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Session: 267. Microbiome, Antibiotics, and Pathogenesis
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Background: Antimicrobials disrupt the gut microbiota by reducing gut microbiome diversity and quantity. *Galleria mellonella* provides an invertebrate model that is inexpensive, easy to maintain, and does not require specialized equipment. This study investigated the feasibility of using *G. mellonella* as an *in vivo* model to evaluate the effect of different antimicrobials on gut microbiota.

Methods: To determine baseline gut microbiota composition, the gut contents of *G. mellonella* were extracted and genomic DNA underwent shotgun meta-genomic sequencing. To determine the effect of infection and antibiotic use, 30 larvae were injected (left proleg) with $\sim 1 \times 10^5$ colony-forming unit (cfu) of methicillin-resistant *Staphylococcus aureus* (MRSA) and were randomized 1:1:1 to treatment with vancomycin (20 mg/kg) or a natural antimicrobial (*Nigella sativa* seed oil, 70 mg/kg; NS oil), or a combination. The larvae were kept at 37°C post-infection and monitored daily for 72 hours for activity, extent of cocoon formation/growth, melanization, and survival. Two larvae from each group were randomly selected and homogenized with PBS as controls. After 24 hours of incubation, gut contents were extracted and plated for MRSA and *Enterococcus* cfu counts.

Results: Metagenomics analysis showed the gut microbiota composition of *G. mellonella* larvae was dominated by a subset of closely-related *Enterococcus* species. After 24 hours of exposure, mean *Enterococcus* counts were 4×10^3 cfu in the vancomycin arm and 6.2×10^4 cfu in the NS oil arm. Mean MRSA counts were 3.3×10^5 cfu in vancomycin arm and 1.5×10^4 cfu in NS oil arm. The combination of vancomycin and NS oil had higher *Enterococcus* counts than the vancomycin alone arm (6.3×10^4 cfu vs. 4×10^3 cfu, respectively), suggesting that NS oil may have a role in protecting the 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.

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2582. The Association Between Dietary Fiber and Diet and Gut Colonization with *Clostridium difficile*

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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 and cultured for *C. difficile*. Dietary components were standardized to 1,000 kcal energy intake. Logistic regression was used to examine diet factors associated with *C. difficile* colonization. The quasi-conditional association test (QCAT) was performed to identify taxa that were significantly associated with fiber intake.

Results: In our general population sample of adults [(N = 238; 58% female; mean (range) age = 54 (18–94)], the prevalence of gut colonization with *C. difficile* was 9.2% (18 toxigenic/3 non-toxicogenic). After adjusting for age, sex, and antibiotic use, *C. difficile* colonization was associated with usual daily fiber consumption over the last year. ORs (95% CI) in the highest vs. lowest quartile were 0.18 (0.03, 0.89) for total fiber, 0.09 (0.01, 0.77) for soluble fiber, and 0.10 (0.1, 0.80) for insoluble fiber. Lower odds of *C. difficile* colonization were associated with greater consumption of dark green vegetables and less consumption of solid fats, total saturated fats, and added sugar, but not significantly. Omega 3 fatty acids and fruit consumption were either non-monotonically or not associated with *C. difficile* colonization. Higher levels of total dietary fiber intake were also associated with increased colonization by bacteria within the order Clostridiales, the families Coriobacteriaceae, Lactobacillaceae, and Veillonellaceae, and the genera *Bifidobacterium*, and *Lactobacillus*.

Conclusion: Higher average daily dietary fiber (total, soluble, and insoluble) appears to be associated with lower odds of gut colonization with *C. difficile*. Future research should examine the impact of dietary interventions on *C. difficile* colonization and infection.

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2583. Short-term Impact of Antimicrobial Exposure on Fecal Carriage of Resistant Microorganisms

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Background: 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 microorganisms. 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.

Methods: 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 22 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).

Results: 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 organisms (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 ($P = .009$). 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.

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2584. Effects of Fecal Microbiota Transplantation for Decolonizing Multidrug-Resistant Organism

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Background: Increasing prevalence of multidrug-resistant microorganisms (MDRO) results in poor clinical outcomes, longer hospitalizations and higher health-care costs. It is likely that MDRO colonization can lead infections to vulnerable patients. Currently, however, MDRO decolonization strategies are lacking. The purpose of this study was to prove 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 unrelated 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 outcome 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 1 (75.0% 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 colonizer (75.0% vs. 38.5% 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