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

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 genomics DNA was sequenced using Illumina MiSeq platform. 16S rRNA sequencing was performed. Gut microbiota composition was analyzed using QIIME2.

Results: After 24 hours of exposure, mean Enterococcus counts were 4 × 10^4 cfu in the vancomycin arm and 6.2 × 10^3 cfu in the NS oil arm. Mean MRSA counts were 3.3 × 10^4 cfu in vancomycin arm and 3.1 × 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 × 10^4 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 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 C. difficile infection. Animal studies have shown potential benefits of dietary fiber in modulating C. difficile infection.

Methods: In 2006–2016, 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 from DNA being sequenced for 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 associated with colonization.

Results: Logistic analysis revealed increasing abundance of Bacteroidetes and Firmicutes was associated with colonization. Higher levels of total dietary fiber intake were also associated with lower odds of gut colonization with C. difficile. Future research should examine the impact of diet on colonization with 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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Session: 267. Microbiome, Antibiotics, and Pathogenesis Saturday, October 5, 2019: 12:15 PM

Background: The relationship between antimicrobial use and subsequent resistance is complicated; this study assesses the short-term impact of antimicrobial use on colonization with 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. Enterococcus species were the most common isolate (35%). Resistance analysis quantifies the effect of 1–2 weeks of systemic antimicrobial use on the fecal flora within 1 week of completing therapy. For each antimicrobial, the rates of decolonization were significantly different between CPE, VRE and CPE/VRE patients. Furthermore, microbiome analyses were performed to assess the effect of a natural and synthetic antimicrobial on 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 Organisms

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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 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 colonization with CPE, VRE, or CPE/VRE patients. BV and C. difficile were the primary outcomes. The parent study has enrolled 216 subjects, with 178 enrolled in the open-label, uncontrolled, single-center pilot study of FMT for digestive tract colonization CPE, VRE, or CPE/VRE patients between March 2018 and February 2019. Fecal sample obtained from healthy unrelated donors was infused to recipient’s gut. Fecal samples of recipients were collected before and after FMT until 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.

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 groups (75.0% vs. 38.5% vs. 66.7%, P = 0.018). Gut microbiota composition 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
decreasing abundance of Proteobacteria at 1 month after FMT in responders. However, those changes of microbial composition did not occur in non-responders.

**Conclusion:** FMT is an effective way to decolonize CPE and VRE by restoration of the gut microbiome.

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2585. Changing Epidemiological Profile of Infantile Parechovirus-A3 Infection in Japan

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**Session:** 268. Neonatal Infections - non CMV/HSV
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**Background:** Parechovirus-A3 (PeV-A3) causes severe disease, including sepsis and meningoencephalitis in young infants. The first case of PeV-A3 was reported in Japan in 1999 and, although epidemics have been reported every 2 to 3 years in more than 20 countries, no major epidemic has occurred in Japan since 2014.

**Methods:** This prospective study included febrile infants (<4 months of age) admitted at Niigata University and its affiliated hospitals, which serve about 2.5 million people, during the period from 2014 to 2018. Neonates and infants younger than 4 months presenting with fever and suspected of having viral sepsis underwent serum and/or cerebrospinal fluid (CSF) testing by real-time PCR for parechovirus-A (PeV-A) and enteroviruses (EVs), and for herpes simplex viruses, if suspected. Bacterial infection was excluded on the basis of the results of bacterial culture of blood, urine, and/or CSF. PeV-A genotype was identified by examining the viral protein 1 (VP1) sequence, and the phylogenetic tree of the VP1 sequence was constructed.

**Results:** Of the 277 patients evaluated, 135 (49%) were positive for PeV-A \( (n = 74, 27%) \) or EVs \( (n = 61, 22%) \). Among PeV-A patients, most had PeV-A3 \( (n = 69; 93\%) \), followed by PeV-A4 \( (n = 4; 5\%) \). There was a PeV-A3 epidemic in 2014 \( (n = 43) \); however, no cases were reported in 2015. In 2016–2018, small numbers of PeV-A3 cases were reported: 10 in 2016, 7 in 2017, and 9 in 2018. In contrast, EV cases were reported throughout this period: 8 in 2014, 22 in 2015, 10 in 2016, 5 in 2017, and 16 in 2018. When data were analyzed by season, the PeV-A3 detection rate in summer (June-August) was 93% \( (40/43) \) in 2014 and 65% \( (17/26) \) during 2016–2018, indicating an increase in the number of PeV-A3 cases in seasons other than summer. Phylogenetic analysis showed that PeV-A3 strains during 2016–2018 were part of a cluster of epidemics in 2011 and differed from those in 2014.

**Conclusion:** After the major PeV-A3 epidemics in 2014, we observed changes in the PeV-A3 epidemic profile, namely, a small, but constant, number of cases every year in Niigata, Japan. A future study should investigate if this trend has continued in Japan and other countries and identify the causes of this change in epidemic profile.

**Table 2. Impact of FMT on complete and partial MRDo decolonization, with or without ATB during the first 3 weeks after transplantation**

| Time Period | Complete MRDo Decolonization | Partial MRDo Decolonization |
|-------------|------------------------------|----------------------------|
| [0, 1] months | [2, 3] months | [4, 6] months | [0, 1] months | [2, 3] months | [4, 6] months |
| Number (%) | Number (%) | Number (%) | Number (%) | Number (%) | Number (%) |

**Figure 1. Decolonization delay of carbapenem-producing enterobacteriaceae (CPE) vs vancomycin-resistant enterococci (VRE) vs CPE/VRE**

**Figure 2. Changes of microbiome composition by phylum level.**

**Figure 2-1. Responders**

**Figure 2-2. Non-responders**

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