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Summary

ANALYSIS OF INTESTINAL TISSUE FROM NEWLY DIAGNOSED PATIENTS WITH INFLAMMATORY BOWEL DISEASE REVEALS DISTINCT PROTEOMIC PROFILES

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UEG Week Copenhagen 2023 | Poster

IBD

October 15, 2023

High-throughput proteomic analysis of treatment-naive IBD intestinal tissue identified nearly 3,000 proteins and revealed dysregulated pathways including mitochondrial dysfunction, neutrophil extracellular trap signaling, and oxidative phosphorylation in Crohn's disease and ulcerative colitis.

KEY POINTS

- Analysis included 193 formalin-fixed paraffin-embedded intestinal samples from 40 active ulcerative colitis patients, 67 active Crohn's disease patients, and 46 healthy controls, all newly diagnosed before treatment.
- A total of 2,903 proteins were identified, with 1,010 differentially expressed between Crohn's disease left colon and controls, 1,242 between ulcerative colitis left colon and controls, and 956 between Crohn's disease ileum and controls.
- Pathway analysis revealed alterations in EIF2 signaling, mitochondrial dysfunction, oxidative phosphorylation, neutrophil extracellular trap signaling, fatty acid oxidation, sirtuin signaling, and tRNA charging depending on disease type and gut location.
- The results serve as a starting point for hypotheses to understand IBD pathogenesis and search for therapeutic targets.

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