

Microbiome: From IBS and the Gut-Brain Axis to IBD Outcomes

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The speakers presented evidence that Western lifestyle-driven changes in gut microbial auxotrophy and tryptophan metabolism link microbiome alterations to both IBS and IBD, with emerging diagnostic and therapeutic implications through metabolite analysis.

KEY POINTS

- The speakers reported that in twin studies using 16S RNA analysis, age and sharing a household were the most important factors determining microbial composition, more so than host genetics.
- Higher microbial auxotrophy (inability to synthesize essential compounds like amino acids) correlated with less industrialized microbiomes, and the speakers stated that tryptophan auxotrophs were dramatically reduced in IBD cohorts.
- Combining microbiome and metabolome analysis provided higher discrimination for IBS versus healthy controls than either method alone, according to studies from the speakers' colleagues in Maastricht.
- The speakers described enterochromaffin cells with neuropods, recently discovered structures that form synapse-like connections with nerve endings and can transduce microbial signals like flagellin into vagal neuron stimulation affecting feeding behavior in mice.
- Fecal volatile organic compound analysis differentiated IBS phenotypes and predicted response to low-FODMAP diet in work by Chris Broberg's group, as stated by the speakers.
- The speakers noted that while systematic reviews show probiotics have a positive effect above placebo in IBS, the effect is small and most studies have not been reproduced, limiting evidence-based recommendations for specific formulations.

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