Section: Microbiology

Original Research Article

A CROSSSECTIONAL STUDY TO FIND OUT THE PROPORTION OF MICROORGANISMS AND THEIR ANTIMICROBIAL RESISTANCE PATTERN OF CENTRAL LINE ASSOCIATED BLOOD STREAM INFECTIONS IN INTENSIVE CARE UNIT PATIENTS OF TERTIARY CARE HOSPITAL

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ABSTRACT

Background: Bloodstream infections are a serious concern in health-care settings, especially with the increasing use of invasive devices in intensive care unit (ICU) patients. The most common organisms associated with CLABSI includes a variety of Gram-positive and Gram negative bacteria as well as yeasts notably Klebsiella spp., Acinetobacter spp., Candida spp., Staphylococcus aureus, Enterococcus spp., and coagulase negative Staphylococci spp. as per reports.

Materials and Methods: This is a cross sectional study involving 211 samples to find out the proportion of Central Line Associated Blood Stream Infections (CLABSI) in intensive care unit patients and to isolate, identify and to determine the antimicrobial resistance pattern of isolated organisms in culture positive samples..

Results: The incidence rate of CLABSI in our study is 9.48%. Klebsiella spp. (35%) are the most commonly isolated micro-organism and other organisms isolated are Acinetobacter baumannii (15%), Pseudomonas aeruginosa (10%), Escherichia coli (10%), Staphylococcus aureus (10%), Candida tropicalis (15%) and Candida krusei (5%) with alarming resistance patterns to critical antibiotics such as carbapenems..

Conclusion: A robust antimicrobial stewardship program apart from a good infection control practices, including hand hygiene is needed to help combat this rise in antimicrobial resistance.

Keywords: Central Line-Associated Bloodstream Infections, Gram-negative bacteria, antimicrobial resistance, Intensive Care Units, multidrug-resistant, extensively drug-resistant.

INTRODUCTION

Central Line-Associated Bloodstream Infections (CLABSIs) have emerged as a critical concern globally, with significant variations in incidence, causative agents, and outcomes across regions. despite these advancements, the global burden remains substantial, particularly in resource-limited settings where healthcare infrastructure and infection control practices are often inadequate (Saharman et al., 2021).[1-5] In low- and middle-income countries (LMICs), CLABSI rates can be as high as 44.6 per 1,000 central line days, compared to less than 2 per 1,000 central line days in high-income countries.

Developing countries bear a disproportionate burden of CLABSIs due to a combination of factors, including limited access to sterile supplies,

overcrowded ICUs, and suboptimal adherence to aseptic techniques (Zeng et al., 2021).[6]

Various studies in literature showed majority of CRBSI is caused by Gram positive pathogens followed by Gram negative pathogens. Coagulase negative Staphylococcus spp. followed by Staphylococcus aureus and Pseudomonas aeruginosa, Acinetobacter baumannii, Klebsiella spp., Enterobacter spp., Citrobacter frundii, Serratia marcescens, Malassezia furfur, Candida spp. (such as Candida albicans, Candida parapsilosis, and Candida tropicalis) Enterococcus spp., Corynebacterium spp.[1,7-10]

Currently the trends have shifted from Gram positive pathogens to Gram negative pathogens in ICU settings.[1,11,12] Gram-negative bacteria were the most common organisms isolated from CLABSI (56%), followed by gram-positive bacteria (41%). Candida was isolated from 3% of the isolates. Pathogens such as Klebsiella pneumoniae, Escherichia coli, Pseudomonas aeruginosa, and Acinetobacter baumannii are frequently isolated in blood cultures from ICU patients (MacVane, 2017).[13] These organisms possess a range of virulence factors and resistance mechanisms, such as the production of extended-spectrum beta-lactamases (ESBLs) and carbapenemases, which enable them to evade commonly used antibiotics. The ICU environment, characterized by prolonged hospital stays, invasive procedures, and high antibiotic use, creates an ideal setting for the proliferation of these pathogens. Studies have shown that infections caused by Gram-negative bacteria are associated with higher mortality rates than those caused by Gram-positive organisms, emphasizing the need for targeted therapeutic strategies and robust infection control measures in ICU settings (MacVane, 2017).[13]

The rising trend of antimicrobial resistance (AMR) among CLABSI-causing pathogens in tertiary care hospitals poses a significant threat to patient outcomes. A research from a multidisciplinary ICU in India highlighted the prevalence of multidrug-resistant organisms, with Klebsiella pneumoniae and Acinetobacter baumannii being the most common culprits (Kumar et al., 2022).[14] These findings align with global reports of emerging resistance to last-resort antibiotics, such as colistin, further complicating the management of CLABSIs. The studies emphasize the importance of antimicrobial stewardship programs, which involve the judicious use of antibiotics and the implementation of strict infection control protocols to curb the spread of resistant strains in hospital settings.

MATERIALS AND METHODS

This study employed a cross-sectional design to determine the proportion of microorganisms in Central Line-Associated Bloodstream Infections (CLABSIs) and analyze their antimicrobial resistance patterns providing a comprehensive overview of the current burden of CLABSIs in the ICU.

Setting And Duration

This study was conducted in the Department of Microbiology, Mahatma Gandhi Memorial Medical College and associated hospitals, Indore (M.P) for a period of one year from December 2022 to December 2023.

Participants

The study included ICU patients with central venous catheters in place for more than 48 hours, as prolonged catheterization is a well-documented risk factor for CLABSIs. Patients were enrolled based on specific inclusion criteria:

- Age >1 year.
- No bloodstream infections at the time of catheter insertion.
- Willingness to provide informed consent.

Data Collection

Data collection was systematic and involved multiple steps to ensure accuracy and reliability

1. **Microbiological Sampling:**
   - Patients were identified (who fulfil the criteria of CLABSI) and their blood samples were collected in BHI broth.
   - Then the BHI broth was incubated overnight aerobically at 37°C.
   - The sample was inoculated onto Blood Agar, MacConkey Agar and Sabouraud's Dextrose Agar.
   - If there is no growth then the sample is sub-cultured on alternate days for 7 days before reporting it as sterile.
2. **Pathogen Identification:**

Standard microbiological protocols, including Gram staining, culture on blood agar and MacConkey agar, and biochemical tests, were used for pathogen identification.

3. **Antibiotic Susceptibility Testing:**

Isolates underwent antibiotic susceptibility testing using the Kirby-Bauer disk diffusion method. Resistance profiles were categorized as sensitive, intermediate, or resistant based on CLSI Guidelines 2022 breakpoints.

Data Analysis

Statistical analysis was conducted using SPSS (Statistical Package for the Social Sciences) software. Descriptive statistics were used to calculate the prevalence of Gram-negative bacteria and their resistance patterns. Chi-square test was applied to determine associations between patient demographics, catheter duration and infection rates. Results were presented as percentages, means, and standard deviations, with a significance threshold set at $p < 0.05$.

RESULTS

Table 1: Incidence rate of CLABSI

	Number	Percentage
No. of culture positive patients	20	9.48%
Total no.of patients with central line	211	

The incidence rate of CLABSI is 9.48%.
CLABSI Rate
In our study the CLABSI rate is 13.5 CVC days.
(Number of CLABSI cases/ Number of central line days) X 1000
(20/1480)X100 = 13.5 per 1000 Central line days

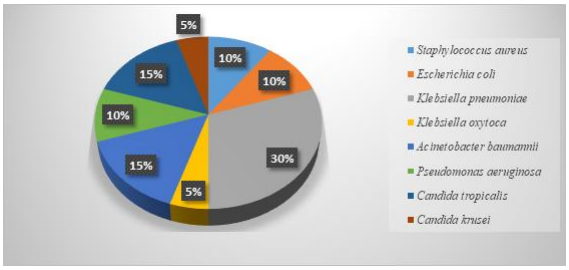

Figure 1: Proportion of micro-organisms isolated in CLABSI patients.

Table 2: a. Antimicrobial resistance pattern of Gram negative Bacteria isolated in CLABSI patients

Antibiotics	R/T (Resistance %)			
	Klebsiella spp.(N=7)	Escherichia coli(N=2)	Acinetobacter baumannii(N=3)	Pseudomonas aeruginosa(N=2)
Ampicillin	NA	2/2(100)	NA	NA
Ciprofloxacin	5/7(71.42)	1/2(50)	1/3(33.33)	0/2(0)
Amikacin	5/7(71.42)	1/2(50)	3/3(100)	2/2(100)
Gentamicin	6/7(85.71)	1/2(50)	0/3(0)	1/2(50)
Cefipime	7/7(100)	1/2(50)	1/3(33.33)	0/2(0)
Ceftriaxone	6/7(85.71)	2/2(100)	3/3(100)	NA
Ceftazidime	7/7(100)	2/2(100)	3/3 (100)	0/2 (0)
Imipenem	5/7(71.42)	2/2(100)	1/3(33.33)	0/2 (0)
Meropenem	3/7(42.86)	1/2(50)	2/3(66.67)	0/2 (0)
Piperacillin-tazobactum	6/7(85.71)	2/2(100)	3/3(100)	0/2 (0)
Cotrimoxazole	5/7(71.42)	1/2(50)	3/3(100)	NA
Aztreonam	7/7(100)	2/2(100)	NA	(1/2) 50

R/T=No. of Resistant isolate/Total No. Isolate
NA=Not Applicable due to intrinsic resistance

Table 2B: Antimicrobial resistance pattern of Gram positive Bacteria isolated in CLABSI patients

Antibiotics	R/T (Resistance %)
	Staphylococcus aureus(N=2)
Penicillin	2/2(100)
Erythromycin	2/2(100)
Clindamycin	1/2(50)
Doxycyclin	1/2(50)
Linezolid	0/2(0)
Cefoxitin	2/2(100)
Ciprofloxacin	2/2(100)
Gentamicin	1/2(50)
Tetracyclin	0/2(0)

Table 2C: Antimicrobial resistance pattern of Candida spp. isolated in CLABSI patients

Antifungal Drugs	R/T (Resistance%)	
	Candida tropicalis(N=3)	Candida krusei(N=1)
Fluconazole	0/3(0)	0/1(0)
Itraconazole	1/3(33.33)	1/1(100)
Voriconazole	0/3(0)	0/1(0)
Caspofungin	1/3(33.33)	1/1(100)

DISCUSSION

Our study was conducted in the Department of Microbiology, MGM Medical College, Indore (M.P.). A total of 211 blood samples were tested for CLABSI during the study period among which 20 samples were culture positive. Keeping in mind objectives of the study, statistical analysis was carried out.

In our study, the incidence rate of 9.48% is observed. This is in agreement with the study conducted by Maqbool et al,[9] 2023, which have similar incidence rate of CLABSI (9.3 %). In our study, the CLABSI rate is 13.5 per 1000 central line days which is almost

similar to the CLABSI rate of 12.1 per 1000 central line days obtained in the multicentric surveillance study conducted in 2022 by Purva Mathur et al.[1] Single-center and some multicentric Indian studies have reported CLABSI rates usually centring around 7–14.[15-17]

The common pathogenic bacteria isolated in our study were Klebsiella spp. (35%), Acinetobacter baumannii (15%), Pseudomonas aeruginosa (10%), Escherichia coli(10%), Staphylococcus aureus(10%), Candida tropicalis(15%) and Candida krusei (5%). This is in concordant with the result obtained in the multicentric study,[1] conducted under ICMR's Antimicrobial Resistance Surveillance and Research Network and the NCDC's National Antimicrobial Resistance Surveillance Network, coordinated by the All India Institute of Medical Sciences, New Delhi in 2022 which concluded Klebsiella spp. (24.8%) were the most frequently identified pathogen among CLABSI patients, followed by Acinetobacter spp. (21·3%) and Candida spp. (11·8%). Our observation of gram negative bacilli, chiefly Klebsiella spp. being the most common cause of CLABSI is a finding similar to that reported from various previous Indian studies.[15-17] However, there are several Indian studies that reported gram-positive bacteria, chiefly S.aureus and CONS as the common isolates.[17] Data from the Western countries implicates CONS , S.aureus, Enterococci and Candida spp. as common pathogens causing CLABSI with gram-negative bacilli accounting for only 20% of the infections.[10] The finding of predominant non albicans Candida as a cause of candidemia in our study is in agreement with the study by Chakrabarti et al.[18]

One of the most notable findings of this study is the high prevalence of antimicrobial resistance accounted for the majority of CLABSI cases which aligns with global trends of rising resistance (MacVane, 2017; Zeng et al., 2021).[6,13] Klebsiella spp. isolated were highly resistant to 3rd and 4th generation cephalosporins i.e. 85.71% and 100% repectively. They were also resistant to aminoglycosides like amikacin (71.42%), gentamicin (85.71%). Piperacillin-tazobactum shows 85.71% resistance while co-trimoxazole and meropenem shows71.42% and 42.85% resistance respectively. Escherichia coli isolated were 100% resistant to 3rd generation cephalosporins, ampicillin, piperacillin-tazobactum and imipenem whereas 50% resistant to meropenem, fluoroquinolones, 4th generation cephalosporins, co-trimoxazole and aminoglycosides. Pseudomonas aeruginosa isolated were completely sensitive to of the used drugs except aminoglycosides and aztreonam. Acinetobacter baumannii were 100% resistant to amikacin, ceftazidime,co-trimoxazole and piperacillin tazobactum. They were also resistant to meropenem (67%), 4th generation cephalosporins (33.3%), ciprofloxacin (33.3%) and imipenem (33.3%). the isolates of Staphylococcus aureus were cefoxitin resistant therefore categorised under methicillin resistant Staphylococcus aureus. They were 100% sensitive to linezolid and tetracyclin, 50% resistant to gentamycin, doxycycline and clindamycin and 100% resistant to macrolides, fluoroquinolones and penicillin. The Candida spp. isolated were 100% sensitive to fluconazole and voriconazole whereas 50% sensitive to caspofungin and itraconazole. These organisms, armed with sophisticated resistance mechanisms, pose a significant threat to patient outcomes, leading to prolonged hospital stays, increased healthcare costs, and higher mortality rates.

CONCLUSION

In our study, a total of 211 patients were taken into consideration who were having central line for more than two calendar days in all age groups (except <1 year). The incidence rate of CLABSI in our study is 9.48%. Central line duration varied from patient to patient with an average of 7 days and we obtained a CLABSI rate of 13.5 per 1000 CVC days. *Klebsiella spp.* were the most commonly isolated micro-organism. According to our study, the trend has been shifted from Gram positive bacteria to Gram negative bacteria. And also the changing trend of *Candida spp*. from albicans to non albicans is also clearly visible in our study. Most of the micro-organisms isolated were multidrug resistant. The clinical implications of these findings are both profound and urgent. Treating infections caused by multidrug-resistant (MDR) and extensively drug-resistant (XDR) Gram-negative bacteria remains a significant challenge. The limited efficacy of last-resort antibiotics such as colistin and tigecycline, coupled with their toxicity, underscores the critical need for alternative therapeutic options. Without effective treatment, these infections result in higher mortality rates and place an unsustainable burden on healthcare systems, particularly in resource-limited settings. Prevention and control of infection is one of the most important and most cost-effective parameter to contain and reduce the burden of antimicrobial selective pressure. It is time to establish antibiotic surveillance systems, having its own antibiotic policy and adhering to good infection control practices, including hand hygiene.

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