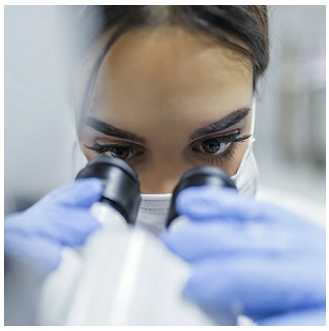
ICU
MANAGEMENT & PRACTICE

Metabolic profiling for monitoring intestinal dysbiosis



Bacteria that reside in the intestinal tract are believed to have several metabolic, endocrine, and immune functions. The composition and diversity of the intestinal microbiome in critical illness can be impacted by poor intestinal perfusion, hypoxia, lack of enteral feeds, and antimicrobial therapy. This could potentially result in adverse outcomes, including secondary infection and mortality.

Detailed information about the intestinal microbiome can be obtained through the capture of metabolic outputs so that greater insight can be obtained with respect to host-microbe interactions in the human system. This information could also help clinicians understand the clinical impact of intestinal dysbiosis in critical illness.

A study was conducted to examine whether metabolic profiling is a feasible method of monitoring intestinal dysbiosis in critically ill children. The goal was to characterise the functional capacity of the intestinal microbiome through multi-compartmental metabolic profiling. The researchers examined the changes in bacterial and host metabolites in urine and faeces in order to characterise the gut microbiota-host relationship in critically ill patients.

The study included critically ill children between the ages of 1 and 16 years. Urine samples were collected on day 3-5 and days 6-8. Faecal samples were collected within the first two days of PICU admission and then between days 5-8. All the children included in the study had received one or more broad-spectrum antibiotics at the time of sampling.

Findings showed a statistically significant increase in primary bile acid concentrations in samples from critically ill children compared to healthy children. Healthy children had a higher prevalence of bacteroids, aecalibacterium, and Ruminococcus genera while critically ill children had an increased presence of noncommensals (e.g., Enterococcus and Streptococcus), and of normally low prevalence microbial genera. The abundance of enterococcus genus in the critically ill patient samples directly correlated with the number of antibiotic classes administered to these patients. There were no microbial or metabolic signatures of nonsurvival. But in previous research conducted in adults, pathogen colonisation of the faecal microbiome has been shown to be associated with death.

The findings from this study demonstrate that profiling of bacterial metabolites offers an insight into the functional capacity of the intestinal microbiome. Disease severity may be linked to the level of these metabolites. There is a need to explore dietary and microbiome-based therapies to support the recovery of healthy gut commensal populations in critically ill patients.

Source: Critical Care Medicine
Image Credit: iStock

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