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Summary

FECAL MICROBIOTA SIGNATURES ARE ASSOCIATED WITH DISEASE SEVERITY AND LOCATION IN INFLAMMATORY BOWEL DISEASE

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IBD

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Analysis of 1,417 IBD patients from the SPARC IBD cohort reveals distinct stool microbiome signatures associated with disease activity and anatomic location in Crohn's disease and ulcerative colitis.

KEY POINTS

- Oral commensals including Veillonella, Klebsiella, Rothia, and Megasphaera were enriched in patients with active disease in both CD and UC, while 21 genera including butyrate-producing species such as Anaerostipes, Ruthenibacterium, Faecalibacterium and Roseburia were more abundant in patients with inactive disease.
- In CD, 32 of 33 disease-specific genera showed differential enrichment by disease location (ileal, colonic, or ileocolonic), suggesting location-specific pathologies.
- UC-specific active disease signatures included enrichment of Escherichia, Haemophilus, and Anaerococcus, while inactive disease was associated with Lactococcus, Proteobacteria_unclassified, Parasutterella, and Gemella.
- The cohort comprised 926 CD and 491 UC patients, predominantly Caucasian females, with approximately 70% in remission; among CD patients with location data, 83% had ileal involvement.

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