

Fecal microbial transplants show lack of predictability when no prior antibiotic treatment is given to recipient

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A fecal microbial transplant—giving a recipient fecal matter from a donor to change the recipient's gut microbial community in the colon—has been a successful last resort therapy for people with recurrent *Clostridium difficile* infection after multiple rounds of suppressive antibiotics have eliminated the recipient microbial community.

However, fecal microbial transplants have also been given to alter a recipient's metabolism to reduce obesity or alter immunity to fight cancer, and in those transplants recipients are not given suppressive antibiotics to eliminate the microbial community prior to the transplant. In these cases, the initial gut community after transplant is a consortium of [donor](#) and recipient microbes that have to compete as new microbial strains are introduced into an established community.

University of Alabama at Birmingham researchers now [report](#) in the journal *PLOS One* that there is a lack of predictability for fecal microbial transplants to change the gut microbial community to correspond to that of the donor when there is no preconditioning to reduce the recipient microbe community. This contrasts with the *C. difficile* fecal microbial transplants after suppressive antibiotic therapy, where stable long-term colonization of donor strains is seen as long as two years post-transplant.

"The practical translation of our analysis suggests the use of pre-fecal microbial transplant treatments to reduce recipient microbial communities to facilitate a donor microbial strain-dominated gut microbial community following fecal microbial transplant," said UAB

researchers Hyunmin Koo, Ph.D., and Casey Morrow, Ph.D. "In addition, longitudinal sampling of individual fecal microbial transplant patients in combination with strain tracking analysis to monitor the status of the post-fecal microbial transplant microbial community would also be important to assess the stability and, ultimately, the success of the fecal microbial transplant."

Koo and Morrow analyzed metagenomic sequencing published by Davar et al. in Science in 2021, using two established strain tracking methods, the WSS strain-tracking method developed at UAB and the strain-level population genomics tool StrainPhlAn. WSS can detect whether a donor strain or recipient strain of a particular species of gut microbes is dominant after fecal microbial transplants, and StrainPhlAn provides a phylogenetic tree of donor-related microbes or recipient-related microbes.

The Davar group gave fecal microbial transplants from patients who responded to anti-PD-1 immunotherapy for melanoma to recipient patients who were resistant to the immunotherapy, since it had been seen that the composition of the gut microbiota correlates with efficacy of anti-PD-1 therapy in animal models and [cancer patients](#). Six out of 15 patients benefited.

Koo and Morrow analyzed five fecal microbial transplants by the Davar group where the recipient microflora was sampled multiple times for as long as 535 days post-fecal microbial transplant. This published metagenomic data allowed a time-series strain tracking analysis.

The UAB researchers found that three *Alistipes* [bacterial species](#) and one *Parabacteroides* species all had patterns, post-fecal microbial transplant, of either dominant donor or dominant recipient strains in the feces.

In contrast, *Bacteroides uniformis* and *Bacteroides vulgatus* showed inter-individual oscillation over time with the appearance of either donor or recipient fecal strain dominance. Adding further to the complexity, there were some instances of dominant strains of the two *Bacteroides* species that were unrelated to either the donor or the recipient strains. Also, one *Bacteroides vulgatus* strain showed a possible genetic recombination event between the donor and recipient strains.

"The complex oscillating patterns of the appearance of fecal dominant donor, recipient or unrelated strains following extended times post-fecal microbial transplant provide new insights into the dynamics of the microbial community interactions with the recipients following fecal microbial transplant," Morrow said. "The result from our analysis has implications for the use of fecal microbial [transplant](#) to predictably change the biological functions of the gut community in metabolism and host immunity."

More information: Hyunmin Koo et al, Time series strain tracking analysis post fecal transplantation identifies individual specific patterns of fecal dominant donor, recipient, and unrelated microbial strains, *PLOS ONE* (2022). [DOI: 10.1371/journal.pone.0274633](https://doi.org/10.1371/journal.pone.0274633)

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