Biomedical and Biopharmaceutical Research
Abbreviation: Biomed. Biopharm. Res.
Volume: 21: Issue: 02 |Year: 2024
Page Number: 744-750

A STUDY ON BACTERIOLOGICAL PROFILE OF SEPTICEMIA IN PATIENTS ATTENDING A TERTIARY CARE HOSPITAL

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Received: 03-10-2024

Accepted: 20-12-2024

ABSTRACT

Background: Septicemia is a life-threatening condition characterized by the presence of pathogenic organisms in the bloodstream, often leading to severe systemic complications, prolonged hospitalization, and increased healthcare costs. Timely identification of causative organisms and their antibiotic susceptibility is critical for effective treatment.

Aim: To isolate and identify bacterial pathogens causing septicemia and to determine their antimicrobial susceptibility patterns in patients attending a tertiary care hospital.

Methods: This observational cross-sectional study was conducted over a 12-month period (June 2023–June 2024). Blood samples from 596 patients clinically suspected of septicemia were cultured using Brain Heart Infusion broth, followed by subculturing on appropriate media. Bacterial isolates were identified using standard biochemical tests and antibiotic susceptibility was determined by the Kirby-Bauer disc diffusion method, as per CLSI guidelines.

Results: Of 596 samples, 122 (20.4%) were blood culture positive. The highest positivity was seen in the 1–5 years age group (45%), with a male predominance (M:F ratio = 1.6:1). Gram-negative organisms accounted for 58.2% of isolates, with *Escherichia coli* (28.7%) being the most common, followed by *Acinetobacter spp*. (15.6%) .Gram-positive organisms constituted 39.3%, predominantly *Staphylococcus aureus* (21.3%)—including MSSA (15.5%) and MRSA (5.8%).Antimicrobial susceptibility testing revealed high resistance to beta-lactams among Enterobacteriaceae and moderate to high sensitivity to tetracycline, meropenem, and amikacin. Among Gram-positive isolates, linezolid, vancomycin, and clindamycin were highly effective.

Conclusion: Gram-negative bacteria, particularly *Escherichia coli*, are the leading cause of septicemia in this region. The emergence of multidrug resistance underscores the importance of regular surveillance, rational antibiotic use, and formulation of effective antimicrobial stewardship programs to combat rising resistance and improve clinical outcomes.

Keywords: Septicemia, Blood culture, Antibiotic susceptibility, *Escherichia coli*, MRSA, Gram-negative bacteria, Antimicrobial resistance.

INTRODUCTION

Blood stream infections, ranging from self-limiting bacteraemia to life threatening septicaemia.[1]Septicemia is a major cause of morbidity and mortality in the world and associated with longer hospitalization and elevated cost.[2]When bacteria are introduced directly into the circulatory system, especially in a person who is ill or undergoing aggressive medical treatment, the immune system may not be able to cope with the invasion, and symptoms of blood stream infections may develop.[3]Symptoms are widely variable and include fever, chills, hypotension, hypothermia (especially in the elderly), diaphoresis, apprehension, change in mental status, tachypnea , tachycardia, hyperventilation, reduced vascular tone, and the possibility of organ dysfunction.[4]A wide spectrum of organisms has been described that cause blood stream infections and this spectrum is subject to geographical alteration.[5]

The leading Gram positive organisms isolated were *S.aureus, Enterococcus* species*, S.pneumoniae* while organisms such as *E.coli,K.pneumoniae, Acinetobacter baumannii* and *Pseudomonas* species constituted the most common Gram negative species.[6]Bacteriological cultures to isolate the offending pathogens and knowledge about sensitivity pattern of the isolates remains the mainstay of definite diagnosis and management of septicaemia.[7]Many studies have found that inadequate empirical therapy of bacteraemia infections is associated with adverse outcomes,including increased mortality and increased drug resistance emergence.[8]Monitoring the antibiotic susceptibility pattern of most frequently isolated bacteria according to local epidemiology which helps clinicians to choose empirical therapies and develop rational prescription policy for antibiotics.[9]
The present study was undertaken to determine the various bacterial organisms causing septicaemia and their antibiotic susceptible patterns, as it would be a useful guide for clinicians initiating the empiric antibiotic therapy.

AIM AND OBJECTIVE
The aim and objective of this study is to isolate and identify the bacterial pathogens causing septicemia from blood cultures and to determine the antibiotic sensitivity pattern of the bacterial isolates

MATERIAL AND METHODS
This was an observational cross-sectional study carried out over a 12-month period, from June 2023 to June 2024. Approval was obtained from the Institutional Ethics Committee prior to the study. A total of 596 samples were collected. Samples were obtained from patients across all age groups, selected based on specific inclusion and exclusion criteria. Patients clinically suspected of septicemia, presenting with symptoms such as fever, and admitted were included. Samples were taken from individuals admitted to various clinical departments. Patients started with antibiotics usage will be excluded. Detailed patient histories were recorded, and informed consent was obtained from all participants.

A set of blood cultures was collected via venepuncture from two distinct anatomical sites under strict aseptic conditions. Specimens were obtained prior to the initiation of antimicrobial therapy and were inoculated into two separate Brain Heart Infusion (BHI) broth bottles. For adult patients, 5–10 mL of blood was drawn and inoculated into 50–100 mL of BHI broth. In pediatric patients, the volume of blood collected was adjusted according to body weight and total blood volume, maintaining a blood-to-broth ratio of 1:5 to 1:10. All inoculated media were incubated aerobically at 37°C.(13)

A subculture was performed after 24 hours by inoculating a drop of blood from the BHI broth onto blood agar and MacConkey agar plates, which were then incubated at 37°C for 16 to 24 hours. If no growth was observed in the initial subculture, further subcultures were carried out on the 3rd, 4th, and 7th days. A report indicating no growth was issued only if the culture remained negative for a total of 7 days.(18)

A Gram stain was prepared and examined during the subculture stage, and any positive findings were promptly communicated to the clinician to help guide the initiation of antimicrobial therapy.(12)

All positive cultures were further subjected to various biochemical testing like oxidase, catalase, Indole, Citrate, Urease, Triple sugar iron, Methyl red test, Voges-Proskauer test and sugar fermentation tests, Coagulase and Oxidative fermentative tests for species-level identification, and antimicrobial susceptibility was tested by inoculating the isolate onto Mueller-Hinton agar plates by Kirby-Bauer disc diffusion method with appropriate antibiotics selected based on CLSI guidelines.(10)(11)

RESULT
A total of 596 samples were included in the study. Of these, 122 samples (20.4%) tested positive for blood culture ,highest number of isolates were observed in 1-5yrs of age group,55(45%)age group. Among the positive cases, 75 (61.5%) were males and 47 (38.5%) were females, resulting in a male-to-female ratio of 1.6:1. The remaining 474 samples were negative for blood culture.
Among 122 isolates, the majority were Gram-negative bacteria (71 isolates, 58.2%), followed by Gram-positive bacteria (48 isolates, 39.3%), and *Candida* species (3 isolates, 2.5%).
Among the 71 Gram-negative isolates, the most frequently identified organism was *Escherichia coli*, accounting for 35 isolates (28.7%), followed by *Acinetobacter* species with 19 isolates (15.6%), *Pseudomonas* species with 9 isolates (7.4%), *Salmonella Typhi* with 5 isolates (4.1%), *Klebsiella* species with 2 isolates (1.6%), and only 1 isolate of *Citrobacter koseri* (0.8%).
Of the 48 Gram-positive isolates, *Staphylococcus aureus* was the predominant organism, detected in 26 isolates (21.3%), of which 19(15.5%) were methicillin-sensitive (MSSA) and 7(5.8%) were methicillin-resistant (MRSA). Coagulase-negative staphylococci (CoNS) were identified in 17 samples (13.9%), while *Enterococcus* species were isolated in only 5 samples (4.1%).

Figure 1: **Distribution of isolates**

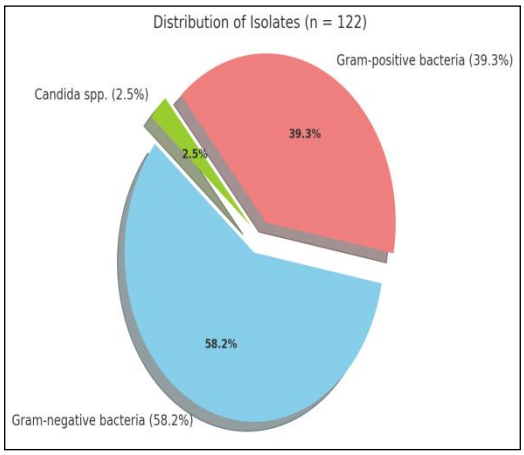

Figure 2: Isolation of gram negative and gram positive organisms

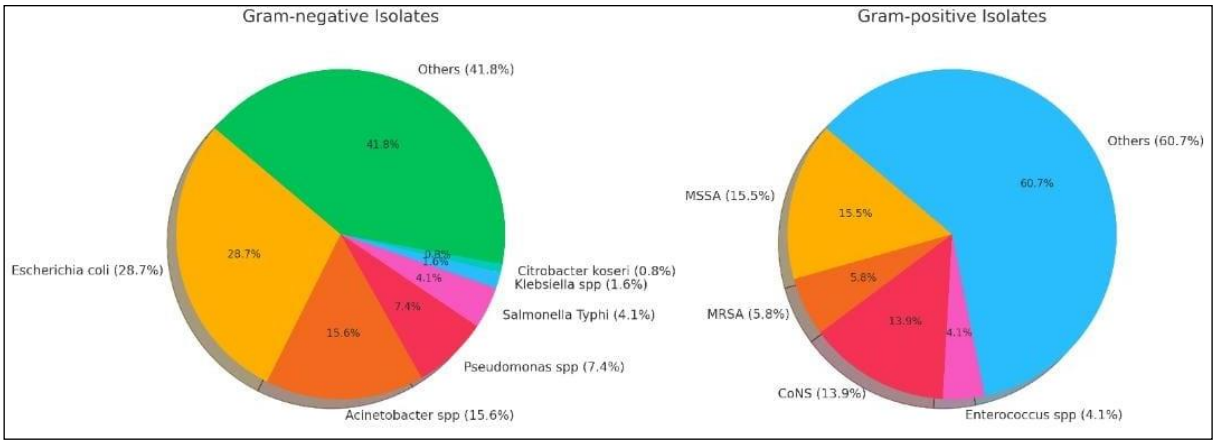

Table 1:Age-wise Distribution of Positive Blood Culture Isolates (n = 122)

Age Group	Number of Isolates	Percentage (%)
<1 year	14	11.4%
1–5 years	55	45.0%
6–15 years	22	18.0%
16–45 years	15	12.2%
46–60 years	12	9.8%
61–80 years	4	3.27%
Total	122	100%

Table 2:Antibiotic Sensitivity Pattern of Gram-Positive Isolates (n = 48)

Antibiotic	MSSA (n = 19)	MRSA (n = 7)	CONS (n=17)	*Enterococcus* species (n = 5)
Cefoxitin	100%	0	84%	-
Gentamicin	68%	52%	70%	-
Ciprofloxacin	30%	28%	64%	98%
Clindamycin	86%	70%	100%	-
Erythromycin	28%	48%	78%	88%
Linezolid	94%	94%	100%	100%
vancomycin	-	-	-	100%
Tetracycline	83%	68%	80%	100%
Cotrimoxazole	77%	52%	65%	-

Table 3:Antibiotic Sensitivity Pattern of *Enterobacterales* (n=43)

Antibiotic	*E. coli* (n = 35)	*K. pneumoniae* (n = 2)	*Citrobacter spp.* (n = 1)	*S.Typhi* (n = 5)
Ampicillin	20%	0	40%	88%
Cefazolin	30%	-	-	-
Cefotaxime	80%	76%	88%	-
Amoxicillin-clavulanate	40%	58%	78%	-
Piperacillin-tazobactam	48%	36%	69%	-
Ciprofloxacin	50%	42%	63%	66%
Gentamicin	40%	30%	62%	70%
Cotrimoxazole	60%	40%	30%	78%
Tetracycline	84%	77%	90%	80%
Meropenem	60%	55%	84%	100%
Amikacin	68%	63%	77%	-
Cefepime	75%	79%	88%	-

Table 4:Antibiotic Sensitivity Pattern of Non fermenters(n=28)

Antibiotics	*P.aeruginosa* (n = 9)	*Acinetobacter spp.* (n = 19)
Ceftazidime	60%	55%
Cefepime	40%	38%
Piperacillin-tazobactam	48%	42%
Ciprofloxacin	50%	69%
Tobramycin	70%	80%
Meropenem	-	62%
amikacin	58%	62%
Ampicillin-sulbactam	-	72%

DISCUSSION

In our study, the majority of blood culture-positive cases were found in the 1–5 years age group (45%), followed by the 6–15 years group (18%), with a higher prevalence among males compared to females. Similarly, **Shefah et al**.[15] reported a higher incidence in the 0–10 years age group (18.01%), also with male predominance.

Gram-negative organisms were more predominant among the positive samples compared to Gram-positive ones in our study, which is consistent with the findings of **Asma Ejaz et al.**[16] Among the Gram-negative isolates, *E. coli* showed the highest growth rate (28.7%), followed by *Acinetobacter* spp. (15.6%). This pattern is similar to the study by **Asma Ejaz et al.,**[16] where *E. coli* and *Acinetobacter* spp. accounted for 19.04% of isolates. However, in contrast, the study by **Jyoti Sonwane et al**[17]. reported a higher prevalence of *Klebsiella* spp. (22.38%). Among the Gram-positive isolates, *Staphylococcus aureus* showed the highest growth (39.3%), with MSSA (15.5%) being more prevalent than MRSA (5.8%). This was followed by coagulase-negative *Staphylococcus* species (13.9%) and *Enterococcus* species (4.1%). These findings are comparable to those reported by **Dr. B.V. Sivamma et al**.,[18] who observed similar rates of 24.88% and 9.95%, respectively

ANTIBIOTIC SENSITIVITY PATTERN:

In this study, among the Gram-positive isolates—***Staphylococcus aureus*** *(MSSA and MRSA),* ***coagulase-negative Staphylococcus*** *(CONS),* and ***Enterococcus*** *species*—the observed antimicrobial resistance patterns highlight significant therapeutic concerns and align with both local and global trends.

Cefoxitin reliably indicated methicillin resistance, showing 100% sensitivity in MSSA and complete resistance in MRSA, consistent with findings by **Sharma et al.** [19] **and Kumar et al.** [20] following CLSI guidelines[11]. **Linezolid** demonstrated excellent efficacy across all Gram-positive isolates, with near or complete sensitivity, comparable to reports by **Sivamma et al.,**[18]**, Mehta et al**. [21] Similarly, **Vancomycin** retained full activity against *Enterococcus species*. **Clindamycin** was highly effective against MSSA (86%) and CONS (100%), though slightly less effective against MRSA (70%). Similar findings noted in **Ramakrishna et al.** [22].**Ciprofloxacin** showed limited activity in MSSA (30%) and MRSA (28%), while Enterococcus species were largely sensitive (98%). These trends correspond with findings by **Saxena et al.,** [23]**,** who reported rising fluoroquinolone resistance in MRSA.**Erythromycin** showed poor efficacy against S. aureus strains but better activity against CONS (78%) and Enterococcus (88%), paralleling results from **Sivamma et al.** [18] who documented high macrolide resistance in MRSA.**Tetracycline** maintained good effectiveness across all tested isolates, consistent with data from Jayalakshmi and Gadepalli et al., whereas **Cotrimoxazole** showed moderate sensitivity, especially lower in MRSA, in agreement with studies by **Kumar et al**[20] **and Mukhopadhyay et al.,** [24] indicating emerging resistance.

Among **Enterobacteriaceae**, *E. coli* exhibited high resistance to ampicillin (20%) and amoxicillin-clavulanate (40%), consistent with findings from **Kumar et al.** [20] who attributed this to β-lactamase-mediated resistance . *K. pneumoniae* was completely resistant to ampicillin and showed only moderate sensitivity to cefotaxime (76%) and amoxicillin-clavulanate (58%), reflecting the global trend of increasing ESBL production [3]. Similarly, *Citrobacter* spp. demonstrated better sensitivity to cefotaxime (88%) and piperacillin-tazobactam (69%), comparable to findings reported by **Mehta et al**. [21] .*T*etracycline showed high efficacy across all Enterobacteriaceae, with sensitivity ranging from 77–90%, consistent with results from **Chopra and Roberts** [18]**,** who highlighted its retained activity despite widespread use [5]. Meropenem and amikacin remained highly effective against *E. coli* (60%, 68%) and *K. pneumoniae* (55%, 63%), in line with data from **Gupta et al.,**[26]who reported carbapenem and aminoglycoside efficacy in MDR isolates [6]. *S. Typhi* showed excellent susceptibility to older drugs like ampicillin (88%), cotrimoxazole (78%), and meropenem (100%), supporting findings **by Dutta et al.** [18]**and Sinha et al.** [18] suggesting re-emergence of susceptibility due to reduced empirical use [7,8].**Fluoroquinolone resistance** was evident, especially in *E. coli* (50%) and *K. pneumoniae* (42%), correlating with studies by **Saxena et al.**[23] who reported declining ciprofloxacin effectiveness . Despite this, *S. Typhi* retained moderate ciprofloxacin sensitivity (66%), reflecting partial efficacy in typhoidal salmonellosis.

Among **non-fermenters**, *P. aeruginosa* showed moderate susceptibility to ceftazidime (60%) and piperacillin-tazobactam (48%), with lower sensitivity to cefepime (40%). *Acinetobacter* spp. showed similar resistance trends, with cefepime (38%) and piperacillin-tazobactam (42%) sensitivity, as reported in studies by **Mehta et al.** [21]**and Tripathi et al.** [30]. Tobramycin was the most effective aminoglycoside, showing 70% sensitivity in *P. aeruginosa* and 80% in *Acinetobacter* spp., supporting findings from **Bhat et al.**[31]Meropenem retained moderate activity in *Acinetobacter* (62%) and amikacin showed consistent efficacy in both *P. aeruginosa* (58%) and *Acinetobacter* spp. (62%), corroborating earlier observations **by Gupta et al**[26]**.** on their role in treating MDR non-fermenters [6]. Notably, ampicillin-sulbactam was relatively effective against *Acinetobacter* spp. (72%), in agreement with the results by **Singhal et al**.,[32] supporting its use in targeted therapy [14].

CONCLUSION

Septicemia remains a significant cause of morbidity and mortality, particularly in pediatric and immunocompromised populations. In our study, septicemia was most prevalent in the **1–5 years age group**, with a **higher incidence in males**, highlighting the need for early clinical suspicion and timely microbiological diagnosis in vulnerable groups. **Gram-negative organisms** were more frequently isolated than Gram-positive bacteria, with *Escherichia coli* being the most common pathogen. In conclusion, regular blood culture monitoring, early identification of the causative agents, and appropriate antibiotic stewardship are essential for effective management of septicemia and for reducing the burden of antimicrobial resistance.

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