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Research article

Microbiological Profile of Bloodstream Infections in ICU Sepsis Patients: A Hospital-Based Study

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ABSTRACT

Background: Severe sepsis remains a critical medical condition with high morbidity and mortality rates. Identifying the causative pathogens is essential for effective treatment. This study aimed to determine the bacterial profile isolated from blood cultures of severe sepsis patients admitted to intensive and respiratory care units in Al-Hilla hospitals. **Methods**: A total of 100 severe sepsis patients (aged 13–90 years) were enrolled from August 2023 to January 2024. Blood samples (7 mL) were collected from patients with abnormal complete blood counts (CBC) and C-reactive protein (CRP) levels >10 mg/L. Blood cultures were cultured on selective media (blood agar, MacConkey, etc.), then processed using the automated VITEK2 system (bioMérieux), followed by Ethical approval was obtained from the Babylon Health Directorate. **Results**: Among 100 patients (mean age 59.60 ± 18.314 years), 25 (25%) had positive blood cultures. The most prevalent isolates were *Stenotrophomonas maltophilia* and *Pseudomonas stutzeri* (16% each), followed by *Kocuria kristinae* (12%). *Staphylococcus aureus*, *S. epidermidis*, and *Escherichia coli* each accounted for 8%, while other species (*Streptococcus pneumoniae*, *Salmonella typhi*, etc.) were detected in single cases (4% each). **Conclusion**: Gram-negative bacteria, particularly *S. maltophilia* and *P. stutzeri*, were the predominant pathogens in sepsis patients. Continuous surveillance of microbial patterns is crucial for guiding empirical antibiotic therapy and improving clinical outcomes in sepsis management.

Keywords:
Pseudomonas stutzeri; bloodstream infection; community-onset; epidemiology; mortality, Bacteremia, BSIs, sepsis.

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INTRODUCTION

Bloodstream infections (BSIs) represent a significant global health challenge, contributing substantially to morbidity and mortality worldwide. Early and accurate identification of causative pathogens is crucial for effective patient management, guiding appropriate antimicrobial therapy, and improving clinical outcomes. Blood culture remains the gold standard for diagnosing BSIs, despite advancements in molecular and rapid diagnostic techniques [1, 2].

The interpretation of blood culture results, however, can be complex, often requiring careful consideration of clinical context, patient risk factors, and the microbiological characteristics of isolated organisms [3]. Coagulase-negative staphylococci (CoNS), such as *Staphylococcus epidermidis* and *Staphylococcus hominis*, are frequently isolated from blood cultures. While they are common skin commensals and often represent contamination, they can also cause true infections, particularly in immunocompromised patients or those with indwelling medical devices [4, 5].

Differentiating between contamination and true infection is a critical aspect of interpreting these results to avoid unnecessary antibiotic exposure and prolonged hospital stays [6]. Gram-negative

bacteria, including *Escherichia coli*, *Klebsiella pneumoniae*, *Stenotrophomonas maltophilia*, *Morganella morganii*, and *Pseudomonas* species, are also significant causes of BSIs, often associated with severe clinical presentations and higher mortality rates [7, 8].

The emergence of multidrug-resistant (MDR) strains among these pathogens further complicates treatment strategies, necessitating continuous surveillance of antimicrobial susceptibility patterns [9]. *Stenotrophomonas maltophilia*, for instance, is an opportunistic pathogen increasingly recognized for its intrinsic resistance to many commonly used antibiotics [10]. Similarly, *Pseudomonas stutzeri*, though less common, has been implicated in serious infections, including bacteremia [11].

This research paper aims to provide a comprehensive analysis of bacterial blood culture results from a study involving 100 patients, focusing on the prevalence of various bacterial species and their clinical significance. By examining the identified pathogens and drawing upon recent scientific literature, we seek to enhance the understanding of BSI epidemiology and the challenges associated with their diagnosis and management. The findings will contribute to the broader knowledge base, aiding clinicians in the accurate interpretation of blood culture data and optimizing therapeutic interventions.

MATERIALS AND METHODS:

A total of 100 severe sepsis patients were participated in this study; they were all hospitalized to the ICU & RCU of Al-Hilla hospitals from August 2023 to January 2024. They were between the ages of 13 and 90 years. Each patient's symptoms, body temperature, complete blood count results (CBC), C-reactive protein (CRP), procalcitonin (PCT), and the site of infection were documented at the time of admission. In this investigation, a volume of 7mL of blood was withdrawn from patients who had a history of an abnormal CBC count, and a CRP level above 10 mg/L. The blood culture tests were performed by bacteriologist staff in the microbiology unit using the automated VITEK2 device (bioMérieux) for species identification.

The first step must be informed consent, in which a patient agrees to participate in a study and authorizes the collection of information and a patient's history without fear of compulsion. The ethical stance received approval from the Babylon Health Directorate. During sample collection and processing, safety and health precautions were taken.

RESULTS:

During the study period, the 100 patients who participated in the study had a mean age of 59.60 ± 18.314 years, with a range of 13-90. Blood samples from those patients were collected and cultivated with in strict aseptic methods, When the blood samples were inoculated in the BHI vials then Only 25 (25%) of 100 samples had positive blood culture (turbid vials) when monitoring daily during the BHI incubation period. Afterward, the bacterial growth in broth media were transferred to several selective and differential media to be re-incubated. Blood agar, Chocolate, MacConkey, Mannitol salt, Xylose lysine deoxycholate, and Eosin methylene blue agar were used. After a 24-hour of incubation at 37 °C is completed, all 25 positive BHI vials gave positive results and demonstrated the morphological form and biochemical properties of different bacterial species.

As shown in [Table 1 and Figure 1], *Stenotrophomonas maltophilia* and *Pseudomonas stutzeri* were the most frequently isolated pathogens, each accounting for 16% (n=4) of the positive cultures. *Kocuria kristinae* was the next most common isolate, representing 12% (n=3) of the cases. *Staphylococcus aureus*, *Staphylococcus epidermidis*, and *Escherichia coli* each constituted 8% (n=2) of the positive cultures. The remaining bacterial species, including *Streptococcus pneumoniae*, *Salmonella typhi*, *Staphylococcus hemolyticus*, *Klebsiella pneumoniae*, *Morganella morganii*, *Pseudomonas aeruginosa*, *Staphylococcus hominis*, and *Enterobacter aerogenes*, were each isolated in one case, accounting for 4% of the positive cultures individually.

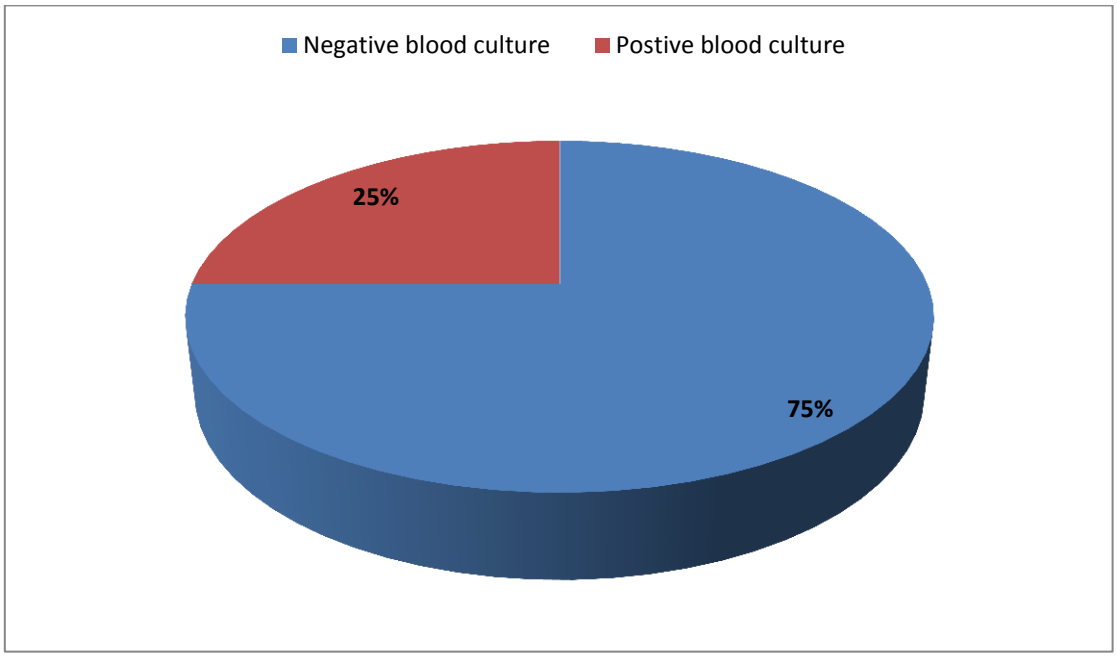

Figure 1: Distribution of Bacterial Species

Table 1: Distribution of Bacterial Species Isolated from Positive Blood Cultures (n=25)

Bacterial species	No.
Staphylococcus aureus	2 (8%)
Staphylococcus epidermidis	2 (8%)
Stenotrophomonas maltophilia	4 (16%)
Escherichia coli	2 (8%)
Streptococcus pneumonia	1 (4%)
Salmonella typhi	1(4%)
Staphylococcus hemolyticus	1(4%)
Klebsiella pneumonia	1(4%)
Morganella morganii	1(4%)
Pseudomonas aeruginosa	1(4%)
Staphylococcus hominis	1(4%)
Kocuria kristinae	3(12%)
Enterobacter aerogenes	1(4%)
Pseudomonas stutzeri	4(16%)
Total	25 (100%)

DISCUSSIONS:

The findings of this study provide valuable insights into the spectrum of bacterial pathogens causing bloodstream infections in the studied patient population. The overall positivity rate of 25% from 100 blood samples aligns with rates reported in various clinical settings, reflecting the challenges in diagnosing BSIs and the potential for both true infections and contaminants [12]. The mean age of the patient cohort (59.60 ± 18.314 years) suggests that BSIs are prevalent across a broad age range, including older adults who may be more susceptible

due to comorbidities.

The prominence of *Stenotrophomonas maltophilia* (16%) and *Pseudomonas stutzeri* (16%) as the most frequently isolated pathogens is a notable finding. *Stenotrophomonas maltophilia* is an opportunistic, multidrug-resistant Gram-negative bacterium increasingly recognized as a significant cause of healthcare-associated infections, particularly in immunocompromised patients [13].

Its high prevalence in this study underscores the need for vigilant surveillance and appropriate antimicrobial stewardship, given its intrinsic resistance to many common antibiotics [10]. Similarly, *Pseudomonas stutzeri*, though less commonly reported than *P. aeruginosa*, has been implicated in various infections, including bacteremia, often in patients with underlying conditions [11]. The significant presence of these two species highlights their emerging importance in the local epidemiology of BSIs.

Kocuria kristinae, accounting for 12% of isolates, is another interesting finding. Traditionally considered a commensal of the skin and mucous membranes, *Kocuria* species are increasingly recognized as opportunistic pathogens, particularly in immunocompromised individuals or those with indwelling devices [14]. While often dismissed as contaminants, their isolation, especially in multiple blood culture sets or in patients with clinical signs of infection, warrants careful evaluation to differentiate true infection from contamination [15]. The relatively high percentage in this study suggests a potential underestimation of its pathogenic role or a specific patient population susceptible to *Kocuria* infections.

The isolation of *Staphylococcus aureus* (8%) and *Escherichia coli* (8%) is consistent with their well-established roles as leading causes of BSIs globally [16, 17]. *S. aureus* bacteremia is associated with high morbidity and mortality and often requires aggressive management due to its potential for metastatic infection [18]. *E. coli* is a common cause of Gram-negative bacteremia, frequently originating from urinary tract or intra-abdominal infections [19]. The presence of these common pathogens in this study reaffirms their continued clinical significance.

Other Gram-negative bacteria such as *Klebsiella pneumoniae* (4%), *Morganella morganii* (4%), *Pseudomonas aeruginosa* (4%), and *Enterobacter aerogenes* (4%) were also identified. These organisms are known to cause severe infections, particularly in healthcare settings, and their presence underscores the diverse etiology of BSIs [20, 21, 22]. The isolation of *Salmonella typhi* (4%) is significant, as it is the causative agent of typhoid fever, a systemic infection that can lead to severe complications if not promptly treated [23].

Among the coagulase-negative staphylococci, *Staphylococcus epidermidis* (8%) and *Staphylococcus hominis* (4%) were identified. While these are common skin flora, their presence in blood cultures necessitates careful clinical correlation to distinguish between true infection and contamination. Factors such as the number of positive bottles, time to positivity, and clinical signs of infection are crucial in making this distinction [5, 6]. *Staphylococcus hemolyticus* (4%) is another coagulase-negative staphylococcus that is increasingly recognized as a cause of nosocomial infections, often exhibiting multidrug resistance [24].

This study has several limitations. Firstly, it is a single-center study with a relatively small sample size (n=100), which may limit the generalizability of the findings to other populations or geographical regions. Secondly, the study design did not include detailed clinical data for each patient, such as underlying comorbidities, presence of indwelling devices, or prior antibiotic exposure, which could influence the spectrum of isolated pathogens and their clinical significance. Thirdly, while standard microbiological methods were used for identification, advanced molecular techniques (e.g., PCR, whole-genome sequencing) were not employed, which could provide more precise identification and characterization of bacterial strains, including their resistance mechanisms.

CONCLUSION

This study highlights the diverse bacterial etiology of bloodstream infections, with a notable prevalence of opportunistic pathogens such as *Stenotrophomonas maltophilia*, *Pseudomonas stutzeri*, and *Kocuria kristinae*, alongside more commonly recognized pathogens like

Staphylococcus aureus and *Escherichia coli*. The findings underscore the importance of accurate microbiological diagnosis and continuous surveillance of local epidemiological patterns and antimicrobial resistance. Further large-scale, multi-center studies with comprehensive clinical data and advanced molecular characterization are warranted to better understand the epidemiology, risk factors, and optimal management strategies for these infections.

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