

Summary: Compositional and Temporal Changes in the Gut Microbiome of Pediatric Ulcerative Colitis Patients Are Linked to Disease Course (Schirmer, et.al)

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The incidence of Inflammatory Bowel Disease (IBD) is quickly rising, though despite the prevalence of disease, treatment options for patients are limited. Our current approach to treatment consists of pharmacologic immunosuppression, which is often only partially effective, or surgical removal of diseased portions of the intestine. These interventions often come with significant comorbidities for the patient, and are poorly tailored to their individual disease phenotypes as we still struggle to understand the pathophysiology of IBD.

The current research and future of IBD treatment is focused on understanding the interplay between the gut microbiome and the development and progression of disease. Research has consistently demonstrated how the microbiomes of IBD patients are less diverse compared to healthy control, and lack populations of protective, healthy bacteria. We have yet to understand, however, exactly how this dysbiosis of intestinal bacteria contributes to disease progression, and subsequently how it can be harnessed for treatment.

A new study, published in *Cell Host & Microbe* by Schirmer et.al., brings us one step closer to the future of a more tailored, elegant approach to IBD therapeutics. Investigators looked at pediatric patients diagnosed with Ulcerative Colitis (UC), a form of IBD, to understand the correlation between disease severity and microbiome characteristics, and how this changes over time with treatment. More specifically, researchers followed a population of newly diagnosed, treatment-naïve children, treated with one of two immunosuppression regimens (corticosteroids or 5-ASA), and monitored changes in fecal microbial populations and disease progression. They collected stool samples and tissue biopsies before, during, and after treatment over the course of a year.

During their investigation, researchers uncovered several important associations between microbiome characteristics, disease severity, and response to treatment. In the pre-treatment population, they found that disease severity correlated with increased populations of oral cavity bacteria (that do not typically colonize the intestine) and depleted populations of protective, commensal bacteria (such as Ruminococcaceae and Lachnospiraceae species). Several of these disease-associated microbiome characteristics, furthermore, were predictive of refractory disease and seen in patients who ultimately required colectomy for treatment. In patients who did respond to medical therapy, the investigators observed similar changes in microbiome characteristics over time in both treatment arms, challenging prior research that suggested treatment response was highly individualized. These findings provided an important step forward in predicting individual prognosis and response to treatment based on pre-treatment microbiome characteristics.