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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 ≥1 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.
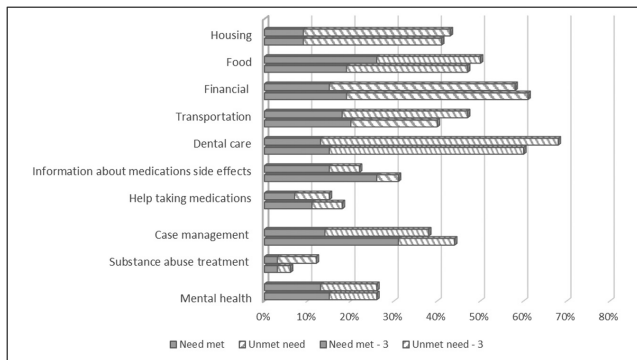

Figure 1. Percentage of participants with a specific need that was met or unmet at baseline (n=417), top bar, and the percentage of participants with a specific need that was met at both time points or unmet at either time point at 3-month follow-up, bottom bar (n = 320).

Disclosures. All authors: No reported disclosures.

1771. Gut Resistome Changes in Response to Prophylactic Antibiotic Administration During Chemotherapy in Children With Acute Lymphoblastic Leukemia

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Session: 215. Translating Microbiome Science into Practice
Saturday, October 6, 2018: 10:30 AM

Background. Antibiotic resistance harbored in gut microbiome 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 chemothearpy. A third of patients ($n = 69$) underwent protocol-driven antibiotic prophylaxis: Levofloxacin (LV) given once neutropenia develops. With neutropenic fever patients on prophylaxis stopped LV and all patients received cefepime. Using metagenomic sequencing, we identified bacterial community composition and after alignment to the Comprehensive Antibiotic Resistance Database were able to determine the presence of bacterial resistance genes in 168 stool samples from 49 patients.

Results. Expected changes in the community composition were discovered with LV prophylaxis, including the loss of many *Enterobacteriaceae* and *Enterococcaceae*

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 imparts 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 *Enterococcaceae* species via direct killing or loss of synergistic partners. The lack of increase in target (FQ) or off-target resistance suggests that prophylaxis altered community selective pressures or prophylaxis drug concentrations were sufficient to limit the outgrowth of resistant mutants.

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

1772. Vancomycin-Resistant Enterococcus Alters 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 *Blautia 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 MDR Gram-negatives, defined as those with nonsusceptibility to 3 or more antibiotic 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 (LefSe) 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-negative compared with VRE-positive samples (0.0012% vs. 8.48×10^{-6}%, $P = 0.03$). On LefSe 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 not with the copresence of MDR Gram-negative bacteria (29.4% if cocolonized 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 co-colonization with MRSA but not with MDR Gram-negative bacteria. *B. producta* may have promise as a probiotic designed to prevent VRE colonization.

Disclosures. All authors: No reported disclosures.

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. Antibiotics (ABX) are frequently inappropriately used to treat non-bacterial causes of respiratory illnesses. The goal of this prospective cohort study was to characterize the impact of ABX used to treat community-acquired pneumonia (CAP) on the fecal microbiome and resistome in healthy volunteers (HV).

Methods. Twenty HVs were randomized to receive 5 days of levofloxacin (LV), azithromycin (AZ), cefpodoxime (CF), or AZ+CF. Stool was collected before, during, and after ABX, then underwent microbiologic culture and shotgun sequencing. DNA was extracted, then sequenced using the Illumina NextSeq platform. Relative abundance of bacterial taxa was estimated by MetaPhlAn and antibiotic resistance gene (ARG) composition by ShortBRED. Analysis was in R.

Results. The mean HV age was 37 (range 24–59) and 10 were female. Species diversity measured via Shannon Index and richness were significantly lower in samples taken from all HVs 3 days post-ABX ($P < 0.01$ for all). While nonmetric