2570. A Randomized Controlled Trial of Lactobacillus rhamnosus GG on Multidrug-Resistant Organism (MDRO) Colonization
Adriana M. Rauseo, MD;1 Tiffany Hink, BS, MT, ASCP2; Kimberly Reske, MPH1; Sondra Seiler, BA1; Kerry Bommarito, PhD3; Victoria J. Fraser, MD;4 Carey-Ann D. Burnham, PhD5; Erik R. Dubberke, MD, MPH6,1; Washington University at St. Louis, St. Louis, Missouri,3
Session: 267. Microbiome, Antibiotics, and Pathogenesis
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Background. MDRO present a greater threat to public health than ever before, and antimicrobial options are decreasing. Altered colonic microbiota following antimicrobial exposure allows for subsequent colonization by MDRO. Ingestion of probiotics such as Lactobacillus rhamnosus GG (LGG) could be an approach to prevent the spread of, and subsequent infection due to MDRO, by promoting a healthy bacterial milieu within the colon.
Methods. This is a prospective, double-blinded, randomized clinical trial in which a total of 87 subjects on broad-spectrum antibiotics were randomized to receive LGG twice daily (n = 43) vs placebo (n = 44). Stool or rectal swab specimens were collected for culture at enrollment, every 3 days during admission, and at discharge. Selective media were used to detect the following MDRO: Clostridium difficile (CD), vancomycin-resistant Enterococcus (VRE), and antibiotic-resistant Gram-negatives (GN). The primary outcome was MDRO acquisition. Secondary outcomes included analysis for loss of any MDRO if colonized at enrollment, and acquisition or loss of individual MDRO.
Results. Subjects in both groups had similar prevalence of colonization with any MDRO at study enrollment (LGG 40% vs. placebo 39%), with similar colonization prevalence for individual MDRO (Figure 1). There was no difference in any MDRO acquisition (LGG 27%, placebo 33%, OR 1.36, 95% CI 0.42–4.41) or any individual MDRO acquisition (Figure 2). There was also no difference in any MDRO (LGG 18%, placebo 24%, OR 0.77, 95% CI 0.24–2.72) or any individual MDRO (Figure 2). LGG administration did not prevent acquisition of MDRO or accelerate loss of MDRO colonization.

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2571. Norovirus Infection and Gut Microbiota in Transplant Recipients
Sarah K. Hussain, MD;1 Christina Chong, MS;2 Victoria J. Fraser, MD;2 Carey-Ann D. Burnham, PhD5; Rebecca Brotman, PhD, MPH3,4; Courtney Robinson, MS2; Jacques Ravel, PhD2; Susan Tuddenham, MD, MPH1;3 Johns Hopkins University School of Medicine, Baltimore, Maryland;4 University of Maryland Institute for Genome Sciences, Baltimore, Maryland
Session: 267. Microbiome, Antibiotics, and Pathogenesis
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Background. The impact of antibiotics on the composition of the vaginal microbiota (VMB) is poorly defined. We analyzed the VMB of women before and after the use of antibiotics.
Methods. We used samples from a cohort of reproductive-aged women who submitted vaginal swabs and clinical data over a 2-year period. 16S RNA gene sequencing was conducted, and VMB was categorized into 7 community state types (CSTs): four dominated by Lactobacillus spp. (CST VI), three low in Lactobacillus spp. and three low in Bacteroides spp. (CST VII), or comprising a variety of anaerobes (CST IV). CSTs were further categorized as

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2572. The Impact of Antibiotics on the Composition of the Vaginal Microbiota
Sima L. Sharara, MD;1 Khalid Ghannem, MD, PhD2; Rebecca Brotman, PhD, MPH3; Courtney Robinson, MS2; Jacques Ravel, PhD2; Susan Tuddenham, MD, MPH1;3 Johns Hopkins University School of Medicine, Baltimore, Maryland;2 University of Maryland Institute for Genome Sciences, Baltimore, Maryland
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Background. In vitro studies have shown that enteric viruses require the gut microbiota (specific members of the Enterobacteriaceae family) for efficient infection of the gastrointestinal tract. Human norovirus (NV) infection in transplant recipients may be chronic and severe. The role of gut microbiota has not been defined in this setting. We hypothesized that gut microbiota diversity and composition are different in norovirus-infected transplant patients.
Methods. We recruited a single-center, pilot, prospective cohort study of adult solid-organ transplant and hematopoietic stem cell transplant recipients with diarrhea. Serial fecal samples were collected and processed for gDNA. Norovirus levels were quantified by PCR and gut microbiota profiling determined by 16S rRNA gene sequencing.

Results. Twenty-five transplant recipients were included; 9 with NV infection and 16 without. Age (61 ± SEM 2.3 years vs. 54 ± 3.5 years; P = 0.172), duration of diarrhea prior to diagnosis (105 ± SEM 43 days vs. 20 ± 7 days; P = 0.146), prior cumulative antibiotic use (42 ± 12 days vs. 46 ± 17 days; P = 0.646), anti-anaerobic antibiotic use (7 ± 3 days vs. 11 ± 6 days; P = 0.643) and length of hospitalization (12 ± 6 days vs. 12 ± 6 days; P = 0.649) were not different between transplant recipients with and without NV infection. Interestingly, the relative abundance of Enterobacteriaceae was significantly higher in NV-infected transplant recipients compared with those without NV infection (26 ± 5.8% vs. 6 ± 2.8%; P = 0.017, Mann–Whitney) (Figure 1). In contrast, the abundance of the Phyla Bacteroidetes (11.2 ± 5.3% vs. 26.3 ± 6.5%; P = 0.191), and Firmicutes (26.8 ± 7.6% vs. 24.9 ± 4.7%; P = 0.803), were not significantly different between those who were NV and not NV-infected. Of note, the diversity metrics of Shannon (3.5 ± 0.4 vs. 3.8 ± 0.3; P = 0.637) and inverse Simpson indices (1.3 ± 0.1 vs. 1.13 ± 0.1; P = 0.649) were not significantly different between the two groups.

Conclusion. Norovirus-infected transplant recipients had a significantly higher relative abundance of Enterobacteriaceae in their gut microbiota compared with transplant recipients without norovirus infection. Future studies are needed to explore if this association is mechanistically important for norovirus infection.

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2573. Multidrug-Resistant Organism (MDRO) Colonization
Sarah K. Hussain, MD;1 Christina Chong, MS;2 Victoria J. Fraser, MD;2 Carey-Ann D. Burnham, PhD5; Rebecca Brotman, PhD, MPH3,4; Courtney Robinson, MS2; Jacques Ravel, PhD2; Susan Tuddenham, MD, MPH1;3 Johns Hopkins University School of Medicine, Baltimore, Maryland;4 University of Maryland Institute for Genome Sciences, Baltimore, Maryland
Session: 267. Microbiome, Antibiotics, and Pathogenesis
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Background. The impact of antibiotics on the composition of the vaginal microbiota (VMB) is poorly defined. We analyzed the VMB of women before and after the use of antibiotics.
Methods. We used samples from a cohort of reproductive-aged women who submitted vaginal swabs and clinical data over a 2-year period. 16S RNA gene sequencing was conducted, and VMB was categorized into 7 community state types (CSTs): four dominated by Lactobacillus spp. and three low in Lactobacillus spp., dominated by Streptococcus spp. (CST VI), Bifidobacterium spp. (CST VII), or comprising a variety of anaerobes (CST IV). CSTs were further categorized as

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began in a LD state transitioned to a non-LD state after antibiotics. 12 controls were in an NLD state at baseline, of these 11 remained NLD at the second time point. 44 controls started in an LD state and all remained in LD at the second time point.

**Conclusion.** In the short term, metronidazole results in a transition of the VMB from a NLD to a L. iners-dominated state. There was little impact of non-nitromida-

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