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Gut microbiome composition and its association with dietary factors in Crohn's disease

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Introduction: The gut microbiota plays a crucial role in the pathogenesis and progression of Crohn’s Disease (CD) by maintaining intestinal homeostasis, supporting metabolic and immune functions, and influencing overall health. An imbalance in the gut microbiota is associated with CD, as disruptions in microbial composition can be further impacted by dietary factors, highlighting the connection between nutrition and gut health. **Aim:** This study aimed to evaluate the gut microbiota composition and its interactions with dietary factors to identify potential opportunities for targeted probiotic interventions in CD management. **Methods:** The study included 53 participants, of whom 20 had CD in remission, 18 had active disease, and 15 were healthy controls. CD activity was evaluated by colonoscopy assessment or by nuclear magnetic resonance scan enterography. All participants aged between 18 and 60 years were assessed using 24-hour dietary recall and gut microbiome profiling through 16S rRNA gene sequencing. Patients had confirmed diagnoses of CD with ileal and/or colonic involvement. The local ethics committee approved this study. **Results:** Microbial composition analyses (beta diversity) revealed significant differences between groups. At the Operational Taxonomic Unit (OTU) level, healthy microbiome differed significantly from both remission and active CD patients, with healthy controls showing a more similar microbial composition compared to remission ($p = 0.001$) and active disease ($p = 0.001$). In addition, Shannon diversity analyses demonstrated that healthy individuals exhibited significantly higher OTU diversity compared to CD patients, further highlighting the microbial imbalance associated with the disease. Among specific taxa, *Eubacterium hallii*, a key butyrate producer, was significantly reduced in patients with active CD. This microorganism is integral to intestinal metabolic balance, playing essential roles in energy homeostasis, colonic motility, immunomodulation, and inflammation suppression. Furthermore, *E. hallii* plays a critical role in bile acid and cholesterol metabolism, highlighting its importance in gut health. Disease severity was associated with changes in microbial abundance, with specific taxa colonizing the gut at higher levels as disease activity increased, including *Escherichia coli*, *Escherichia-Shigella*, and taxa from the *Enterobacteriaceae*, *Lachnospirales*, and *Bacteroides*. This growth may be linked to inflammatory processes and intestinal dysbiosis, suggesting a potentially pathogenic role. Furthermore, dietary components such as saccharin, an artificial sweetener, were significantly associated with alterations in microbial composition. **Conclusions:** These findings underline the potential for probiotics targeting specific taxa, such as *E. hallii*, to restore microbial balance and improve clinical outcomes in CD. The study also highlights the impact of dietary components, such as saccharin, in disrupting the gut microbiome, suggesting that certain dietary factors may contribute to microbial imbalance and inflammation in CD. Future research should focus on integrating dietary patterns with probiotic development to optimize gut health and mitigate inflammation in CD patients.

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