

FECAL MICROBIOME COMPOSITION IN ACTIVE ULCERATIVE COLITIS IS ASSOCIATED WITH LABORATORY FINDINGS AND CAN PREDICT DISEASE SEVERITY

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In 108 patients with active ulcerative colitis, blood haemoglobin levels were the most prominent factor associated with gut microbial composition, and *Blautia* abundance negatively correlated with disease severity.

KEY POINTS

- Blood haemoglobin levels, serum albumin levels and antibiotic intake were the strongest factors influencing alpha diversity in the multivariate model
- Blood haemoglobin levels and aminosalicylate intake were the main influencing factors for beta diversity
- Nine genera including *Blautia*, *Enterococcus*, *Alistipes*, *Coprococcus*, *Dorea*, *Fusicatenibacter*, *Parasutterella*, *Eubacterium hallii* group, and *Ruminococcus torques* group were most strongly associated with blood haemoglobin levels
- Aminosalicylate intake was associated with increased relative abundance of butyrate-producing genera *Bifidobacterium* and *Blautia*
- *Blautia* abundance negatively correlated with fecal calprotectin and CRP and predicted disease severity according to the Truelove and Witts score with an AUC of 0.81

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