with IBS who were not responsive to traditional treatment and who underwent FMT between October 2011 and October 2012 were identified. Diagnosis of IBS was based on Rome III Criteria and nonresponsive IBS was defined as failure to achieve symptomatic relief with dietary changes, antidepressants, probiotics, antibiotics, or other therapeutic modalities.

Donors were chosen by the FMT recipient and were screened in accordance with current recommendations (5). A fecal suspension of 50–100 ml was infused into the distal duodenum or proximal jejunum by esophagogastroduodenoscopy in all patients. A 41-item questionnaire soliciting demographic and pre- and post-FMT data were administered; study outcomes included the length of symptom-free intervals, abdominal pain, bloating, flatus, dyspepsia, frequency of bowel movements, and overall well-being before and after FMT.

A total of 13 patients (mean age of 45 years; 54% female) were identified and completed the study questionnaire. Of these patients, nine had diarrhea-predominant IBS, three had constipation-predominant IBS, and one had mixed IBS. Mean time from initial diagnosis of IBS until FMT was 73 months, and mean time between FMT and data collection was 11 months.

In our study, 70% of the patients experienced resolution or improvement of symptoms after FMT, specifically those with abdominal pain (72%), dyspepsia (67%), bloating (50%), and flatus (45%). A long-term treatment goal in patients with IBS is improvement of overall well-being, which was achieved in nearly half of our patients (46%). The only adverse event reported was a transient increase in flatus; there were no long-term side effects, and none of the participants developed any new diseases.

Limitations of our study include its retrospective design, small sample size, and use of a questionnaire that had not previously been validated. Future studies should comprise prospective, randomized controlled trials and fecal microbiome analyses before and after FMT. This pilot study suggests that FMT may be beneficial for the treatment of IBS and calls for carefully designed studies to support or refute our findings.

CONFLICT OF INTEREST

Dr Brandt is a consultant for CIPAC.

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[1]Beth Israel Medical Center, New York City, New York, USA; [2]Division of Gastroenterology, Montefiore Medical Center, New York City, New York, USA. Correspondence: Lawrence J. Brandt, MD, MACG, Division of Gastroenterology, Montefiore Medical Center, 111 East 210th Street, Bronx, New York, New York 10467, USA. E-mail: lbrandt@montefiore.org

Therapeutic Modulation and Reestablishment of the Intestinal Microbiota With Fecal Microbiota Transplantation Resolves Sepsis and Diarrhea in a Patient

Qiurong Li, MD, PhD[1], Chenyang Wang, MA[1], Chun Tang, BA[1], Qin He, MA[1], Xiaofan Zhao, BA[1], Ning Li, MD[1] and Jieshou Li, MD[1]

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To the Editor: We read with great interest the article regarding the therapeutic value of fecal microbiota transplantation (FMT) in ulcerative colitis (1). FMT has emerged as an accepted treatment for recurrent *Clostridium difficile*-associated diarrhea (2–4). It represents a therapeutic protocol that allows reconstitution of a normal composition of gut microbial community. Dysbiosis of gut microbiota is probably relevant for the etiology of sepsis, raising an interesting possibility of microbiota-targeted therapy in these cases. Here, we describe the case of a sepsis patient with severe diarrhea who received FMT and report findings.

A 29-year-old woman was admitted to our hospital because of high fever and uncontrollable watery diarrhea. The patient was diagnosed with ulcerative colitis and underwent a colectomy in November 2010. She subsequently developed intermittent diarrhea and thus antibiotics, including cefradine or ornidazole, were discontinuously administered for 2 years after the colectomy. On admission, the temperature was 39.3 °C, the pulse 118, the respirations 23, and the blood pressure 79/55 mm Hg. Laboratory results showed white-cell count 2900/mm^3, blood lactate 3.2 mmol/l, prothrombin time 17.9 s, activated partial thromboplastin time 44.5 s, and platelets 68,000/mm^3. An analysis of arterial blood gas revealed a pH of 7.365, a partial pressure of oxygen of 92.8 mm Hg, and of carbon dioxide of 23.8 mm Hg; the base excess was −6.7 mmol/l. The findings were compatible with clinical signs of septic shock, and supportive intensive care plus intravenous antibiotics were given. Blood cultures were negative until 7 days, when yielded *Acinetobacter baumannii*. Despite 20-day interventions with antibiotics, probiotics, and supportive strategies, the fever and diarrhea failed to improve. Considering the possibility of intestinal dysbiosis, we applied 16S rRNA gene-based molecular techniques to characterize the fecal bacterial composition of the patient. We showed that the microbiota was extensively disturbed, characterized by a profound deficiency of the commensals in Firmicutes and Bacteroidetes and by an overgrowth of opportunistic organisms in Proteobacteria, especially *Enterobacter cloacae*, *Enterobacteriaceae bacterium*, *Klebsiella pneumoniae* and *Alpha proteobacterium* (**Figure 1**). The findings led to the decision to correct the imbalance *via* FMT. We administered a suspension of donor feces through a

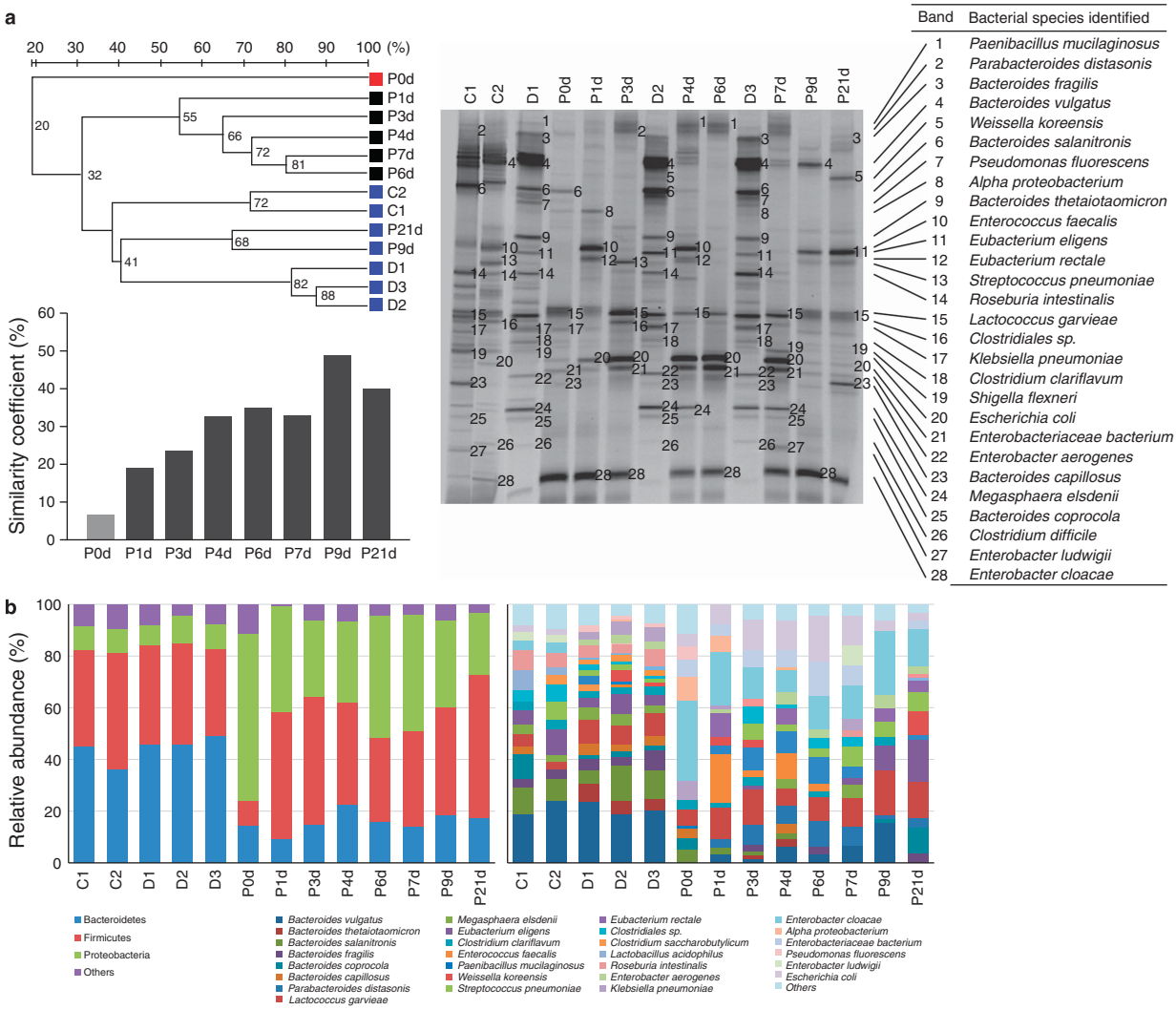

Figure 1. Molecular characterization of the fecal bacterial microbiotas. (**a**) Analysis of the fecal microbiotas by denaturing gradient gel electrophoresis (DGGE). Right panel: representative fingerprints of the fecal microbiotas. The profiles are generated from DGGE analyses of 16S rRNA gene fragments with universal V3 region-targeted primers. The numbers 1 to 28 represent the bands for DNA sequencing, and the bacterial species identified are shown in the right panel. Upper left: clustering dendrogram based on the profiles. The scale bar indicates similarity (%). Lower left: shifts of bacterial community similarities compared with the donor. Similarity indices between samples were represented by the Dice coefficient. The data presented here indicate the mean values of the similarity values between the patient and the donor (D1, D2, and D3). (**b**) Variations of the predominant bacterial composition in the fecal microbiotas. Left panel: the phylum level; right panel: the species level. The relative intensity of each band is expressed as a proportion (%) of the sum of all fragments in the same lane of the gel. P0d, P1d, P3d, P4d, P6d, P7d, P9d, and P21d represent the samples collected from the patient at 0, 1, 3, 4, 6, 7, 9, and 21 days. C and D indicate the samples from healthy controls and the donor.

nasoduodenal tube and withdrew antibiotics. In the next day, the fever went down, and the stool output had a marked reduction. Blood cultures became sterile. At 21 days, the stool volume ultimately declined to less than half of pre-FMT. Significantly, the patient's microbiota with a very low similarity (6.5%) shifted toward a donor-like microbial pattern following FMT (**Figure 1a**). The bacterial species in Firmicutes and Bacteroidetes, including *Eubacterium spp.*, *Lactococcus garvieae*, *Weissella koreensis*, and *Bacteroides spp.*, were remarkably expanded, whereas opportunistic organisms in Proteobacteria were significantly depleted (**Figure 1b**). Interestingly, specific FMT-induced alterations in gut microbiotas were associated with clinical benefits (**Figure 2**). On the basis of data, we reasoned that FMT could counterbalance dysbiosis, induce recovery of gut microbial barrier, and aid in the treatment of sepsis.

In conclusion, we report our initial experience of treating sepsis with FMT. The dysbiosis of intestinal micobiota in the patient is defined, providing potentially useful diagnostic indicators for microbiota-based therapeutic intervention. The patient benefits from the unconventional approach, which is, at least in part, due to FMT being able to facilitate the reestablishment of normal microbiota. This is the first description of FMT as a potentially

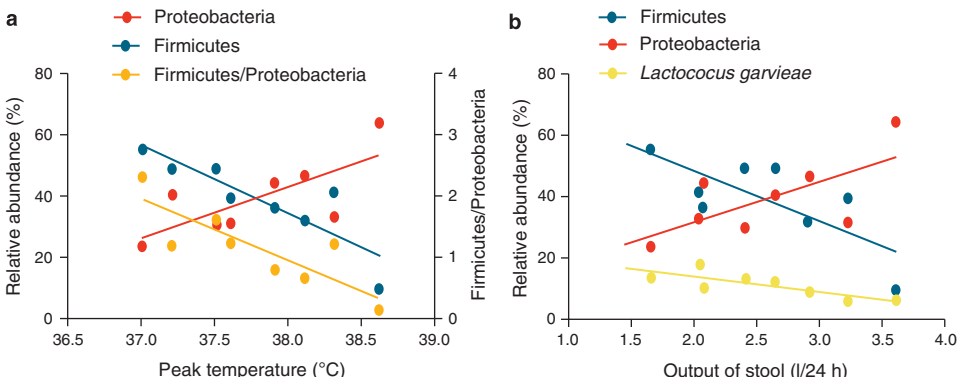

Figure 2. Correlative analyses between specific bacterial phylogroups and clinical features. (**a**) Correlations of the relative proportion of Firmicutes (blue), Proteobacteria (red), and the ratio Firmicutes/Proteobacteria (orange) with daily peak temperature of the patient. (**b**) The relationship between specific bacterial taxas and stool volume each day. The phylum Firmicutes (blue) and the species *Lactococcus garvieae* (yellow) show strong correlation with the output of stools in the patient, whereas Proteobacteria shows a weak association with it (red).

therapeutic alternative for sepsis and provides a wonderful example of using the cutting-edge technique into clinical practice. Although the donor stool is tested negative to minimize the risk, transmission of potentially pathogenic organisms to the patient may exist. Future studies with a larger number of patients are required to validate the efficacy and safety of the procedure in sepsis and also toward broader clinical use.

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CONFLICT OF INTEREST

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Specific author contribution: Qiurong Li and Jieshou Li conceived and designed the study. Chenyang Wang, Chun Tang, Qin He, and Xiaofan Zhao performed the experiments. Ning Li contributed to interpretation of data. Qiurong Li and Chenyang Wang analyzed data and wrote the manuscript. All of the authors have approved the final draft submitted.
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[1]Jinling Hospital, Research Institute of General Surgery, Nanjing University School of Medicine, Nanjing, China. Correspondence: Qiurong Li, MD, PhD, or Jieshou Li, MD, Jinling Hospital, Research Institute of General Surgery, Nanjing University School of Medicine, No. 305 East Zhongshan Road, Nanjing 210002, China. E-mail: liqiurongjue@126.com or lijieshounj@163.com

Evaluation of TNM Status Changes Between the First Two CT Scans in Patients With Pancreatic Cancer

Douglas G. Adler, MD, FACG, AGAF, FASGE[1], Geetha Nallamothu, MD[1], Kristen Cox, MS, RN[1], Marta Heilbrun, MD[2], Ashish Sharma, MD[1] and Todd H. Baron, MD[3]

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To the Editor: There is no universally agreed upon time frame for obtaining the first follow-up computed tomography (CT) scan following a diagnosis of pancreatic cancer, although imaging before diagnosis has been previously studied (1–3). The aim of this study was to try to determine the optimal time to obtain a follow-up CT scan in patients with pancreatic cancer.

A total of 122 patients were included (60F, 62M). Fifty percent of patients received oncologic treatment between their initial and follow-up CT scan and were assigned to the treatment group. The remaining patients were assigned to the observation group. The average time interval between CT scans in all patients was 68.5±48.3 days. In the treatment group, the average time interval was 93.5±40.2 days; the average time interval in the observation group was 42.8±42.6 days (P<0.0001).

For patients in the treatment group, mean tumor size significantly decreased by 0.28 cm: 3.9 cm (range 0.7–8.7) compared with 3.6 cm (0–10.7) (P=0.05). Nodal stage was not changed: 27 patients in the treatment group had findings consistent with malignant lymphadenopathy on the first CT scan as compared with 28 by the post-treatment CT scan (P=0.66). Metastatic disease was significantly more frequent on the follow-up scan in the treatment group. A total of 22 patients had metastatic disease on the first CT and 35 patients had metastatic disease on the second CT scan (P value <0.0001). Overall, in the treatment