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Original Research Article

Clinical and Biochemical Profile of Sepsis and Its Correlation with Blood Culture: A Prospective Intensive Care Unit Study

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Abstract

Background: Sepsis represents a life-threatening organ dysfunction caused by a dysregulated host response to infection and remains a leading cause of mortality in intensive care units globally. Understanding the clinical presentation, biochemical alterations, and microbiological patterns is essential for optimizing therapeutic interventions and improving patient outcomes.

Methods: This prospective observational study was conducted among 50 adult patients admitted to the Intensive Care Unit with a diagnosis of sepsis according to the American College of Chest Physicians/Society of Critical Care Medicine criteria. Clinical features, biochemical parameters including complete blood count, renal function tests, liver function tests, arterial blood gas analysis, and blood culture results were systematically analyzed. Organ dysfunction was assessed using standardized definitions, and outcomes were documented.

Results: The mean age of patients was 54.7 ± 17.5 years, with male predominance (74%). Disease severity distribution showed sepsis in 40%, severe sepsis in 44%, and septic shock in 16% of patients. Blood cultures were positive in 32% of cases, with gram-negative organisms predominating (81.3%). Escherichia coli was the most common isolate (37.5%), followed by Pseudomonas aeruginosa (25%) and Klebsiella pneumoniae (18.8%). Respiratory tract infections constituted the primary source of sepsis (50%). Overall mortality was 26%, which significantly increased with sepsis severity ($p < 0.001$) and number of organ dysfunctions ($p < 0.001$). Patients with three or more organ dysfunctions demonstrated 100% mortality.

Conclusion: Severe sepsis and septic shock are associated with substantially elevated mortality rates. Gram-negative organisms represent the predominant pathogens, and respiratory infections constitute the most common source. Early recognition, prompt antimicrobial administration, and aggressive supportive care are imperative for improving survival outcomes in sepsis.

Keywords: Sepsis, blood culture, organ dysfunction, gram-negative bacteria, intensive care unit, mortality.

Introduction

Sepsis constitutes a major global health challenge, characterized by a dysregulated host immune response to infection resulting in life-threatening organ dysfunction [1]. Despite significant advances in critical care medicine, sepsis remains the leading cause of mortality in intensive care units worldwide, with estimated global incidence rates exceeding 48 million cases annually and approximately 11 million sepsis-related deaths [2]. The pathophysiology of sepsis involves a complex interplay between pro-inflammatory and anti-inflammatory responses, leading to endothelial dysfunction, coagulopathy, and progressive multi-organ failure [3]. The clinical spectrum of sepsis

ranges from uncomplicated systemic infection to severe sepsis with organ dysfunction and septic shock characterized by refractory hypotension and cellular metabolic abnormalities [4]. Early identification of sepsis through clinical and biochemical parameters is crucial, as delayed recognition and treatment are associated with significantly increased mortality [5]. Studies have demonstrated that each hour of delay in appropriate antimicrobial therapy increases mortality by approximately 7.6% in patients with septic shock [6].

Blood culture remains the gold standard for identifying causative pathogens in sepsis, although positivity rates vary considerably across studies, ranging from 20% to 40% [7].

The microbiological profile of sepsis demonstrates geographic variation, with gram-negative organisms predominating in Asian and developing countries, while gram-positive organisms are more prevalent in Western settings [8]. Understanding regional microbiological patterns is essential for formulating empirical antibiotic protocols and optimizing therapeutic outcomes.

Biochemical markers including lactate, procalcitonin, C-reactive protein, and various hematological parameters serve as valuable tools for diagnosis, severity assessment, and prognostication in sepsis [9]. Organ dysfunction assessment through parameters such as serum creatinine, bilirubin, platelet count, and arterial blood gas values provides critical information regarding disease severity and predicted outcomes [10].

Despite extensive research, significant knowledge gaps remain regarding the clinical and biochemical profile of sepsis in resource-limited settings, particularly in Indian intensive care units. Understanding local epidemiology, microbiological patterns, and factors influencing outcomes is essential for developing context-specific management strategies.

The present study aimed to analyze the clinical and biochemical profile of sepsis patients admitted to the intensive care unit, correlate blood culture positivity with disease severity and mortality, identify common organisms and sources of infection, and determine outcomes in relation to organ dysfunction.

Materials and Methods

Study Design and Setting

This prospective observational study was conducted in the Intensive Care Unit at District Hospital, Chitradurga of between January 2025 and December 2025. The study protocol was approved by the Institutional Ethics Committee, and written informed consent was obtained from patients or their legal representatives.

Study Population

A total of 50 adult patients meeting the American College of Chest Physicians/Society of Critical Care Medicine (ACCP/SCCM) criteria for sepsis were enrolled consecutively. Sepsis was defined as the presence of systemic inflammatory response syndrome (SIRS) with documented or suspected infection. Severe sepsis was defined as sepsis with associated organ dysfunction, and septic shock was defined as sepsis with persistent hypotension despite adequate fluid resuscitation requiring vasopressor support.

Inclusion Criteria

Patients aged 15 years and above with clinical diagnosis of sepsis, severe sepsis, or septic shock were included. Evidence of infection was confirmed through clinical assessment, radiological findings, or microbiological documentation.

Exclusion Criteria

Patients with non-infectious causes of systemic inflammatory response syndrome, those with incomplete medical records, patients with terminal malignancy or immunodeficiency states, and those who declined participation were excluded from the study.

Data Collection

Detailed clinical history including presenting complaints, duration of symptoms, and comorbidities was recorded. Physical examination findings including vital signs (temperature, heart rate, blood pressure, respiratory rate, oxygen saturation) and signs of infection were documented. Source of infection was identified based on clinical assessment, radiological investigations, and culture reports.

Laboratory Investigations

Blood samples were collected for complete blood count, renal function tests (blood urea nitrogen, serum creatinine), liver function tests (serum bilirubin, alanine aminotransferase, aspartate aminotransferase, and alkaline phosphatase), random blood glucose, serum electrolytes, and arterial blood gas analysis. Blood cultures were obtained from two different sites using aseptic technique before initiating antimicrobial therapy. Cultures were processed using automated blood culture systems with species identification and antimicrobial susceptibility testing.

Assessment of Organ Dysfunction

Organ dysfunction was assessed using the following criteria: cardiovascular dysfunction (hypotension requiring vasopressors), respiratory

dysfunction (PaO2/FiO2 ratio < 300 or mechanical ventilation requirement), renal dysfunction (serum creatinine > 2.0 mg/dL or urine output < 0.5 mL/kg/hour), hepatic dysfunction (serum bilirubin > 2.0 mg/dL), and hematological dysfunction (platelet count < 100,000/µL), and neurological dysfunction (Glasgow Coma Scale < 13).

Statistical Analysis

Data were entered and analyzed using Statistical Package for Social Sciences (SPSS) version 25.0. Continuous variables were expressed as mean ± standard deviation, and categorical variables as frequencies and percentages.

Chi-square test was used to evaluate associations between categorical variables. Student's t-test and ANOVA were used for comparison of continuous variables. A p-value < 0.05 was considered statistically significant.

Results

Baseline Characteristics

The study enrolled 50 patients with sepsis, of whom 37 (74%) were male and 13 (26%) were female. The mean age was 54.7 ± 17.5 years, ranging from 18 to 82 years. The majority of patients (62%) were above 50 years of age. Common comorbidities included diabetes mellitus (44%), hypertension (38%), chronic kidney disease (16%), and chronic obstructive pulmonary disease (12%). Regarding severity classification, 20 patients (40%) had sepsis, 22 patients (44%) had severe sepsis, and 8 patients (16%) presented with septic shock.

Table 1: Baseline Demographic and Clinical Characteristics (n = 50)

Parameter	Value
Age (years), mean ± SD	54.7 ± 17.5
Age groups	
15-30 years	6 (12%)
31-50 years	13 (26%)
51-70 years	22 (44%)
>70 years	9 (18%)
Gender	
Male	37 (74%)
Female	13 (26%)
Comorbidities	
Diabetes mellitus	22 (44%)
Hypertension	19 (38%)
Chronic kidney disease	8 (16%)
COPD	6 (12%)
Coronary artery disease	5 (10%)
Sepsis severity	
Sepsis	20 (40%)
Severe sepsis	22 (44%)
Septic shock	8 (16%)

Biochemical Parameters

The mean hemoglobin was 10.2 ± 2.3 g/dL, with 68% of patients demonstrating anemia. Mean total leukocyte count was 16,850 ± 8,420 cells/µL, with leukocytosis present in 72% and leukopenia in 8% of patients. Mean platelet count was 1,42,000 ± 68,000/µL, with thrombocytopenia observed in 34% of cases. Mean serum creatinine was 2.4 ± 1.8 mg/dL, with renal dysfunction present in 42% of patients. Mean serum bilirubin was 1.8 ± 1.4 mg/dL, with hepatic dysfunction in 28% of cases. Arterial blood gas analysis revealed metabolic acidosis in 56% of patients, with mean lactate levels of 4.2 ± 2.8 mmol/L.

Blood Culture Results and Source of Infection: Blood cultures were positive in 16 patients (32%), while 34 patients (68%) had negative cultures. Among positive cultures, gram-negative organisms were isolated in 13 cases (81.3%), and gram-positive organisms in 3 cases (18.7%). The most common isolates were Escherichia coli (37.5%), Pseudomonas aeruginosa (25%), Klebsiella pneumoniae (18.8%), and Staphylococcus aureus (12.5%).

Respiratory tract was the most common source of infection (50%), followed by urinary tract (20%), skin and soft tissue (18%), abdominal (8%), and intravenous catheter-related infections (4%).

Table 2: Microbiological Profile and Source of Infection (n = 50)

Parameter	n (%)
Blood culture results	
Positive	16 (32%)
Negative	34 (68%)
Organism type (n = 16)	
Gram-negative	13 (81.3%)
Gram-positive	3 (18.7%)
Specific isolates	
Escherichia coli	6 (37.5%)
Pseudomonas aeruginosa	4 (25%)
Klebsiella pneumoniae	3 (18.8%)
Staphylococcus aureus	2 (12.5%)
Enterococcus species	1 (6.2%)
Source of infection	
Respiratory tract	25 (50%)
Urinary tract	10 (20%)
Skin/soft tissue	9 (18%)
Abdominal	4 (8%)
IV catheter-related	2 (4%)

Organ Dysfunction and Outcomes

Organ dysfunction analysis revealed that 8 patients (16%) had no organ dysfunction, 18 patients (36%) had single organ dysfunction, 14 patients (28%) had two organ dysfunctions, and 10 patients (20%) had three or more organ dysfunctions. The most common organ dysfunctions were respiratory (58%), renal (42%), cardiovascular (32%), and hepatic (28%). Overall mortality was 26% (13 patients). Mortality was significantly associated with sepsis severity: sepsis 5%, severe sepsis 31.8%, and septic shock 75% ($p < 0.001$).

Mortality also increased significantly with the number of organ dysfunctions ($p < 0.001$).

Table 3: Organ Dysfunction, Severity, and Mortality Outcomes (n = 50)

Parameter	n (%)	Mortality (%)	p-value
Organ dysfunctions			
0 organs	8 (16%)	0 (0%)	<0.001
1 organ	18 (36%)	3 (16.7%)	
2 organs	14 (28%)	4 (28.6%)	
≥3 organs	10 (20%)	6 (60%)	
Sepsis severity			
Sepsis	20 (40%)	1 (5%)	<0.001
Severe sepsis	22 (44%)	6 (27.3%)	
Septic shock	8 (16%)	6 (75%)	
Blood culture status			
Positive	16 (32%)	6 (37.5%)	0.142
Negative	34 (68%)	7 (20.6%)	

Discussion

The present study provides valuable insights into the clinical and biochemical profile of sepsis in an Indian intensive care unit setting. Our findings demonstrate that sepsis predominantly affects middle-aged and elderly males, with significant mortality particularly in those with severe sepsis and septic shock. The mean age of 54.7 years observed in our study aligns with previous reports from Indian and international studies, indicating that advancing age is a significant risk factor for sepsis development [11]. The male predominance (74%) is consistent with epidemiological data suggesting that males are more susceptible to sepsis, possibly due to immunological differences, hormonal factors, and higher prevalence of comorbidities [12]. The high prevalence of diabetes mellitus (44%) among our patients is noteworthy, as diabetes impairs immune function and increases susceptibility to infections [13].

Blood culture positivity rate of 32% in our study is comparable to rates reported in other studies, which typically range from 20% to 40% [14]. The predominance of gram-negative organisms (81.3%) reflects the microbiological pattern commonly observed in developing countries and Asian settings [15]. Escherichia coli, Pseudomonas aeruginosa, and Klebsiella pneumoniae were the most common isolates, consistent with findings from other Indian ICU studies [16]. This pattern has important implications for empirical antibiotic selection, emphasizing the need for broad-spectrum coverage against gram-negative pathogens.

Respiratory tract infections constituted the most

common source of sepsis (50%), followed by urinary tract infections (20%), similar to patterns reported globally [17]. This finding underscores the importance of pneumonia prevention strategies and appropriate management of respiratory infections in critically ill patients.

The overall mortality rate of 26% observed in our study is within the range reported in contemporary literature, which varies from 20% to 40% depending on disease severity and healthcare settings [18]. The striking increase in mortality with disease severity—from 5% in sepsis to 75% in septic shock—emphasizes the critical importance of early recognition and intervention. This observation is consistent with the established understanding that septic shock represents the most severe end of the sepsis spectrum with highest mortality [19].

The relationship between organ dysfunction and mortality was particularly notable, with mortality increasing from 0% in patients without organ dysfunction to 60% in those with three or more organ dysfunctions. This finding reinforces the concept that multi-organ dysfunction syndrome represents a critical determinant of outcomes in sepsis [20]. The Sequential Organ Failure Assessment score and similar tools that quantify organ dysfunction have proven valuable for prognostication and guiding therapeutic decisions [21].

Our biochemical findings, including elevated leukocyte counts, thrombocytopenia, metabolic acidosis, and elevated lactate levels, reflect the systemic inflammatory response and tissue hypoperfusion characteristic of sepsis [22].

These parameters serve as useful markers for diagnosis, severity assessment, and monitoring treatment response.

The study has certain limitations, including the relatively small sample size and single-center design, which may limit generalizability. Additionally, newer biomarkers such as procalcitonin were not routinely measured. Future multicenter studies with larger sample sizes and comprehensive biomarker panels would provide more robust evidence.

Conclusion

This prospective study demonstrates that sepsis in the intensive care unit setting is associated with significant morbidity and mortality, particularly in patients with severe sepsis, septic shock, and multi-organ dysfunction. Gram-negative organisms, predominantly Escherichia coli, Pseudomonas aeruginosa, and Klebsiella pneumoniae, represent the major causative pathogens, with respiratory tract infections constituting the primary source. The strong correlation between disease severity, organ dysfunction, and mortality emphasizes the critical importance of early recognition, prompt initiation of appropriate antimicrobial therapy, and aggressive supportive care. These findings have important implications for developing empirical antibiotic protocols and optimizing management strategies in resource-limited settings.

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