may have many explanations. Future studies should consider how chronic AD could change the microbial ecology of the mouth and lead to further infection as well as utilizing multiple oral sites and a larger sample size to better understand the relationship between AD and periodontal disease.

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2578. Narrow-Spectrum Antibiotic Treatment of Clostridium difficile Infection Improves Preservation of Intestinal Metabolic Profile

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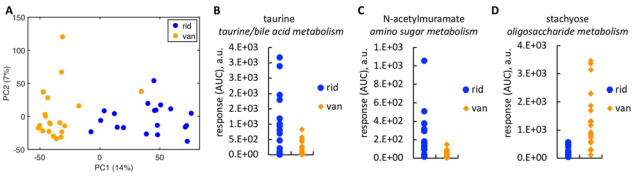
Background: Commensal gut bacteria are thought to protect against *C. difficile* infection (CDI) by producing metabolites that inhibit *C. difficile* germination and growth. Alternatively, the protective effect could reflect nutrient competition or other mechanisms of chemical communication that also involve the host. CDI treatment using a broad-spectrum antibiotic such as vancomycin (VAN) dramatically depletes commensal bacteria. This dysbiosis can persist for several weeks after end-of-therapy (EOT), and is associated with increased recurrence risk. In this study, we investigate the hypothesis that treating CDI with a more selective antibiotic reduces collateral damage to the intestinal microbiota, preserving or restoring a CDI-inhibitory metabolic profile.

Methods: Stool samples were collected from CDI patients treated with either a narrow- (RDZ) or broad-spectrum antibiotic (VAN) at days 1, 10 (EOT), 25, and 40. Global metabolite profiles were measured by untargeted LC-MS.

Results: Untargeted metabolite analysis showed broad differences in the metabolic activity of intestinal microbiota of RDZ- and VAN-treated subjects (Figure 1). At EOT, 28% of LC-MS features detected in both RDZ and VAN samples were differentially present (FDR corrected *P*-value <0.05). Over 80% of the differentially present features were elevated in the RDZ group, indicating diminished capacity of microbiota from VAN subjects to generate diverse metabolic products. Pathway analysis found significant differences in purine, taurine, tyrosine, and bile acid metabolites. The VAN group showed a 5-fold decrease in free taurine, a major conjugation substrate of primary bile acids released by bacterial bile salt hydrolases. VAN treatment also decreased fermentation products of aromatic amino acids and amino sugars derived from mucin degradation. Oligosaccharides were the major metabolite class elevated in VAN subjects.

Conclusion: Our data suggest that RDZ treatment correlates with enhanced preservation of bacteria-derived ligands regulating intestinal immune function and substrates of bacterial metabolism. These metabolic profile differences between a narrow- and broad-spectrum antibiotic may contribute to their varying efficacy in preventing CDI recurrence.



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

2579. Impact on the Gut Microbiota of the Prolonged Antimicrobial Therapy in Patients with Bone and Joint Infection (BJI): Results From the OSIRIS Prospective Study in France

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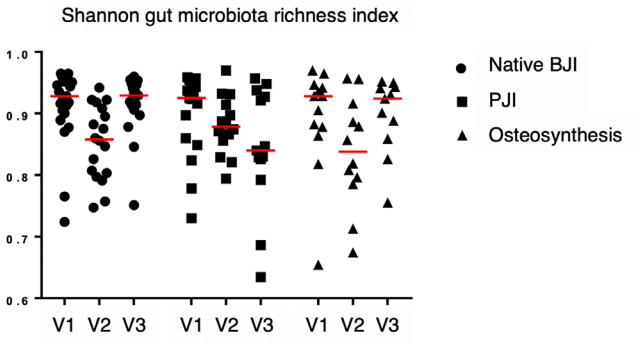
Background: There is growing interest about the deleterious impact of antibiotics on loss of gut symbiosis, called dysbiosis. As patients with BJI require antibiotics usually during 6 to 12 weeks, it is of interest to determine whether dysbiosis is frequent in this population, and if it could potentially reversible or not.

Methods: Multicentric prospective cohort study in France (EudraCT 2016-003247-10) including patients with 3 categories of BJI: native, osteosynthesis-related and prosthetic joint infection (PJI). At the time of suspicion (V1), at the end of therapy (V2) and then 2 weeks after stopping therapy (V3), blood and fecal samples were collected. Extracted DNA from stool was sequenced using shotgun metagenomic sequencing based on illumina library and Iseq instrumentation. Data run through a dedicated pipeline in order to produce microbiome indexes such as Sympson or Shannon diversities indexes. Gut microbiome and inflammation markers were analyzed including fecal neopterin, a maker of gut inflammation.

Results: Concerning the 62 patients included (mean age, 60 years; mean duration of antibiotics, 66 days), 27 had native, 14 had osteosynthesis and 21 had PJI. The most frequently prescribed drug was a fluoroquinolone, followed by a third-generation cephalosporin and vancomycin. Stools from 42 of them were analyzed as per protocol. Overall, the mean Shannon richness index decreased from 0.904 at V1 to 0.845 at V2; the Bray-Curtis index underlined the difference in microbiome reconstitution at V3 in comparison with V1. We report significant microbiome loss of diversity at V2, that was reversible at V3 in patients with native BJI and osteosynthesis-related BJI, but not in patients with PJI (figure). Fecal neopterin increased between V1 and V2 (mean 221.6 and 698.1 pmol/g of feces, respectively) and then decreased at V3 (422.5 pmol/g), and could be a potential surrogate marker of gut dysbiosis. Of note, patients with abnormal CRP at the end of antibiotics had high neopterin values, that raises the hypothesis that abnormal CRP at the end of antibiotics could be in relation with gut dysbiosis rather than uncured BJI.

Conclusion: The impact of antibiotics on the gut microbiota of patients with BJI seems to be significant, especially in patients with PJI who could be candidate for fecal microbiota transplantation.



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

2580. Serial Microbiome Analysis in a Patient with Multiple Failed Fecal Microbiome Transplantations

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Background: Fecal microbiota transplantation (FMT) is recommended to treat refractory or recurrent cases of *Clostridioides difficile* infection (CDI) through restoration of a healthy intestinal microbiome. The procedure has reported success rates of 90% or higher for CDI, but several risk factors for FMT failure have been identified. Here we present a case of a patient failing four FMT procedures over a 2-year period, with accompanying microbiome and metagenomic analyses.

Methods: Seven serial *C. difficile*-positive stool samples were collected as part of an ongoing surveillance system in Texas. Samples, including the index case, represented independent CDI episodes interspersed between four separate FMT procedures between 2016 and 2018. PCR ribotype (RT) testing, 16S rRNA gene sequencing, MIC testing, multidrug-resistant organism (MDRO) screening, and shotgun metagenome sequencing were conducted for each of the samples.

Results: The patient was a 42-year-old female with various comorbidities, including systemic lupus erythematosus. She received continuous non-CDI antibiotic courses throughout her CDI therapy for a variety of infections. The vancomycin MICs in infecting *C. difficile* strains increased with cumulative vancomycin exposure. Multidrug-resistant organisms were detected in stool, including *Enterococcus* spp., MRSA, and *Candida glabrata*. The first five of the seven strains were RT 078–126, one was mixed RT 002 and RT 054, and one was RT 002. The analysis of 16S rRNA gene sequences demonstrated that microbial diversity was never restored after FMT procedures. A strong correlation between microbial and functional gene compositions suggests that fecal samples share many microbial species with associated functional genes.

Conclusion: A number of systems biology changes were observed in a patient with persistent CDI despite multiple FMTs. The lack of FMT engraftment was most likely due to continuous broad-spectrum antibiotic exposure in an immunocompromised patient.

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2581. An Invertebrate Model to Study Gut Microbiome Dysbiosis

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