

CHARACTERISTICS OF PATIENTS UNDERGOING FECAL MICROBIOTA TRANSPLANTATION FOR CLOSTRIDIUM DIFFICILE INFECTION: ONE INSTITUTION'S STORY

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**Background:** *Clostridium difficile* infection (CDI) accounts for 20%-30% of cases of antibiotic-associated diarrhea and is the most commonly recognized cause of infectious diarrhea in healthcare settings. Based on previous experience at our institution, fecal microbiota transplantation (FMT) represents an effective therapeutic option for the treatment of recurrent CDI, with worldwide cure rates reported as high as 93%. It is generally safe and well tolerated by most patients and has applicability for patients with mild to complicated disease and appears to be useful even in high-risk populations. Our hope is that one institution's experience can elucidate potential clinically relevant risk factors that present a common theme among our 106 patients that have undergone the procedure thus far. **Methods:** We performed a retrospective chart review of selected patient data on the 106 patients that have undergone FMT at Ochsner Clinic Foundation from August 2012 to February 2016. **Results:** FMT was performed in 106 CDI patients. The 83 female and 23 male patients ranged in age from 17 to 94 years (mean 61 years), with 93 (88%) Caucasian patients, 10 (9%) African Americans, 2 (2%) Hispanic patients, and 1 (1%) Asian patient. One hundred patients (94%) had FMT done for recurrent CDI and 6 (6%) patients had severe/complicated CDI, with African Americans accounting for 2 of the 6 patients. In our 3.5 years performing the procedure we have repeated FMT in 4 patients for recurrence. Forty (38%) patients had undergone prior cholecystectomy. Seventy five (71%) patients had antibiotic use prior to their first CDI episode. At least 49 (46%) of our patients were on PPIs or H2 blockers, with 4 of these patients on both. Of the 21 (20%) patients considered immunosuppressed, 12 (11%) were on corticosteroid therapy and 6 (6%) were organ transplant recipients. The average distance traveled by our patients to receive FMT was 90 miles (range 3 - 463 miles). We had 78 patients (74%) that had to travel > 40 miles to undergo the procedure and 57 patients (54%) that traveled > 80 miles. **Conclusions:** Based on our experience, Caucasians, older adults, and women had a higher incidence of recurrent CDI and African Americans had a higher proportion of severe/complicated CDI with a greater number of risk factors overall in the patients observed. The small number of patients requiring repeat FMT each had unique clinical scenarios with several risk factors for recurrent disease. Similar to other studies we noted a high rate of antibiotic use and acid suppression therapy. Of interest, we report a significantly elevated cholecystectomy rate compared to national data, however this finding merits further inquiry. Finally, given the overall success of treatment and significant travel burden apparent in our population, increased access to this valuable treatment option is essential.

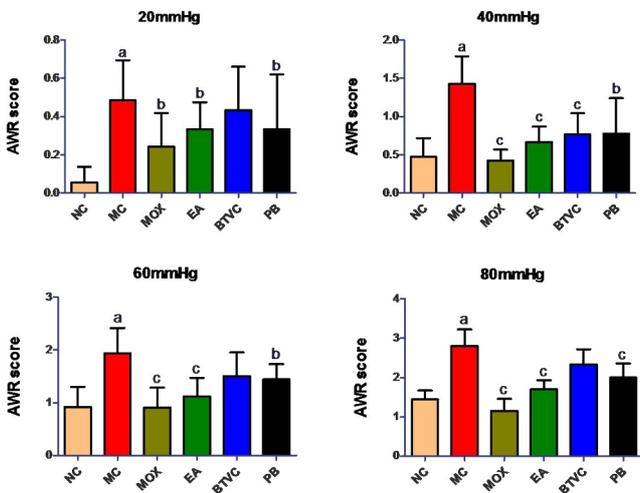


Fig. 1 AWR scores by treatment group (M, Q<sub>25</sub>-Q<sub>75</sub>). <sup>a</sup>P < 0.01, versus normal group; <sup>b</sup>P < 0.05, <sup>c</sup>P < 0.01, versus model group. NC: normal group; MC: IBS model group; MOX: moxibustion group; EA: electroacupuncture group; BTVC: Bifid-triple Viable Capsule group; PB: Pinaverium Bromide group.

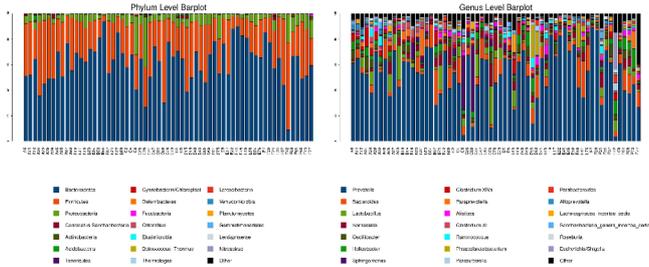


Fig. 2 Microbiota comparison at phylum and genus level. A: normal group; B: IBS model group; C: moxibustion group; D: electroacupuncture group; E: Bifid-triple Viable Capsule group; F: Pinaverium Bromide group.

Su2027

THE INFLUENCE OF HELICOBACTER PYLORI ERADICATION THERAPY ON INTESTINAL MICROBIOTA

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*H. pylori* eradication therapy including antibiotics as well as *H. pylori* itself can influence the normal intestinal microbiota content. The aim of the study was to describe the gut microbiota composition in *H. pylori*-positive and *H. pylori*-negative patients as well as the influence of eradication therapy on gut microbiota. 198 stool samples were taken for analysis: 74 samples from *H. pylori*-positive patients before eradication therapy, 74 - from the same patients after eradication, 50 - from *H. pylori*-negative patients (control group). Total DNA was isolated from the stool samples and subjected to whole-genome sequencing on SOLiD 5500 Wildfire platform. Intestinal microbiota was evaluated based on number of species, qualitative composition, Shannon diversity index and Bray-Curtis metrics. **Results.** Bacterial community was quite similar in all groups: *Bacteroides*, *Prevotella*, *Eubacterium*, *Roseburia*, *Faecalibacterium* and *Clostridium* genera were predominant in all samples. The spread in variations of the prevailing Firmicutes and Bacteroides phyla was wider after the treatment than in control samples. In about half of patients eradication therapy led to the decrease of both the number of species and the Shannon index indicating a decrease in the overall bacterial diversity with a possible predominance of individual species. Eradication therapy resulted in the reduction of the relative representation of *Bifidobacterium*, *Collinsella*, *Coprococcus* genera, accompanied with the increase of *Clostridium*, *Bacteroides*, *Coprobacillus* and *Flavonifractor* genera. Evaluation of taxonomic diversity changes based on Shannon index and Bray-Curtis metrics allows to differentiate patients into the groups with mild, moderate and severe changes. In 82% of cases mild and moderate changes in microbial community content were found - increased level of *Bacteroides* genus, decreasing levels of *Bifidobacterium* and *Eubacterium* genus, simultaneously. *Escherichia* genus had the increased abundance in the majority of patients with severe microbial shifts after eradication therapy. Changes in the composition of intestinal microbiota after *H. pylori* eradication therapy depend mostly on the initial content of the intestinal microbiota: the closer initial microbial state of *H. pylori*-positive patients to the control samples is, the milder changes could be detected after eradication therapy. Gene-centric analysis of the functional composition in paired samples taken before and after therapy showed an increase of the relative abundance of genes conferring antibiotic resistance. **Conclusions.** Evaluation of intestinal microflora content prior to treatment can probably predict the incidence of side effects related to changes in microbial composition. This work was financially supported by the Ministry of Education and Science of Russian Federation (agreement #14.575.21.0076, ID RFMEFI571514X0076).

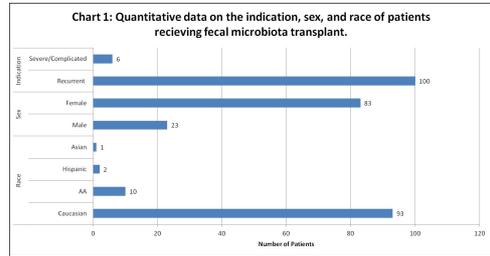


Chart 1: Quantitative data on the indication, sex, and race of patients receiving fecal microbiota transplant.

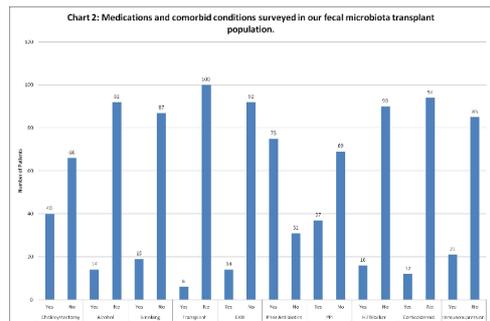


Chart 2: Medications and comorbid conditions surveyed in our fecal microbiota transplant population.

Su2029

EFFECTS OF LIRAGLUTIDE ON GASTRIC EMPTYING, GASTRIC ACCOMMODATION, SATIATION AND SATIETY AFTER 16 WEEKS' TREATMENT: A SINGLE-CENTER, RANDOMIZED, PLACEBO-CONTROLLED TRIAL IN 32 PATIENTS

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**Background:** We previously showed that a short-acting GLP-1 agonist, exenatide, 5µg, SQ, BID, for 30 days, delays gastric emptying and induces weight loss (PMID: 26542264). Gastric emptying was delayed after 3 weeks of treatment with the long-acting GLP-1 agonist, liraglutide, escalated to 1.8mg/day, but not delayed after 24 weeks' treatment (PMID: