

ANALYSIS OF MICROBIOTA CHANGES IN DIFFERENT SEGMENTS OF THE COLON AND TERMINAL ILEUM IN MICROSCOPIC COLITIS

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Mucosa-associated microbiome profiling in microscopic colitis reveals distinct bacterial signatures in collagenous colitis (CC) and lymphocytic colitis (LC), with microbiome composition at baseline predicting budesonide response and disease behaviour in CC but not LC.

KEY POINTS

- Study included 20 CC patients, 20 LC patients, and 50 controls undergoing 16S rRNA sequencing of biopsies from terminal ileum and six colonic segments.
- CC showed consistent alterations in three bacterial families throughout the colon (Erysipelatoclostridiaceae and Coriobacteriaceae decreased, Pasteurellaceae increased), plus 35 families with segment-specific changes and 25 families altered in the terminal ileum.
- LC exhibited consistent increase in Erysipelotrichaceae across the colon, with 38 families showing segmental changes and 12 families altered in the terminal ileum; LC showed lower abundance across many families compared to CC, particularly in the right colon and terminal ileum.
- In CC, incomplete response to budesonide (3 of 15 treated patients) was associated with increased abundance of genus Paucibacter and significant differences in beta diversity in the ascending and left colon.
- CC patients with relapsing or chronic active disease (13 of 20) showed significant beta diversity differences in transverse, descending colon and rectum, with medium correlation in the descending colon, while no significant microbiota-disease behaviour correlation was observed in LC.
- Bacterial alterations in both CC and LC were not consistent throughout the colon but varied between different colonic segments.

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