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Original Article

Microbiology Section

Microbiological and Clinical Profiles of Bloodstream Infections in Adult Intensive Care Unit Patients: A Prospective Observational Study from a Tertiary Care Teaching Hospital of Rural Gujarat, India

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ABSTRACT

Introduction: Bloodstream Infections (BSIs) are among the most severe healthcare-associated infections encountered in Intensive Care Units (ICUs) and are associated with increased morbidity, mortality, prolonged hospital stays, and higher healthcare costs. The emergence of Multidrug-Resistant (MDR) organisms has further complicated the management of these infections, particularly in ICUs.

Aim: To evaluate the microbiological and clinical profile of BSIs among adult ICU patients in a tertiary care teaching hospital.

Materials and Methods: This prospective observational study was conducted from February 2023 to January 2024 in the adult ICU of Shree Krishna Hospital, Karamsad, Gujarat, India. A total of 100 non duplicate BSI isolates were included in the study. Blood culture samples were processed as per standard microbiological procedures. Identification of isolates and Antimicrobial Susceptibility Testing (AST) were performed using the VITEK® 2 Compact automated system. Relevant demographic details, clinical characteristics, and outcomes were recorded and analysed. Descriptive statistical analysis was performed; categorical variables are expressed as percentages.

Results: Primary BSIs accounted for 72% (72/100) of the BSI cases. Among the 100 BSI isolates, *Escherichia coli* (32%) was the most common pathogen, followed by *Enterococcus faecium* (12%), *Klebsiella pneumoniae* (10%), and *Staphylococcus aureus* (10%). Extended-spectrum β-lactamase (ESBL) production was detected in 24 (75%) *E. coli* and in 7 (70%) *K. pneumoniae* isolates. All the *Enterococcus faecium* (12/12) demonstrated 100% resistance to penicillin, whereas 100% *Enterococcus faecalis* (4/4) and *Staphylococcus aureus* isolates (10/10) were uniformly susceptible to linezolid, teicoplanin, and vancomycin. Postoperative complications were the most frequent reason for ICU admission. Among 100 BSIs, the overall mortality rate was 28%, while 54% of patients were discharged against medical advice and 18% showed clinical improvement.

Conclusion: BSIs in adult ICU patients are predominantly caused by Gram-negative organisms with a high prevalence of antimicrobial resistance. Early microbiological diagnosis and regular surveillance of resistance patterns are essential for optimising empirical therapy, improving patient outcomes, and strengthening antimicrobial stewardship in ICU settings.

Keywords: Antimicrobial resistance, Blood culture, Multidrug-resistant pathogens, Sepsis

INTRODUCTION

The BSIs are among the most serious and potentially fatal infections encountered in clinical practice, particularly in ICUs [1,2]. BSIs are categorised into intravascular and extravascular infections depending on the source of infection. Intravascular BSI stems from the cardiovascular system, such as infective endocarditis, catheter-associated bacteraemia, whereas extravascular BSI results from the dissemination of the pathogen into the bloodstream from a distant primary infection site [3]. BSI may occur either as healthcare-associated or community-associated infections, depending on where the infection was acquired. Healthcare-associated BSI are commonly observed among hospitalised patients, such as ICU patients [4,5]. Inadequate or delayed management of BSI may lead to the development of sepsis, septic shock, multiorgan dysfunction and mortality [5]. ICUs are considered high-risk settings as patients admitted to ICUs are critically-ill patients and especially vulnerable due to their compromised immunophysiological status and frequent exposure to invasive procedures [2]. Previous reports suggest that more than 10% of BSIs develop within the first four weeks of ICU admission, with mortality rates ranging between 20-50% [2,4,6]. Gamit MA et al., reported in their study that BSI is the third most encountered infection in ICU settings worldwide after urinary and respiratory infections [7]. BSIs are recognised worldwide as a major cause of hospital-acquired morbidity and mortality, contributing to prolonged hospital stay, increased healthcare expenditure, and significant therapeutic challenges. Even in patients with septic shock, outcomes may remain poor despite early initiation of appropriate antimicrobial therapy and adequate source control measures [8]. The elevated risk of infection in ICU settings is largely attributable to the widespread use of invasive medical devices, including central venous catheters, mechanical ventilation, urinary catheters, and other indwelling devices. Central line-associated BSIs and secondary bacteraemia resulting from Ventilator-Associated Pneumonia (VAP) are among the most common sources of infection in critically-ill patients [9]. The growing prevalence of MDR organisms further complicates management. Globally, frequently reported pathogens include Gram-negative bacilli such as *Klebsiella pneumoniae*, *Escherichia coli*, *Acinetobacter baumannii* complex, and *Pseudomonas aeruginosa* [8,10] as well as Gram-positive organisms including coagulase-negative staphylococci, *Staphylococcus aureus*, and *Enterococcus* species. Although several studies have described BSIs in different healthcare settings, microbiological profiles and resistance trends

vary significantly across institutions and as per different geographic areas [2,5,8]. The study was conducted at a tertiary care teaching hospital that serves a large patient population from Anand and surrounding rural areas. Recent institution-specific data on BSIs among ICU patients were not available, highlighting the need for local surveillance. Such epidemiological data and local antibiogram are important for clinicians to understand the prevailing pathogens and their resistance patterns, thereby facilitating appropriate empirical antimicrobial treatment, especially in the context of MDR infections where therapeutic options may be limited, particularly in critically-ill patients in the ICU. It also supports and strengthens antimicrobial stewardship initiatives.

The current study aimed to evaluate the microbiological spectrum, antimicrobial resistance patterns and clinical profile of BSIs among adult ICU patients in a tertiary care teaching hospital. The primary objectives of the study were to determine the incidence of BSIs among adult ICU patients, along with the distribution of pathogenic isolates and to analyse their antimicrobial susceptibility patterns, with special emphasis on MDR, Extensively Drug-Resistant (XDR), and Pan-Drug-Resistant (PDR) organisms. Secondary objectives were to identify clinical risk factors present in patients with BSIs and to assess patient outcomes and final clinical outcome.

MATERIALS AND METHODS

This prospective observational study was conducted at a tertiary care teaching hospital, Shree Krishna Hospital, Karamsad, Gujarat, India affiliated with Bhaikaka University, and included a total of 100 laboratory-confirmed non-duplicate BSI cases from the adult ICU from February 2023 to January 2024. Microbiological investigations were carried out at an NABL-accredited Central Diagnostic Laboratory following standard quality control procedures.

Prior approval was obtained from the Institutional Ethics Committee, Approval letter no: (IEC/BU/143/Faculty/04/72/2023), H.M. Patel Centre for Medical Care and Education, Bhaikaka University, Karamsad. Informed consent requirement was waived by the Institutional ethics committee due to the pure observational nature of the study, and no additional investigation or intervention had been performed on patients.

This was a time-bound study, and all eligible BSI cases meeting the inclusion criteria during the study period were taken into consideration.

Inclusion criteria: Adult patients admitted to the ICU during the study period with laboratory-confirmed BSI during their first ICU admission were included in the study.

Exclusion criteria: Patients with laboratory-confirmed viral, parasitic, or mycobacterial BSIs were excluded. Readmissions to the ICU during the study period, blood cultures interpreted as skin contaminants after clinical correlation, and cases with incomplete or inconsistent clinical data were also excluded from the study.

Study Procedure

Demographic, clinical, microbiological, and outcome data were prospectively collected using a structured Case Record Form (CRF) and/or electronic medical records. Information recorded included age, sex, reasons for admission, dates of hospital and ICU admission, duration of hospital and ICU stay, co-morbid conditions or risk factors present including renal failure, hepatic failure, malignancy, immunosuppression, diabetes mellitus, Human Immunodeficiency Virus (HIV) infection, chronic lung disease, malnutrition, and organ transplantation, surgical history (elective or emergency), suspected source of infection, ventilatory support, urinary catheterisation, presence of other invasive devices, antimicrobial therapy administered, blood culture results, antimicrobial susceptibility patterns and clinical outcomes categorised as discharge, Discharge Against Medical Advice (DAMA), or death. All the above-mentioned details were retrieved from hospital's electronic medical record system (SOLACE), which was maintained and documented by treating clinical teams. The diagnosis of BSI was based on clinical assessment, laboratory findings, and consultation with the treating intensivist. Considerations included clinical features of sepsis, specimen collection practices, blood volume collected, number and timing of cultures, and supporting diagnostic evidence.

Blood culture bottles were incubated in the BacT/ALERT system (bioMérieux) following standard laboratory protocol. Positive bottles were sub-cultured onto 5% sheep blood agar, MacConkey agar, and chocolate agar. Culture plates were incubated at 35-37°C for 16-18 hours; chocolate agar and 5% sheep blood agar were incubated at 35-37°C for 16 to 18 hours in a CO_2-enriched environment. Gram staining was performed from positive bottles, and significant findings were immediately communicated to the treating clinicians as critical alerts and documented in the Laboratory Information System (LIS).

Identification and Antimicrobial Susceptibility Tests (AST) with VITEK®2 Compact systems

Identification of isolates and AST were performed using the VITEK® 2 Compact automated system (bioMérieux). Appropriate identification cards for bacterial and yeast identification were used, including Gram-positive (GP), Gram-negative (GN), and yeast (YST) cards.) and AST cards (P628 and ST03 for Gram-positive cocci; N405 for Gram-negative oxidase-negative bacilli; N406 for Gram-negative oxidase-positive bacilli; and YS08 for yeasts were used. Minimum Inhibitory Concentrations (MICs) were interpreted according to Clinical and Laboratory Standards Institute (CLSI) guidelines M 100 34th Edition 2024 [11].

Antimicrobial Susceptibility Tests (AST) with the Kirby-Bauer disk diffusion method

Selected antibiotics, including doripenem, ampicillin–sulbactam, tetracycline, tobramycin, levofloxacin, and ceftazidime, were additionally tested using the Kirby–Bauer disc diffusion method in accordance with CLSI M 100 34th Edition 2024 recommendations [11]. The inoculum was prepared by directly suspending the colony in normal saline. Turbidity of inoculum was set according to the 0.5 McFarland standard, and lawn culture was done on Mueller Hinton Agar plates (MHA) using a sterile cotton swab dipped in suspension. Plates were incubated at 35-37°C overnight, and after incubation, the plates were examined for the inhibition zones under reflected light with the help of an antibiotic zone scale. The diameter of the discs was measured referring to CLSI M 100, 2024 recommendations [11].

Extended-spectrum β-lactamases (ESBLs) are enzymes produced by certain Gram-negative bacteria, particularly Enterobacterales that hydrolyse extended-spectrum cephalosporins (such as cefotaxime, ceftriaxone, ceftazidime) and aztreonam, but are inhibited by β-lactamase inhibitors such as clavulanic acid [12].

MDR/XDR/PDR organisms are defined as per the expert group of the Centres for Disease Prevention and Control (CDC) and the European Centres for Disease Control and Prevention (ECDC) [13].

Multidrug-Resistant organism (MDR organism): Acquired non-susceptibility to at least one agent in three or more antimicrobial categories [13].

Extensively Drug-Resistant (XDR): Non-susceptibility to at least one agent in all but two or fewer antimicrobial categories (i.e., bacterial isolates remain susceptible to only one or two categories) [13].

Pandrug-Resistant (PDR): Non-susceptibility to all agents in all antimicrobial categories [13].

Duplicate isolates: Repeated isolation of the same microorganism with a similar antimicrobial susceptibility pattern from the same patient during the study period.

Potential contaminants: Microorganisms commonly considered as skin commensals, for example, Coagulase-negative Staphylococci,

Micrococcus, Corynebacterium spp. (diphtheroids), *Bacillus* species etc., isolated in a single blood culture and clinically insignificant after correlation with the patient's clinical findings and discussion with treating physicians.

Quality control: Quality control procedures were strictly followed using American Type Culture Collection (ATCC) reference strains whenever new identification cards, AST cards, or antibiotic discs were introduced. Test kits were used for patient samples only after satisfactory quality control results were obtained. In cases of deviation, repeat testing and documentation were performed as per laboratory protocol. All final results were entered into the Hospital Information System and reported as per the standard institutional microbiology laboratory protocol. *S. saprophyticus* ATCC BAA 750 for GP card, *S. aureus* ATCC 25923 and *E. faecalis* ATCC 29212 for AST P628, *S. maltophilia* ATCC 17666 for GN card, *E. coli* ATCC 25922 for AST N405, *P. aeruginosa* ATCC 27853 for AST N406, *C. albicans* ATCC 14053 for YST card and *C. parapsilosis* ATCC 22019 strains were used for quality control.

STATISTICAL ANALYSIS

Data were entered into Microsoft Excel and analysed using IBM Statistical Package for the Social Sciences (SPSS) version 20.0. Descriptive statistical analysis was performed; categorical variables are expressed as percentages. As the study involves primarily descriptive analysis, no inferential statistical tests were applied.

RESULTS

A total of 1,169 blood cultures were received from various ICUs during the study period. Of these, 171 cultures were positive, yielding an overall culture positivity rate of 14.62%. The detailed study analysis was restricted to 100 non-duplicate laboratory-confirmed BSI that fulfilled the study eligibility criteria.

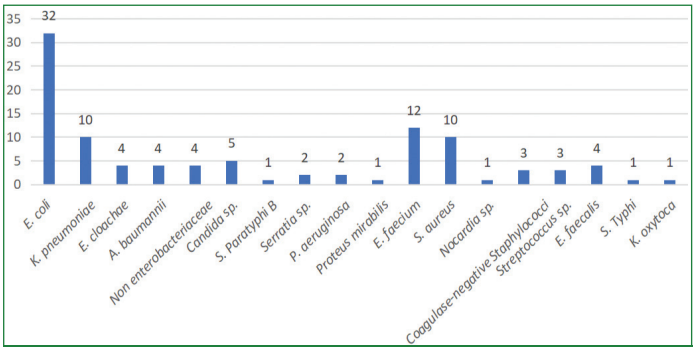
Based on 16,407 patient days of ICU stay, the BSIs in the ICU were 6.09 episodes per 1000 patient days.

The highest number of BSI cases was observed in patients aged >50 years. Among the 100 patients with BSI, 57 (57%) were male patients and 43 (43%) were female patients [Table/Fig-1].

Gender	Age (in years)							
	11-20	21-30	31-40	41-50	51-60	61-70	>70	Total (n=100)
Male	0	3	5	7	15	10	17	57
Female	2	2	0	5	11	14	9	43
Total	2	5	5	12	26	24	26	100

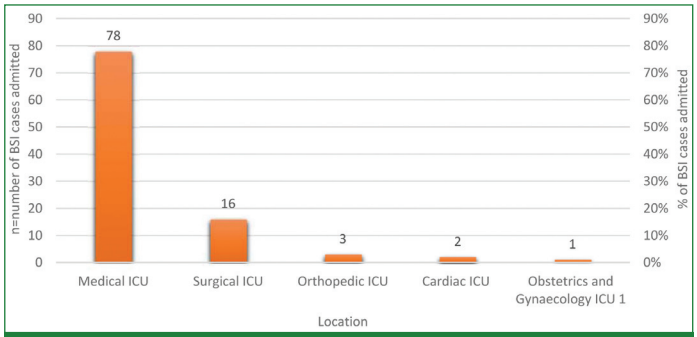
[Table/Fig-1]: Age and gender-wise distribution of Bloodstream Infections (BSI) (n=100).

Among the 100 isolates of BSI, the four major leading pathogens were; *Escherichia coli* 32 (32%) was the most common pathogen, followed by *Enterococcus faecium* 12 (12%), *Klebsiella pneumoniae* 10 (10%), and *Staphylococcus aureus* 10 (10%). *Candida* species accounted for 5% (n=5) of total isolates [Table/Fig-2].



[Table/Fig-2]: The distribution of bacterial and fungal isolates (n=100).
*As total isolates were 100, % corresponds numerically to absolute counts

Among the BSI cases, 78 (78%) of BSI reported in Medical ICU (MICU) followed by 16 (16%) from the Surgical ICU (SICU), [Table/Fig-3].



[Table/Fig-3]: Distribution of blood stream infections (n=100) across different Intensive Care Units (ICU).
*As total isolates were 100, % corresponds numerically to absolute counts

The majority of *E. coli* (n=32) were isolated from blood cultures received from MICU 30 (30%) followed by SICU 02 (2%). Another leading organism *K. pneumoniae* (n=10) was isolated predominantly from MICU i.e., 7 (7%) followed by SICU 3 (3%).

Among the 100 BSI cases, the median duration of ICU stay was seven days, with a range of 1-80 days. (IQR: 2.75-15 days)

Out of 100 BSI patients, Postoperative complications 28 (28%) were the most common indication for ICU admission, followed by renal diseases 16 (16%), decompensated heart failure 15 (15%), infective exacerbation of COPD 14 (14%), neutropenic sepsis 10 (10%), hepatic diseases 6 (6%), and diabetic ketoacidosis 2 (2%) [Table/Fig-4].

S. No.	Reasons for ICU admission	Total number of BSI n (%)
1	Postoperative complications	28 (28)
2	Renal diseases	16 (16)
3	Decompensated heart failure	15 (15)
4	Infective exacerbation of Chronic Obstructive Pulmonary Disease (COPD)	14 (14)
5	Neutropenic sepsis	10 (10)
6	Hepatic diseases	6 (6)
7	Diabetic ketoacidosis	2 (2)
8	Complete heart block	1 (1)
9	Gastrointestinal diseases	1 (1)
10	Hypoxia	1 (1)
11	COVID-19 infection	1 (1)
12	Aspiration pneumonia	1 (1)
13	Disseminated intravascular coagulation	1 (1)
14	Skin and soft-tissue infection	1 (1)
15	Seizures	1 (1)
16	Pleural effusion	1 (1)
Total		**100**

[Table/Fig-4]: Reasons for admission to Intensive Care Unit (ICU) among patients with Bloodstream Infection (BSI) n (%).

Primary BSI was the most common source, accounting for 72% of cases. Other suspected primary foci of infection are detailed in [Table/Fig-5].

Out of 100 BSI cases, mechanical ventilation was the most common risk factor present in 13 cases (13%), either alone or in combination with other factors. Other frequently observed risk factors included chronic kidney disease present in 12 (12%), diabetes mellitus 11 (11%), and recent surgery 11 (11%) [Table/Fig-6].

Suspected source of infection	n (%)
Primary blood stream infection	72 (72)
Urinary tract infection	14 (14)
Respiratory tract infection	04 (04)
Central line associated blood stream infection	04 (04)
Skin and soft tissue infections	03 (03)
BSI developed postoperatively	03 (03)
Total	100 (100)

[Table/Fig-5]: Suspected primary foci of infection contributing to Bloodstream Infection (BSI) in ICU patients (n=100).

S. No.	Risk factors	Total number of BSI n (%)
1	Mechanically ventilated	13 (13)
2	Chronic kidney disease	12 (12)
3	Surgical admission	11 (11)
4	Diabetes mellitus	11 (11)
5	High-risk equipment/procedures	7 (7)
6	Surgical admission and diabetes mellitus	7 (7)
7	Liver disease	6 (6)
8	Mechanically ventilated and high-risk procedure	6 (6)
9	COPD	5 (5)
10	Mechanically ventilated and Surgical admission	4 (4)
11	Malignancy	3 (3)
12	Diabetes mellitus and renal disease	3 (3)
13	Mechanically ventilated and Malignancy	3 (3)
14	Mechanically ventilated and COPD	3 (3)
15	Mechanically ventilated and Diabetes mellitus	2 (2)
16	Chronic kidney disease and COPD	1 (1)
17	Surgical admission and malignancy	1 (1)
18	Mechanically ventilated, diabetes mellitus and chronic kidney disease	1 (1)
19	Diabetes mellitus and COPD	1 (1)

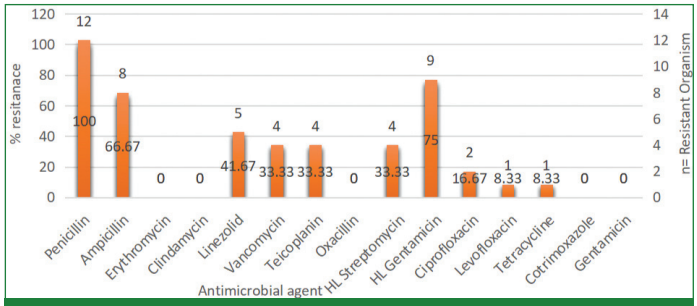
[Table/Fig-6]: Risk factors associated with BSI.

E. coli showed the highest resistance against ceftriaxone and cefuroxime 25/32 (78.12%), followed by ciprofloxacin 23/32 (71.87%). For the resistance profile of *K. pneumoniae* isolates (n=10), 7 out of 10 (70%) showed resistance to cefepime, ceftriaxone, cefuroxime, and ceftazidime, while six out 10 (60%) were resistant to ciprofloxacin [Table/Fig-7]. All (4/4) *Enterobacter cloacae* isolates demonstrated 100% resistance to amoxicillin-clavulanic acid, with variable resistance (25-75%) to other antimicrobial agents. *Acinetobacter baumannii* exhibited resistance ranging from 25% to 75% against most tested antimicrobials.

Antimicrobial agent	*E. coli* n=32 (%)	*K. pneumoniae* n= 10 (%)
Ampicillin-sulbactam	15 (46.87)	5 (50)
Aztreonam	8 (25)	3 (30)
Amikacin	1 (3.12)	3 (30)
Amoxicillin-clavulanic acid	14 (43.75)	5 (50)
Ampicillin	10 (31.25)	1 (10)
Cefepime	18 (56.25)	7 (70)
Cefotaxime	0	0
Ceftriaxone	25 (78.12)	7 (70)
Cefuroxime	25 (78.12)	7 (70)
Ceftazidime	20 (62.5)	7 (70)
Cefoperazone-sulbactam	8 (25)	5 (50)
Trimethoprim-sulfamethoxazole	13 (40.62)	4 (40)
Ciprofloxacin	23 (71.87)	6 (60)
Ertapenem	8 (25)	5 (50)
Imipenem	6 (18.75)	4 (40)
Meropenem	20 (62.5)	4 (40)
Doripenem	6 (18.75)	3 (30)
Levofloxacin	20 (62.5)	4 (40)
Gentamycin	6 (18.75)	3 (30)
Piperacillin/tazobactam	13 (40.62)	5 (50)
Tetracycline	17 (53.12)	4 (40)
Tobramycin	8 (25)	3 (30)
Colistin	0	0

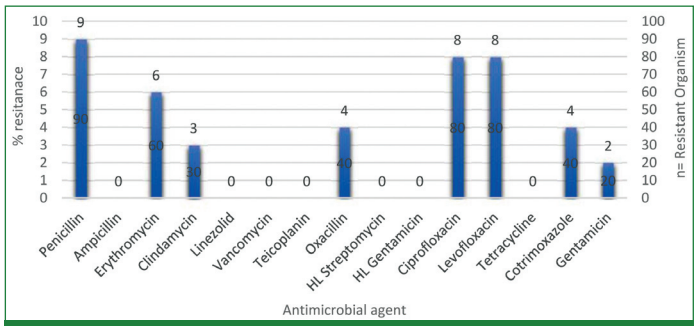
[Table/Fig-7]: Antimicrobial drug resistance of most common Gram-negative organisms (n=50).

Among Gram-positive organisms, *E. faecium* (n=12) showed 100% resistance to penicillin [Table/Fig-8] and *E. faecalis* (n=4) isolates were 100% susceptible to linezolid, teicoplanin, and vancomycin [Table/Fig-8].



[Table/Fig-8]: Antimicrobial drug resistance pattern of *E. faecium* (n=12).

S. aureus isolates (n=10) demonstrated 100% susceptibility to linezolid, teicoplanin, and vancomycin [Table/Fig-9].



[Table/Fig-9]: Antimicrobial drug resistance pattern of *S. aureus* (n=10).

Antifungal Susceptibility

Total n=5 *Candida* species isolated, *Candida parapsilosis* (n=1) was resistant to fluconazole 1/1 (100%) but remained susceptible to amphotericin-B, micafungin, flucytosine, voriconazole, and caspofungin. *Candida glabrata* (n=2) demonstrated 2/2 (100%) resistance to caspofungin but was susceptible to other antifungal agents. *Candida lucitaniae* (n=2) was fully susceptible to all tested antifungal drugs.

Distribution of ESBL-producing and non-producing *E. coli* and *K. pneumoniae* in BSI: Among 32 isolates of *E. coli,* 24 (75%) isolates were ESBL producers and 8 (25%) isolates were ESBL non-producers. Among 10 isolates of *K. pneumoniae*, 7 (70%) were ESBL producers and 3 (30%) isolates were ESBL non-producers.

Distribution of MDR, XDR, and PDR isolates among Bloodstream Infection (BSI)

The distribution of MDR, XDR, and PDR isolates among 38 resistant strains, MDR isolates were most common (22/38; 57.89%), followed by PDR (11/38; 28.94%) and XDR (5/38; 13.15%). *E. coli* was the predominant MDR organism, accounting for 15/22 (68.18%). Among 11 PDR isolates, *Klebsiella* spp. and *Enterococcus* spp.

each accounted for 4 (36.4%) isolates and again *E. coli* constitutes 60% (3/5) of XDR.

Clinical Outcomes

The overall mortality rate was 28%. DAMA was observed in 54% of cases, while 18% of patients showed clinical improvement.

DISCUSSION

Globally, sepsis continues to impose a substantial burden on healthcare systems [14]. Septicaemia remains a highly fatal condition, and rapid diagnosis along with timely determination of the antimicrobial susceptibility pattern, is essential for early initiation of appropriate therapy. Blood culture remains the gold standard for identifying aetiological agents of sepsis. The present study provides important insights into the distribution of bacterial isolates causing septicaemia and their antimicrobial susceptibility patterns, which are crucial for guiding effective clinical management.

The overall blood culture positivity rate in the present study was 14.62%. A similar finding was observed in the study conducted by Kaur C and Sharma S, where the culture positivity rate observed was 14.5% [15], whereas a study conducted by Sonawane J et al., had shown a culture positivity rate of 19.95% [2]. Culture positivity rate depends on a variety of factors such as different geographical area, difference in the distribution of various aetiological agents, the amount of over-the-counter use of antimicrobial agents before visiting hospital, and population characteristics [15]. Collecting multiple sets of blood culture bottles and adequate blood volume per bottle increase the rate of isolating the organism for suspected BSI [3]. Di Franco S et al., mentioned in their study that approximately 5-7% of ICU admissions are reported to result in BSIs, translating to 6-10 episodes per 1000 patient-days in critically-ill patients [8]. In the present study, the rate was 6.09 episodes per 1000 patient-days, which falls within the reported global range.

Gender-wise distribution showed male predominance (57%) compared with females (43%), similar to study done by Komori A et al., reporting 56.4% males affected [16]. Gamit MA et al., has also mentioned male predominance (60%) in blood culture positivity [7], Sonawane J et al., showed 66% of male patients and 33% female patients affected in their study population [2]. The higher susceptibility in males has been attributed to possible genetic factors. As mentioned in study done by Nowak TJ and Muehlenbein MP, a gene located on the X chromosome, involved in thymic function or immunoglobulin synthesis, has been postulated. Females, having two X chromosomes, may possess enhanced immunological protection, potentially explaining their relatively lower susceptibility [17].

The present study demonstrated that patients aged >50 years was the most commonly affected age group, which was commonly found and comparable to other studies. Sonawane J et al., reported higher prevalence of BSI among patients aged >60 year and Robinson P et al., reported 46-60 years of age group is most commonly affected [2,3].

Similar to the findings of few previous studies, Gram-negative organisms were the predominant causative pathogens of BSIs [18-20]. Out of 100 isolates of BSI, Gram-negative organisms were the predominant pathogens causing BSI, among which *E. coli* was the most common isolated pathogen. In the study conducted by Robinson P et al., where Gram-negative pathogens predominate the causative agents for adult blood stream infections which was similar finding as the present study [3]. As per review study done by Di Franco S et al., *Klebsiella pneumoniae* and *Escherichia coli* are among the most frequently reported pathogens causing BSIs, followed by *Acinetobacter baumannii* complex and *Pseudomonas aeruginosa* [8]. This variation may reflect local epidemiological patterns and antimicrobial practices. A comparative distribution of common organisms isolated in various studies is shown in [Table/Fig-10] [2-4,7].

Regarding the source of infection, Pradipta IS et al., reported in their study, respiratory tract 35.7% as the most common source of infection, followed by intra-abdominal source 26.18%, skin and soft-tissue 11.90%, urinary tract infection 4.76% and in 21.43% cases, source remained unknown [21]. A study conducted by Komori A et al., from Japan reported lung (20.9%), renal (25.2%), skin and soft-tissue (20.5%), and central line infections (3.1%) as common sources [16]. In comparison, the present study showed corresponding rates of 4%, 14%, 3%, and 4%, respectively. The same Japanese study reported risk factors such as Chronic Obstructive Pulmonary Disease (COPD) (5.2%), chronic kidney disease (7.7%), diabetes mellitus (16.8%), malignancy (12.7%), and liver disease (4.9%). In the present study, these were observed in 5%, 12%, 11%, 3%, and 6% of cases, respectively. Vincent JL et al., reported COPD (20.2%), chronic renal failure (10.7%), Diabetes mellitus (10.3%), malignancy (15.7%), liver disease (3.7%) co-morbid conditions as risk factors in their study [1]. These differences may reflect regional variation in comorbidity profiles and healthcare settings.

In the present study, vancomycin demonstrated 100% sensitivity against *S. aureus*, indicating its continued effectiveness. However, resistance to penicillin 9/10 (90%), ciprofloxacin 8/10 (80%), erythromycin 6/10 (60%), clindamycin 3/10 (30%), and gentamicin 2/10 (20%) was observed. Similar findings of high vancomycin effectiveness against Gram-positive organisms have been reported in other studies conducted by Chopra S et al., Garg A et al., and Mehta M et al., [18-20]. Nevertheless, the continued efficacy of vancomycin cannot be assumed indefinitely, as reports of Vancomycin-Resistant *S. aureus* (VRSA) have emerged in the study conducted by Pradipta IS et al., [21].

Gram-negative organisms were predominant in this study, and most were MDR. *E. coli* exhibited high resistance to ceftriaxone and cefuroxime 25/32 (78.12%), and ciprofloxacin 23/32 (71.87%). Amikacin remained effective against *E. coli* in this study. These findings highlight the therapeutic challenges posed by increasing resistance among Gram-negative pathogens. In the present study 75% *E. coli* (24/32) and 70% *Klebsiella pneumoniae* were ESBL producers. Study conducted by Sonawane J et al., showed 89.65% (26/29) *E. coli* and 94.59% (35/37) *Klebsiella pneumoniae* were ESBL producers [2]. 34.61% *E. coli* and 54.76% *Klebsiella pneumoniae* were found to be ESBL producers in the study conducted by Robinson P et al., [3].

Common organisms isolated	Ladani KD et al.,	Sonawane JP et al., [2]	Tatte PS et al., [5]	Gamit MA et al., [7]	Robinson P et al., [3]	Bhabhor H et al., [4]
Escherichia coli	32%	17.36%	13.47%	3.86%	13.26%	8.09%
Klebsiella pneumoniae	10%	22.15%	5.71%	14.97%	21.93%	15.02%
Staphylococcus aureus	10%	6.59%	21.22%	11.6 %	18.36%	41.61%
Enterococcus sp.	16%	8.38%	3.67%	13.04%	5.61%	1.73%
Acinetobacter sp.	4%	18.56%	3.26%	12.07%	9.69%	9.82%
Pseudomonas sp.	3%	9.58%	11.83%	13.04%	9.18%	9.82%
Coagulase Negative Staphylococcal species (CONS)	3%	2.40%	11.02%	28.98%	2.04%	8.67%
Candida sp.	5%	9.58%	19.19%	4.60%	2.55%	-

[Table/Fig-10]: Common organisms isolated in different studies [2-5,7].

Emerging non-*albicans Candida* species have been associated with increased virulence, higher mortality, and resistance to commonly used antifungal agents such as fluconazole and ketoconazole [22]. In the present study, *Candida parapsilosis* showed 100% resistance to fluconazole, and *Candida glabrata* demonstrated 100% resistance to caspofungin. Tatte PS et al., demonstrated varying degree of resistance towards commonly prescribed antifungal agents in *Candida albicans* and non-*albicans* species [5]. These findings emphasise the need for species-level identification and susceptibility testing in fungal BSIs.

The high frequency of MDR organisms observed in this study may reflect inappropriate antimicrobial use, limited availability of advanced diagnostic tools, and lack of updated antibiotic guidelines. The increasing prevalence of MDR organisms underscores the urgent need for rational antibiotic use, implementation of antimicrobial stewardship programs, formulation of institutional antibiotic policies, and strict infection control practices.

The findings of the present study provide institution-specific data on the microbiological profile and antimicrobial susceptibility patterns of BSIs among ICU patients. Such data may help guide clinicians in selecting appropriate empirical antimicrobial therapy, particularly in the context of MDR infections where therapeutic options may be limited, and support antimicrobial stewardship initiatives.

Limitation(s)

The study was conducted at a single tertiary care teaching hospital with limited sample size. So the findings of the study may not be generalisable to all health care settings. In addition, the study was restricted to ICU setting, the observed pathogen distribution and their antimicrobial susceptibility pattern may differ from non-ICU setting and other hospitals.

CONCLUSION(S)

Septicaemia remains an important cause of morbidity and mortality. The present study demonstrated that both Gram-positive and Gram-negative organisms contribute to septicaemia, with a predominance of MDR strains, limiting therapeutic options. Timely detection and awareness of prevalent pathogens and their antimicrobial susceptibility patterns are essential to guide appropriate treatment decisions. Strengthening surveillance systems, implementing antibiotic stewardship policies, and reinforcing infection control measures are crucial steps toward effective management and prevention of antimicrobial resistance.

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