



GUT MICROBIOME CHANGES AND TREATMENT RESPONSE FOLLOWING FECAL MICROBIOTA TRANSPLANTATION IN ULCERATIVE COLITIS

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ABSTRACT

FMT could influence the gut microbiome of patients with ulcerative colitis (UC), though the relationship between changes in the microbiome and response is unclear. This exploratory analysis included ten patients with UC (4 of which were responders and 6 nonresponders) with paired phylum-level profiles. The unit of analysis was the patient. Medians were used for summarization of relative abundances, and exact label-permutation tests were used for comparing within-patient changes between groups, with adjustment for seven comparisons. Median abundance of Bacteroidetes increased by 13.55 points and Firmicutes decreased by 22.05 points among responders. The changes in nonresponders were -19.15 and +18.44 points. Proteobacteria saw a decrease in both groups, and a greater median decrease in the responders. There were also differences in baseline abundances between groups, and no between-group difference was statistically significant following multiple testing adjustment. These results reflect the different pairs of microbial patterns based on the recorded response status and do not indicate the treatment effects nor clinical biomarkers. More larger cohorts with known clinical outcome, donor details and more detailed microbial data are required to determine if patterns are repeatable.

Keyword: ulcerative colitis, fecal microbiota transplantation, gut microbiome, treatment response, microbial abundance.

Introduction

Ulcerative colitis (UC) is a condition where the colon becomes inflamed and has a tendency to flare up and go into remission. It is a course that reflects the interactions between the intestinal microbiota, the mucosal immune system and environmental exposures. So, disruption of the gut microbial community has become an interest in the potential role of inflammation and has been targeted for therapeutic approaches. Fecal microbiota transplantation (FMT) involves transplantation of donor material into the recipient's gastrointestinal tract to alter the recipient microbiota. Changes in the microbes have been reported in studies of patients prior to and following FMT, which also showed changes in clinical outcomes (Tikunov et al., 2023). Microbial changes after FMT have also been associated with changes in the ratio of Th17 and regulatory T cells (Huang et al., 2022). These correlations enable further study, but provide no evidence of the mechanism causing clinical improvement.

There is some promising, yet inconsistent, evidence that FMT is effective in UC. A systematic review of double-blind randomized trials showed that the FMT group had more clinical and endoscopic remission compared to the control group (El Hage Chehade et al., 2023). Another meta-analysis also found a benefit across randomized studies, but they pointed out some variability in treatment and outcomes (Feng et al., 2023). Another review reported the emerging clinical trial evidence for FMT in UC (Huang et al., 2022). However, inducing remission and maintaining remission are two different things. In a review specific to induction, issues regarding delivery and patient selection were not addressed (Saleh et al., 2023). A single FMT did not appear to be superior to autologous transplantation after 1 year in a randomized maintenance trial (Lahtinen et al., 2023).

Depending on the patient's characteristics and treatment approach, a response might happen. A comparison of FMT to glucocorticoids in mild to moderate UC exemplifies the importance of considering outcomes in a clinically circumscribed group of patients (Huang, et al., 2022). For refractory ulcerative proctitis and distal colitis, clinical parameters in the pretreatment period were correlated with treatment response (Raja et al., 2025). Microbial outcomes may also be influenced by the selection of donors and associated interventions. FMT from diet conditioned donors followed by dietary intervention resulted in better gut microbial profile than FMT alone (Leibovitzh et al., 2024). In a randomized study, donor composition and diet fiber were correlated with bacterial strain engraftment (Gogokhia et al., 2025). Differences make comparisons difficult if treatment data is not available.

Resolution of microbial measurements is important to describe variation in response. Successful FMT outcomes were correlated with a microbial state that included control of a Prevotellaceae community, not detectable from phylum-level measurements, by longitudinal profiling (Pinto et al., 2025). The study of encapsulated FMT with specific bacterial group and metabolite differences (Chen et al., 2023). Metagenomic analysis of the donors' oral flora revealed both taxonomic and functional shifts,

highlighting the distinct information provided by the composition and activity of the microbial communities in the donor's mouth (Raich et al., 2025). Wang et al., (2023) performed additional clinical work on both intestinal flora and inflammatory factors after transplantation. It has also been examined in immune checkpoint inhibitor-associated colitis, which is a different type of colitis than UC (Halsey et al., 2023). These finer taxonomic, metabolic or immune results cannot be directly tested by the broad abundance categories.

The detection of microbial features associated with the response is still a research goal. A systematic review identified potential biomarkers for candidates but highlighted the need for better validation (Rees et al., 2022). Inflammatory bowel disease (IBD) was reviewed, and the authors found that while there are features of the microbiome that predispose to FMT response, there is no single reliable profile for all patients (Zhang et al., 2022). Comparisons between two patients can help determine if a change occurred in that patient, or if there was a difference between the patients prior to treatment. Patterns can be seen at the phylum level and might need further research, but only within the limits of the measurements available.

The current study compares the gut microbial composition of paired gut microbial samples from ten patients with UC before and after FMT, based on the patient's response to the procedure. It takes into account six reported phyla of bacteria and an 'Others' category. Four persons responded, and six did not respond (or refused); the analysis is exploratory. The available data do not specify how response was clinically determined. The objectives are to:

1. Describe differences in reported phylum-level abundances before and after transplantation within each recorded response group.
2. Compare within-patient changes in microbial abundance between recorded responders and nonresponders following fecal microbiota transplantation.
3. Identify baseline microbial patterns that warrant further investigation as potential correlates of subsequent recorded response.

2. Materials and Methods

2.1 Study design and population

A paired gut microbiome analysis was performed in an observational secondary analysis of 10 patients who underwent fecal microbiota transplantation (jaijje, 2022). Every patient had two observations, one prior to treatment and one following: 20 observations. Four persons responded and six did not to the recorded response question. Patient identifiers tied measurements together over time, and comparisons of change were based on patients instead of samples. There was no documentation of criteria used to give

the response status nor was it inferred from available records, nor was there any documentation of interval between samples.

2.2 Microbial variables and data checks

The abundance profile consisted of Actinobacteria, Bacteroidetes, Firmicutes, Fusobacteria, Proteobacteria, Verrucomicrobia, and Others. Values were analysed as percentages as reported. The data were examined for missing or nonnumeric values, duplicate patient–time pair, and inconsistent response labels for pairs. The seven abundance values were added together to recognize the profiles that did not come close to adding up to 100%. This profile was not rescaled and based on the unaccounted portion, it was not possible to identify it. Zeros were included in the records and were not presumed to represent positive biological findings.

2.3 Descriptive and paired analyses

Each category was then ranked for median abundance, for both time points in each group. The group profiles were also determined with arithmetic means. Pairing "change" was calculated as "after-treatment" abundance minus "before-treatment" abundance, both in percentage points, for each patient. These individual changes were summarized as their typical change by calculating the median, directly based on the pairs of patients, not based on the medians of the time points. Positive, negative and zero changes were all counted. Pre and post treatment profiles were used to give context to the differences between pre and post treatment.

2.4 Change across the microbial profile

Half of the sum of the absolute differences between the paired changes in all seven categories were summarized for the entire profile to represent the magnitude of change recorded by each patient. This shift towards the aggregate was only used as a descriptive measure of the available values as some recorded profiles did not sum to 100%. Abundances of bacteria were presented separately, the direction of the change of Bacteroidetes and Firmicutes shifts, and the distribution of the change of the bacteria aggregates within the groups of responses. These changes were kept at a patient level throughout the calculations.

2.5 Statistical comparisons

Between-group contrasts for each abundance category were the median paired change for responders compared with the median paired change for nonresponders. This comparison was performed using two-sided exact permutation testing, which involved calculating the number of all possible assignments of 4 responder labels for the 10 patient-level changes observed. The p value was the percentage of the assignments in the sample with an absolute median difference that was equal to or greater than the observed difference. The Benjamini–Hochberg adjustment was carried out for the seven categories. With

the small groups and the observational response labels, estimates and adjusted probabilities were interpreted as exploratory evidence.

3. Results

3.1 Records and data completeness

There were 20 observations in the file, and 1 observation before and 1 observation after each identifier. Response status was the same across the two records with four patients classified as R and six NR. Neither were there any missing abundance values nor were there duplicate time labels within any patient. The category totals were found to be between 94.54% and 100.00% for all samples as indicated in Table 1. The totals of the three samples were less than 99% compared to a complete compositional total. Only ten pairs were available for analysis.

Table 1. Patient records and abundance-data checks

Measure	Responders	Nonresponders	Total
Patients	4	6	10
Before-treatment records	4	6	10
After-treatment records	4	6	10
Complete patient pairs	4	6	10
Missing abundance cells	0	0	0
Samples with listed abundances <99%	1	2	3
Minimum listed-abundance sum (%)	98.94	94.54	94.54
Maximum listed-abundance sum (%)	100.00	100.00	100.00

3.2 Microbial composition before treatment

Prior to treatment, there was variation in the proportions of several reported groups of microorganisms across the response groups. As presented in Table 2, the median abundance of Actinobacteria in the responders group was 37.81%, while it was 11.13% in nonresponders group. The abundance of median Bacteroidetes was 3.15% and 43.03%, while the medians of Firmicutes were 52.69% and 38.54%, respectively. The median of Proteobacteria was 6.50% in the responders and 3.42% in the nonresponders. The patients who were later given different response labels are described in these baseline comparisons. The differences between the small groups and lack of clinical covariates make it difficult to attribute any differences in the groups to a specific patient characteristic at baseline (Figure 1).

Table 2. Median reported relative abundance before and after treatment (%)

Category	Responders before	Responders after	Nonresponders before	Nonresponders after
Actinobacteria	37.81	51.88	11.13	11.69
Bacteroidetes	3.15	19.72	43.03	27.34
Firmicutes	52.69	28.75	38.54	50.62
Fusobacteria	0.00	0.00	0.00	0.00
Proteobacteria	6.50	1.77	3.42	2.00
Verrucomicrobia	0.00	0.00	0.00	0.00
Others	0.05	0.04	0.02	0.01

Note. Each column reports the median at that time point, not the median within-patient change.

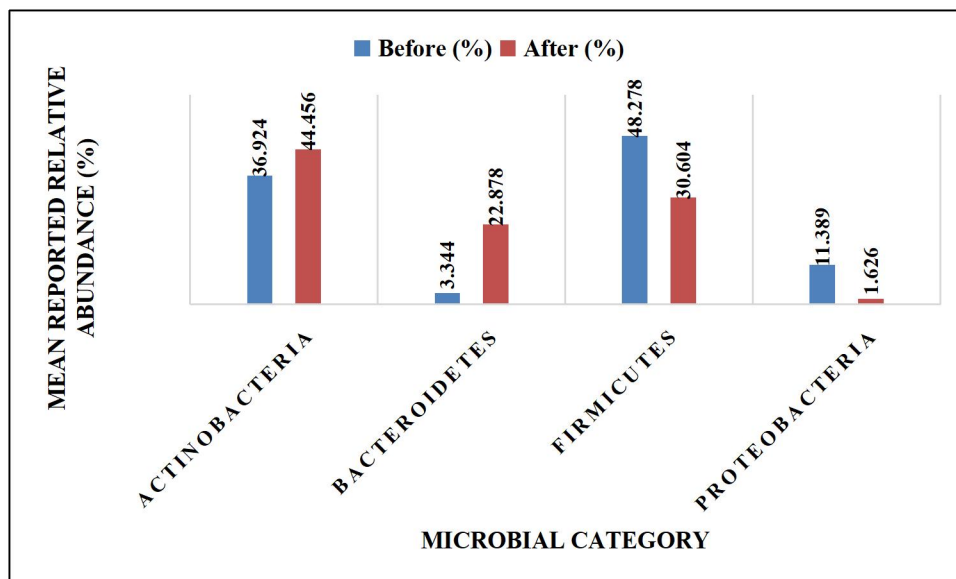


Figure 1. Mean abundance among responders

3.3 Microbial composition after treatment

Median abundance of Actinobacteria was 51.88% in responders and 11.69% in nonresponders after treatment. The medians of the Bacteroidetes were 19.72% and 27.34%, while the medians of the Firmicutes were 28.75% and 50.62%, respectively. The median Proteobacteria level was 1.77% and 2.00% in responders and nonresponders, respectively. The medians of fusobacteria and Verrucomicrobia were both zero at both time points in both groups. The “Others” category was also minimal for both groups. These after-treatment values represent group distributions and median changes within patients are not necessarily equal to differences from the baseline medians (Table 3) (Figure 2).

Table 3. Distribution of reported microbial abundance after treatment

Category	Responders > 0, n	Responders min (%)	Responders max (%)	Nonresponders >0, n	Nonresponders min (%)	Nonresponders max (%)
Actinobacteria	4	16.870	57.186	6	1.880	82.915
Bacteroidetes	4	13.081	38.985	6	0.157	50.406
Firmicutes	4	23.004	41.922	6	16.641	65.366
Fusobacteria	0	0.000	0.000	2	0.000	0.628
Proteobacteria	4	1.052	1.909	6	0.276	12.449
Verrucomicrobia	1	0.000	0.314	0	0.000	0.000
Others	4	0.001	0.142	3	0.000	0.249

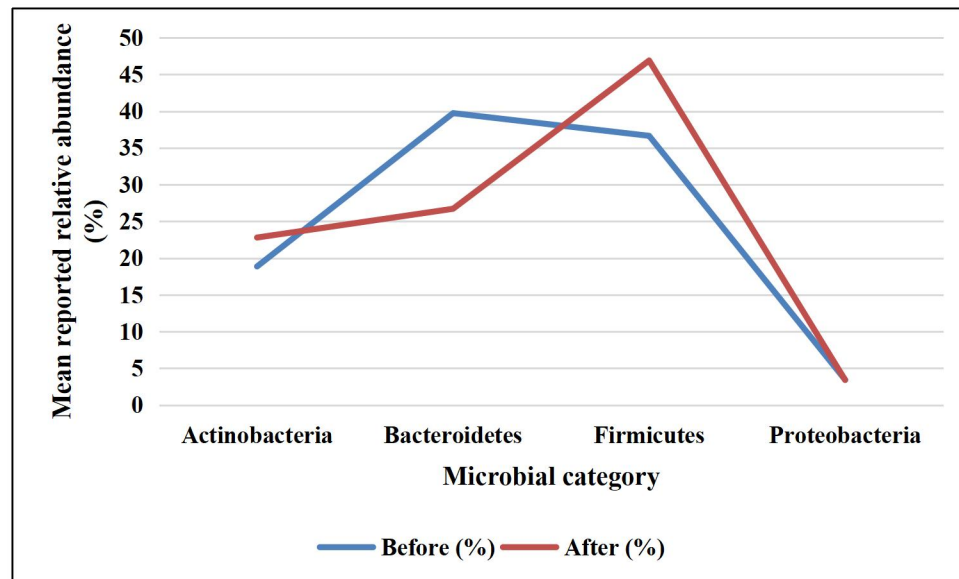


Figure 2. Mean abundance among nonresponders

3.4 Within-patient microbial changes

There were significant intra-individual differences in the direction of change for the major categories when compared within patients. The abundance of Bacteroidetes in all four responders and two of six nonresponders and Firmicutes in three responders and two nonresponders. In both responders and nonresponders, Proteobacteria was decreased in all four instances. Median increases/decreases of +13.55 and -19.15 percentage points of Bacteroidetes were recorded for responders and nonresponders, respectively, as shown in Table 4. The changes in the levels of Firmicutes were -22.05 and +18.44 points. Changes in Actinobacteria were not as uniform in individual patients, especially in nonresponders. These counts and medians are paired observations, but do not imply a treatment mechanism (Figure 3).

Table 4. Median paired changes and exploratory response-group comparisons

Category	Responder change (pp)	Nonresponder change (pp)	Difference (pp)	Exact p	Adjusted p
Actinobacteria	+13.317	-2.835	+16.152	0.271	0.475
Bacteroidetes	+13.552	-19.148	+32.700	0.110	0.256
Firmicutes	-22.051	+18.437	-40.488	0.086	0.256
Fusobacteria	+0.000	+0.000	+0.000	1.000	1.000
Proteobacteria	-5.078	-1.086	-3.992	0.043	0.256
Verrucomicrobia	+0.000	+0.000	+0.000	1.000	1.000
Others	+0.005	-0.004	+0.009	0.848	1.000

Note. Change = after minus before; pp = percentage points. Difference = responder median change minus nonresponder median change. Adjusted *p* values use the Benjamini–Hochberg procedure across seven categories.

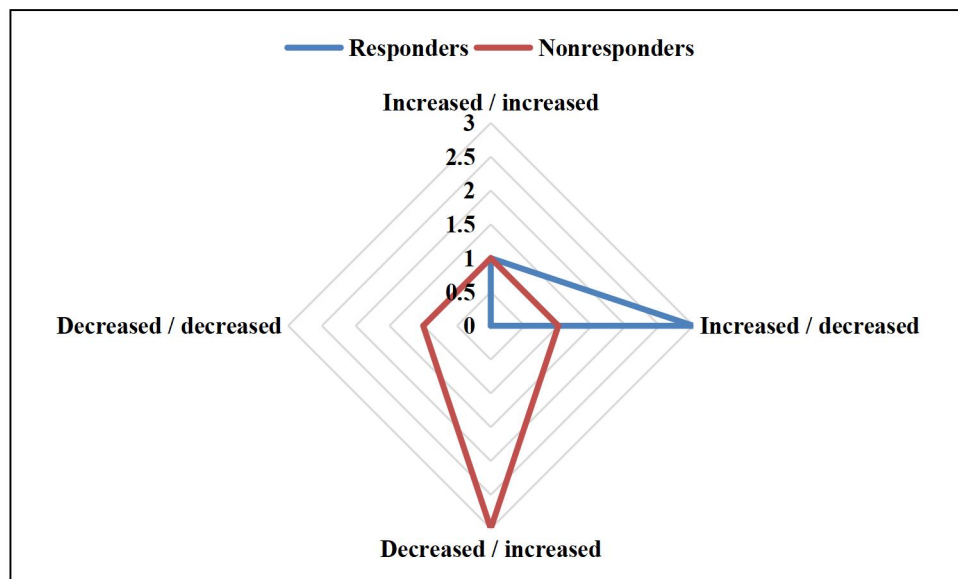


Figure 3. Combined directions of *Bacteroidetes* and *Firmicutes* change

3.5 Exploratory comparison of response groups

Exploratory comparisons of the changes between the two response groups. Firmicutes had the highest absolute median difference (40.49 points), with Bacteroidetes coming in second (+32.70 points). The unadjusted multiplicity p value for Proteobacteria was 0.043 and the multiplicity adjusted value was 0.256. None of the categories were adjusted to values less than 0.05. In both groups, there were no changes in the median for Fusobacteria and Verrucomicrobia. Because these patterns are based on a limited number of patients and an undefined definition of response to treatment, they cannot reliably serve as microbial markers of response to treatment (Table 5) (Figure 4).

Table 5. Number of patients with increased, decreased, or unchanged abundance

Category	Responders increased	Responders decreased	Responders unchanged	Nonresponders increased	Nonresponders decreased	Nonresponders unchanged
Actinobacteria	3	1	0	2	4	0
Bacteroidetes	4	0	0	2	4	0
Firmicutes	1	3	0	4	2	0
Fusobacteria	0	1	3	1	2	3
Proteobacteria	0	4	0	1	5	0
Verrucomicrobia	1	0	3	0	0	6
Others	2	2	0	2	3	1

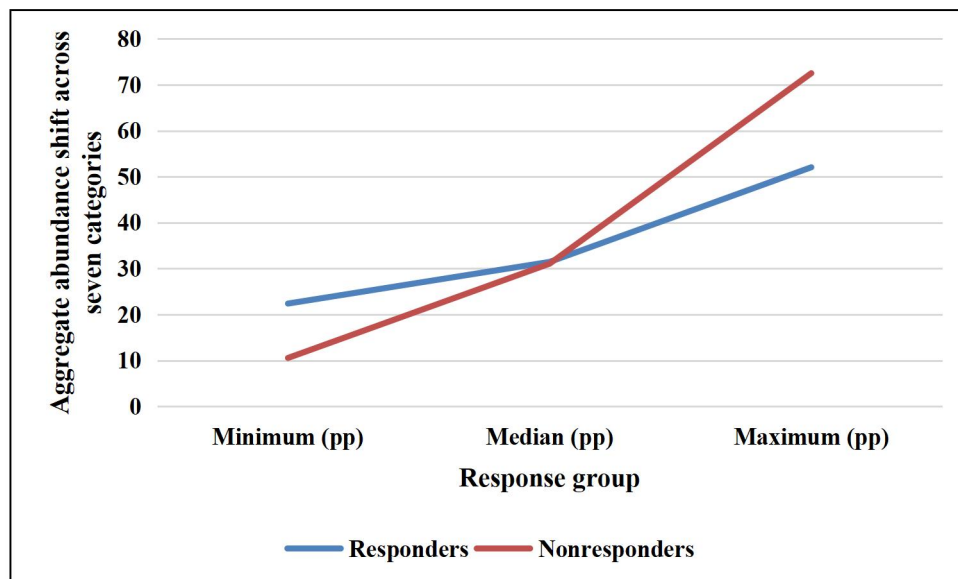


Figure 4. Range of aggregate abundance shift

4. Discussion

A comparison of the paired profiles revealed distinct responder and nonresponder profiles of change. The abundance of the median *Bacteroidetes* increased by 13.55 percentage points in the four responders and decreased by 19.15 points in the six nonresponders. Changes in Median *Firmicutes* were opposite, with -22.05 and $+18.44$ points, respectively. The growth of actinobacteria in responders was higher and it was a little lower in nonresponders. These opposing findings indicate that the groups of responders did not experience a consistent microbial change after fecal microbiota transplantation (FMT). They don't prove that a change in a whole phylum was clinically beneficial. The measurements referred to the general categories of microbes, and no clinical scores or classification rule were included with the labels that were reported for the response.

The median abundance of *Actinobacteria* was greater in responders than nonresponders before transplantation, and the median abundance of *Bacteroidetes* was significantly lower in responders compared to nonresponders prior to transplantation. There was thus a certain separation among groups prior to treatment. In the case of a randomized pilot study with preselected donors, donor engraftment was not correlated with clinical response, yet donor identity and the transfer of specific taxa was more informative (van Lingen et al., 2024). That explanation cannot be tested with the present data since there were no donor profiles or strain-level engraftment information. They do demonstrate the importance of accounting for any differences in abundances prior to the treatment. Paired changes give a better idea of what happened in each patient, but cannot tell us why such changes happened.

Observed shifts of the *Bacteroidetes* and *Firmicutes* also need to be compared with other research that has used different treatment protocols and clinical results. The randomized trial of FMT combined with

mesalazine showed that FMT led to greater changes in the microbiota, but there were no significant differences between the groups at 8 weeks (Tkach et al., 2023). In the present analysis there is no standard care comparator as there was with that trial. It can't distinguish if the changes were caused by FMT, background treatment or over time. A metaanalysis of randomized studies revealed that FMT had higher clinical and endoscopic remission rates than the control group, while the numerical difference in the direction of change within a specific phylum was not considered. (Wei et al., 2022). An overview of systematic reviews also supported the possibility of remission induction and highlighted delivery, dosage, frequency, and donor selection as remaining unanswered questions (Liu et al., 2023).

The decline in Proteobacteria was significantly higher among those that responded. There was no significant difference between abundance categories at the $p=0.043$ exploratory unadjusted level, however the comparison did not hold after Bonferroni adjustment across the seven abundance categories. No other category did. This contrast is therefore a finding (not a response marker) for replication, not a validated response marker. A more recent systematic review and analysis of randomized trials showed that FMT had a higher clinical remission and endoscopic response than did control therapy (Doukas et al., 2026). That level of treatment evidence is insufficient to support that the changes in Proteobacteria are responsible for the outcomes recorded in this small group. Another factor that complicates the situation are relative abundances, where a category's percentage can drop in comparison to another category even though the number of microbes in that category does not drop.

Comparisons with other biological information bring the boundaries of measuring in the phylum to light. The metabolomic profiling of patients' serum examined metabolic changes associated with treatment and whether they could be used to predict efficacy in those with extensive UC (Wu et al., 2023). Serum metabolites, inflammatory markers, or species-level measurements are not available in the present data so these relationships can not be assessed here. Antibiotic-associated diarrhea (AAD) is reported to have changes in specific bacterial genera in studies investigating FMT (Wang et al., 2024). This is not UC; the findings are instead a relevant guide to the ability to measure the microbial change, not a direct comparison with treatment response. No consensus on the replication of taxa or effect on clinical disease should be taken as the sense of the broad consensus that communities change after FMT.

All of the patients in the program had before/after records and changes calculated within patients and baseline differences analyzed separately. However, these four responders and six nonresponders offer little precision especially in the categories with many zero or near zero values. The reported abundances for three samples were less than 99%, which further restricted the interpretation of the reported categories as a complete community composition. No clinical response criteria, no donor information, no concomitant medication and no longer follow up makes it impossible to assess remission, engraftment, durability and safety. The defensible finding is that the recorded response categories agreed with different patterns of paired phylum-level responses in this sample. Future studies should confirm the response with

specific clinical endpoints and explore the association of paired microbiome profiles within the context of donor characteristics and more detailed taxonomic information.

5. Conclusion

A comparison of the paired profiles revealed distinct responder and nonresponder profiles of change. The abundance of the median Bacteroidetes increased by 13.55 percentage points in the four responders and decreased by 19.15 points in the six nonresponders. Changes in Median Firmicutes were opposite, with -22.05 and $+18.44$ points, respectively. The growth of actinobacteria in responders was higher and it was a little lower in nonresponders. These opposing findings indicate that the groups of responders did not experience a consistent microbial change after fecal microbiota transplantation (FMT). They don't prove that a change in a whole phylum was clinically beneficial. The measurements referred to the general categories of microbes, and no clinical scores or classification rule were included with the labels that were reported for the response.

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Observed shifts of the Bacteroidetes and Firmicutes also need to be compared with other research that has used different treatment protocols and clinical results. The randomized trial of FMT combined with mesalazine showed that FMT led to greater changes in the microbiota, but there were no significant differences between the groups at 8 weeks (Tkach et al., 2023). In the present analysis there is no standard care comparator as there was with that trial. It can't distinguish if the changes were caused by FMT, background treatment or over time. A metaanalysis of randomized studies revealed that FMT had higher clinical and endoscopic remission rates than the control group, while the numerical difference in the direction of change within a specific phylum was not considered. (Wei et al., 2022). An overview of systematic reviews also supported the possibility of remission induction and highlighted delivery, dosage, frequency, and donor selection as remaining unanswered questions (Liu et al., 2023).

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References

1. Chen, Q., Fan, Y., Zhang, B., Yan, C., Zhang, Q., Ke, Y., ... & Xu, H. (2023). Capsulized fecal microbiota transplantation induces remission in patients with ulcerative colitis by gut microbial colonization and metabolite regulation. *Microbiology Spectrum*, 11(3), e04152-22.
2. Doukas, P. G., Doukas, S. G., & Broder, A. (2026). Effectiveness and safety of fecal microbiota transplantation for ulcerative colitis treatment: a systematic review and meta-analysis. *Digestive Diseases*, 44(1), 85-98.
3. El Hage Chehade, N., Ghoneim, S., Shah, S., Chahine, A., Mourad, F. H., Francis, F. F., ... & Hashash, J. G. (2023). Efficacy of fecal microbiota transplantation in the treatment of active ulcerative colitis: a systematic review and meta-analysis of double-blind randomized controlled trials. *Inflammatory Bowel Diseases*, 29(5), 808-817.
4. Feng, J., Chen, Y., Liu, Y., Lin, L., Lin, X., Gong, W., ... & Xiao, C. (2023). Efficacy and safety of fecal microbiota transplantation in the treatment of ulcerative colitis: a systematic review and meta-

- analysis. *Scientific Reports*, 13(1), 14494.
5. Gogokhia, L., Tran, N., Grier, A., Nagayama, M., Xiang, G., Funez-dePagnier, G., ... & Longman, R. S. (2025). Donor composition and fiber promote strain engraftment in a randomized controlled trial of fecal microbiota transplant for ulcerative colitis. *Med*, 6(9).
 6. Halsey, T. M., Thomas, A. S., Hayase, T., Ma, W., Abu-Sbeih, H., Sun, B., ... & Wang, Y. (2023). Microbiome alteration via fecal microbiota transplantation is effective for refractory immune checkpoint inhibitor-induced colitis. *Science Translational Medicine*, 15(700), eabq4006.
 7. Huang, C., Huang, Z., Ding, L., Fu, Y., Fan, J., Mei, Q., ... & Zeng, Y. (2022). Fecal microbiota transplantation versus glucocorticoids for the induction of remission in mild to moderate ulcerative colitis. *Journal of Translational Medicine*, 20(1), 354.
 8. jaijee. (2022). FMT-treated patients with ulcerative colitis (UC) [Data set]. Kaggle. <https://www.kaggle.com/datasets/jaijee/uc-fmt>
 9. Lahtinen, P., Jalanka, J., Mattila, E., Tillonen, J., Bergman, P., Satokari, R., & Arkkila, P. (2023). Fecal microbiota transplantation for the maintenance of remission in patients with ulcerative colitis: a randomized controlled trial. *World journal of gastroenterology*, 29(17), 2666.
 10. Leibovitch, H., Sarbagili Shabat, C., Hirsch, A., Zittan, E., Mentella, M. C., Petito, V., ... & Maharshak, N. (2024). Faecal transplantation for ulcerative colitis from diet conditioned donors followed by dietary intervention results in favourable gut microbial profile compared to faecal transplantation alone. *Journal of Crohn's and Colitis*, 18(10), 1606-1614.
 11. Liu, H., Li, J., Yuan, J., Huang, J., & Xu, Y. (2023). Fecal microbiota transplantation as a therapy for treating ulcerative colitis: an overview of systematic reviews. *BMC microbiology*, 23(1), 371.
 12. Pinto, S., Šajbenová, D., Benincà, E., Nooij, S., Terveer, E. M., Keller, J. J., ... & Steyerberg, E. W. (2025). Dynamics of gut microbiota after fecal microbiota transplantation in ulcerative colitis: success linked to control of prevotellaceae. *Journal of Crohn's and Colitis*, 19(2), jjae137.
 13. Raich, S. S., Majzoub, M. E., Haifer, C., Paramsothy, S., Shamim, M. M. I., Borody, T. J., ... & Kaakoush, N. O. (2025). Bacterial taxonomic and functional changes following oral lyophilized donor fecal microbiota transplantation in patients with ulcerative colitis. *Msystems*, 10(10), e00991-25.
 14. Raja, S. S., Costello, S. P., Rayner, C. K., Day, A., Portmann, L., Uylaki, W., ... & Bryant, R. V. (2025). Examining the role of fecal microbiota transplantation for inducing remission in resistant ulcerative proctitis and distal ulcerative colitis (ulcerative proctitis-fecal microbiota transplantation). *Journal of Crohn's and Colitis*, 19(10), jjaf169.
 15. Rees, N. P., Shaheen, W., Quince, C., Tselepis, C., Horniblow, R. D., Sharma, N., ... & Quraishi, M. N. (2022). Systematic review of donor and recipient predictive biomarkers of response to faecal microbiota transplantation in patients with ulcerative colitis. *EBioMedicine*, 81.
 16. Saleh, A., Parsa, S., Garza, M., Quigley, E. M., & Abraham, B. P. (2023). The role of fecal microbiota transplantation in the induction of remission in ulcerative colitis. *Digestive Diseases*, 41(4), 656-665.
 17. Tikunov, A. Y., Fedorets, V. A., Shrainer, E. V., Morozov, V. V., Bystrova, V. I., & Tikunova, N. V. (2023). Intestinal microbiome changes and clinical outcomes of patients with ulcerative colitis after fecal microbiota transplantation. *Journal of Clinical Medicine*, 12(24), 7702.
 18. Tkach, S., Dorofeyev, A., Kuzenko, I., Falalyeyeva, T., Tsyryuk, O., Kovalchuk, O., ... & Boccuto, L. (2023). Efficacy and safety of fecal microbiota transplantation via colonoscopy as add-on therapy in patients with mild-to-moderate ulcerative colitis: a randomized clinical trial. *Frontiers in Medicine*, 9, 1049849.
 19. van Lingen, E., Nooij, S., Terveer, E. M., Crossette, E., Prince, A. L., Bhattarai, S. K., ... & Keller, J. J. (2024). Faecal microbiota transplantation engraftment after budesonide or placebo in patients with active ulcerative colitis using pre-selected donors: a randomized pilot study. *Journal of Crohn's and Colitis*, 18(9), 1381-1393.
 20. Wang, L., Guo, G., Xu, Y., Li, L., Yang, B., Zhao, D., ... & Chen, Q. (2024). The effect of fecal microbiota transplantation on antibiotic-associated diarrhea and its impact on gut microbiota. *BMC microbiology*, 24(1), 160.
 21. Wang, Z., Yang, L., & Sun, S. (2023). Effect of intestinal microbiota transplantation on intestinal flora and inflammatory factor levels in patients with ulcerative colitis. *Infection and Drug Resistance*, 1183-1191.
 22. Wei, Z. J., Dong, H. B., Ren, Y. T., & Jiang, B. (2022). Efficacy and safety of fecal microbiota

- transplantation for the induction of remission in active ulcerative colitis: a systematic review and meta-analysis of randomized controlled trials. *Annals of Translational Medicine*, 10(14), 802.
23. Wu, X., Li, P., Wang, W., Xu, J., Ai, R., Wen, Q., ... & Zhang, F. (2023). The underlying changes in serum metabolic profiles and efficacy prediction in patients with extensive ulcerative colitis undergoing fecal microbiota transplantation. *Nutrients*, 15(15), 3340.
24. Zhang, J., Guo, Y., & Duan, L. (2022). Features of gut microbiome associated with responses to fecal microbiota transplantation for inflammatory bowel disease: a systematic review. *Frontiers in Medicine*, 9, 773105.

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