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Summary

MULTI-COHORT CROSS-DISEASE METAGENOMIC ANALYSIS OF IMMUNE-MEDIATED INFLAMMATORY DISEASES IDENTIFIES SHARED OR UNIQUE GUT MICROBIAL SIGNATURES AND THEIR POTENTIAL CLINICAL IMPLICATIONS IN INFLAMMATORY BOWEL DISEASE

Jongsik Chun

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Digestive Oncology | Gut Microbiota | IBD

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Multi-cohort gut metagenome analysis of 2,252 samples across six immune-mediated inflammatory diseases identified both shared and disease-specific microbial signatures, with trained models achieving an average AUC of 0.818 in external IBD validation.

KEY POINTS

- Cross-cohort validation showed significantly higher prediction performance within the same disease (W=23278, p<0.001) than across diseases, though inter-disease prediction remained comparable, suggesting both shared and disease-specific gut microbiome contributions to IMIDs.
- Several bacterial features were commonly enriched across at least five IMIDs, including Enterocloster bolteae and pyridine nucleotide-disulfide oxidoreductase (K21739) in cases, and Faecalibacterium sp. and Oscillibacter sp. in controls.
- IBD-specific control-enriched signatures included Gemmiger formicilis and Alistipes shahii, which were not consistently enriched in non-gastrointestinal IMIDs such as MS, AS, COPD, and PsO.
- Dysosmobacter welbionis showed negative correlation with Harvey Bradshaw Index in two CD sub-cohorts (Spearman's rho=-0.5 and -0.26, p=0.009 and 0.039), suggesting potential clinical relevance for disease activity monitoring.

– The study used uniform taxonomic and functional profiling across 28 discovery case-control sub-cohorts (10 CD, 9 UC, 4 AS, 2 COPD, 2 MS, 1 PsO) and validated findings in 253 external IBD samples from seven sub-cohorts.

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