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Summary

MUCOSA-ASSOCIATED COLLAGENOUS COLITIS MICROBIOTA IN-DEPTH ANALYSIS IDENTIFIES POTENTIAL DISEASE TRIGGERS

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Shotgun metagenomic analysis of subepithelial mucosa in collagenous colitis found overall microbial similarity to healthy controls but identified specific bacterial associations including biofilm-forming Anoxybacillus and Barnesiella in disease samples.

KEY POINTS

- Laser microdissection was used to isolate subepithelial mucosa from formalin-fixed paraffin-embedded samples of collagenous colitis patients (n=7-10) and healthy controls for shotgun metagenomic sequencing.
- Bray-Curtis and Jaccard similarity coefficients showed that collagenous colitis subepithelial microbiome was similar to healthy controls, though microbial metabolic pathways and molecular functions could differ.
- Microbiota associated with collagenous colitis included Anoxybacillus and Barnesiella, while healthy controls were associated with Bacteroides, Leuconostoc, and Lactobacillus.
- The authors suggest their results point to a relation of collagenous colitis with biofilm-forming bacteria (Anoxybacillus) and bacteria affecting colitis development variability (Barnesiella), requiring validation and follow-up.
- This work may interest researchers investigating microbial triggers in microscopic colitis and mucosal microbiome analysis methods.

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