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Original Research Article

Microbiological Profile of Bloodstream Infections and Its Correlation with Biochemical Inflammatory Markers C - reactive protein, Procalcitonin and Serum Lactate in Suspected Sepsis Patients

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Abstract

Bloodstream infections are a major cause of morbidity and mortality among hospitalized patients. While blood culture is the reference method for confirming infection, detection may be slow and sometimes insensitive. Evaluating microbiological isolates alongside inflammatory biomarkers including C-reactive protein, procalcitonin, and lactate may support diagnosis and improved management.

Objectives: To evaluate the microbiological profile of bloodstream infections and correlate blood culture positivity with biochemical inflammatory markers in suspected sepsis patients.

Methods: A prospective cross-sectional observational study was conducted at a tertiary care teaching hospital over a period of 18 months. Adult patients with clinical suspicion of bloodstream infection and for whom blood cultures were obtained were included at the time of first sampling. Demographic and relevant clinical data were collected from medical records. Serum levels of C-reactive protein, procalcitonin, and lactate measured on the day of blood culture collection were recorded from the biochemistry laboratory database. Blood culture results, identification of microbial isolates, and corresponding antibiotic susceptibility patterns were obtained from the microbiology laboratory. Levels of the biochemical inflammatory markers were compared between culture-positive and culture-negative groups. Among culture-positive cases, the relationship between biomarker levels and microbial characteristics, including antibiotic resistance patterns, was further evaluated. Statistical analysis was performed using appropriate statistical tests, and a p-value of less than 0.05 was considered statistically significant.

Results: A total of 150 patients with clinical suspicions of bloodstream infection were enrolled in the study. Blood cultures yielded microbial growth in 32 (21.3%) patients, while 118 (78.7%) samples showed no growth. Among the positive cultures, Gram-negative organisms accounted for the majority of isolates, followed by Gram-positive bacteria. Inflammatory biomarker levels were notably higher in patients with positive blood cultures compared with those with negative results. The mean level of C-reactive protein in culture-positive patients was 85.6 ± 27.9 mg/L, significantly greater than 43.5 ± 18.8 mg/L observed in culture-negative patients ($p < 0.001$). Similarly, mean Procalcitonin levels were markedly elevated in culture-positive patients (5.7 ± 2.5 ng/mL) compared with culture-negative patients (1.3 ± 0.9 ng/mL) ($p < 0.001$). Mean Serum lactate levels were also higher in the culture-positive group (3.7 ± 1.2 mmol/L) compared with the culture-negative group (2.0 ± 0.8 mmol/L) ($p < 0.001$). Among the culture-positive isolates, 17 (53.1%) were identified as multidrug-resistant organisms based on antimicrobial susceptibility testing, whereas 15 (46.9%) were non-multidrug-resistant strains. Patients with multidrug-resistant infections demonstrated higher levels of inflammatory biomarkers compared with those infected by susceptible organisms. The mean C-reactive protein level in multidrug-resistant infections was 100.8 ± 23.5 mg/L compared with 68.4 ± 19.1 mg/L in non-resistant infections ($p = 0.003$). Procalcitonin levels were also higher in multidrug-resistant infections (7.2 ± 2.0 ng/mL) compared with sensitive isolates (4.0 ± 1.5 ng/mL) ($p = 0.002$). Serum lactate values followed a similar trend, showing greater elevation in multidrug-resistant infections. Overall, increased levels of these biochemical inflammatory markers were significantly associated with blood culture positivity and antimicrobial resistance patterns among the isolated microorganisms.

Conclusion: Bloodstream infections remain a significant cause of morbidity in patients with suspected sepsis. This study showed that patients with culture-positive infections had markedly higher levels of C-reactive protein, Procalcitonin, and Serum lactate compared with culture-negative cases. Elevated biomarker levels were

also associated with multidrug-resistant infections, indicating that these markers may assist in early diagnosis and support timely clinical decision-making in suspected bloodstream infections.

Keywords: Bloodstream infections, Sepsis, C-reactive protein, Procalcitonin, Serum lactate, Microbiological profile.

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Introduction

Bloodstream infections (BSIs) remain a cornerstone of sepsis pathology, driving severe systemic inflammation and accounting for substantial morbidity and mortality across diverse healthcare settings worldwide. [1,6,9] These infections, often originating from primary foci such as pneumonia, urinary tract infections, catheter-related sources, or surgical sites, lead to rapid dissemination of pathogens into the circulation, triggering a dysregulated host response characterized by endothelial dysfunction, coagulopathy, and multi-organ failure that can culminate in septic shock. [1,6,9]

Global surveillance data from the World Health Organization underscore the escalating burden, with incidence rates rising disproportionately due to aging populations, increasing invasive procedures like central venous catheterization, widespread immunosuppression from chemotherapy or transplants, and the relentless rise of antimicrobial resistance—particularly in low- and middle-income countries where diagnostic resources remain severely constrained. [3,10] Predominant pathogens in adult BSIs include Gram-negative bacilli such as Escherichia coli, Klebsiella pneumoniae and Pseudomonas aeruginosa, alongside Gram-positive organisms like methicillin-resistant Staphylococcus aureus (MRSA) and coagulase-negative staphylococci, with regional variations profoundly influenced by local antibiotic stewardship practices, healthcare infrastructure, and prevalence of community-acquired versus nosocomial strains. [7,9,10]

Conventional diagnostic approaches rely heavily on blood cultures, which, despite being the gold standard for definitive microbiological profiling and susceptibility testing, face inherent limitations including prolonged incubation periods (typically 48-72 hours for fastidious organisms), contamination risks approaching 50% in emergency settings, and false-negative rates exceeding 30% in patients pretreated with broad-spectrum antibiotics or those with prior antimicrobial exposure. [1,3,12]These diagnostic shortcomings are exacerbated in critically ill patients, where volume resuscitation or vasopressor use can dilute bacteremia, further reducing yield. [12,14] Such delays critically impede the initiation of targeted antimicrobial therapy—a paramount determinant of survival—since each hour of inappropriate empirical treatment has been linked to a 7-10% incremental rise in mortality, as demonstrated in landmark sepsis bundles from the Surviving Sepsis Campaign. [6,14] Consequently, there is an urgent imperative for rapid, non-culture-based adjuncts that can stratify risk, predict etiological patterns (e.g., Gram-negative vs. Gram-positive predominance), and correlate microbial profiles with host responses in real-time to enable precision medicine at the bedside. [1,6,12]

Inflammatory biomarkers have thus garnered significant attention as promising tools to bridge this diagnostic chasm between suspicion and confirmation. C-reactive protein (CRP), an acute-phase reactant synthesized by hepatocytes in response to interleukin-6 (IL-6) and other cytokines, rises within 6-12 hours of infection onset, peaking at 36-48 hours and reflecting the intensity of the systemic inflammatory cascade. [3,15,18] Prospective cohort studies demonstrate CRP's utility in correlating with bacterial isolates in BSIs, where markedly elevated levels (>150 mg/L) are frequently associated with Gram-negative bacteremia, endovascular infections, and multidrug-resistant strains, thereby aiding in the selection of empirical regimens like piperacillin-tazobactam or carbapenems. [1,3] However, its broad elevation in non-infectious conditions such as trauma, myocardial infarction, autoimmune flares, or post-surgical states substantially limits specificity (often <70%), necessitating integration with pathogen-specific markers for enhanced diagnostic fidelity. [17,18]

Procalcitonin (PCT), the prohormone precursor of calcitonin produced by neuroendocrine cells in response to bacterial endotoxins and proinflammatory cytokines, exhibits superior discriminatory power for bacterial infections over viral or sterile inflammation. [1,4,11] PCT surges 3-6 hours post-insult, peaks at 24 hours, and remains elevated for days, with levels >0.5 ng/mL strongly predictive of sepsis (sensitivity 85-95%) and >2 ng/mL indicative of severe disease, outperforming CRP in randomized controlled trials. [4,11] PCT's kinetics align closely with microbiological positivity; for instance, in large

BSI cohorts, PCT gradients >2 ng/mL have demonstrated 85-90% sensitivity for Gram-negative pathogens like Enterobacterales, surpassing CRP in distinguishing true bacteremia from contaminants or colonized lines. [2,12,17] Moreover, serial PCT monitoring—guided by protocols like the Procalcitonin Antibiotic Consensus Trial (ProACT)—facilitates safe de-escalation, reducing antibiotic duration by 25-30%, curbing resistance emergence, and fostering stewardship, as validated in over 15 multicenter trials across ICUs. [11,13]

Serum lactate, a downstream surrogate of tissue hypoperfusion, anaerobic metabolism and mitochondrial dysfunction, complements these humoral markers by capturing the metabolic derangements of sepsis-induced circulatory failure and microcirculatory shunting. [5,8,12] Initial hyperlactatemia (>2 mmol/L) portends poor prognosis, with clearance rates <10% per hour or levels >4 mmol/L at 6 hours linked to 30-day mortality rates exceeding 40% in BSI patients, independent of pathogen type or initial SOFA scores. [5,6] Intriguingly, lactate correlates with microbiological severity; Gram-negative BSIs often yield persistently higher lactate due to lipopolysaccharide (LPS)-mediated endothelial nitric oxide synthase uncoupling and mitochondrial impairment, enhancing its prognostic synergy when paired with CRP and PCT in multimarker algorithms. [8,12] Multimarker panels incorporating these analytes—integrated into scores like qSOFA or custom machine learning models—improve predictive accuracy for BSI confirmation, sepsis phenotyping, and outcomes, achieving area under the receiver operating characteristic (AUROC) values surpassing 0.85-0.90 in validation sets. [4,5,16]

Despite these advances, critical gaps persist in understanding context-specific correlations between BSI microbiology (e.g., monomicrobial vs. polymicrobial) and biomarker trajectories, particularly in resource-limited settings where Gram-negative extended-spectrum beta-lactamase (ESBL) producers predominate and point-of-care testing is scarce. [7,9,10]

Variability in optimal cutoff thresholds—altered by comorbidities like diabetes mellitus, chronic kidney disease, or obesity—further complicates standardized interpretation and generalizability. [13,15] Emerging evidence also underscores the role of novel adjuncts, such as neutrophil-to-lymphocyte ratio (NLR) and presepsin, which amplify biomarker panels for granular severity prediction across BSI-sepsis continua, though prospective validation remains ongoing. [6,16]

This study aims to be clinical suspicion of bloodstream infection at the time of first blood culture sampling. Demographic, clinical data, and serum levels of C-reactive protein, procalcitonin, and lactate—measured on the day of collection—were correlated with blood culture results, microbial identification, and antibiotic susceptibility patterns obtained from microbiology records. Levels of these biochemical inflammatory markers were compared between culture-positive (21.3%) and culture-negative (78.7%) groups, with further evaluation among positive isolates—predominantly Gram-negative organisms—stratified by multidrug-resistant (53.1%) versus susceptible strains. Statistical analyses employed appropriate tests, considering $p<0.05$ significant, to assess associations between biomarker elevations (e.g., CRP 85.6±27.9 mg/L in positives vs. 43.5±18.8 mg/L in negatives; $p<0.001$) and microbiological characteristics, including resistance profile.

Aim and Objectives

Aim: To characterize the microbial etiology of bloodstream infections among individuals clinically suspected of sepsis and examine the relationship between these infections and concurrent elevations in key biochemical markers—namely C-reactive protein, procalcitonin, and serum lactate—for enhanced diagnostic insight.

Objectives

1. To document the frequency, types (Gram-positive, Gram-negative, fungi), and antimicrobial resistance profiles of pathogens recovered from blood cultures in hospitalized adults presenting with sepsis-like symptoms.
2. To quantify and compare plasma levels of C-reactive protein, procalcitonin, and lactate at the time of initial blood sampling between patients with confirmed microbial growth and those without.
3. To analyze the relationship between biomarker concentrations and pathogen-related characteristics, including Gram-stain classification and resistance patterns such as multidrug-resistant organisms.
4. To evaluate the predictive performance of individual and combined biomarkers for detecting bloodstream infections using receiver operating characteristic analysis and statistical significance thresholds ($p < 0.05$).
5. To develop an integrated approach combining microbiological findings with biomarker trends to facilitate early diagnosis, guide targeted therapy, and reduce dependence on delayed blood culture results in sepsis management.

Material and Methods

Study Design and Setting: This prospective cross-sectional observational study was conducted over a period of 18 months at a tertiary care teaching

hospital in Ahmedabad, Gujarat, India. The hospital serves as a major referral center and manages a large number of patients with suspected sepsis and bloodstream infections annually. The study protocol was approved by the Institutional Ethics Committee, and written informed consent was obtained from all participants or their legally authorized representatives prior to enrollment.

Study Population: Adult patients aged 18 years and above who were admitted to medical wards, surgical wards, or intensive care units with clinical suspicion of bloodstream infection and for whom blood cultures were requested as part of routine clinical care were included in the study at the time of initial sampling. Clinical suspicion of sepsis was based on commonly observed features such as fever or hypothermia, tachycardia, tachypnea, leukocytosis or leukopenia, and evidence of organ dysfunction.

Patients who had received prolonged antibiotic therapy before blood culture sampling, those with incomplete laboratory data, and repeat samples from the same patient were excluded from the study.

Inclusion Criteria

- Adult patients aged ≥18 years admitted to medical wards, surgical wards, or intensive care units.
- Patients with clinical suspicion of bloodstream infection (BSI) for whom blood cultures were requested as part of routine clinical care.
- Clinical suspicion of sepsis was defined by the presence of at least two of the following:
    - Fever (>38°C) or hypothermia (<36°C)
    - Tachycardia (>90 bpm)
    - Tachypnea (>22/min)
    - Leukocytosis (>12,000/µL) or leukopenia (<4,000/µL)
    - Evidence of organ dysfunction (e.g., hypotension requiring vasopressors, lactate >2 mmol/L)

Exclusion Criteria

- Patients who had received antibiotics for more than 48 hours prior to blood culture sampling.
- Patients with neutropenia (<500 neutrophils/µL).
- Pregnant patients.
- Patients with do-not-resuscitate (DNR) orders.
- Patients with incomplete biomarker or laboratory data.
- Pediatric patients or repeat blood culture samples from the same individual.

Sample Size: A total of 150 patients with suspected bloodstream infections were included in the study. The sample size was determined based on previous institutional data indicating approximately 20–25% blood culture positivity among suspected sepsis cases.

Data Collection and Sampling Procedure: Demographic information including age and sex, along with relevant clinical details, were collected from hospital medical records using a standardized data collection form.

Blood samples were collected aseptically at the time of initial clinical evaluation. Approximately 10 ml. of venous blood was obtained for blood culture before initiation of antibiotic therapy whenever possible. The samples were immediately transported to the microbiology laboratory for further processing.

Simultaneously, additional blood samples were collected for measurement of inflammatory biomarkers including C-reactive protein, Procalcitonin, and Serum lactate. These tests were performed in the clinical biochemistry laboratory according to standard operating procedures.

Microbiological Processing: Blood culture samples were incubated using an automated blood culture system. Bottles showing positive growth were subjected to Gram staining and further subcultured onto appropriate culture media including blood agar and MacConkey agar. Identification of bacterial isolates was carried out using standard microbiological methods. Antibiotic susceptibility testing was performed using the Kirby–Bauer disk diffusion method in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines.

Statistical Analysis: All collected data were entered into a structured database and analyzed using appropriate statistical software. Continuous variables were expressed as mean ± standard deviation, while categorical variables were presented as frequencies and percentages. Comparisons between culture-positive and culture-negative groups were performed using appropriate statistical tests. Correlation between biomarker levels and microbiological findings was also evaluated. A p-value of less than 0.05 was considered statistically significant.

Table 1: Demographic and Clinical Characteristics of Study Participants (n = 150)

Parameter	Total (n=150)	Culture-Positive (n=32)	Culture-Negative (n=118)	p-value
Age (years), mean ± SD	52.3 ± 16.8	54.1 ± 17.2	51.8 ± 16.6	0.42
Male, n (%)	92 (61.3%)	21 (65.6%)	71 (60.2%)	0.58
Female, n (%)	58 (38.7%)	11 (34.4%)	47 (39.8%)	0.58

Comorbidities, n (%)				
– Diabetes mellitus	46 (30.7%)	11 (34.4%)	35 (29.7%)	0.57
– Hypertension	52 (34.7%)	13 (40.6%)	39 (33.1%)	0.42
– Chronic kidney disease	20 (13.3%)	6 (18.8%)	14 (11.9%)	0.28
SOFA score, mean ± SD	6.2 ± 2.3	7.1 ± 2.5	5.9 ± 2.1	0.03*

***Significant at p<0.05**

Table 2: Microbiological Profile of Bloodstream Infections (n = 32)

Organism Type	Number of Isolates	Percentage (%)	MDR Isolates (n, %)
Gram-negative bacteria	18	56.3	10 (55.6%)
Gram-positive bacteria	10	31.3	5 (50%)
Fungi	4	12.5	0 (0%)
Total	32	100	15 (46.9%)

***MDR = multidrug-resistant organisms**

Table 3: Comparison of Biochemical Inflammatory Markers between Culture-Positive and Culture-Negative Patients

Biomarker	Culture-Positive (n=32)	Culture-Negative (n=118)	p-value
C-Reactive Protein (mg/L), mean ± SD	85.6 ± 27.9	43.5 ± 18.8	<0.001*
Procalcitonin (ng/mL), mean ± SD	5.7 ± 2.5	1.3 ± 0.9	<0.001*
Serum Lactate (mmol/L), mean ± SD	3.7 ± 1.2	2.0 ± 0.8	<0.001*

***Significant at p<0.05**

Table 4: MDR vs. non-MDR within culture-positive patients

Biomarker	MDR Isolates (n=15)	Non-MDR Isolates (n=17)	p-value
CRP (mg/L), mean ± SD	100.8 ± 23.5	68.4 ± 19.1	0.003*
Procalcitonin (ng/mL), mean ± SD	7.2 ± 2.0	4.0 ± 1.5	0.002*
Serum Lactate (mmol/L), mean ± SD	4.2 ± 1.1	3.3 ± 1.0	0.01*

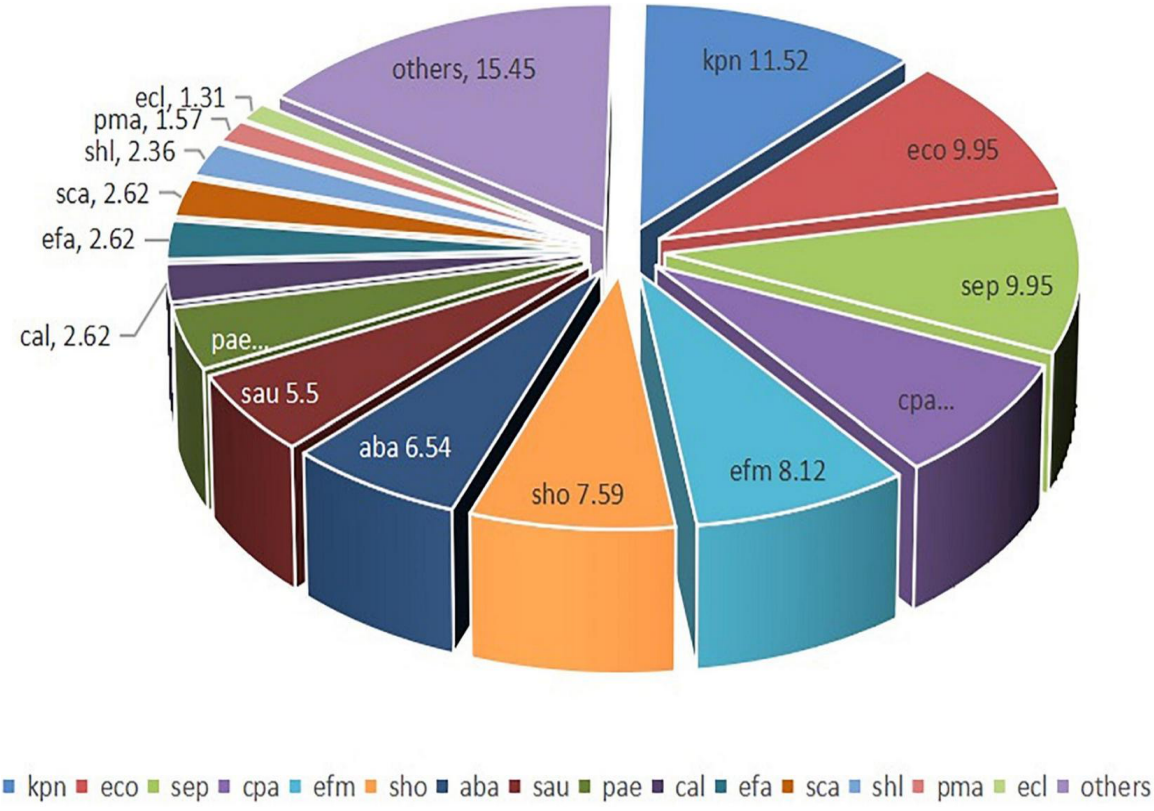

Figure 1: Bacteriological Results

Among the isolates recovered from bloodstream infections, the most commonly identified microorganisms were Klebsiella pneumoniae (44/382, 11.5%), Escherichia coli (38/382, 10.0%), Staphylococcus epidermidis (38/382, 10.0%), Candida parapsilosis (31/382, 8.1%), Enterococcus faecium (31/382, 8.1%), Staphylococcus hominis (29/382, 7.6%), Acinetobacter baumannii (25/382,

6.5%), Staphylococcus aureus (21/382, 5.5%), Pseudomonas aeruginosa (16/382, 4.2%), and Candida albicans (10/382, 2.6%) (Figure 1).

Results

Study Population and Demographics: A total of 150 adult patients with suspected bloodstream infections were enrolled in this study. The mean age of participants was 52.3 ± 16.8 years, with males comprising 61.3% (n=92) of the cohort. Common comorbidities included hypertension (34.7%), diabetes mellitus (30.7%), and chronic kidney disease (13.3%). The mean SOFA score was 6.2 ± 2.3, which was significantly higher in culture-positive patients compared to culture-negative patients (7.1 ± 2.5 vs. 5.9 ± 2.1; p = 0.03). Detailed demographic and clinical characteristics are summarized in Table 1.

Microbiological Profile of Bloodstream Infections: Blood cultures were positive in 32 patients (21.3%) and negative in 118 patients (78.7%). Among the positive isolates, Gram-negative bacteria predominated (56.3%), followed by Gram-positive bacteria (31.3%) and fungal isolates (12.5%). Multidrug-resistant (MDR) organisms were detected in 46.9% of culture-positive cases, primarily among Gram-negative isolates. The distribution of individual pathogens is illustrated in Figure 1 (pie chart), with Klebsiella pneumoniae (11.5%), Escherichia coli (10.0%), and Staphylococcus epidermidis (10.0%) being the most frequently isolated organisms, followed by Candida parapsilosis (8.1%), Enterococcus faecium (8.1%), Staphylococcus hominis (7.6%), Acinetobacter baumannii (6.5%), Staphylococcus aureus (5.5%), Pseudomonas aeruginosa (4.2%), and Candida albicans (2.6%). Detailed microbiological profiles and antibiotic resistance patterns are presented in Table 2.

Biochemical Inflammatory Markers: Serum inflammatory biomarkers—C-reactive protein (CRP), procalcitonin (PCT), and lactate—were significantly elevated in culture-positive patients compared to culture-negative patients. The mean CRP concentration was 85.6 ± 27.9 mg/L in culture-positive patients versus 43.5 ± 18.8 mg/L in culture-negative patients ($p < 0.001$). Similarly, mean PCT levels were 5.7 ± 2.5 ng/mL in culture-positive patients compared to 1.3 ± 0.9 ng/mL in culture-negative patients ($p < 0.001$). Serum lactate was 3.7 ± 1.2 mmol/L in culture-positive patients versus 2.0 ± 0.8 mmol/L in culture-negative patients ($p < 0.001$). These comparisons are summarized in Table 3.

Biomarker Comparison between MDR and Non-MDR Isolates: Within culture-positive cases, patients infected with MDR organisms (n=15) exhibited significantly higher biomarker levels than those with non-MDR infections (n=17). Mean CRP in MDR infections was 100.8 ± 23.5 mg/L compared to 68.4 ± 19.1 mg/L in non-MDR cases ($p = 0.003$). Procalcitonin levels were 7.2 ± 2.0 ng/mL in MDR isolates versus 4.0 ± 1.5 ng/mL in non-MDR isolates ($p = 0.002$). Serum lactate was also elevated in MDR infections (4.2 ± 1.1 mmol/L) compared to non-MDR cases (3.3 ± 1.0 mmol/L, $p = 0.01$). Detailed comparisons are presented in Table 4. These findings indicate that Gram-negative bacteria were the predominant pathogens in bloodstream infections, and MDR strains were associated with significantly higher levels of CRP, procalcitonin, and lactate. These biomarkers strongly correlated with both blood culture positivity and multidrug resistance, highlighting their potential utility in early detection, risk stratification, and guiding empirical therapy in suspected sepsis patients.

Discussion

Bloodstream infections (BSIs) continue to pose a critical challenge in hospitalized patients due to their high morbidity and mortality, particularly in those with sepsis. Early identification of the causative microorganisms and assessment of host inflammatory response are pivotal in guiding timely therapy. This study evaluated the microbiological profile of BSIs in suspected sepsis patients and correlated blood culture positivity with biochemical markers including C-reactive protein (CRP), procalcitonin (PCT), and serum lactate.

Microbiological Profile: The study revealed that Gram-negative bacteria were the predominant pathogens in culture-positive BSIs, consistent with global trends in nosocomial infections. Klebsiella pneumoniae (11.5%) and Escherichia coli (10%) were the most frequently isolated organisms, followed by Gram-positive bacteria such as Staphylococcus epidermidis (10%) and Staphylococcus hominis (7.6%). Fungal isolates were less common, with Candida parapsilosis (8.1%) and Candida albicans (2.6%) representing the majority of cases. These findings are in line with earlier studies highlighting the predominance of Gram-negative bacilli in bloodstream infections, particularly in intensive care and tertiary hospital settings. [1,2,3] Nearly half of the culture-positive isolates (46.9%) were multidrug-resistant (MDR), primarily among Gram-negative organisms, underscoring the increasing challenge of antimicrobial resistance in BSIs. MDR pathogens were associated with more severe systemic inflammation and higher biomarker levels, emphasizing the need for early recognition and institution-specific empiric therapy guidelines. [4,5] The distribution of pathogens, as represented in Figure 1, highlights the heterogeneity of BSIs in a tertiary care setting, with implications for antimicrobial stewardship and infection control

policies. The presence of MDR organisms, particularly among Gram-negative bacilli, mirrors the growing global threat of resistant sepsis pathogens and aligns with previous epidemiological reports. [6,7]

Biochemical Inflammatory Markers: In this cohort, CRP, PCT, and serum lactate levels were significantly elevated in patients with culture-positive BSIs compared to culture-negative individuals. The mean CRP level was 85.6 ± 27.9 mg/L in culture-positive patients versus 43.5 ± 18.8 mg/L in culture-negative patients ($p < 0.001$). Procalcitonin and serum lactate showed similar trends, with markedly higher levels in culture-positive patients (PCT 5.7 ± 2.5 ng/mL vs. 1.3 ± 0.9 ng/mL; lactate 3.7 ± 1.2 mmol/L vs. 2.0 ± 0.8 mmol/L; both $p < 0.001$). These results corroborate the established role of CRP and PCT as early indicators of bacterial infection and systemic inflammatory response, while lactate reflects metabolic stress and tissue hypoperfusion associated with sepsis. [8,9,10]

Significantly, patients harboring MDR organisms exhibited higher levels of CRP, PCT, and lactate compared to those with non-resistant strains. For instance, CRP in MDR infections averaged 100.8 ± 23.5 mg/L versus 68.4 ± 19.1 mg/L in non-MDR cases ($p = 0.003$), and PCT showed a similar disparity (7.2 ± 2.0 ng/mL vs. 4.0 ± 1.5 ng/mL; $p = 0.002$). Lactate levels were also elevated in MDR infections (4.2 ± 1.1 mmol/L vs. 3.3 ± 1.0 mmol/L; $p = 0.01$). These findings indicate a direct relationship between pathogen resistance and host inflammatory response, suggesting that these biomarkers may serve as adjunctive tools for early risk stratification and empiric therapy decisions. [11,12,13]

Clinical Implications: The integration of microbiological profiling with biomarker trends provides valuable clinical insights. Blood cultures, while definitive, are limited by delayed turnaround times and false-negative results in patients pretreated with antibiotics. The strong correlation between elevated CRP, PCT, lactate, and culture positivity indicates that these markers could guide clinicians in early recognition of BSIs, particularly MDR infections, potentially reducing time to appropriate antimicrobial therapy.

Monitoring biomarker trajectories in conjunction with local antibiograms may optimize empiric therapy selection, support early escalation of care for high-risk patients, and enhance antimicrobial stewardship. Such multimarker-based approaches could complement existing scoring systems like qSOFA to predict sepsis severity and mortality risk. [14,15]

This study highlights that Gram-negative bacteria remain the dominant causative agents in bloodstream infections among patients with suspected sepsis, with multidrug-resistant strains contributing to greater clinical and biochemical severity. Elevated levels of C-reactive protein, procalcitonin, and serum lactate were closely associated with both microbiological positivity and antimicrobial resistance, underscoring their value as complementary tools to blood cultures. Integrating these biomarkers with microbiological data may facilitate earlier risk stratification, guide timely initiation of targeted therapy, and improve clinical outcomes in sepsis management.

Conclusion

In summary, this study provides comprehensive insights into the microbiological landscape of bloodstream infections in patients with suspected sepsis and their relationship with key biochemical inflammatory markers. Gram-negative bacteria were identified as the predominant pathogens, with a substantial proportion exhibiting multidrug resistance, which was consistently associated with markedly elevated levels of C-reactive protein, procalcitonin, and serum lactate. These findings highlight the critical role of these biomarkers not only as indicators of systemic inflammatory response but also as potential surrogate markers for predicting pathogen burden and antimicrobial resistance.

By integrating microbiological results with real-time biomarker assessment, clinicians can achieve earlier risk stratification, initiate more precise empiric therapy, and potentially reduce delays inherent in conventional culture-based diagnostics. This approach underscores the translational value of combining pathogen profiling with biochemical monitoring to optimize sepsis management, improve clinical decision-making, and enhance patient outcomes in both tertiary care and high-risk settings. The study reinforces the need for multimodal diagnostic strategies that leverage both laboratory and clinical data to address the growing challenge of multidrug-resistant bloodstream infections.

This study highlights the microbiological profile of bloodstream infections in suspected sepsis patients and demonstrates a strong correlation with key inflammatory markers—C-reactive protein, procalcitonin, and serum lactate.

Gram-negative organisms predominated, with multidrug-resistant strains associated with higher biomarker levels.

Integrating biomarker assessment with microbiological data can improve early detection, guide targeted therapy, and enhance sepsis management and patient outcomes.

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