

## Fecal Microbial Transplants Reduce Antibiotic-resistant Genes in Patients With Recurrent *Clostridium difficile* Infection

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### Abstract

**Background.** Recurrent *Clostridium difficile* infection (RCDI) is associated with repeated antibiotic treatment and the enhanced growth of antibiotic-resistant microbes. This study tested the hypothesis that patients with RCDI would harbor large numbers of antibiotic-resistant microbes and that fecal microbiota transplantation (FMT) would reduce the number of antibiotic-resistant genes.

**Methods.** In a single center study, patients with RCDI (n = 20) received FMT from universal donors via colonoscopy. Stool samples were collected from donors (n = 3) and patients prior to and following FMT. DNA was extracted and shotgun metagenomics performed. Results as well as assembled libraries from a healthy cohort (n = 87) obtained from the Human Microbiome Project were aligned against the NCBI bacterial taxonomy database and the Comprehensive Antibiotic Resistance Database. Results were corroborated through a DNA microarray containing 354 antibiotic resistance (ABR) genes.

**Results.** RCDI patients had a greater number and diversity of ABR genes compared with donors and healthy controls. Beta-lactam, multidrug efflux pumps, fluoroquinolone, and antibiotic inactivation ABR genes were increased in RCDI patients, although donors primarily had tetracycline resistance. RCDI patients were dominated by Proteobacteria with *Escherichia coli* and *Klebsiella* most prevalent. FMT resulted in a resolution of symptoms that correlated directly with a decreased number and diversity of ABR genes and increased Bacteroidetes and Firmicutes with reduced Proteobacteria. ABR gene profiles were maintained in recipients for up to a year following FMT.

**Conclusions.** RCDI patients have increased numbers of antibiotic-resistant organisms. FMT is effective in the eradication of pathogenic antibiotic-resistant organisms and elimination of ABR genes.