

METABOLOMIC BIOMARKERS OF INFLAMMATORY BOWEL DISEASE AND ITS DAMP HEAT SYNDROME IN COMPARING WITH FUNCTIONAL DIARRHEA OF CHINESE PATIENTS AND HEALTHY CONTROLS--- PRELIMINARY FINDINGS

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Poster

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Pseudotargeted metabolomics analysis of 60 IBD patients identified distinct plasma and urine metabolite profiles differentiating active IBD from healthy controls, functional diarrhea, and distinguishing traditional Chinese medicine syndrome subtypes.

KEY POINTS

- In IBD versus healthy controls, 73 plasma and 98 urine differential metabolites were identified, with increased acylcarnitines (ACar 16:1, ACar 18:1, ACar 20:4), LPC P-18:0, and malate, and decreased PC 33:3, glycocholic acid, hippuric acid, and p-cresol; L-glutamic acid, ACar 18:1, and lactic acid emerged as potential IBD diagnostic biomarkers.
- Comparing IBD to functional diarrhea, 48 plasma and 69 urine differential metabolites were found, predominantly fatty acids, acylcarnitines, aromatic amino acid metabolites, bile acids, and glycerophospholipids; ACar 6:0 and 5b-cholestane-3a,7a,12a,24,25-pentanol showed potential to differentiate organic IBD from functional diarrhea.
- Between IBD damp heat syndrome and spleen deficiency syndrome, 28 plasma and 15 urine differential metabolites were identified, with aromatic amino acids and glycerophospholipids predominating; indolelactate, tyramine, L-tryptophan, LPC 16:0-2, PC 38:7-sn1, and itaconic acid distinguished the two syndrome subtypes.
- This study recruited 60 active IBD patients, 23 functional diarrhea patients, and 30 healthy volunteers from May 2020 to July 2021, using ultra-high performance liquid chromatography-high-resolution mass spectrometry and triple-quadrupole mass spectrometry for metabolomic profiling.

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