

Figure 3: Effect of the monitoring interval during TI (days) on the reported adverse events. The area of circles is proportional to the sample size.

Disclosures. All authors: No reported disclosures.

1768. Efficacy and Safety of Switching From Boosted-Protease Inhibitors (bPI) Plus Emtricitabine/Tenofovir Disoproxil Fumarate (F/TDF) Regimens to the Once Daily (QD), Single-Tablet Regimen (STR) of Darunavir/Cobicistat/Emtricitabine/Tenofovir Alafenamide (D/C/F/TAF) in Virologically Suppressed, HIV-1-Infected Adults: Week 96 Results of the Phase 3, Randomized, Non-Inferiority EMERALD Trial

Joseph Eron Jr., MD¹; Chloe Orkin, MBBCh²; Douglas Cunningham, DO³; Federcio Pulido, MD⁴; Frank Post, MD PhD⁵; Stéphane De Wit, MD⁶; Erkki Lathouwers, PhD⁷; Veerle Hufkens, MSc⁷; Romana Petrovic, MSc⁷; Erika Van Landuyt, MD⁷ and the EMERALD Study Group, ¹The University of North Carolina at Chapel Hill, School of Medicine, Chapel Hill, North Carolina, ²Department of Infection and Immunity, Royal London Hospital and Queen Mary University, Barts Health NHS Trust, London, UK, ³Pueblo Family Physicians, Phoenix, Arizona, ⁴HIV Unit, Hospital 12 de Octubre, Madrid, Spain, ⁵King's College Hospital NHS Foundation Trust, London, UK, ⁶Saint-Pierre University Hospital, Université Libre de Bruxelles, Brussels, Belgium and ⁷Janssen Pharmaceutica NV, Beerse, Belgium

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

Background. The QD STR D/C/F/TAF 800/150/200/10 mg was noninferior to bPI + F/TDF at 48 weeks in EMERALD. Efficacy and safety of D/C/F/TAF through week 96 are presented.

Methods. EMERALD (NCT02269917) is a randomized, active-controlled, open-label, international, multicenter noninferiority trial. Virologically suppressed (VL < 50 c/mL for ≥ 2 months) ART experienced (previous non-DRV VF allowed) HIV-1-infected adults were randomized (2:1) to switch to D/C/F/TAF or continue bPI + F/TDF over 48 weeks. Patients could then continue on D/C/F/TAF or switch from bPI + F/TDF to D/C/F/TAF at week 52 (Late switch, 44 weeks D/C/F/TAF exposure) in a single-arm extension phase until week 96. The percentage of patients with virologic rebound (confirmed VL ≥ 50 c/mL) cumulative through week 48 and week 96 were primary and secondary endpoints, respectively.

Results. Of 1141 randomized and treated patients (58% had received ≥ 5 previous ARVs including screening ARVs; 15% had previous non-DRV VF), 1,080 continued in the extension phase (N = 728 D/C/F/TAF; N = 352 late switch). Few patients had virologic rebound cumulative through week 96 in the D/C/F/TAF arm (3.1%, 24/763). Virologic rebound occurred in 2.3% (8/352) in the late switch arm over 44 weeks D/C/F/TAF treatment. Many rebounders (14/24 and 2/8) resuppressed by week 96. At week 96 a high percentage of patients in the D/C/F/TAF arm (90.7%, 692/763) were suppressed (VL < 50 c/mL). In the late switch arm, 93.8% (330/352) maintained virologic suppression after 44 weeks of treatment. No DRV, primary PI, TFV, or FTC RAMs were seen post baseline. Few serious AEs and AE related discontinuations occurred in either arm (Table 1). Improvements in renal and bone parameters were maintained in the D/C/F/TAF arm and seen in the late switch arm (week 52–96), with a small change in TC/HDL-C ratio (Table 1).

Conclusion. Switching to D/C/F/TAF maintained high virologic suppression rates (>90%) at week 96 with no resistance development, and was well tolerated over 96 weeks with bone, renal, and lipid safety consistent with known TAF and cobicistat profiles. Efficacy and safety results in the late switch arm were consistent with week 48 results in the D/C/F/TAF arm. D/C/F/TAF combines the efficacy and high genetic barrier to resistance of DRV with the safety benefits of TAF, even in patients with a history of non-DRV VF.

Table 1: Treatment-emergent AEs and changes in renal, lipid and bone parameters of Week 96

Treatment-emergent AEs, n (%)	D/C/F/TAF (n=728)		P-value ¹	D/C/F/TAF (n=352)		P-value ²
	Number	%		Number	%	
AEs by organ system						
GI	103 (14)	14.1	NS	50 (14)	14.2	NS
Gen	14 (2)	1.9	NS	10 (3)	2.8	NS
Respiratory	10 (1)	1.4	NS	10 (3)	2.8	NS
DERM	9 (1)	1.2	NS	1 (0)	0	NS
Other	10 (1)	1.4	NS	10 (3)	2.8	NS
AEs by severity						
AEs, all levels (n=)	117	16.1	NS	74	21.0	NS
AEs, all levels (%)	16.1	2.2	NS	21.0	6.0	NS
AEs, grade 1-2 (n=)	103	14.1	NS	50	14.2	NS
AEs, grade 1-2 (%)	14.1	1.9	NS	14.2	4.0	NS
AEs, grade 3-4 (n=)	14	1.9	NS	10	2.8	NS
AEs, grade 3-4 (%)	1.9	0.3	NS	2.8	0.8	NS
AEs, grade 5 (n=)	0	0	NS	0	0	NS
AEs, grade 5 (%)	0	0	NS	0	0	NS
AEs, grade 6 (n=)	0	0	NS	0	0	NS
AEs, grade 6 (%)	0	0	NS	0	0	NS
AEs, grade 7 (n=)	0	0	NS	0	0	NS
AEs, grade 7 (%)	0	0	NS	0	0	NS
AEs, grade 8 (n=)	0	0	NS	0	0	NS
AEs, grade 8 (%)	0	0	NS	0	0	NS
AEs, grade 9 (n=)	0	0	NS	0	0	NS
AEs, grade 9 (%)	0	0	NS	0	0	NS
AEs, grade 10 (n=)	0	0	NS	0	0	NS
AEs, grade 10 (%)	0	0	NS	0	0	NS
AEs, grade 11 (n=)	0	0	NS	0	0	NS
AEs, grade 11 (%)	0	0	NS	0	0	NS
AEs, grade 12 (n=)	0	0	NS	0	0	NS
AEs, grade 12 (%)	0	0	NS	0	0	NS
AEs, grade 13 (n=)	0	0	NS	0	0	NS
AEs, grade 13 (%)	0	0	NS	0	0	NS
AEs, grade 14 (n=)	0	0	NS	0	0	NS
AEs, grade 14 (%)	0	0	NS	0	0	NS
AEs, grade 15 (n=)	0	0	NS	0	0	NS
AEs, grade 15 (%)	0	0	NS	0	0	NS
AEs, grade 16 (n=)	0	0	NS	0	0	NS
AEs, grade 16 (%)	0	0	NS	0	0	NS
AEs, grade 17 (n=)	0	0	NS	0	0	NS
AEs, grade 17 (%)	0	0	NS	0	0	NS
AEs, grade 18 (n=)	0	0	NS	0	0	NS
AEs, grade 18 (%)	0	0	NS	0	0	NS
AEs, grade 19 (n=)	0	0	NS	0	0	NS
AEs, grade 19 (%)	0	0	NS	0	0	NS
AEs, grade 20 (n=)	0	0	NS	0	0	NS
AEs, grade 20 (%)	0	0	NS	0	0	NS
AEs, grade 21 (n=)	0	0	NS	0	0	NS
AEs, grade 21 (%)	0	0	NS	0	0	NS
AEs, grade 22 (n=)	0	0	NS	0	0	NS
AEs, grade 22 (%)	0	0	NS	0	0	NS
AEs, grade 23 (n=)	0	0	NS	0	0	NS
AEs, grade 23 (%)	0	0	NS	0	0	NS
AEs, grade 24 (n=)	0	0	NS	0	0	NS
AEs, grade 24 (%)	0	0	NS	0	0	NS
AEs, grade 25 (n=)	0	0	NS	0	0	NS
AEs, grade 25 (%)	0	0	NS	0	0	NS
AEs, grade 26 (n=)	0	0	NS	0	0	NS
AEs, grade 26 (%)	0	0	NS	0	0	NS
AEs, grade 27 (n=)	0	0	NS	0	0	NS
AEs, grade 27 (%)	0	0	NS	0	0	NS
AEs, grade 28 (n=)	0	0	NS	0	0	NS
AEs, grade 28 (%)	0	0	NS	0	0	NS
AEs, grade 29 (n=)	0	0	NS	0	0	NS
AEs, grade 29 (%)	0	0	NS	0	0	NS
AEs, grade 30 (n=)	0	0	NS	0	0	NS
AEs, grade 30 (%)	0	0	NS	0	0	NS
AEs, grade 31 (n=)	0	0	NS	0	0	NS
AEs, grade 31 (%)	0	0	NS	0	0	NS
AEs, grade 32 (n=)	0	0	NS	0	0	NS
AEs, grade 32 (%)	0	0	NS	0	0	NS
AEs, grade 33 (n=)	0	0	NS	0	0	NS
AEs, grade 33 (%)	0	0	NS	0	0	NS
AEs, grade 34 (n=)	0	0	NS	0	0	NS
AEs, grade 34 (%)	0	0	NS	0	0	NS
AEs, grade 35 (n=)	0	0	NS	0	0	NS
AEs, grade 35 (%)	0	0	NS	0	0	NS
AEs, grade 36 (n=)	0	0	NS	0	0	NS
AEs, grade 36 (%)	0	0	NS	0	0	NS
AEs, grade 37 (n=)	0	0	NS	0	0	NS
AEs, grade 37 (%)	0	0	NS	0	0	NS
AEs, grade 38 (n=)	0	0	NS	0	0	NS
AEs, grade 38 (%)	0	0	NS	0	0	NS
AEs, grade 39 (n=)	0	0	NS	0	0	NS
AEs, grade 39 (%)	0	0	NS	0	0	NS
AEs, grade 40 (n=)	0	0	NS	0	0	NS
AEs, grade 40 (%)	0	0	NS	0	0	NS
AEs, grade 41 (n=)	0	0	NS	0	0	NS
AEs, grade 41 (%)	0	0	NS	0	0	NS
AEs, grade 42 (n=)	0	0	NS	0	0	NS
AEs, grade 42 (%)	0	0	NS	0	0	NS
AEs, grade 43 (n=)	0	0	NS	0	0	NS
AEs, grade 43 (%)	0	0	NS	0	0	NS
AEs, grade 44 (n=)	0	0	NS	0	0	NS
AEs, grade 44 (%)	0	0	NS	0	0	NS
AEs, grade 45 (n=)	0	0	NS	0	0	NS
AEs, grade 45 (%)	0	0	NS	0	0	NS
AEs, grade 46 (n=)	0	0	NS	0	0	NS
AEs, grade 46 (%)	0	0	NS	0	0	NS
AEs, grade 47 (n=)	0	0	NS	0	0	NS
AEs, grade 47 (%)	0	0	NS	0	0	NS
AEs, grade 48 (n=)	0	0	NS	0	0	NS
AEs, grade 48 (%)	0	0	NS	0	0	NS
AEs, grade 49 (n=)	0	0	NS	0	0	NS
AEs, grade 49 (%)	0	0	NS	0	0	NS
AEs, grade 50 (n=)	0	0	NS	0	0	NS
AEs, grade 50 (%)	0	0	NS	0	0	NS
AEs, grade 51 (n=)	0	0	NS	0	0	NS
AEs, grade 51 (%)	0	0	NS	0	0	NS
AEs, grade 52 (n=)	0	0	NS	0	0	NS
AEs, grade 52 (%)	0	0	NS	0	0	NS
AEs, grade 53 (n=)	0	0	NS	0	0	NS
AEs, grade 53 (%)	0	0	NS	0	0	NS
AEs, grade 54 (n=)	0	0	NS	0	0	NS
AEs, grade 54 (%)	0	0	NS	0	0	NS
AEs, grade 55 (n=)	0	0	NS	0	0	NS
AEs, grade 55 (%)	0	0	NS	0	0	NS
AEs, grade 56 (n=)	0	0	NS	0	0	NS
AEs, grade 56 (%)	0	0	NS	0	0	NS
AEs, grade 57 (n=)	0	0	NS	0	0	NS
AEs, grade 57 (%)	0	0	NS	0	0	NS
AEs, grade 58 (n=)	0	0	NS	0	0	NS
AEs, grade 58 (%)	0	0	NS	0	0	NS
AEs, grade 59 (n=)	0	0	NS	0	0	NS
AEs, grade 59 (%)	0	0	NS	0	0	NS
AEs, grade 60 (n=)	0	0	NS	0	0	NS
AEs, grade 60 (%)	0	0	NS	0	0	NS
AEs, grade 61 (n=)	0	0	NS	0	0	NS
AEs, grade 61 (%)	0	0	NS	0	0	NS
AEs, grade 62 (n=)	0	0	NS	0	0	NS
AEs, grade 62 (%)	0	0	NS	0	0	NS
AEs, grade 63 (n=)	0	0	NS	0	0	NS
AEs, grade 63 (%)	0	0	NS	0	0	NS
AEs, grade 64 (n=)	0	0	NS	0	0	NS
AEs, grade 64 (%)	0	0	NS	0	0	NS
AEs, grade 65 (n=)	0	0	NS	0	0	NS
AEs, grade 65 (%)	0	0	NS	0	0	NS
AEs, grade 66 (n=)	0	0	NS	0	0	NS
AEs, grade 66 (%)	0	0	NS	0	0	NS
AEs, grade 67 (n=)	0	0	NS	0	0	NS
AEs, grade 67 (%)	0	0	NS	0	0	NS
AEs, grade 68 (n=)	0	0	NS	0	0	NS
AEs, grade 68 (%)	0	0	NS	0	0	NS
AEs, grade 69 (n=)	0	0	NS	0	0	NS
AEs, grade 69 (%)	0	0	NS	0	0	NS
AEs, grade 70 (n=)	0	0	NS	0	0	NS
AEs, grade 70 (%)	0	0	NS	0	0	NS
AEs, grade 71 (n=)	0	0	NS	0	0	NS
AEs, grade 71 (%)	0	0	NS	0	0	NS
AEs, grade 72 (n=)	0	0	NS	0	0	NS
AEs, grade 72 (%)	0	0	NS	0	0	NS
AEs, grade 73 (n=)	0	0	NS	0	0	NS
AEs, grade 73 (%)	0	0	NS	0	0	NS
AEs, grade 74 (n=)	0	0	NS	0	0	NS
AEs, grade 74 (%)	0	0	NS	0	0	NS
AEs, grade 75 (n=)	0	0	NS	0	0	NS
AEs, grade 75 (%)	0	0	NS	0	0	NS
AEs, grade 76 (n=)	0	0	NS	0	0	NS
AEs, grade 76 (%)	0	0	NS	0	0	NS
AEs, grade 77 (n=)	0	0	NS	0	0	NS
AEs, grade 77 (%)	0	0	NS	0	0	NS
AEs, grade 78 (n=)	0	0	NS	0	0	NS
AEs, grade 78 (%)	0	0	NS	0	0	NS
AEs, grade 79 (n=)	0	0	NS	0	0	NS
AEs, grade 79						

Effectiveness, and Safety, Michael E. DeBakey Veterans Affairs Medical Center, Houston, Texas, ³Department of Medicine, Section of Health Services Research, Baylor College of Medicine, Houston, Texas, ⁴School of Public Health, University of Michigan, Ann Arbor, Michigan and ⁵Department of General Internal Medicine, The University of Texas M.D. Anderson Cancer Center, Houston, Texas

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.

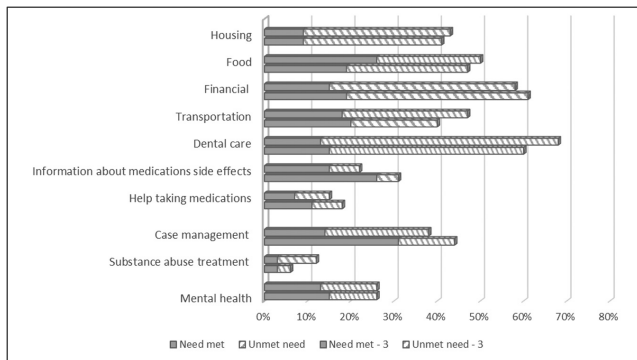


Figure 1. Percentage of participants with a specific need that was met or unmet at baseline ($n=417$), top bar, and the percentage of participants with a specific need that was met at both time points or unmet at either time point at 3-month follow-up, bottom bar ($n = 320$).

Disclosures. All authors: No reported disclosures.

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

Ellie Margolis, MD PhD¹; Hana Hakim, MD, MS¹; Jiangwei Yao, PhD¹; Jason Rosch, PhD¹; Li Tang, PhD²; Yilun Sun, MS²; Ronald Dallas, PhD¹ and Joshua Wolf, MBBS FRACP³, ¹Infectious Diseases, St. Jude Children's Research Hospital, Memphis, Tennessee, ²Biostatistics, St. Jude Children's Research Hospital, Memphis, Tennessee and ³St. Jude Children's Research Hospital, Memphis, Tennessee

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 chemotherapy. 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

Edward Cuaresma, MD¹; Monica Laszkowska, MD²; Stephanie Stump, BS²; Dagmara Moscoso, BS²; David Chong, MD² and Daniel Freedberg, MD, MS³, ¹Medicine, Columbia University Medical Center, New York, New York, ²Columbia University Medical Center, New York, New York and ³Division of Digestive and Liver Diseases, Columbia University Medical Center, New York, New York

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. $8.48 \times 10^{-6}\%$, $P = 0.03$). 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 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 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

Winston Anthony, BS¹; Bin Wang, MS²; Candice Cass, AA³; Tiffany Hink, BA⁴; Kimberly Reske, MPH⁵; Sondra Seiler, BA⁶; Erik R. Dubberke, MD, MSPH⁷; Carey-Ann D. Burnham, PhD⁷; Gautam Dantas, PhD⁸ and Jennie H. Kwon, DO, MSCI⁹, ¹Division of Biology and Biomedical Sciences, Washington University School of Medicine, St. Louis, Missouri, ²Department of Pathology and Immunology, Washington University School of Medicine, St. Louis, Missouri, ³Washington University School of Medicine, St. Louis, Missouri, ⁴Washington University School of Medicine, St. Louis, Missouri, ⁵Department of Infectious Diseases, Washington University School of Medicine, St. Louis, Missouri, ⁶Washington University, St. Louis, Missouri, ⁷Department of Pathology and Immunology, Washington University School of Medicine, St. Louis, Missouri, ⁸Washington University in St. Louis, St. Louis, Missouri and ⁹Department of Medicine, Washington University School of Medicine, St. Louis, Missouri

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