Differential Gut Microbiota Composition Between Sepsis and Shock Patients

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Introduction

Sepsis is an exacerbated immune response to infection that may progress to septic shock, leading to hypotension and organ dysfunction. Hospitalization-related stressors can alter the gut microbiota in critically ill patients. Identifying key microbial taxa involved in this process may inform clinical management and guide antimicrobial therapy.

Aim

This study aimed to compare the intestinal microbiota of patients with sepsis and with septic shock.

Methodology

Patients presenting with systemic inflammatory response syndrome (SIRS) at the Hospital de Clínicas de Porto Alegre (HCPA) were enrolled following informed consent between August 2022 and August 2023. Those meeting SEPSIS-3 criteria underwent stool sample collection for gut microbiota analysis using 16S rRNA gene sequencing. Differential taxonomic abundance was evaluated with the ANCOM-BC2 package in R.

Results

Stool samples were collected from 38 sepsis patients within the first 10 days of antibiotic therapy, of whom 11 developed shock requiring vasopressors. The respiratory tract was the most common primary infection site, observed in 25.9% (7/27) of sepsis cases and 54.5% (6/11) of shock cases. Renal dysfunction predominated in sepsis patients (70.4%; 19/27), whereas hypotension and hypoxemia were most frequent in shock cases (72.7%; 8/11). Regarding clinical outcomes, 18.5% (5/27) of sepsis patients required intensive care unit (ICU) admission within 10 days of hospitalization, compared to 54.5% (6/11) of those with shock. Piperacillin-tazobactam was the most prescribed antibiotic in both groups (sepsis: 37.0%; shock: 45.5%). No significant differences were observed in alpha diversity (Shannon index: sepsis 2.53; shock 2.65; $p = 0.66$) or beta diversity ($p = 0.15$). However, patients in the shock group exhibited a significantly higher differential abundance of *Holdemania* and *Bilophila*, whereas the genera *Massiliomicrobiota* and *Clostridium* were significantly decreased in this group.

Conclusion

In summary, *Holdemania* may contribute to epithelial damage via excess H_2S production, while *Bilophila* is linked to dysbiosis and immune disturbance. *Clostridium* includes both harmful and beneficial species, as SCFA-producing species. Although *Massilimicrobiota* is a rare commensal, elucidating key taxa may

provide valuable insights for microbiota-targeted strategies aimed at improving clinical outcomes.