Unraveling microbial dynamics in inflammatory bowel diseases

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Inflammatory bowel diseases (IBD), comprising Crohn's disease (CD), ulcerative colitis (UC), and pouchitis, are complex conditions influenced by genetic, environmental, immunological, and microbial factors. Patients with complicated and severe UC that do not respond to medications undergo complete large bowel resection with pouch reconstruction using a healthy small bowel segment. In many of these patients, inflammation of the pouch (pouchitis) later develops, manifesting as recurrent cycles of inflammation (flares) and remission. We tracked fecal metagenomic data from 16 patients with pouchitis, during an inflammatory flare, immediately followed by antibiotic treatment, and throughout a year of follow-up, during which some patients experienced additional flares. Since *E. coli* is considered a potentially harmful agent in IBD, we also isolated *E. coli* strains from a subset of fecal samples and obtained their complete genomes including their plasmid profile.
Genomic analysis revealed that subsets of *E. coli* were associated with disease flares in a patient-specific manner. Moreover, the analysis showed that multiple *E. coli* strains coexist in most samples. Some strains persisted over time while others were quickly replaced by different ones. Notably, plasmids acquired by several strains during the pouchitis follow-up exhibited diverse profiles, contributing to microbiome variability.

Through this research, we aim to elucidate the causative factors driving inflammation in pouchitis, thereby advancing our understanding of disease pathogenesis and informing potential therapeutic interventions.