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The microbiology of sepsis: Identifying culprits in critical care.

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Introduction

Sepsis is a life-threatening organ dysfunction caused by a dysregulated host response to infection. It remains a major challenge in critical care, responsible for significant morbidity and mortality worldwide. Despite advances in supportive care and antimicrobial therapy, early identification of the microbial culprits behind sepsis is essential for effective treatment and improved outcomes. Clinical microbiology plays a pivotal role in diagnosing sepsis, guiding targeted therapy, and informing infection control strategies. Sepsis can arise from infections in virtually any part of the body, including the lungs, urinary tract, abdomen, and bloodstream. The condition is not caused by a single pathogen but rather a wide array of bacteria, fungi, and occasionally viruses. *Staphylococcus aureus*, including methicillin-resistant strains (MRSA), and *Streptococcus pneumoniae* are frequent causes [1].

Host factors such as age, comorbidities, immune status, and prior antibiotic exposure influence susceptibility to specific pathogens. For example, neutropenic patients are more prone to infections with *Pseudomonas* and *Candida*, while elderly patients may present atypically and harbor resistant organisms. Routine microbiological surveillance in hospitals helps track pathogen prevalence and resistance trends. This data informs empiric therapy guidelines and supports antimicrobial stewardship programs aimed at optimizing antibiotic use and reducing resistance. *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* are prominent in hospital-acquired infections. *Candida* species, particularly *Candida albicans*, are increasingly recognized in immunocompromised patients. Though less common, organisms like *Bacteroides fragilis* and *Mycoplasma* can contribute to sepsis. Bloodstream infections (BSIs) are a primary source of sepsis. Bacteremia—the presence of bacteria in the blood—is a hallmark of systemic infection. Blood cultures remain the gold standard for identifying pathogens in sepsis, though they are limited by time delays and sensitivity. Studies show that up to 30% of septic patients may have negative blood cultures, especially if antibiotics were administered prior to sample collection [2].

Traditional blood cultures require 24–72 hours for growth and identification. While essential for antimicrobial susceptibility testing (AST), they may miss fastidious or slow-growing organisms. PCR-based assays detect microbial DNA directly from blood samples, offering rapid results. Multiplex PCR panels can identify multiple pathogens and resistance genes simultaneously, improving diagnostic speed and accuracy. MALDI-TOF enables rapid identification of bacteria and fungi from positive blood cultures based on protein profiles. It significantly reduces turnaround time compared to conventional biochemical methods [3].

NGS provides comprehensive analysis of microbial genomes and metagenomes, identifying pathogens even in culture-negative sepsis. Though currently limited by cost and complexity, NGS holds promise for future diagnostics. Antimicrobial resistance (AMR) complicates sepsis management. Multidrug-resistant organisms (MDROs) such as MRSA, extended-spectrum beta-lactamase (ESBL)-producing *E. coli*, and carbapenem-resistant *Klebsiella* are increasingly implicated in sepsis cases. Rapid detection of resistance markers is crucial for guiding effective therapy and preventing treatment failure [4].

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Commonly caused by *S. pneumoniae*, *Legionella*, and *P. aeruginosa*. Frequently involves *E. coli*, *Klebsiella*, and *Enterococcus* species. Often polymicrobial, including anaerobes like *Bacteroides* and facultative organisms like *Enterobacteriaceae*. Typically involves skin flora such as *S. epidermidis* and *S. aureus*. Understanding these patterns helps clinicians anticipate likely pathogens and tailor empiric therapy accordingly. Fungal sepsis, particularly due to *Candida* species, is rising in prevalence among ICU patients, especially those with central venous catheters, broad-spectrum antibiotic use, or immunosuppression. *Candida auris*, a multidrug-resistant yeast, has emerged as a global threat due to its persistence in healthcare environments and resistance to multiple antifungal agents [5].

Conclusion

Sepsis is a complex syndrome with diverse microbial etiologies. Accurate and timely identification of pathogens is critical for effective treatment and improved outcomes in critical care. While traditional culture methods remain essential, molecular diagnostics and emerging technologies are enhancing our ability to detect and characterize sepsis-causing microbes. A multidisciplinary approach that integrates clinical microbiology, infectious disease expertise, and critical care is vital to combat this global health challenge.

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