SJR 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

Simi Thomas. Hurst, PhD[1]; James Martorano, MBA[2]; Dale N. Gerding, MD[3]; [1]Medscape Education, Oxford, New Jersey; [2]Medscape Education, New York, New York; [3]Hines VA Medical Center, Hines, Illinois

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 = .555). Improvements were also observed in several specific areas of assessment (table). 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.

Assessment of Educational Effectiveness			
Area of Assessment	% relative improvement (% of ID specialists selecting the correct response at pre- vs post-assessment)	*P*-value for change	Cramer's V for the magnitude of the change
Applying the most current IDSA guidelines for *C. difficile* testing	88% improvement (52% vs 98%)	*P* <.0001	V=.521 (Extensive)
Selecting an appropriate management strategy for an elderly patient with recurrent *C. difficile* infection	230% improvement (23% vs 76%)	*P* <.0001	V=.524 (Extensive)
Developing a step-wise treatment strategy for patients at increased risk for recurrence	232% improvement (28% vs 93%)	*P* <.0001	V=.660 (Extensive)

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

2566. infection Dynamics of *Pseudomonas aeruginosa* Bloodstream Infections

Kelly E. R. Bachta, MD, PhD; Jonathan P. Allen, PhD; Alan R. Hauser, MD PhD; Feinberg School of Medicine, Northwestern University, Chicago, Illinois

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 significant cause of morbidity and mortality, especially in immunocompromised patients; However, little is known about the in-host infection dynamics of PA bacteremia and the impact of individually infected patients on transmission in the healthcare environment.

Methods. We utilized animal modeling in conjunction with sequencing technology to dissect the infection dynamics of PA bloodstream infections. BALB/c mice were challenged intravenously with a human bacteremia isolate, PABL012. At various time points post infection, organs were harvested and the surviving PA enumerated. In parallel, PABL012 engineered to express the luciferase cassette was used to track PA in live mice over time using the IVIS imaging system. STAMP (sequence tag-based analysis of microbial populations) analysis was then applied to define the population dynamics of PA bloodstream infection.

Results. Bacterial enumeration and IVIS imaging revealed that systemically infected mice have a focus of bacterial expansion in their gallbladders (GB). Surprisingly, the same mice also shed PA in their gastrointestinal tract (GI), a phenomenon not previously appreciated following bloodstream infection. 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

Cheleste M. Thorpe, MD[1]; Xi Qian, PhD[2]; Karin Yanagi, BS[2]; Anne Kane, MD[3]; Nicholas Alden[2]; David R. Snydman, MD[3]; Kyongbum Lee, PhD[2]; [1]Tufts Medical Center and Tufts University School of Medicine, Boston, Massachusetts; [2]Tufts University, Boston, Massachusetts; [3]Tufts Medical Center, Boston, Massachusetts

Session: 267. Microbiome, Antibiotics, and Pathogenesis
Saturday, October 5, 2019: 12:15 PM

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, stool composition became dominated by conjugated primary bile acids and decreased levels of secondary bile acids compared with baseline; the ratio of stool conjugated bile acids to secondary bile acids significantly predicted treatment arm. This ratio was also associated with predicted BSH gene abundance in ridinilazole-treated subjects.

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

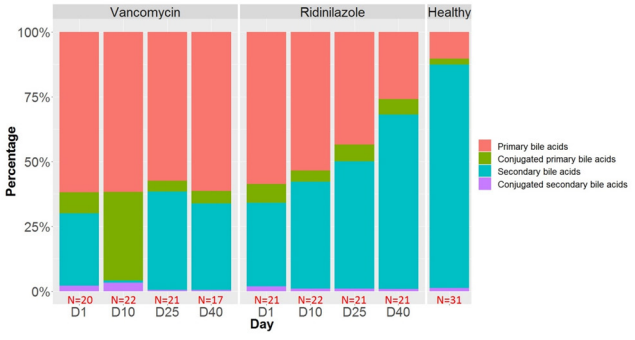

Figure 1. Changes in stool bile acid composition over time following treatment with vancomycin or ridinilazole, and in healthy subjects.

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

2568. Mechanisms of a Specific Probiotic Comprised of *Lactobacillus acidophilus* CL1285, *L. casei* LBC80R and *L. rhamnosus* CLR2 that Interferes with *Clostridioides difficile* 20291 Toxin Production

Sathursha Gunaratnam, MSc[1]; Carine Diarra, MSc[2]; Patrick D. Paquette, MSc[2];