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Summary

MUCOSA-ASSOCIATED MICROBIAL SIGNATURES DISCRIMINATE RESPONSE TO BIOLOGICALS IN CROHN'S DISEASE

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Prospective study of 117 Crohn's disease patients identified distinct mucosal microbiome signatures in colon and ileum biopsies that discriminate responders from non-responders to three classes of biological therapies prior to treatment initiation.

KEY POINTS

- Colonic biopsies from 117 CD patients and ileal biopsies from 107 patients were collected at baseline before starting anti-TNF, vedolizumab, or ustekinumab treatment, with response defined by endoscopic improvement (≥50% SES-CD reduction), steroid-free clinical response, and/or biochemical response.
- In the anti-TNF cohort, responders showed significantly higher alpha diversity and species richness in colonic biopsies, with 13 genera more abundant and 4 genera less abundant compared to non-responders, while vedolizumab and ustekinumab cohorts showed no significant diversity differences but revealed 10 and 15 discriminatory genera respectively.
- Analysis established three categories of microbial signatures: treatment-specific genera (discriminatory for one biological only), treatment-aspecific response supporters (discriminatory across at least two biologicals with shared direction), and treatment-drivers (discriminatory across cohorts with contradicting direction), with patterns distinct between ileum and colon.
- Ileal biopsies showed no baseline diversity differences between responders and non-responders across cohorts, but genus-level analysis identified 14, 25, and 13 discriminatory genera in anti-TNF, vedolizumab, and ustekinumab cohorts respectively.

– The authors suggest that microbial evaluation of these taxa could support treatment selection decisions, and note that amplicon sequence variant-level modeling is underway to address species-level differences within genera.

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