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Comparing pathogenic signatures of inflammatory bowel disease with enterotype-specific microbial network changes

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Inflammatory bowel disease (IBD) is a chronic inflammatory disorder driven by complex interactions among genetic, environmental, dietary, and immunological factors, with gut microbiome dysbiosis playing a critical role. Microorganisms assemble into communities that form intricate interaction networks, and characterizing how network structures change is critical for uncovering IBD pathogenesis and identifying therapeutic targets. In this study, we analyzed the gut microbiome of healthy controls, at-risk individuals, and IBD patients to investigate disease-associated alterations in microbial interaction networks. Using dimensionality reduction (t-SNE) and clustering, we identified four distinct enterotypes with differing proportions of IBD patients, and then inferred microbial interaction networks using FastSpar. The enterotype with the lowest proportion of IBD patients exhibited a healthy-like network, characterized by greater microbial richness and denser interactions. In contrast, enterotypes enriched with IBD patients showed reduced microbial diversity and simplified network structures; notably, patients with this enterotype exhibited poorer clinical outcomes. These results suggest that alterations in microbial interaction networks are associated with IBD and that stratifying patients by enterotype may provide novel insights into disease etiology and guide the development of personalized therapeutic strategies.