Microbiota Dynamics in Patients Treated with Fecal Microbiota Transplantation for Recurrent Clostridium difficile Infection


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Introduction

One of a major hospital-acquired disease is caused by the bacterium known as Clostridium difficile. This pathogen is normally found in the gut microbiome of some healthy individuals, but they can become dangerous when antibiotics that is used to treat infections also eliminates healthy bacteria that can keep them in check. This disruption can lead to conditions known as pseudomembranous colitis (PC) and antibiotic-associated diarrhea (AAD). This study by Yang et al. investigates increasing evidence to suggest an imbalance in the microbiome can contribute to various diseases such as PC and AAD. Current therapeutic option such as administration of metronidazole, vancomycin, and fidaxomicin are not sufficient, as the rate of recurrent C. difficile infection (RCDI) is about 20%. As such, an alternative method of fecal microbiota transplantation (FMT) can help restore RCDI individuals gut microbiome to its homeostatic state and improve their overall health.

Methods

• 14 pairs of healthy donors and RCDI individuals who were successfully treated with FMT were analyzed by their fecal microbiota using 16S rRNA gene amplicon pyrosequencing method.
• Continual longitudinal study of post-FMT patient and healthy donor samples were analyzed after one year.
• Using Principal coordinates analysis (PCoA) to identify differences among microbial communities.
• Rarefaction curves to analyzed microbial groups based on operational taxonomic units (OTUs).
• Microbiota diversity (Shannon) and richness (ACE).

Results and Future Work

• Microbiota rarefactor curves and microbiota diversity data shows that those who are healthy are associated with a more diverse microbial species in the gut and those who has RCDI are less diverse (Figure 2 & 3).
• Though, there is some overlap between the microbial species of RCDI versus healthy individuals, but overall, PCoA Unifrac analysis shows that individuals with RCDI have different microbial species in the guts than when compared with those who are healthy (Figure 5A).
• C difficile is actually less abundant in those with RCDI when compared with healthy individuals (Figure 4 & 6). This means that the data supports that there’s more than one group (more than one microbiota composition) of microbe that’s causing RCDI. This suggests RCDI may be caused by multiple mixtures of different gut bacteria and not just one particular species (Figure 5B).
• Other microbial species such as Enterococcus, Venilonella, and Klebsiella are generally associated with those who have RCDI but not those who have a healthy gut (Figure 6). Again, this may indicate that certain particular microbial species are contributing to individuals with RCDI.
• Overall, these results indicate that those with healthy guts have a different composition of microbial species than when compared with RCDI and that fecal microbiota transplantation (FMT) may help restore RCDI individuals gut microbiome.

Further study on other species other than such as the one mentioned (Enterococcus, Venilonella, and Klebsiella ) may help explains how they may be contributing to C difficile symptoms.