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Original Research Article

Microbiological Study of Septicemia in a Tertiary Care Teaching Hospital, Kachchh

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Abstract

Background: Septicemia remains a major cause of morbidity and mortality worldwide, with increasing concerns regarding antimicrobial resistance.

Aim: To identify the common bacterial pathogens associated with septicemia in adult patients and analyze their antibiotic susceptibility patterns.

Methods: A hospital-based prospective observational study was conducted on 150 clinically suspected adult septicemia cases. Blood cultures were processed using standard microbiological techniques, antimicrobial susceptibility testing and identification of the isolated organisms were performed using the VITEK 2 system.

Results: Culture positivity was observed in 73.3% cases. Gram-negative organisms (60%) predominated, with Escherichia coli (29.1%) being the most common isolate. High resistance was observed to commonly used antibiotics, including gentamicin and aztreonam, along with significant resistance to carbapenems.

Conclusion: The study highlights a predominance of Gram-negative pathogens and an alarming rise in antimicrobial resistance in septicemia, emphasizing the need for continuous surveillance and rational antibiotic use.

Keywords: Septicemia, bloodstream infection, antimicrobial resistance, Gram-negative bacteria, antibiotic susceptibility.

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Introduction

Septicemia, also referred to as bloodstream infection (BSI), is a life-threatening condition characterized by the presence of pathogenic microorganisms in the blood, leading to a systemic inflammatory response and potential organ dysfunction [1,2]. It remains a major cause of morbidity and mortality worldwide, particularly among hospitalized patients, critically ill individuals, and those with compromised immune status [3]. Despite advances in medical care and antimicrobial therapy, septicemia continues to pose significant clinical and public health challenges, especially in developing countries [4].

The clinical presentation of septicemia can vary widely, ranging from nonspecific symptoms such as fever, chills, malaise, and weakness to severe manifestations including hypotension, septic shock, and multi-organ failure [5]. Early diagnosis is often challenging due to the variability in clinical features, which may lead to delays in appropriate treatment and increased risk of adverse outcomes [6]. Therefore, prompt identification of causative pathogens and timely initiation of effective antimicrobial therapy are critical for improving patient survival.

The microbiological profile of septicemia varies depending on geographical location, hospital settings, and patient populations. Both Gram-negative and Gram-positive organisms are commonly implicated. Among Gram-negative bacteria, Escherichia coli, Klebsiella pneumoniae, and Pseudomonas aeruginosa are frequently isolated, while Gram-positive organisms such as Staphylococcus aureus, coagulase-negative Staphylococci, and Enterococcus species also play a significant role [7,8]. The distribution of these pathogens is influenced by factors such as hospital-acquired infections, invasive procedures, and underlying comorbid conditions. A major concern in the management of septicemia is the increasing prevalence of antimicrobial resistance (AMR). Many pathogens have developed resistance to commonly used antibiotics, including beta-lactams, aminoglycosides, and even higher-end drugs such as carbapenems. The emergence of multidrug-resistant (MDR) organisms, including extended-spectrum beta-lactamase (ESBL) producers and carbapenem-resistant strains, has significantly limited treatment options and is associated with higher morbidity, mortality, and healthcare costs [9].

Empirical antibiotic therapy is often initiated before microbiological confirmation due to the rapid progression of septicemia. However, irrational and widespread use of antibiotics has contributed substantially to the development of resistance. Therefore, continuous surveillance of bacterial pathogens and their antibiotic susceptibility patterns is essential to guide appropriate empirical therapy and ensure better clinical outcomes [10].

Blood culture remains the gold standard for the diagnosis of septicemia, enabling the identification of causative organisms and determination of their antimicrobial susceptibility patterns. Knowledge of local bacteriological profiles is crucial for developing effective treatment protocols and implementing antibiotic stewardship programs aimed at reducing the burden of antimicrobial resistance.

In this context, the present study aims to identify the common bacterial pathogens associated with septicemia in adult patients and to evaluate their antibiotic susceptibility patterns in a tertiary care teaching hospital in Kachchh, thereby aiding in the optimization of therapeutic strategies and improving patient outcomes.

Material and Methods

The present study was designed as a hospital-based prospective observational study conducted in the Department of Microbiology of a tertiary care teaching hospital in Kachchh from October 2025 to February 2026 after obtaining necessary institutional permissions. A total of 150 adult patients clinically suspected of septicemia were included in the study.

Patients aged 18 years and above presenting with clinical features suggestive of septicemia, such as fever, chills, hypotension, tachycardia, altered sensorium, or other signs of systemic infection, were enrolled.

Patients who had received prolonged antibiotic therapy prior to admission or those who did not provide consent were excluded from the study. After obtaining informed written consent, detailed demographic and clinical data including age, sex, comorbidities, and presenting symptoms were recorded using a predesigned proforma. Under strict aseptic precautions, venous blood samples (5–10 mL) were collected from each patient prior to the initiation of antibiotic therapy and inoculated into sterile blood culture bottles containing appropriate culture media. The samples were incubated under standard laboratory conditions and processed using conventional microbiological techniques. Positive cultures were identified based on colony morphology and Gram staining.

Antimicrobial susceptibility testing and identification of the isolated organisms were performed using the VITEK 2 system and the results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. The antibiotic panel included commonly used antibiotics such as ampicillin, gentamicin, cefotaxime, ceftriaxone, amikacin, piperacillin-tazobactam, and carbapenems. The isolates were categorized as sensitive, intermediate, or resistant based on zone diameter interpretation.

The data obtained were entered into Microsoft Excel and analyzed using the Statistical Package for the Social Sciences (SPSS) software version 25.0. Descriptive statistics such as mean, standard deviation, frequencies, and percentages were used to summarize demographic and clinical characteristics. The prevalence of different bacterial isolates and their antibiotic susceptibility patterns were expressed in percentages. Inferential statistical tests such as the Chi-square test were applied to assess associations between categorical variables, and a p-value of less than 0.05 was considered statistically significant.

Ethical clearance for the study was obtained from the Institutional Ethics Committee prior to the commencement of the study. The study adhered to the ethical principles outlined in the Declaration of Helsinki. Confidentiality of patient information was strictly maintained, and participation in the study was entirely voluntary.

Results

The distribution of bacterial isolates obtained from blood cultures of 150 clinically suspected sepsis cases is summarized in Table 1. Out of the total sample, 110 cases (73.3%) were culture positive, indicating a high prevalence of confirmed sepsis. Among these isolates, Escherichia coli was the most predominant organism accounting for 32 cases (29.1%), followed by Staphylococcus aureus with 24 cases (21.8%) and Klebsiella species with 20 cases (18.2%). Pseudomonas aeruginosa was isolated in 14 cases (12.7%), while Enterococcus species contributed to 12 cases (10.9%). Coagulase-negative Staphylococci (CoNS) were the least common isolates, accounting for 8 cases (7.3%). Overall, Gram-negative organisms constituted 66 cases (60%), whereas Gram-positive organisms accounted for 44 cases (40%), clearly indicating a predominance of Gram-negative bacterial infections in sepsis. The antibiotic resistance pattern among Gram-negative isolates is detailed in Table 2. A high degree of resistance was observed across multiple antibiotics. Escherichia coli showed maximum resistance to gentamicin and aztreonam (93.7% each), followed by piperacillin/tazobactam (87.5%) and amikacin (84.3%). Klebsiella species demonstrated extremely high resistance to imipenem and aztreonam (95% each) and piperacillin/tazobactam (90%), indicating significant multidrug resistance. Pseudomonas aeruginosa showed complete resistance to gentamicin and aztreonam (100%), with very high resistance to polymyxin-B (92.8%) and piperacillin/tazobactam (85.7%). Notably, colistin showed comparatively lower resistance, particularly in Pseudomonas (21.4%), suggesting its retained effectiveness as a last-resort antibiotic. The antibiotic resistance pattern among Gram-positive isolates is shown in Table 3. A considerable level of resistance was observed among these organisms as well. Staphylococcus aureus demonstrated resistance of 62.5% to vancomycin and 58.3% to teicoplanin, while resistance to linezolid was 50%. CoNS showed equal resistance of 50% to vancomycin, teicoplanin, and linezolid. Among Enterococcus species, resistance to vancomycin and teicoplanin was 66.6%, with linezolid resistance at 50%. Alarmingly, 100% resistance was observed across all Gram-positive isolates for antibiotics such as amikacin, netilmicin, cefoxitin, erythromycin, gentamicin, and polymyxin-B, indicating a high prevalence of multidrug-resistant strains.

Table 1: Isolated bacterial species and their percentage from blood samples (n = 110)

Isolated Bacteria	Number of Cases	Percentage (%)
Escherichia coli	32	29.1%
Klebsiella species	20	18.2%
Pseudomonas aeruginosa	14	12.7%
Staphylococcus aureus	24	21.8%
Coagulase-negative Staph	8	7.3%
Enterococcus species	12	10.9%
Total	110	100%

Table 2: Antibiotic resistance pattern among Gram-negative bacterial isolates (n = 66)

Antibiotic	E. coli (n=32) n (%)	Klebsiella (n=20) n (%)	Pseudomonas (n=14) n (%)
Meropenem	22 (68.7%)	13 (65%)	9 (64.3%)
Imipenem	24 (75%)	19 (95%)	13 (92.8%)
Colistin	15 (46.8%)	11 (55%)	3 (21.4%)
Polymyxin-B	25 (78.1%)	14 (70%)	13 (92.8%)
Piperacillin/Tazobactam	28 (87.5%)	18 (90%)	12 (85.7%)
Amikacin	27 (84.3%)	16 (80%)	2 (14.3%)
Netilmicin	26 (81.2%)	17 (85%)	4 (28.6%)
Aztreonam	30 (93.7%)	19 (95%)	14 (100%)
Gentamicin	30 (93.7%)	19 (95%)	14 (100%)

Table 3: Antibiotic resistance pattern among Gram-positive bacterial isolates (n = 44)

Antibiotic	S. aureus (n=24) n (%)	CoNS (n=8) n (%)	Enterococcus (n=12) n (%)
Vancomycin	15 (62.5%)	4 (50%)	8 (66.6%)
Teicoplanin	14 (58.3%)	4 (50%)	8 (66.6%)
Linezolid	12 (50%)	4 (50%)	6 (50%)
Amikacin	24 (100%)	8 (100%)	12 (100%)
Netilmicin	24 (100%)	8 (100%)	12 (100%)
Cefoxitin	24 (100%)	8 (100%)	12 (100%)
Erythromycin	24 (100%)	8 (100%)	12 (100%)
Gentamicin	24 (100%)	8 (100%)	12 (100%)
Polymyxin-B	24 (100%)	8 (100%)	12 (100%)

Discussion

The present study demonstrates a high culture positivity rate of 73.3% among adult patients with suspected septicemia, indicating a significant burden of bloodstream infections in the hospital setting. This high rate of culture positivity reflects the clinical relevance of early microbiological investigation in suspected cases and is comparable to findings reported in recent studies conducted in tertiary care centers, where similar positivity rates have been observed due to improved diagnostic techniques and patient selection criteria [11].

In the current study, Gram-negative organisms (60%) predominated over Gram-positive organisms (40%), which is consistent with recent epidemiological trends showing a shift towards Gram-negative pathogens as the leading cause of septicemia in hospitalized adult patients. Among the isolates, Escherichia coli (29.1%) was the most frequently identified organism, followed by Staphylococcus aureus (21.8%) and Klebsiella species (18.2%). These findings are in agreement with other contemporary studies where E. coli and Klebsiella pneumoniae have been reported as major contributors to bloodstream infections, particularly in patients with underlying comorbidities or hospital-acquired infections [11,12].

The presence of Staphylococcus aureus and coagulase-negative Staphylococci highlights the significant role of Gram-positive organisms in septicemia, especially in patients with invasive devices, prolonged hospital stay, or compromised immunity. Although coagulase-negative Staphylococci accounted for a smaller proportion (7.3%), their role as opportunistic pathogens in nosocomial infections is well recognized. Similarly, the isolation of Enterococcus species (10.9%) in this study reflects emerging trends in adult septicemia, where these organisms are increasingly implicated in healthcare-associated infections [13].

A major concern highlighted by this study is the alarming level of antimicrobial resistance observed among both Gram-negative and Gram-positive isolates. Gram-negative organisms demonstrated very high resistance to commonly used antibiotics such as gentamicin and aztreonam, with resistance rates approaching 100% in some isolates. Additionally, resistance to piperacillin/tazobactam exceeded 85% across Gram-negative organisms, indicating a high prevalence of multidrug-resistant strains. These findings are comparable to recent studies that have documented increasing resistance to first-line and second-line antibiotics, posing serious challenges in the management of septicemia [11,14].

The high level of carbapenem resistance observed in this study, particularly among Klebsiella species and Pseudomonas aeruginosa, is of significant clinical concern. Resistance rates as high as 95% for imipenem suggest the emergence of carbapenem-resistant organisms, which are associated with limited therapeutic options and poor clinical outcomes. Similar trends have been reported globally, emphasizing the growing threat of carbapenem-resistant Enterobacteriaceae (CRE) in hospital settings [14]. However, relatively lower resistance to colistin observed in certain isolates suggests that last-resort antibiotics may still retain some effectiveness, although their use must be judicious due to potential toxicity and risk of emerging resistance.

Among Gram-positive isolates, moderate to high resistance was observed to key antibiotics such as vancomycin and teicoplanin, particularly among Enterococcus species. This raises concerns regarding the emergence of vancomycin-resistant enterococci (VRE), which have been increasingly reported in hospital-acquired infections. Furthermore, the uniform high resistance observed to multiple antibiotics including aminoglycosides and macrolides among Gram-positive organisms indicates a significant burden of multidrug resistance. These findings are in concordance with recent reports highlighting increasing resistance even among traditionally susceptible Gram-positive pathogens [13,15].

The overall findings of this study underscore the critical importance of continuous surveillance of microbial patterns and antibiotic susceptibility profiles in hospital settings. The high prevalence of multidrug-resistant organisms necessitates the implementation of strict antibiotic stewardship programs and infection control measures to curb the spread of resistant pathogens. Early diagnosis through blood culture and timely initiation of appropriate, targeted antimicrobial therapy based on local sensitivity patterns remain essential strategies in reducing morbidity and mortality associated with septicemia [11,15].

Conclusion

The present study concludes that Gram-negative organisms, particularly Escherichia coli and Klebsiella species, are the predominant causative agents of septicemia in adult patients admitted to a tertiary care teaching hospital. Gram-positive organisms, including Staphylococcus aureus and Enterococcus species, also contribute significantly to the burden of bloodstream infections.

A high level of antimicrobial resistance was observed among both Gram-negative and Gram-positive isolates, including resistance to commonly used antibiotics as well as higher-end drugs such as carbapenems. The presence of multidrug-resistant organisms highlights the growing challenge in the effective management of septicemia and underscores the need for judicious use of antibiotics.

The findings of this study emphasize the importance of continuous surveillance of microbial patterns and antibiotic susceptibility profiles in guiding empirical therapy. Implementation of strict antibiotic stewardship programs, early diagnosis through blood culture, and timely initiation of targeted antimicrobial treatment are essential to improve clinical outcomes and reduce morbidity and mortality associated with septicemia.

References

1. Singer M, Deutschman CS, Seymour CW, Shankar-Hari M, Annane D, Bauer M. The third international consensus definitions for sepsis and septic shock (Sepsis-3). JAMA. 2016;315(8):801–810.
2. Rhodes A, Evans LE, Alhazzani W, Levy MM, Antonelli M, Ferrer R. Surviving sepsis campaign: international guidelines for management of sepsis and septic shock. Intensive Care Med. 2017;43(3):304–377.
3. Fleischmann C, Scherag A, Adhikari NKJ, Hartog CS, Tsaganos T, Schlattmann P. Assessment of global incidence and mortality of hospital-treated sepsis. Am J Respir Crit Care Med. 2016;193(3):259–272.
4. Rudd KE, Johnson SC, Agesa KM, Shackelford KA, Tsoi D, Kievlan DR. Global, regional, and national sepsis incidence and mortality. Lancet. 2020;395(10219):200–211.
5. Vincent JL, Opal SM, Marshall JC, Tracey KJ. Sepsis definitions: time for change. Lancet. 2013;381(9868):774–775.
6. Cheng MP, Stenstrom R, Paquette K, Stabler SN, Akhter M, Davidson AC. Blood culture results before and after antimicrobial administration in patients with severe sepsis. Clin Infect Dis. 2019;69(4):654–661.
7. Laupland KB, Church DL. Population-based epidemiology and microbiology of community-onset bloodstream infections. Clin Microbiol Rev. 2014;27(4):647–664.
8. Diekema DJ, Hsueh PR, Mendes RE, Pfaller MA, Rolston KV, Sader HS. The microbiology of bloodstream infection: 20-year trends. Clin Infect Dis. 2019;69(Suppl 1):S13–S21.
9. Laxminarayan R, Matsoso P, Pant S, Brower C, Røttingen JA, Klugman K. Access to effective antimicrobials: a worldwide challenge. Lancet. 2016;387(10014):168–175.
10. O'Neill J. Tackling drug-resistant infections globally: final report and recommendations. Rev Antimicrob Resist. 2016;1–84.
11. Huynh BT, Padget M, Garin B, Delarocque-Astagneau E, Guillemot D. Bacterial epidemiology and antimicrobial resistance in bloodstream infections. J Glob Antimicrob Resist. 2021;26:145–153.
12. Banerjee R, Ozenci V, Patel R. Individualized approaches to bloodstream infection diagnosis. Clin Microbiol Rev. 2016;29(4):883–901.
13. Murray BE. The life and times of the Enterococcus. Clin Microbiol Rev. 1990;3(1):46–65.
14. Logan LK, Weinstein RA. The epidemiology of carbapenem-resistant Enterobacteriaceae. J Infect Dis. 2017;215(Suppl 1):S28–S36.
15. Tong SYC, Davis JS, Eichenberger E, Holland TL, Fowler VG. Staphylococcus aureus infections: epidemiology and clinical manifestations. Clin Microbiol Rev. 2015;28(3):603–661.