was to describe the microbiologic and epidemiologic characteristics of CZA-resistant (CZA-R) CRE. **Methods:** From 2015 to 2017, 9 states participated in laboratory- and population-based surveillance for carbapenem-resistant *Escherichia coli*, *Klebsiella pneumoniae*, *K. oxytoca*, *K. aerogenes*, and *Enterobacter cloacae* complex isolates from a normally sterile site or urine. A convenience sample of isolates from this surveillance were sent to the CDC for antimicrobial susceptibility testing (AST) using reference broth microdilution (BMD) including an MBL screen, species confirmation with MALDI-TOF, and real-time PCR to detect *bla*KPC, *bla*NDM, and *bla*OXA-48–like genes. Additional AST by BMD was performed on CZA-R isolates using meropenem-vaborbactam (MEV), imipenem-relebactam (IMR), plazomicin (PLZ), and eravacycline (ERV). Epidemiologic data were obtained from a medical record review. Community-associated cases were defined as having no healthcare exposures in the year prior to culture, no devices in place 2 days prior to culture, and culture collected before calendar day 3 after hospital admission. Data were analyzed in 3 groups: CRE that were CZA-susceptible (CZA-S), CZA-R that were due to *bla*NDM, and CZA-R without *bla*NDM. **Results:** Among 606 confirmed CRE tested with CZA, 33 (5.4%) were CZA-R. Of the CZA-R isolates, 16 (48.5%) harbored a *bla*NDM gene, of which 2 coharbored *bla*NDM and *bla*OXA-48-like genes; 9 (27.3%) harbored only a *bla*KPC gene. Of the 17 CZA-R isolates without *bla*NDM, all were MBL screen negative. CZA-R due to *bla*NDM were more frequently community-associated (43.8%) than CZA-S or CZA-R without *bla*NDM (11.0% and 5.9%, respectively); a higher percentage of CZA-R cases due to *bla*NDM also had recent international travel (25%) compared to the other groups (1.8% and 5.9%, respectively). CZA-R without *bla*NDM were more susceptible to MEV (76%), IMR (71%), PLZ (88%), and ERV (65%) compared to CZA-R due to *bla*NDM (19%, 6%, 56%, and 44%, respectively). **Conclusions:** The emergence of CZA-R isolates without *bla*NDM are concerning; however, these isolates are more susceptible to newer antimicrobials than those with *bla*NDM. In addition to high rates of resistance to newer antimicrobials, isolates with *bla*NDM are more frequently community-associated than other CRE. This underscores the need for more aggressive measures to stop the spread of CRE.

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Poster Presentation

Chemical, Mechanical, and Heat Cleaning to Decontaminate Hospital Drains Harboring Carbapenemase-Producing Enterobacteriales

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Background: Carbapenemase-producing Enterobacteriales (CPE) outbreaks have been linked to contaminated wastewater drainage systems in hospitals. The optimal strategy for CPE decontamination of drains is unknown. In this randomized controlled trial, we aimed to determine whether combining chemical, mechanical, and heat cleaning was superior to routine cleaning for drain decontamination. **Methods:** We enrolled CPE-contaminated hospital drains at 2 geographic locations. Eligible drains were those initially found to be culture positive in a 2017 study and that remained positive (by RT-PCR) when retested twice in August 2018. Drains were stratified by type (sink versus shower) and randomized with a 1:1 allocation ratio (as per computer-generated randomization) to standard-of-care cleaning (comparator) or combined chemical, mechanical, and heat cleaning (intervention) on day 0. Drain tail pieces were swabbed on days 0 (before administration of the intervention), 1, 2, 3, 7, and 14, and at months 1, 2, 3, 4, 5, and 6. Swabs were placed into brain heart infusion with 10% Dey-Engley neutralizing broth and incubated overnight. Direct RT-PCR was performed to detect KPC, VIM, NDM, OXA-48–like, IMP, GES, and SME genes. The primary outcome was drain decontamination, defined as no detectable carbapenemase gene in the drain from day 1 to 7 (inclusive). **Results:** Overall, 33 CPE-contaminated drains were enrolled (7 sink and 26 shower); 17 and 16 drains were randomized to the intervention and comparator, respectively. Moreover, 12 (36%) drains met the primary outcome of decontamination, 18 (55%) remained contaminated, and 3 (9%) could

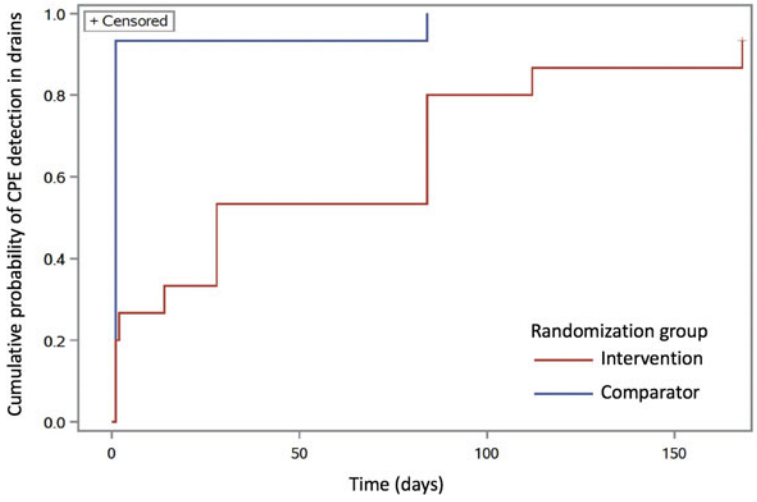

Fig. 1.

not be assessed. Among drains that could be assessed, 11 of 15 (74%) in the intervention group met the primary outcome of decontamination compared to 1 of 15 (7%) in the comparator group ($P = .0005$). Of the 11 drains in the intervention group that were decontaminated, the carbapenemase gene present at enrollment was subsequently detected in 10 (91%): 1 (10%) at day 14, 3 (30%) at month 1, 4 (40%) at month 3, 1 (10%) at month 4, and 1 (10%) at month 6. The median time to a swab yielding CPE was 1 day in the comparator group versus 14 days in the intervention group (Fig. 1). Overall, 24 drains (73%) had a carbapenemase gene (that was not detectable at enrollment) appear in the follow-up. Of patients identified as CPE colonized or infected during this study, none occupied rooms with these drains. **Conclusions:** Chemical, mechanical, and heat cleaning were superior to standard cleaning for CPE decontamination of hospital drains at 7 days, but these trends were not sustained. Such cleaning may be useful if applied repeatedly.

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***Clostridioides difficile* Strains in the Gut by Next-Generation Shotgun Sequencing: Innocent Bystander or Villain?**

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Background: Pathogenic *Clostridioides difficile* is the most common cause of nosocomial infections in the United States. However, the prevalence of *C. difficile* colonization in the general population is poorly understood. **Objective:** In this study, we sought to determine the presence and nature of various strains of *Clostridioides difficile* colonizing a representative sample of 121 asymptomatic adult volunteers from around the globe, consisting of 110 healthy and 11 stable Crohn's patients. **Methods:** Next-generation sequencing was performed on fecal samples from 121 study participants. Stool samples were collected by patients utilizing a Zymo collection kit, which preserves bacterial DNA and RNA. Following collection, DNA was extracted, quantitated, and then normalized for downstream library fabrication utilizing shotgun methodology. Prepared and indexed libraries were subsequently pooled and sequenced on the Illumina NextSeq 550 System. **Results:** All 121 of 121 subjects (100%) were found to possess the bacterium *Clostridioides difficile* as identified by the NGS bioinformatics metagenomic pipeline. To visualize comparative abundances of *Clostridioides difficile* present in study participants, normalized read counts were highlighted (Fig. 1). **Conclusions:** NGS provides a unique opportunity to increase the resolution and identification of *Clostridioides difficile* compared to traditional categorizations, such as PCR ribotypes (ie, RT027), restriction endonuclease groups (BI), and North American pulsotypes (ie, NAP1). This is accomplished by its ability to differentiate species based on a nucleotides, while targeting entire bacterial genomes. Our approach for this study was to utilize a bioinformatics pipeline that would provide *Clostridioides difficile* strain-specific resolution when aligning to genomes in the NCBI (National Center for Biotechnology Information) database. In our representative sample of 121 volunteers, all (100%) possessed at least 1 *Clostridioides difficile* strain in their gut. Although it is recognized that some *Clostridioides difficile* strains are pathogenic, our findings suggest that nonpathogenic *Clostridioides difficile* strains make up an important component of the commensal gut microbiome and may perhaps play a protective role. Although symptomatic toxigenic CDI is a clear indication for therapy, *Clostridioides difficile* colonization with nontoxigenic strains is not believed to be a direct precursor for CDI. These findings demonstrate the need to be aware of the existence of numerous strains of *Clostridioides difficile*, and the relevance of sequencing prior to hospitalization

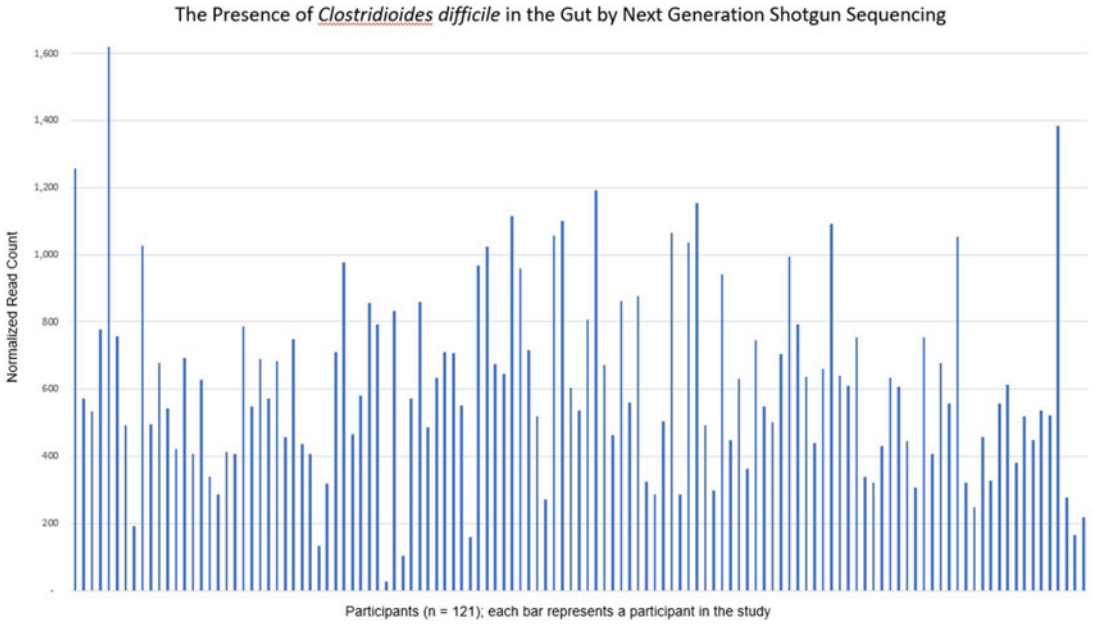

Fig. 1