1016. Long-term Follow-up after Fecal Microbiota Transplantation via Colonoscopy or Freeze-Dried Capsules for Recurrent *Clostridioides difficile* infection

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**Session:** P-57. Microbiome in Health and Disease

**Background.** Fecal microbiota transplantation (FMT) is effective for treatment of recurrent *Clostridioides difficile* infection (CDI). However, limited data are available on the durability of FMT, especially after FMT via capsules and with more than 1 year of follow-up.

**Methods.** A retrospective cohort study was conducted for all patients undergoing FMT from April 2013–November 2020 in a tertiary care hospital. Initial management was considered successful if 1 to 3 FMTs resulted in improved symptoms with no diagnosis of recurrent CDI at 3 months after the initial FMT. Medical record review and telephone interviews were conducted to determine the frequency of recurrent CDI after initial successful management.

**Results.** One-hundred sixty-two patients received 228 FMT procedures (range, 1 to 5), including 78 (34%) via colonoscopy, 144 (63%) via freeze-dried oral capsules, and 6 (3%) via nasogastric-duodenal/PEG tube. The median follow-up time after initial FMT was 61 months (range, 10 to 99 months). Initial management was successful in 132 (81%) patients after 1 FMT and in 24 (14%) patients with 1-2 additional FMTs (Figure). During long-term follow-up, 29 recurrences occurred in 22 of 159 (14%) patients evaluated. Ten (34%) of the recurrences occurred greater than 12 months after the initial FMT. Of the 22 patients with recurrence after 3 months, 16 (73%) were successfully managed with CDI therapy or additional FMT.

**Conclusion.** In our center, FMT via colonoscopy or freeze-dried capsules was very successful in initial management of recurrent CDI and 85% had a durable response with no further recurrences. However, more than 1 FMT procedure was often required to achieve initial success and to manage late recurrences.

**Disclosures.** All Authors: No reported disclosures

1017. Gut Microbiota Diversity and Beneficial Metabolite Production is Reduced in Liver Transplant Recipients and Associated with Post Operative Infection

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**Session:** P-57. Microbiome in Health and Disease

**Background.** Liver transplant (LT) recipients have abnormal microbiota before and after transplantation. (1,2) Associations between fecal microbiota, microbial metabolites, and clinical outcomes in liver transplantation are not well established. We aimed to determine the diversity of the microbiota and metabolites, and clinical outcomes in Liver transplant recipients.

**Methods.** In a prospective observational study, we collected peri-transplant fecal samples and determined microbiota composition by 16S ribosomal RNA gene sequencing in LT recipients. Fecal short chain fatty acid (SCFA) and bile acid concentrations were measured by targeted GC- and LC-MS analyses, respectively. Inverse Simpson index was used to determine microbiota alpha-diversity in subjects and healthy controls. Clinical outcomes including length of stay, ICU admission, liver function, antibiotic use, immunosuppressive requirement and post-operative infection were correlated with microbiota composition.

**Results.** 69 patients were enrolled, 70 liver transplants were performed and 307 peri-transplant fecal samples were collected and analyzed. Compared to healthy controls, the fecal microbiota of LT recipients had reduced alpha-diversity (p < 0.001). (Fig1) Bacteroidetes, Ruminococcaceae, and Lachnospiraceae, three taxa associated with a health-promoting microbiota, and their metabolites, SCFA and secondary bile acids, were markedly diminished 55% of LT patients. (3) Intestinal domination (>30% frequency) by Enterococcus or Proteobacteria species was common and occurred in 36% of LT recipients. 76 post-operative infections occurred in 40 LT recipients, with Enterococci causing 32% and Proteobacteria 41% of bacterial infections. In subjects with fecal samples collected within 5 days of infection, 9/17 infections were caused by the organism dominating the microbiota. (Fig2)

**Microbiota Composition and Metabolite Production**

**Figure.** Outcomes after FMT in 162 patients with recurrent CDI

16s gene sequencing color coded by taxonomy. Each bar represents one stool sample nearest to healthy controls. Alpha diversity measured by inverse simpson index. Absolute values of microbial metabolites and ratio of primary to secondary bile acids.

**Comparison of Microbiota Composition and Post Operative Infection**

**Table.** Outcomes after FMT in 162 patients with recurrent CDI

<table>
<thead>
<tr>
<th>Patient</th>
<th>Infection</th>
<th>Organism</th>
<th>SCFA</th>
<th>Bile Acid</th>
<th>Outcome</th>
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</thead>
<tbody>
<tr>
<td>1</td>
<td>C. difficile</td>
<td>VRE</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>2</td>
<td>C. difficile</td>
<td>VRE</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>3</td>
<td>C. difficile</td>
<td>VRE</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>4</td>
<td>C. difficile</td>
<td>VRE</td>
<td>Yes</td>
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<td>Yes</td>
</tr>
</tbody>
</table>

**Conclusion.** Microbiota diversity and microbially derived metabolites are markedly reduced in >50% of LT recipients. Intestinal domination and post-operative infections caused by antibiotic-resistant Enterococcus and Proteobacteria correlate with loss of Bacteroidetes, Ruminococcaceae, and Lachnospiraceae species, suggesting a potential role for microbiota reconstitution therapy in LT patients.

**Disclosures.** Eric G. Pamer, MD; FIDSA: Nothing to disclose

1018. Bacterial Bioburden Characterization of Infected Diabetic Foot Ulcers in Hospitalized Patients in Association with Clinical Outcomes: Traditional Cultures vs. Molecular Sequencing Methods

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**Session:** P-57. Microbiome in Health and Disease

**Background.** Bacterial bioburden, in terms of infecting pathogens and the bioburden caused by the host’s skin microbiome, plays an important role in the development of diabetic foot ulcers (DFU). The impact of traditional culture methods vs. molecular sequencing methods in understanding DFU bioburden is understudied.

**Methods.** We evaluated 30 patients with a DFU hospitalized at a tertiary care hospital in Israel. Two samples were collected from each ulcer, one for traditional culture methods and the other for molecular sequencing methods. The bacterial bioburden was evaluated using traditional culture methods and molecular sequencing for pathogenic bacterial isolates and the host’s skin microbiome.

**Results.** Comparison of the bacterial bioburden between traditional culture methods and molecular sequencing methods revealed significant differences in the identification of pathogenic bacterial isolates and the host’s skin microbiome. Molecular sequencing methods identified a larger number of bacterial species compared to traditional culture methods, suggesting a more comprehensive understanding of the DFU bioburden.

**Conclusion.** Molecular sequencing methods provide a more comprehensive understanding of the DFU bioburden compared to traditional culture methods. Using molecular sequencing methods may provide insights into the complex interplay between the host’s skin microbiome and pathogenic bacterial isolates in DFU development.

**Disclosures.**nothing to disclose