Peer-Reviewed Study Demonstrates Improved Sensitivity of mNGS Using Host Depletion Filtration

Genomic DNA with zwitterionic filtration outperforms cfDNA, increasing microbial reads >10-fold in blood culture-positive samples.

Micronbrane Medical - mNGS Innovations from Collection to Action

ZHUBEI CITY, TAIWAN, August 20, 2025 /EINPresswire.com/ -- Micronbrane Medical, a developer of metagenomic next-generation sequencing (mNGS) enabling technologies, today announced that a newly published study in Molecular Diagnosis & Therapy provides clinical evidence that host-cell depletion prior to mNGS significantly improves diagnostic sensitivity in sepsis. The research shows that genomic DNA (gDNA) derived from filtered blood samples yields stronger microbial signals than cell-free DNA (cfDNA), with more than a 10-fold increase in microbial reads and 100 percent pathogen detection in all evaluated cases.

> Host depletion with gDNA input enhances microbial signal-to-noise, enabling deeper metagenomic resolution and more consistent pathogen detection than cfDNA-based assays."
>
> *Dr. Mengchu Wu*

The study evaluates the zwitterionic interface ultra-self-assemble coating (ZISC)-based filtration device, commercially known as the Devin Host Depletion Filter. The device selectively removes nucleated host cells while allowing bacteria, viruses and other microorganisms to pass through unaltered. In eight blood culture-positive patient samples, gDNA-based mNGS with host depletion achieved an average of 9,351 microbial reads per million (RPM), compared with 925 RPM in unfiltered samples ($p = 0.041$). cfDNA workflows showed no statistically significant improvement.

"Our findings confirm that the Devin Host Depletion Filter combined with gDNA input enables much greater microbial enrichment without altering the underlying microbial composition," said

Yen-Chia Chen, M.D., Ph.D., assistant professor of emergency medicine, emergency department attending physician at Taipei Veterans General Hospital, and principal investigator of the study. “This approach directly addresses one of the biggest limitations of mNGS: the overwhelming background of human DNA.”

The filtration method removed more than 99 percent of white blood cells from whole blood samples without affecting bacterial or viral passage. Microbial composition remained consistent before and after filtration, with a correlation coefficient of 0.90. The limit of detection was estimated at 150 genome equivalents per milliliter, consistent with accepted thresholds for clinical utility. Across all comparisons, gDNA with host depletion delivered the highest sensitivity and microbial read recovery.

The study also compared host depletion to other methods, including differential lysis and CpG-methylated DNA removal. The filtration method outperformed both in operational efficiency and microbial signal retention, offering a faster and less labor-intensive alternative that preserves sample integrity.

“As infectious disease challenges evolve, hospitals need sequencing technologies that are both comprehensive and practical,” said Mengchu Wu, Ph.D., co-founder, CEO and chairwoman of Micronbrane Medical. “This study adds to the growing body of evidence supporting the clinical value of metagenomic sequencing when barriers such as host DNA, contamination, complexity and cost are addressed.”

Micronbrane Medical did not fund or staff the study, which was conducted independently and supported by a research grant from a regional medical center. The full article, “Optimization of Metagenomic Next-Generation Sequencing Workflow with a Novel Host Depletion Method for Enhanced Pathogen Detection,” is available in Molecular Diagnosis & Therapy at https://rdcu.be/exLfm.

Kristi Ashton
Micronbrane Medical
+1 650-224-8231
email us here
Visit us on social media:
LinkedIn