SIR was associated with study type and sample size, and Altmetric score was associated with ID subfield, journal, and sample size.

**Conclusion.** We present a descriptive overview of the ID literature and identify article factors associated with journal tier and audience engagement after publication. **Disclosures.** All authors: No reported disclosures.

### 2565. Initial and Recurrent Episodes of Clostridioides difficile: Online Education as a Tool to Improve Management Strategies
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**Session:** 266. Medical Education: Medical School to Practice
Saturday, October 5, 2019: 12:15 PM

**Background.** The most common cause of infectious diarrhea in hospitalized patients, *C. difficile* is responsible for nearly half a million infections annually. Among persons over the age of 65 years, 1 in 11 die within a month of diagnosis.

**Methods.** A CME-certified/ABIM MOC educational program was developed to evaluate and improve ID specialists’ application of the latest guideline recommendations for the diagnosis and management of individuals with *C. difficile*. Modeled on the interactive grand rounds approach, the activity blended case-based presentation with multiple-choice questions. Using a “test then teach” approach to elicit cognitive dissonance, the activity provided evidence-based feedback following each learner response. Educational effectiveness was assessed with a repeated-pairs pre-/post-assessment study design; each individual served as his/her own control. A chi-square test assessed changes pre- to post-assessment. *P* values < 0.05 are statistically significant. Effect sizes were evaluated using Cramer’s *V* (< 0.05 modest; 0.06–0.15 noticeable effect; 0.16–0.26 considerable effect; > 0.26 extensive effect). The activity launched on a website dedicated to continuous professional development on May 29, 2018. Data for this initial analysis were collected through March 27, 2019.

**Results.** To date, 3274 HCPs, including 2946 physicians have participated in the activity. Data from the subset of ID specialists (n = 82) who answered all pre-/post-assessment questions during the initial study period were analyzed. Following activity participation, significant improvements were observed in the proportion of ID specialists who answered all assessment questions correctly (4% pre vs. 74% post; *P* < 0.0001; *V* = 0.552). Improvements were also observed in several specific areas of assessment (Table 1). Additionally, 50% of ID specialists indicated they planned to modify their treatment approach and 18% planned to modify their diagnostic strategies for *C. difficile*.

**Conclusion.** Participation in this online, interactive, case-based, educational intervention significantly improved ID specialists’ management strategies for initial and recurrent episodes of *C. difficile*. These findings highlight the positive impact of well-designed online education.

**Disclosures.** All authors: No reported disclosures.

### 2566. Infection Dynamics of Pseudomonas aeruginosa Bloodstream Infections
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**Session:** 267. Microbiome, Antibiotics, and Pathogenesis
Saturday, October 5, 2019: 12:15 PM

**Background.** *Pseudomonas aeruginosa* (PA) is a critically important healthcare-associated pathogen responsible for a variety of infections including bloodstream infection (bacteremia), pneumonia, and urinary tract infection. PA bacteremia is a healthcare-associated pathogen responsible for a variety of infections including bloodstream infections. Finally, STAMP analysis revealed that (1) PA experiences a severe in vivo bottleneck when trafficking to the GB, (2) the population in the GB expands tremendously during infection and (3) this population is ultimately the source of excreted bacteria in the GI tract.

**Conclusion.** Our research, using murine models, provides the first evidence that the GB acts as a sanctuary site for PA replication following systemic infection and links replication with fecal excretion. Fecal excretion of PA from hospitalized patients is observed, but the direct link between acute infection, GI shedding, and transmission remains unclear. Our observations have significant implications on understanding how PA evades initial host clearance, the identity of protected expansion niches, and how PA might exit the human host in the healthcare environment facilitating a transmission event.

**Disclosures.** All authors: No reported disclosures.

### 2567. Effect of Broad vs. Narrow-Spectrum Clostridioides difficile Treatment on Human Stool Bile Acid Composition Over Time
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**Session:** 267. Microbiome, Antibiotics, and Pathogenesis
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**Background.** Secondary bile acid production by a diverse commensal flora may be a critical factor in preventing recurrence of *Clostridioides difficile* infection (CDI). Key enzymes involved are bacterial-encoded bile salt hydrolases (BSHs), felt to be “gatekeepers” to secondary bile acid synthesis. Ridinilazole, a novel narrow-spectrum drug for CDI, demonstrated superior sustained clinical response compared with vancomycin in Phase 2. Longitudinal sampling during this trial allowed for assessment of metabolites differentially present in stools during/after therapy with either broad or narrow-spectrum anti-CDI agent. Previous work characterizing subject’s fecal microbiota in this trial showed that unlike vancomycin, ridinilazole has little effect on commensal flora during and after therapy. We hypothesized that ridinilazole’s microbiota-preserving effect is associated with lack of accumulation of conjugated primary bile acids and/or reaccumulation/persistence of secondary bile acids over the course of CDI treatment, when compared with vancomycin-treated subjects. Furthermore, we hypothesized that we would observe correlations between bile acid profiles and predicted BSH gene abundances.

**Methods.** Sequential stool samples were obtained from 44 subjects treated with either ridinilazole or vancomycin (22 in each arm), ranging from time of CDI diagnosis, at end-of-therapy, and up to 40 days after diagnosis. Bile acids were quantitated by liquid chromatography-mass spectrometry. Using the PICRUST algorithm, metagenomic predictions of BSH gene abundances were performed.

**Results.** Stool bile acid compositions differed between ridinilazole-treated and vancomycin-treated subjects at end-of-therapy. In vancomycin-treated subjects, bile acids were quantitated by liquid chromatography-mass spectrometry. Using the PICRUST algorithm, metagenomic predictions of BSH gene abundances were performed.

**Conclusion.** Microbiota-preserving CDI treatment with ridinilazole preserves bile acid composition, which may decrease likelihood of recurrence.

**Disclosures.** All authors: No reported disclosures.

### 2568. Mechanisms of a Specific Probiotic Comprised of Lactobacillus acidophilus CL12185, L. casei LBC680 and L. rhamnosus CLR2 That Interferes with Clostridioides difficile 20291 Toxin Production
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**Session:** 2066. Microbiome, Antibiotics, and Pathogenesis
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**Background.** *Clostridioides difficile* (CDI) is a major cause of antibiotic-associated diarrhea and colitis in hospitalized patients. CDI affects 500,000 people annually in the United States and is associated with a 25% mortality rate. The two main treatments for CDI are fidaxomicin, a narrow-spectrum antibiotic, and vancomycin, a broad-spectrum antibiotic. Recurrence rates are high, with one in three patients experiencing recurrence in the first 2 months after treatment. The mechanisms through which probiotics interfere with CDI pathogenesis remain unclear. This work aimed to identify the mechanisms by which a mixture of probiotics interferes with CDI pathogenesis.

**Methods.** We characterized the ability of a mixture of probiotics to interfere with CDI pathogenesis using a mouse model of CDI. The probiotic mixture consisted of Lactobacillus acidophilus CL12185, L. casei LBC680, and L. rhamnosus CLR2. These strains were chosen based on their reported beneficial effects in clinical trials and previous studies that demonstrated their ability to interfere with CDI pathogenesis.

**Results.** Our results showed that the probiotic mixture significantly reduced the bacterial load in the gut and reduced the duration of diarrhea in the CDI model. Additionally, we found that the probiotic mixture decreased the production of CDI toxins, which are thought to be key mediators of CDI symptoms and pathogenesis.

**Conclusion.** Our findings suggest that a mixture of probiotics can interfere with CDI pathogenesis by reducing bacterial load and toxin production. These results may provide new insights into the development of probiotics as a potential therapeutic for CDI.

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**Figure 1.** Changes in stool bile acid composition over time following treatment with vancomycin or ridinilazole, and in healthy subjects.