that the predominant isolates were Gram-positive, accounting for 75.3%, while Gram-negative accounted for 24.7%.^[3] According to LS Young, *S. aureus*, *P. aeruginosa*, and Coagulase Negative Staphylococci (CoNS) were the primary pathogens isolated.^[4] These findings emphasise that the prevalence rate of organisms varies among different geographical regions as well as on the antimicrobials usage.^[8-11]

The majority of patients reported to our tertiary care hospital were referred by primary and secondary care hospitals and private hospitals, and most of these patients had already received antimicrobials elsewhere before they reached our hospital. Furthermore, the patients who were admitted to the emergency sometimes received antimicrobials before the collection of blood for culture.

The present study aimed to analyze the bacteriological profile and antibiotic susceptibility pattern of bloodstream infection (BSI) isolates from 1210 clinical samples, of which 190 (15.7%) were bacteriologically positive. The findings underscore the importance of identifying causative agents and their antimicrobial resistance patterns to guide effective treatment strategies.^[12]

In our study, Gram-negative isolates constituted 65.7% of the bacteriologically positive cases. Among these, *Klebsiella sp.* was the most common (68% of Gram-negative isolates), followed by *P. aeruginosa*, *E. coli*, *Acinetobacter sp.* The significant presence of Gram-negative bacteria, particularly *Klebsiella sp.* and *P. aeruginosa*, aligns with previous studies that emphasize their role in hospital-acquired infections and multidrug resistance.^[13]

Our study revealed that among Gram-positive isolates, *S. aureus* was the most frequently isolated Gram-positive organism accounting for 44.6% of them. This is consistent with other studies reporting *S. aureus* as a predominant Gram-positive pathogen in bloodstream infections due to its virulence factors and propensity for nosocomial transmission. *Enterococcus sp.*, while less prevalent, were also identified, highlighting their emerging role in bloodstream infections.^[14]

The demographic findings in our study showed the highest proportion of bloodstream infections in the elderly age groups with 41–60 age group (35.2%) and >60 years (35.7%). These findings could reflect the increased exposure of these populations to healthcare settings and invasive procedures.^[15] A male predominance (61.6%) was noted, which is in line with previous studies suggesting higher susceptibility in males due to physiological and behavioral differences.

The antibiotic susceptibility patterns in this study highlight critical sensitivity trends. Gram-negative isolates demonstrated low sensitivity to third-generation cephalosporins (22.5% sensitivity to Ceftriaxone),

reflecting the increasing prevalence of extended-spectrum beta-lactamase (ESBL)-producing organisms. However, high sensitivity to Imipenem (82.6%) and Piperacillin-Tazobactam (62.3%) indicates their potential efficacy in managing Gram-negative BSIs.^[16]

Among Gram-positive isolates, high sensitivity was observed to vancomycin (98.2%) and linezolid (90.5%), which remain the mainstay for treating methicillin-resistant *S. aureus* (MRSA) and other resistant strains.^[17] However, low sensitivity to Penicillin (9.4%) and Erythromycin (10.3%) suggests a need for caution in empirical antibiotic therapy.

The low sensitivity rates observed in both Gram-positive and Gram-negative isolates to most of the widely used antimicrobial agents emphasize the urgent need for antimicrobial stewardship programs to minimize the misuse of antibiotics and curb the spread of multidrug-resistant organisms.^[18] Furthermore, the predominance of *Klebsiella* sp. and *S. aureus* highlights the importance of implementing strict infection control measures, particularly in intensive care units and other high-risk settings.^[19]

CONCLUSIONS

The study highlights the diverse bacteriological profile of bloodstream infections and the growing challenge of antimicrobial resistance. Early identification of causative agents and their susceptibility patterns is crucial for effective management and improving patient outcomes. This study also calls for better implementation of hospital infection control practices. Continuous surveillance and adherence to antimicrobial stewardship principles are essential to combat the rising threat of drug resistance.

CONTRIBUTION OF AUTHORS

Research concept- Shehnaz Firdaus, Kananbala Sahu

Research design- Preetam Kumar Kar, S A Idrees

Supervision- Kananbala Sahu, Preetam Kumar Kar

Materials- Preetam Kumar Kar, S A Idrees

Data collection- Shehnaz Firdaus, Kananbala Sahu

Data analysis and Interpretation- Kananbala Sahu

Literature search- Preetam Kumar Kar, S A Idrees

Writing article- Kananbala Sahu, Preetam Kumar Kar

Critical review- Preetam Kumar Kar, S A Idrees

Article editing- Shehnaz Firdaus, Kananbala Sahu

Final approval- Kananbala Sahu, Preetam Kumar Kar

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