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Session: 214. Optimizing HIV Treatment
Saturday, October 6, 2018: 10:30 AM

Background. Unmet needs among hospitalized patients with HIV may prevent engagement in HIV care leading to worse clinical outcomes. Our aim was to examine the role of unmet subsistence needs (e.g., housing, transportation, food) and medical needs (e.g., mental health, substance abuse treatment) as barriers for retention in HIV care and viral load (VL) suppression.

Methods. We utilized data from the Mentor Approach for Promoting Patients’ Self-Care intervention study, the enrolled hospitalized HIV+ patients at a large publicly funded hospital between 2010 and 2013, who were out-of-care. We examined the effect of unmet needs on retention in HIV care (attended HIV appointments within 0–30 days and 30–180 days) and viral load suppression, 6 months after discharge.

Results. A total of 417 participants were enrolled, 78% reported having 2+ unmet need at baseline, most commonly dental care (55%), financial (43%), or housing needs (34%). Participants with unmet needs at baseline, compared with those with no needs, were more likely to be African American, have an existing HIV diagnosis, and be uninsured. Among participants who completed a baseline and 3-month survey (n = 320), 45% reported a need for dental care, 42% reported financial needs, and 32% reported housing needs that were unmet at either time point (Figure 1). Having a dental care need at baseline that was met was significantly associated with higher odds of VL improvements at 6-month follow-up (OR: 2.2; 95% CI: 1.04–4.50, P = 0.03) and higher odds for retention in care (OR: 2.06; 95% CI: 1.05–4.07, P = 0.04). An unmet need for transportation was associated with lower odds of retention in care (OR: 0.5; 95% CI: 0.34–0.94, P = 0.03), even after adjusting for other factors. Compared with participants with no need, those who reported ≥3 unmet subsistence needs were less likely to demonstrate viral load improvement (OR: 0.51; 95% CI: 0.28–0.92, P = 0.03) and to be retained in care (OR: 0.52; 95% CI: 0.28–0.95, P = 0.03).

Conclusion. An important and novel finding in our study is that the number of unmet subsistence needs had a significant effect on retention in care and VL suppression. Broader access to programs that can assist in meeting subsistence needs among hospitalized patients could have significant individual and public health benefits.

Disclosures. All authors: No reported disclosures.

1772. Vancomycin-Resistant Enterococcus Alter the Gastrointestinal Microbiome in Critically Ill Patients
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Session: 215. Translating Microbiome Science into Practice
Saturday, October 6, 2018: 10:30 AM

Background. In critically ill patients, rectal colonization with VRE is associated with an increased risk for nosocomial infection or death. In mice, fecal transplantation of Probiotica producta directly inhibits VRE growth and leads to clearance of VRE. We performed a prospective, intensive care unit (ICU)-based study to evaluate the relationship between B. producta and VRE. We also sought to determine the relationship between VRE, MRSA, and other common MDR bacteria.

Methods. This study included 97 adults newly admitted to the ICU between February 2015 and June 2016. Rectal swabs were obtained at time of ICU admission and 72 hours later. VRE rectal colonization status was determined categorically for each sample by culture on selective media. Specimens were also cultured for methicillin-resistant Staphylococcus aureus (MRSA) and for other MDR pathogens, defined as those with nonsusceptibility to 3 or more antibiotics classes. 16S rRNA gene sequencing was performed and the relative abundance was calculated for B. producta. Differentially abundant bacteria taxa between VRE positive and VRE negative specimens were assessed using linear discriminant analysis effect size (LDA) analysis.

Results. Among the 97 patients, 7 (7.2%) were colonized with VRE at the time of ICU admission and 3 (3.3%) of the remaining patients became colonized 72 hours later. The microbiome composition differed significantly when accounting for VRE colonization status. The relative abundance of B. producta was 140-fold higher in VRE-positive compared with VRE-positive samples (0.0012% vs. 8.48 × 10⁻⁶%, P = 0.03). On LDA analysis, there was also significantly lower differential abundance of B. producta when VRE was present (LDA score 4.65). The presence of VRE in culture was significantly associated with the co-presence of MRSA (23.5% co-colonized if VRE positive vs. 8.4% if VRE negative, P = 0.046) but with the co-presence of MDR Gram-negative bacteria (29.4% if colonized if VRE positive vs. 34.3% if VRE negative, P = 0.68).

Conclusion. In this ICU cohort, rectal colonization with VRE was inversely associated with the putatively protective organism B. producta. VRE was associated with rectal colonization with MDR Gram-negative bacteria. B. producta may have promise as a probiotic designed to prevent VRE colonization.

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1773. Impact of Antibiotics Used to Treat Community Acquired Pneumonia on the Gut Microbiome and Resistome in Healthy Volunteers
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Session: 215. Translating Microbiome Science into Practice
Saturday, October 6, 2018: 10:30 AM

Background. Antibiotic resistance harbored in gut microbiota contributes to the emergence of multi-drug-resistant organisms (MDRO). Pediatric leukemia patients typically receive extensive antibiotics and are at higher risk for infection due to MDRO.

Methods. A prospective cohort of children (n = 242) with acute lymphoblastic leukemia self-collected stool samples at diagnosis and after induction chemotherapy. A third of patients initiated an antibiotic-driven probabilistic prophylaxis. Levofloxacin (LV) given once neutropenia develops. With neutropenic fever patients typically receive extensive antibiotics and are at higher risk for infection due to MDRO.

Disclosures. J. Wolf, Karius Inc.: Investigator, Research support.

Figure 1. Percentage of participants with a specific need that was met or continued at baseline (n=477), top bar, and the percentage of participants with a specific need that was met or continued at baseline at each time point at 3 months follow-up, bottom bar (n=230).

Antibiotic resistance harbored in gut microbiota contributes to the emergence of multi-drug-resistant organisms (MDRO). Pediatric leukemia patients typically receive extensive antibiotics and are at higher risk for infection due to MDRO.

Methods. A prospective cohort of children (n = 242) with acute lymphoblastic leukemia self-collected stool samples at diagnosis and after induction chemotherapy. A third of patients initiated an antibiotic-driven probabilistic prophylaxis. Levofloxacin (LV) given once neutropenia develops. With neutropenic fever patients typically receive extensive antibiotics and are at higher risk for infection due to MDRO.

Results. Expected changes in the community composition were discovered with LV prophylaxis, including the loss of many Enterobacteriaceae and Enterococaceae species, offset by increases in Bacteroides species. Unexpectedly, LV prophylaxis reduced the acquisition of VanA cluster of vancomycin resistance genes and did not increase acquisition of β-lactamase or fluoroquinolone (FQ) resistance gene families.

Conclusion. LV prophylaxis during leukemia treatment impacts predictable changes in gut bacterial communities but counter intuitively decreases antibiotic resistance in the gut microbiome reservoir. The reduction in VanA cluster of genes is likely due to depletion of Enterococaceae species via direct killing or loss of synergistic partners. The lack of increase in target (FQ) or off-target resistance suggests that prophylaxis altered common community selective pressures or prophylaxis drug concentrations were sufficient to limit the outgrowth of resistant mutants.

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Recurrence of CDI (rCDI) is associated with perturbation of the human gut microbiome and clinical outcomes is presented. Here correlation of reduced microbiome species diversity and richness, and an increase in ARG abundance across all samples (P < 0.003). Within each ARG, there were unique changes in ARG abundance, and groups with CF had increases in ARG abundance (Figure 2).

Conclusion. ABX used to treat CAP can cause acute microbiome disruptions, as evidenced by decreased microbiome species diversity and richness, and an increase in ARG abundance post-ABX. The duration of this impact is variable. To prevent microbiome disruptions, measures to prevent inappropriate ABX use via ABX stewardship are necessary.

1774. Ridinilazole (RDZ) for Clostridium difficile infection (CDI): Correlation of In Vitro Spectrum of Activity with Human Gut Microbiome Profiles from a Phase 2 Clinical Trial

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Background. Recurrence of CDI (rCDI) is associated with perturbation of the gut microbiome during treatment with vancomycin (VAN) or metronidazole (MTZ). RDZ is a novel, targeted spectrum antibiotic under investigation to treat CDI and reduce rCDI. Here correlation of in vitro spectrum of activity with preservation of the human gut microbiome and clinical outcomes is presented.

Methods. Susceptibility testing was to CLSI standards with VAN, MTZ, and fidaxomycin (FID) comparators. The Phase 2 clinical trial was a double-blind, randomized study of 100 patients assigned 1:1 to 10 days RDZ 200 mg BID or VAN 125 mg QID treatment. Primary endpoint was sustained clinical response (SCR), defined as cure at end of therapy (EOT), and no rCDI for the next 30 days. Relative effects of RDZ and VAN on the gut microbiome were examined by sequencing 165 rRNA amplicons from stool collected at baseline, days 5, 10, 25, and end of study. Bioinformatic analyses were performed in QIIME. Results. RDZ C. difficile (N = 50) MIC range was 0.125–0.25 μg/mL. C. difficile spp. showed varied RDZ susceptibility: C. innocuum MIC50 1 μg/mL, C. ramosum and C. perfringens MIC90 >512 μg/mL. VAN showed potent to moderate growth inhibition of all C. difficile spp. (MIC range 1–16 μg/mL). Limited RDZ activity was observed for Gram-positive anaerobes, including Bifidobacteria, Eubacterium, Peptostreptococcus, and Peptostreptococcus spp. MIC90 >512, 64, and 64 μg/mL compared with VAN (MIC50 1, 4, 0.5, and 0.5 μg/mL). Bacteroides fragilis MIC50 for RDZ and VAN were >512 and 64 μg/mL, respectively. These in vitro data correlate closely with human microbiome profiles. RDZ reduced C. difficile to below detection with other reductions in abundance observed in only 2 families from the Clostridium. VAN at EOT resulted in significant losses, often below detection, in 4 Firmicutes families, Actinobacteria, and Bacteroidetes and a 25-fold increase in Proteobacteria abundance. The preservation of the microbiome by RDZ likely accounted for reduced rCDI compared with VAN with RDZ shown to be superior on SCR to VAN with rates of 66.7% and 42.4%, respectively (pre-specified 90% CI 3.1, 39.1).

Conclusion. These data demonstrate strong translation of in vitro spectrum to human gut microbiome preservation during therapy and support further clinical development of RDZ.