Colonization was associated with increased colonization by bacteria within the order Clostridiales, the genus *Clostridium*, and the family *Coriobacteriaceae*. Higher levels of total dietary fiber intake were also significantly associated with fiber intake. The rates of decolonization were significantly different between CPE, VRE and CPE/VRE. The relationship between antimicrobial use and subsequent resistance is complicated; this study assesses the short-term impact of antimicrobial use on fecal carriage of resistant organisms. This is a sub-study of an ongoing trial comparing 7 vs. 14 days of antimicrobial treatment for male urinary tract infection. This analysis quantifies the effect of 1-2 weeks of systemic antimicrobial use on the fecal flora within 1 week of completing therapy.

Method: The parent study has enrolled 216 subjects, with 178 enrolled in the optional resistance sub-study. Subjects received either ciprofloxacin or trimethoprim/sulfamethoxazole (SXT), randomized to 7 vs. 14 days therapy. Subjects provided 2 stool specimens, 1 during treatment and 1 a week after completing study medication. Samples were plated on media for Gram-positive and negative growth, including T-7 plates with ciprofloxacin and SXT added to select for resistant organisms. Resistance to antimicrobials was assessed, with resistance reported by: number of isolates with any antimicrobial resistance, total number of resistant drugs/isolate, and number of isolates with multi-drug resistance (resistance to 3 or more different antimicrobial classes). Overall, 143 (80%) subjects provided 2 stool samples, with 104 (73%) having growth from at least 1 of the samples. Fifty-one of 143 (36%) had microbial growth from both samples. From these 51 paired samples, there were 255 total strains isolated (117 from the first sample, 138 from the second), with some yielding multiple classes. (range, 1-5). From sample 1, 110/117 (94%) isolates had any antimicrobial resistance, vs. 131/138 (95%) from sample 2 (P = .79). Mean number of resistant drugs/isolate was 7.4 in sample 1 and 5.8 in sample 2 (P = .069). Multi-drug resistance was seen in 102/117 (87%) isolates from sample 1 vs. 85/138 (62%) isolates in sample 2 (P = .001).

Conclusion: The fecal flora of patients on antimicrobial therapy for UTI has a significant increase in resistant microorganisms compared with samples obtained shortly after antimicrobial completion. This may reflect repopulation of the fecal flora with less-resistant strains after the selection pressure of therapy has been removed. After unblinding, we will assess if differences in resistance are affected by therapy duration.

Disclosures: All authors: No reported disclosures.

### 2587. The Association Between Dietary Fiber and Diet and Gut Colonization with *Clostridium difficile*

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Session: 267. Microbiome, Antibiotics, and Pathogenesis
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Background: There is little research on the relationship between diet and *Clostridium difficile* infection. Animal studies have shown potential benefits of dietary fiber in modulating *C. difficile* infection.

Methods: In 2016-2017, we carried out a microbiota study among adults in the Survey of the Health of Wisconsin, a population-based health survey collecting data on a wide range of health determinants and outcomes. We administered the Dietary History Questionnaire and asked about risk factors for *C. difficile* and collected fecal samples for 16S rRNA sequencing of gut microbiota.

Conclusion: This study provides preliminary evidence to support the potential use of *G. mellonella* to assess the in vivo effect of a natural and synthetic antimicrobial on the gut microbiota.

Disclosures: All authors: No reported disclosures.

### 2588. Effects of Fecal Microbiota Transplantation for Decolonizing Multidrug-Resistant Organism

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Session: 267. Microbiome, Antibiotics, and Pathogenesis
Saturday, October 5, 2019: 12:15 PM

Background: Increasing prevalence of multidrug-resistant microorganisms (MDRO) results in poor clinical outcomes, longer hospitalizations and higher healthcare costs. It is likely that MDRO colonization can lead to infections in vulnerable patients. Currently, however, MDRO decolonization strategies are lacking. The purpose of this study was to compare the efficacy of FMT on decolonization of carbapenemase-producing Enterobacteriaceae (CPE) and vancomycin-resistant enterococci (VRE) carriers.

Methods: This study was a prospective, open-label, uncontrolled, single-center pilot study of FMT for digestive tract colonized CPE, VRE, or CPE/VRE patients between March 2018 and February 2019. Fecal solution obtained from healthy unrestrained donors was infused to recipient’s gut. Fecal samples of recipients were collected before and after FMT until 1 year. We compared characteristics of subjects succeed in decolonization during study period (responders) with subjects who failed to decolonize MDRO by FMT (non-responders). Furthermore, microbiome analyses were performed to investigate the influence of microbial characteristics of recipients on the outcomes of FMT.

Results: Decolonization was achieved in 12/23 (52.2%) during study period. Hemoglobin (11.0 vs. 10.0, P = 0.018), low-density lipoprotein cholesterol (102.0 vs. 89.0, P = 0.049), and albumin (3.4 vs. 3.2, P = 0.006) levels were higher in responders. Antibiotic treatment (ATB) within 1 week after FMT were less common in responders (41.7% vs. 90.9%, P = 0.027). Patients with no ATB approached frequent decolonization at 175 (0% vs. 26.7%, P = 0.037) and 3 months (87.5% vs. 33.3%, P = 0.027). The rates of decolonization were significantly different between CPE, VRE and CPE/VRE (87.5% vs. 66.7%, P = 0.018). Gut microbiome of responders showed a higher richness and diversity than non-responders before (294 vs. 274 by Ace; 2.6 vs. 1.8 by Shannon) and after (345 vs. 260 by Ace; 2.9 vs. 2.1 by Shannon) FMT. The microbiota composition analysis revealed increasing abundance of Bacteroidetes and