

Fig. 1.

champions, failure to conduct competency assessments, and inconsistency in performing device insertion practices were commonly reported across facilities. These common gaps have and will continue to inform the development of tools and resources to improve infection prevention practices as well as help to better target the implementation of interventions.

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#### Presentation Type:

Top Oral Award

#### The Gut Microbiome and Resistome of Healthy Volunteers are Restructured After Short Courses of Antibiotics

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**Background:** Antimicrobial exposure is a significant risk factor for the development of antibiotic-resistant organisms (ARO); however, the depth and duration of this impact is not well described. The study goal is to define impact of antibiotics on the gut microbiome of healthy volunteers (HVs). **Methods:** HVs were randomized to receive either 5 days of levofloxacin (LVX), azithromycin (AZM), cefpodoxime (CPD), or AZM + CPD (Fig. 1). Stool samples were collected at 15 time points per patient before, during, and after antibiotics. Remnant stool samples from the microbiology laboratory were collected from patients admitted to the medical intensive care unit (MICU) as a comparison of the microbiome

in a critically ill state. DNA was extracted from samples and was submitted for shotgun sequencing. Relative abundance, resistome, and metabolic pathway abundance of bacterial taxa were determined and statistical analysis conducted in R software. **Results:** In total, 289 stool specimens from 20 HVs, and 26 remnant stool specimens were obtained from patients admitted from the MICU (Fig. 1). Community diversity and richness decreased in the first week post-ABX for all HVs ( $P < .01$ ). Linear discriminant analysis identified *Bacteroides* and *Clostridium* as taxonomic groups enriched after CPD, while AZM and LVX produced a relative abundance increase in diverse *Firmicutes* spp. Longitudinal tracking confirmed that after all antibiotics except LVX, HV microbiomes lost species diversity and shifted toward a state similar to that observed in MICU patients (Fig. 2). The gut microbiome of most HVs exhibited resiliency and returned to a higher diversity level similar to their starting point; however, 10% of HVs did not. Moreover, antibiotic-specific increases in resistance markers reveal innate resistance to  $\beta$ -lactams and macrolides within the gut microbiome of the HVs. Finally, HV microbiomes, which shifted toward a MICU-like taxonomic state, also clustered with microbial metabolic profiles from MICU patients.

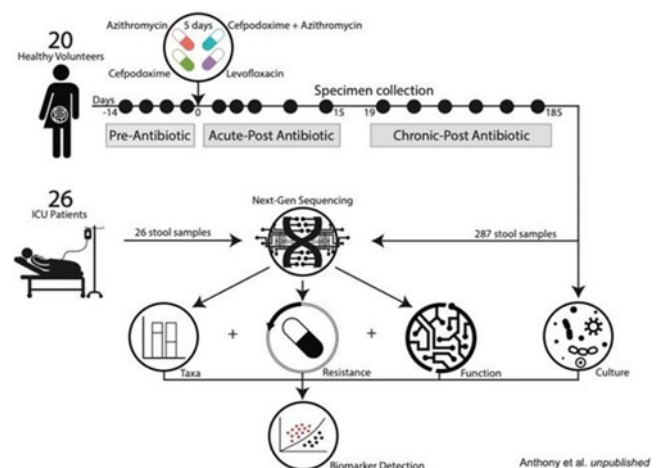
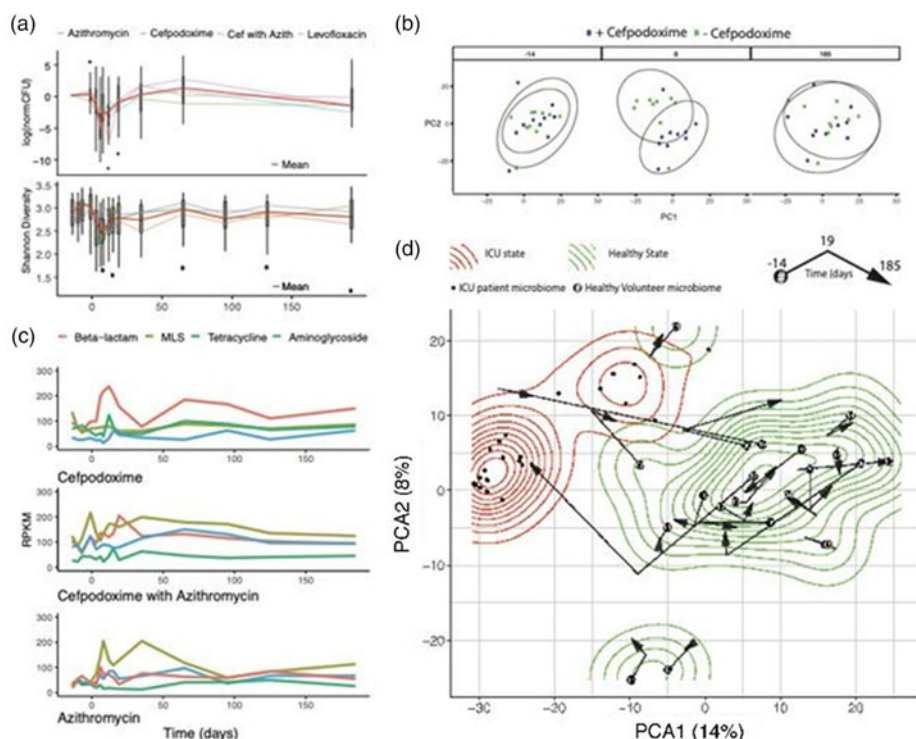


Fig. 1.



**Figure 2.** A. Healthy volunteers exhibit acute perturbation of the log-relative CFUs, and in community diversity (Shannon's index). B. Antibiotic-specific changes in PCA dimensions of taxonomic profiles form clusters 3 days after antibiotic administration, but these differences disappear by 185, suggesting resolution of perturbations to community diversity. Variance explained by both axes is shown on subplot D. C. Antibiotic-specific changes to resistance burden after antibiotic administration demonstrate healthy microbiomes are primed to respond to antibiotics, and burden remains elevated for much of the study. D. Antibiotic perturbation moves healthy volunteer microbiomes towards a state similar to the ICU patients, defined as the density gradient estimated from ICU taxonomic profiles. The healthy state is defined as a density gradient estimated from the taxonomic profiles of healthy volunteers before antibiotics. Arrows track the longitudinal change in healthy volunteer microbiomes over time.

**Fig. 2.**

The HV microbial metabolic profiles were significantly enriched for important biosynthesis pathways producing chorismate and polysaccharides. MICU patient gut microbiomes were enriched for fatty acid regulation and quinolone biosynthesis, and for many degradation pathways important for different aspects of antibiotic resistance such as membrane integrity, alternative respiration, and antibiotic inactivation. **Conclusions:** Short courses of antibiotics can cause acute and chronic microbiome disruptions in HVs, as evidenced by decreased microbiome diversity and increases in specific innate resistance elements. These data support the need for antimicrobial stewardship to support rationale antibiotic use to prevent gut microbiome disruptions.

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#### Presentation Type:

Distinguished Oral

#### A Ten-Year Review of Carbapenemase Producing Enterobacteriales (CPE) in London, United Kingdom

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**Background:** To determine the pattern of CPE observed in a single region in the United Kingdom. **Methods:** From 2009 to 2018, clinical laboratories in England were requested to send suspected CPE from all sites to the national reference laboratory for confirmation and investigation of carbapenem resistance mechanism(s). Isolates of Enterobacteriales from London laboratories and confirmed to have 1 or more carbapenemase genes were included in the analysis. **Result:** Between 2009 and 2018, 5,133 isolates were confirmed to produce a carbapenemase; at least 1 CPE was identified in every London Laboratory and hospital. Confirmations increased from 28 isolates in 2009 to 1857 in 2018 and with a sharp rise after the introduction of the 'PHE toolkit' in 2013 (Fig. 1). Most CPE (2655, 51.7%) were from rectal screens (the 3 most frequently identified carbapenemase families were OXA-48-like in 1,263 isolates, NDM in 971 and IMP in 128), 631 (12.3%) were from urine samples, 180 (3.5%) from blood cultures, 103 (2.0%) from sputum specimens and the remainder (1564, 30.5%) were swabs, fluids and tissues from various body sites. Moreover, 51 CPE (1%) were identified from environmental swabs. Isolates were predominantly *Klebsiella* spp (2,525, 49%; 2,088 were *K. pneumoniae*), followed by *Escherichia coli* (1,434, 27.9%), *Enterobacter* spp (746, 14.5%; 605 were *E. cloacae* complex), and *Citrobacter* spp (349, 6.8%); 10 other species contributed smaller numbers. Within the carbapenemase families, OXA-48-like enzymes predominated overall (2303,