|| ISSN(online): 2589-8698 || ISSN(print): 2589-868X ||
International Journal of Medical and Biomedical Studies
Available Online at www.ijmbs.info
NLM (National Library of Medicine ID: 101738825)
Index Copernicus Value 2018: 75.71
Original Research Article
Volume 3, Issue 5; May: 2019; Page No. 264-267

Bacteriological Profile and Antibiotic Susceptibility Pattern of Bloodstream Infections in Hospitalized Patients: A Cross-Sectional Study

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Article Info: Received 07 April 2019; Accepted 19 May. 2019
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Conflict of interest: No conflict of interest.

Abstract

Background: Bloodstream infections (BSIs) are among the most serious nosocomial infections, often leading to sepsis, prolonged hospital stays, and increased mortality. Identification of causative organisms and knowledge of local antimicrobial susceptibility patterns are essential for guiding empirical therapy.

Objective: To identify bacterial pathogens causing bloodstream infections in hospitalized patients and evaluate their antibiotic resistance profiles using Clinical and Laboratory Standards Institute (CLSI) guidelines.

Methods: This cross-sectional study included 310 blood culture samples collected from suspected septicemic patients over a period of six months. Culture and sensitivity were performed using standard microbiological techniques. Antibiotic susceptibility testing was done using the Kirby-Bauer disk diffusion method and interpreted according to CLSI guidelines. Statistical analysis included descriptive statistics and chi-square test for categorical variables.

Results: Out of 310 blood cultures, 106 (34.2%) were positive. Gram-negative bacilli accounted for 57.5% of isolates, with Klebsiella pneumoniae (25.4%) and Escherichia coli (19.8%) being predominant. Among gram-positive cocci, Staphylococcus aureus was most common (26.4%), with 42.9% being MRSA. High resistance was noted to third-generation cephalosporins and fluoroquinolones. Amikacin, carbapenems, and vancomycin were the most effective agents. Multidrug resistance was significantly associated with prior ICU admission ($p = 0.01$).

Conclusion: Bloodstream infections in hospitalized patients are predominantly caused by gram-negative bacteria. Rising resistance to empirical antibiotics highlights the need for regular surveillance and adherence to antimicrobial stewardship practices.

Keywords: Bloodstream infections, antibiotic resistance, gram-negative bacilli, MRSA,

Introduction

Bloodstream infections (BSIs) are among the most serious and potentially life-threatening infections encountered in hospitalized patients, particularly those in intensive care units (ICUs) and among immunocompromised individuals [1]. These infections, if not promptly recognized and treated, can progress rapidly to sepsis, severe sepsis, or septic shock, contributing significantly to morbidity and mortality [2]. Globally, BSIs remain a major public health concern due to their association with prolonged hospital stays, increased healthcare costs, and poor patient outcomes [3].

The cornerstone of effective BSI management is the early identification of the causative organism and timely initiation of appropriate antimicrobial therapy [4]. However, clinicians are often forced to initiate empirical treatment before culture results are available, increasing the likelihood of using broad-spectrum antibiotics that may not be effective and may contribute to antimicrobial resistance (AMR) [5]. This trend is particularly problematic in countries like India, where high antimicrobial usage in both healthcare and community settings has accelerated resistance rates [6].

Several studies have highlighted a shift in the BSI pathogen profile, with Gram-negative bacilli—notably Klebsiella pneumoniae and Escherichia coli—becoming more dominant over Gram-positive organisms, particularly in nosocomial settings [7,8]. Compounding this problem is the growing prevalence of multidrug-resistant (MDR) organisms, which limits the therapeutic options available and increases reliance on last-resort drugs like carbapenems and glycopeptides [9].

To combat this, periodic surveillance of local bacterial profiles and antibiotic susceptibility patterns is essential for guiding empirical therapy, revising hospital antibiotic policies, and informing antimicrobial stewardship efforts [10]. The present study was undertaken to determine the prevalent bacterial isolates and their resistance patterns in blood cultures of hospitalized patients in a tertiary care setting using CLSI guidelines for antimicrobial susceptibility interpretation.

Materials and Methods

This cross-sectional observational study was carried out in the Department of Microbiology over a period of six months. Blood samples were collected from 310 hospitalized patients who were clinically suspected of having bloodstream infections. Only one blood sample per patient was included, and patients already receiving antibiotics for more than 48 hours were excluded.

Blood was collected aseptically (8–10 mL from adults, 2–5 mL from pediatric patients) and inoculated into BHI broth bottles. Bottles were incubated at 37°C and observed for turbidity or hemolysis daily for up to 7 days. Subcultures were performed on blood agar and MacConkey agar at 24, 48, and 72 hours, and then weekly. Any growth was subjected to Gram staining and identified by standard biochemical tests, including catalase, coagulase, oxidase, TSI, citrate, urease, and motility testing. Final species confirmation was done using commercial identification systems when needed.

Antibiotic susceptibility was tested using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar following CLSI guidelines. For gram-negative isolates, the antibiotics tested included ampicillin, ceftriaxone, ceftazidime, amikacin, ciprofloxacin, piperacillin-tazobactam, and imipenem. For gram-positive cocci, penicillin, erythromycin, clindamycin, cefoxitin (for MRSA screening), vancomycin, and linezolid were included.

Staphylococcus aureus ATCC 25923 and Escherichia coli ATCC 25922 were used as control strains. MDR was defined as resistance to three or more classes of antibiotics. Statistical analysis was performed using SPSS v22.0. Chi-square test was applied to determine associations, with p-value <0.05 considered statistically significant.

Results

Out of 310 blood samples processed, 106 (34.2%) showed significant bacterial growth. Of these, 61 (57.5%) were gram-negative bacilli, and 45 (42.5%) were gram-positive cocci. No fungal isolates were detected during the study period.

Table 1: Distribution of Blood Culture Isolates (n = 106)

Organism	Number (%)
Klebsiella pneumoniae	27 (25.4%)
Escherichia coli	21 (19.8%)
Staphylococcus aureus	28 (26.4%)
Pseudomonas aeruginosa	9 (8.5%)
Acinetobacter baumannii	4 (3.8%)
Enterococcus faecalis	7 (6.6%)
Others	10 (9.4%)

Among the 28 S. aureus isolates, 12 (42.9%) were methicillin-resistant (MRSA) based on cefoxitin disc screening. All MRSA strains were sensitive to vancomycin and linezolid. Of the gram-negative isolates, 84% of K. pneumoniae and 76% of E. coli were resistant to ceftriaxone, and 58% of both were resistant to ciprofloxacin. Amikacin and imipenem showed high sensitivity (>90%) across most gram-negative isolates.

Table 2: Antibiotic Resistance Pattern of Major Isolates (CLSI)

Antibiotic	S. aureus (n=28)	E. coli (n=21)	K. pneumoniae (n=27)
Penicillin	89%	NA	NA
Cefoxitin (MRSA)	42.9%	NA	NA
Erythromycin	64%	NA	NA
Ciprofloxacin	46%	58%	60%
Amikacin	NA	9%	12%
Imipenem	NA	4%	7%
Ceftriaxone	NA	76%	84%
Piperacillin-tazobactam	NA	14%	19%
Vancomycin	0%	NA	NA

MDR was found in 41 isolates (38.7%), more commonly in patients with a prior ICU stay. A statistically significant association was observed between MDR and ICU admission ($p = 0.01$, χ^2 test).

Discussion

This study shows the current microbiological bloodstream infections in a tertiary care hospital, revealing that Gram-negative bacilli were more frequently isolated than Gram-positive cocci, consistent with recent epidemiological trends reported from similar healthcare settings in India and other developing countries [7,11].

Among Gram-negative isolates, Klebsiella pneumoniae and Escherichia coli were predominant, accounting for 25.4% and 19.8% of the total positive cultures, respectively. These findings support earlier reports that highlight a shift from Gram-positive to Gram-negative dominance in nosocomial BSIs [7,12]. The high resistance rates to ceftriaxone (76–84%) and ciprofloxacin (58–60%) among these organisms are alarming and mirror the resistance trends observed in multicentric studies across India [13,14]. These data emphasize the injudicious use of third-generation cephalosporins and fluoroquinolones, which remain common empirical choices despite diminishing effectiveness.

The retained susceptibility of K. pneumoniae and E. coli to amikacin and imipenem (>90%) is encouraging and supports their role as effective agents for severe infections, especially in ICU settings. Nevertheless, reliance on these agents must be cautious and restricted, as their overuse is associated with the emergence of carbapenem-resistant Enterobacteriaceae (CRE) [15].

In Gram-positive isolates, Staphylococcus aureus was the most commonly detected organism (26.4%), with 42.9% of isolates being MRSA, which aligns with previous Indian studies reporting MRSA rates between 30% and 50% in bloodstream infections [6,16]. Notably, all MRSA isolates in our study were 100% sensitive to vancomycin and linezolid, which continues to support their role as first-line agents for invasive MRSA infections. However, judicious prescribing practices and therapeutic monitoring are critical to prevent resistance development, including vancomycin-intermediate or resistant strains (VISA/VRSA).

Importantly, MDR organisms were identified in 38.7% of total isolates, with a statistically significant association with ICU admission ($p = 0.01$). This supports previous literature suggesting that ICU environments, due to high antibiotic usage and invasive procedures, are hotspots for MDR acquisition and spread [9,17]. The findings highlight the need for active infection control programs, surveillance, and strict adherence to antimicrobial stewardship protocols, especially in critical care settings.

However, certain limitations such as the exclusion of anaerobic and fungal pathogens, and lack of molecular confirmation for MRSA, ESBL, or MBL production, should be addressed in future studies to enhance diagnostic accuracy and clinical relevance.

Conclusion

This study underscores the changing trend of bloodstream infections, with gram-negative bacilli now being predominant. The high rate of antimicrobial resistance, particularly among ICU patients, necessitates constant surveillance, timely antibiogram updates, and implementation of robust antibiotic stewardship programs. Empirical therapy should be guided by local data and CLSI-compliant protocols to curb resistance and improve outcomes.

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