

Fig. 2.

**Presentation Type:**

Top Oral Award

**Targeted Assessment for Prevention Facility Assessments: The Most Common CAUTI and CLABSI Infection Prevention Gaps**

Rachel Snyder, Centers for Disease Control and Prevention; Katelyn White, Centers for Disease Control and Prevention; Janet Glowicz, Centers for Disease Control and Prevention; Shannon Novosad, Centers for Disease Control and Prevention; Elizabeth Soda, Centers for Disease Control and Prevention; David Kuhar, Centers for Disease Control and Prevention; Ronda Sinkowitz-Cochran, Centers for Disease Control and Prevention

**Background:** The Targeted Assessment for Prevention (TAP) strategy is a quality improvement framework created by the Centers for Disease Control and Prevention (CDC) to facilitate the reduction of healthcare-associated infections (HAIs). TAP facility assessments are a component of the TAP strategy and are completed by staff across the facility to help identify perceptions of and target infection prevention gaps. We have described the gaps most commonly reported by facilities completing TAP facility assessments for catheter-associated urinary tract infections (CAUTIs) and central-line-associated bloodstream infections (CLABSIs). **Methods:** TAP CAUTI and CLABSI assessments were completed by acute-care facilities across the nation, with CDC technical assistance, from December 2014 to August 2019.

Similar questions across 2 versions of CAUTI assessments and 3 versions of CLABSI assessments were combined. Analysis was limited to facilities with  $\geq 10$  assessments. Infection prevention gaps were defined as  $\geq 33\%$  respondents answering Unknown,  $\geq 33\%$  respondents answering “no,” or  $\geq 50\%$  of respondents answering “no” and “unknown” or “never” and “rarely” “sometimes” “unknown.” The analysis was completed at the facility level, and the gaps most commonly reported across facilities were identified.

**Results:** In total, 1,942 CAUTI assessments from 42 facilities in 12 states and 1,623 CLABSI assessments from 29 facilities in 11 states were included for analysis. The mean numbers of assessments per facility were 46.2 for CAUTIs and 56.0 for CLABSIs. Across both CAUTIs and CLABSIs, commonly reported perceptions about infection prevention gaps included lack of physician and nurse champions for prevention activities, failure to conduct competency assessments, and inconsistency in select device insertion practices (Fig. 1). For CAUTIs, lack of practices to facilitate timely removal of urinary catheters were also commonly reported, with one-third of facilities reporting inconsistency in use of alerts for catheter removal, 78.6% reporting lack of physician response to these alerts, and 90.5% reporting deficiencies in removing unnecessary catheters in the postanesthesia care unit. For CLABSIs, 79.3% of facilities reported failure to replace central lines within 48 hours after emergent insertion, and 62.1% reported that feedback was not provided to staff on central-line device utilization ratios. **Conclusion:** For both assessments, absence of CAUTI and CLABSI prevention

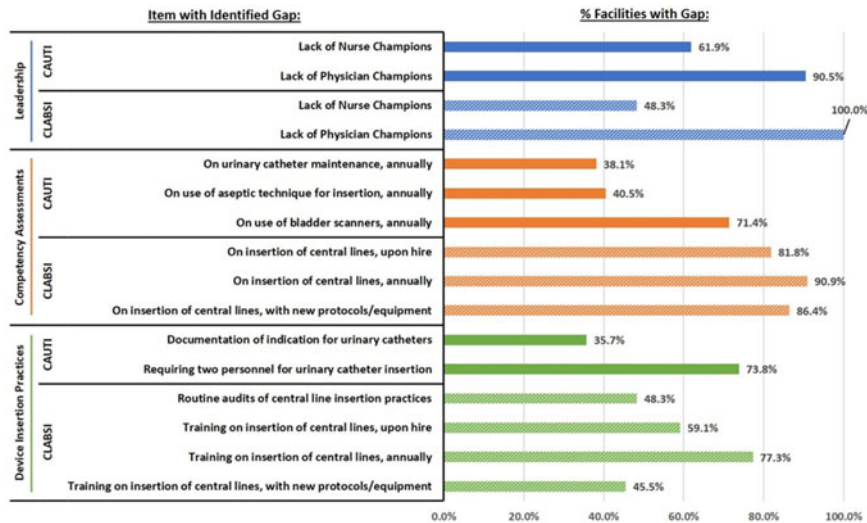


Fig. 1.

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.

**Funding:** None

**Disclosures:** None

Doi:[10.1017/ice.2020.475](https://doi.org/10.1017/ice.2020.475)

#### Presentation Type:

Top Oral Award

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

Winston Anthony, Washington University School of Medicine; Kimberley Sukhum, Washington University School of Medicine; Candice Cass, Washington University School of Medicine; Kimberly Reske, Washington University School of Medicine; Sondra Seiler, Washington University School of Medicine; Tiffany Hink, Washington University School of Medicine; Christopher Coon, Washington University School of Medicine; Alaric D'Souza, Washington University School of Medicine; Bin Wang, Washington University School of Medicine; Sherry Sun, Washington University School of Medicine; Erik Dubberke, Washington University School of Medicine; Carey-Ann Burnham, Washington University School of Medicine; Gautam Dantas, Washington University School of Medicine; Jennie H. Kwon, Washington University – School of Medicine

**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.

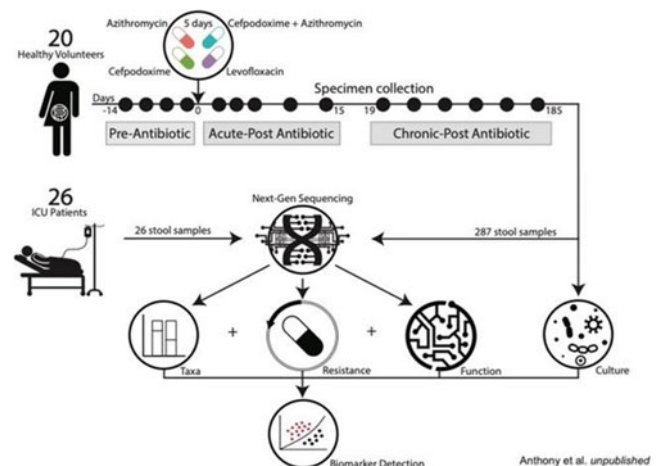


Fig. 1.