

Nasal Microbiota - Potential Diagnostic Biomarker for Sepsis



A new study published in *Microbiology Spectrum* reveals that the nasal microbiota of ICU patients can effectively distinguish between sepsis and non-sepsis cases, outperforming gut microbiota in predicting sepsis.

These findings have implications for developing diagnostic strategies and advancing critical care medicine. Historically, the focus has been more on the intestinal microbiota of sepsis patients, but this study shows that the respiratory microbiota also deserves attention.

Sepsis is a severe illness with a high mortality rate, ranging from 29.9% to 57.5%. Despite the Sepsis-3 definition, further exploration is needed to improve its diagnosis. The evolution of diagnostic criteria from Sepsis-1 to Sepsis-3 underscores the need for continued investigation. The diagnostic criteria for sepsis have shifted from focusing solely on the inflammatory response to including organ failure caused by infection. While progress has been made, no biological indicators with strong sensitivity and specificity have been identified. Additionally, the low culture positivity rate and the presence of few culturable microorganisms limit clinical sepsis diagnosis. Therefore, researchers have been aiming to identify a new, effective, and reliable biomarker for sepsis.

In the new study, researchers recruited 157 subjects (89 with sepsis) at the affiliated hospital of Southern Medical University. They collected nasal swabs and fecal specimens from septic and non-septic patients in the ICU and Department of Respiratory and Critical Care Medicine. The scientists extracted and sequenced DNA using Illumina technology. Bioinformatics analysis, statistical processing, and machine learning techniques were used to differentiate between septic and non-septic patients.

They discovered that the nasal microbiota of septic patients exhibited significantly lower community richness and distinct compositions than non-septic patients. *Corynebacterium*, *Staphylococcus*, *Acinetobacter*, and *Pseudomonas* were identified as enriched genera in the nasal microbiota of septic patients.

The researchers recommend further research, possibly through animal models or larger patient cohorts, to deepen the understanding of microbiota's role in sepsis beyond the antibiotic effect.

Source: [American Society for Microbiology](#)

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