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Summary

MULTI-OMICS BIOMARKERS FOR PREDICTING TREATMENT RESPONSE IN INFLAMMATORY BOWEL DISEASE

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Gut Microbiota | Mechanisms & Personalised Medicine | IBD

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Multi-omics profiling identified therapy-specific biomarkers predicting endoscopic response to advanced therapies in 130 IBD patients, with all markers achieving AUC greater than 0.9.

KEY POINTS

- In Crohn's disease, PDIA1 and IGHV4-28 in serum extracellular vesicles and intestinal tissue predicted anti-TNFα response, while LINC02802 and MIR567 distinguished ustekinumab responders.
- In ulcerative colitis, vedolizumab response was associated with SCIMP and CYP39A1 in intestinal tissue, and tofacitinib response with CAVN2 in serum extracellular vesicles.
- Metagenomic analysis identified genera associated with response including Prevotella and Anaerotruncus for anti-TNFα, Faecalibacterium for ustekinumab, Catenibacterium for vedolizumab, and Phascolarctobacterium for tofacitinib.
- Metabolomic profiling revealed coordinated serum and urinary alterations in amino acids, organic acids, and lipid metabolism linked to therapeutic efficacy.
- The study was a discovery-phase analysis of 58 Crohn's disease and 72 ulcerative colitis patients from 20 Spanish hospitals; validation in a larger independent cohort is required.
- The presenter emphasized that extracellular vesicles were the most promising biomarker source, being non-invasive and easier to analyse, with predictive signals found in four of five treatment groups.

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