Baseline and Longitudinal Microbial Changes Predict Response to Rifaximin and/or Diet Low in Fermentable Oligosaccharides, Disaccharides, Monosaccharides, and Polyols in Irritable Bowel Syndrome

INTRODUCTION: Diarrhea-predominant irritable bowel syndrome (IBS-D) is a chronic, disabling condition. Treatments for IBS-D, including rifaximin, a nonabsorbable antibiotic, and a diet low in fermentable oligosaccharides, disaccharides, monosaccharides, and polyols (FODMAP), improve symptoms in ≤50% of patients. We hypothesized that changes in the gut microbiota predict response to treatment for IBS-D.

METHODS: We randomized 17 subjects meeting Rome IV criteria for IBS-D to receive either rifaximin (550 mg three times daily for 14 days) or a low FODMAP diet for 4 weeks. The primary outcome was proportion of responders to intervention defined by ≥30% improvement in mean daily abdominal pain or bloating scores. The secondary outcome was ≥50% point decrease in IBS-Symptom Scoring (IBS-SSS) compared with baseline. Fecal samples were collected at baseline and 2, 4, and 5 weeks. The microbial community in these specimens was characterized by 16S rRNA encoding gene sequence analysis.

RESULTS: There were 6 subjects (60%) in the rifaximin group and 4 subjects (57.1%) in the low FODMAP group. In the rifaximin group, there were significant improvements in abdominal pain (P = 0.03), bloating (P = 0.02), and IBS-SSS (P = 0.009) compared with baseline. In the low FODMAP group, there was improvement in IBS-SSS only (P = 0.06) at the end of treatment. Responders to treatment had unique inter- and intra-individual temporal characteristics compared with non-responders. Responders to rifaximin and low FODMAP diet showed a distinct microbial community structure at baseline. Many microbiome features at baseline predict response to treatment. Longitudinal analyses show responders have a more resilient community structure to either rifaximin or dietary modification compared with non-responders. The functional significance of these microbial changes in responders vs. non-responders is unclear, but may be the focus of future studies.

Figure 1. Responders to Therapy Demonstrate Differences in Fecal Microbial Community Structure Compared with Non-Responders

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