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.

Presentation Type:
Poster Presentation

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

Sabine Hazan, ProgenaBiome; Andreas Papoutsis, ProgenaBiome; Jordan Daniels, ProgenaBiome

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
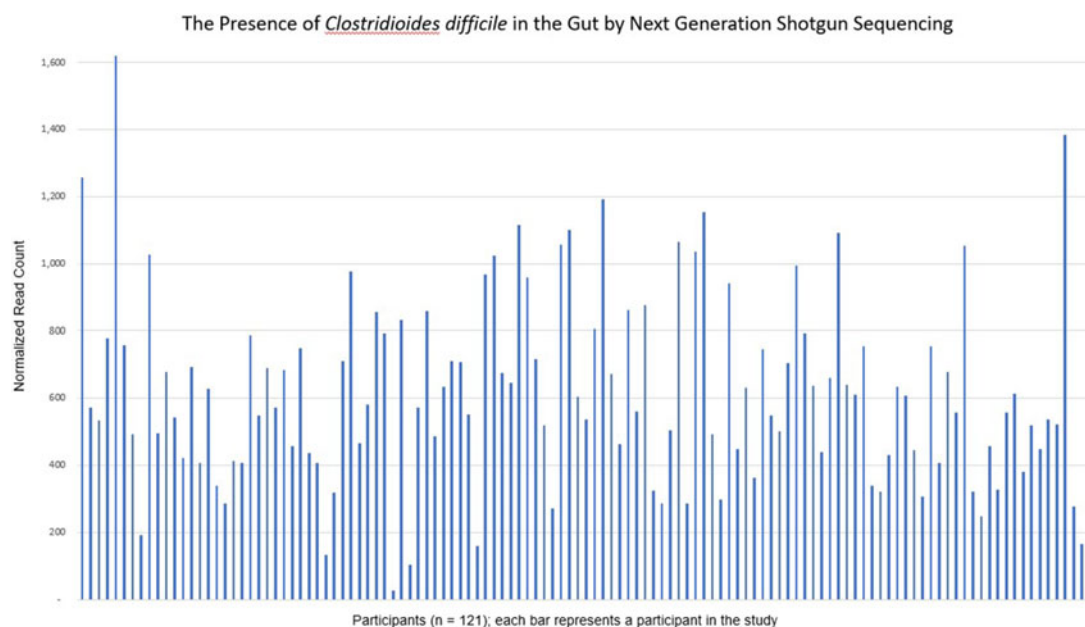

The Presence of *Clostridioides difficile* in the Gut by Next Generation Shotgun Sequencing

Fig. 1

or antibiotic treatment to help predict those at risk of CDI, and after treatment to be aware of any loss of what appear to be protective components of our microbiome.

Presentation Type:
Poster Presentation
Decreasing Blood Culture Contamination Rates Using A Specimen Diversion Device: A Quasi-Experimental Study

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Background: Blood culture contamination rates are frequently higher than the ≤3% standard in the emergency department (ED). Objective: We sought to determine whether the implementation of a blood diversion device that mechanically sequesters the initial aliquot of the blood culture sample decreased blood culture contamination rates. Methods: We performed a quasi-experimental study in two 500-bed hospitals. The blood-diversion device was implemented in the ED in hospital A, but not in hospital B, starting in January 2018. Preintervention data were collected over a 29-month baseline period, and postintervention data were collected for 20 months. Both hospitals provided ongoing feedback on contamination rates. Blood culture contamination was defined as presence of common skin microbiota (eg, coagulase-negative staphylococci) in only 1 of ≥2 blood culture sets collected within 24 hours. Preintervention and postintervention blood culture contamination rates were calculated based on total blood cultures collected and were compared within and between hospitals using the Wilcoxon rank-sum test. Changes in preintervention and postintervention total and ED contamination rates within hospitals were calculated as rate ratios (RRs) using interrupted time series (ITS) analysis with segmented Poisson regression. Results: Among 212,789 total blood cultures (hospital A, 70,005; hospital B, 142,784), 4,025 (1.8%) were contaminated. In hospital A, the intervention resulted in a decrease in overall median blood culture contamination rates (2.4% vs 1.4%; $P < .001$) and ED median blood culture contamination rates (4.7% vs 2.6%; $P < .001$), whereas in hospital B there was no significant change during the same period in overall (2.3% vs 2.0%) or ED (5.0% vs 5.0%) median blood culture contamination rates. In the ITS analysis, the intervention was associated with an immediate decrease in hospital A's contamination rate by 21.3% (level change RR, 0.79; 95% CI, 0.63–0.98; $P = .04$) overall and 21.0% (level change RR, 0.79; 95% CI, 0.62–1.0; $P = .06$) in the ED. After the intervention, there was a continued decrease in hospital A's overall (trend change RR, 0.95; 95% CI, 0.93–0.97; $P < .001$) and ED (trend RR, 0.94; 95% CI, 0.92–0.96; $P < .001$) blood culture contamination rates, but not in hospital B's overall (trend change RR, 1.02; 95% CI, 1.00–1.02; $P = .01$) or ED (RR, 1.00; 95% CI, 0.99–1.02; $P = .30$) blood culture contamination rates during the same period. **Conclusions:** Implementation of the blood diversion device in the ED resulted in a >20% relative reduction from a baseline of 5% of ED blood culture contamination rates. Continued improvement after implementation suggests ongoing efforts to address the workflow and the culture of safety are needed to optimize the use of this device.

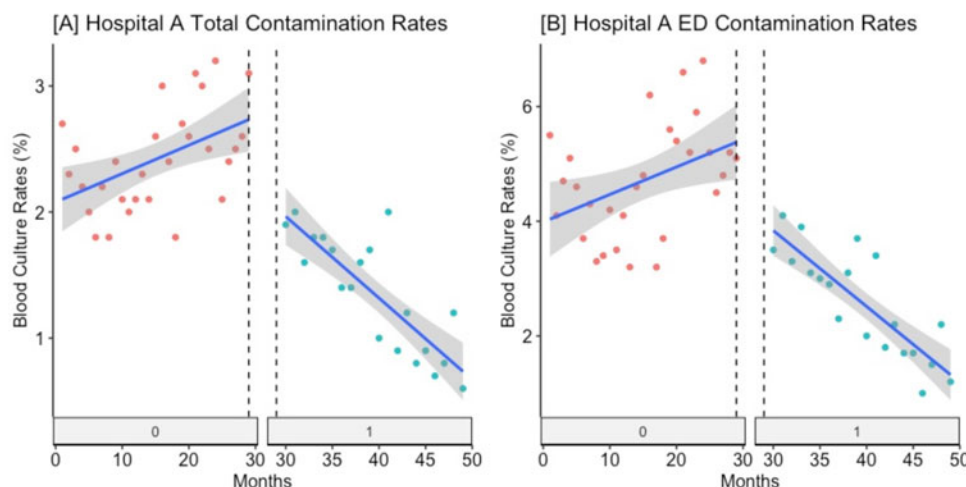**Figure 1A/B: Hospital A Total (A) and ED (B) Blood Culture Contamination Rates**

Figure 1A/B Legend: Blood culture contamination rates before (red dots) and after (turquoise dots) implementation of the intervention (dotted line [Month 29]) at Hospital A.

Fig. 1.