2400. Are Multiple Clostridioides difficile Infections in Pediatric Oncology Patients Related to Recurrence of the Same Isolate or Re-infections with Different isolates?

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Background. Pediatric oncology and hematopoietic stem cell transplant patients (POTP) are at increased risk for *Clostridioides difficile* infection (CDI) and recurrence. It is unknown whether recurrent CDI is related to the same *C. difficile* strain as the initial CDI. We describe genomic relatedness of *C. difficile* strains in patients with multiple CDI using whole-genome sequencing (WGS).

Methods. This was a retrospective cohort study of CDI in POTP in 2016. CDI cases were identified by electronic medical record search for positive *C. difficile* toxin PCR tests. Patients with multiple CDI episodes were identified. CDI episodes were classified as incident, duplicate or recurrent using National Healthcare Safety Network (NHSN) definitions. Retrieved residual stool specimens were cultured anaerobically, toxin-producing *C. difficile* isolates were determined using a cell culture cytotoxicity assay with neutralization and WGS was performed followed by core genome MLST (cgMLST). Variability of the isolates was summarized by strain type (ST), and a minimum spanning tree was constructed, defining genomically related isolates as those with <7 allele difference.

Results. Eighteen patients had 51 positive *C. difficile* samples. CDI were classified as incident in 31 (61%) episodes, recurrent in 18 (36%), and duplicate in 2 (3%). Isolates from 47 (92%) samples were sequenced, identifying 14 different strain types (ST) in 41 (87%) isolates. Of the 31 incident CDI, 13 (42%) episodes occurred 8 weeks or more after the initial incident CDI. Among those 13 incident CDI, 7 (54%) had prior CDI due to a related isolate. Of the 18 recurrent CDIs, 10 (55%) were due to an isolate related to the previous incident CDI and 5 (28%) were due to an isolate unrelated to the incident CDI. The relatedness of the remaining 3 recurrent episodes could not be evaluated because no isolate was available for sequence analysis.

Conclusion. CDI classification of incident vs. recurrent infection using NHSN definition might be not applicable in POTP. WGS showed that more than half of CDI episodes classified as incident were actually a recurrence of a previous *C. difficile* strain. Similarly, some CDI episodes classified as recurrent were actually re-infection with a different stain.

Disclosures: Randall Hayden, MD, Abbott Molecular: Advisory Board; Quidel: Advisory Board; Roche Diagnostics: Advisory Board

2401. Epidemiology of *Clostridium difficile* Infection in Intestinal and Multivisceral Transplant Patients at a Single Transplant Center

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Background. *Clostridium difficile* infection (CDI) is the leading cause of infectious diarrhea in the healthcare setting. Solid-organ transplant (SOT) recipients are at increased risk compared with the general hospitalized population (7.4–20% vs. 0.9%). Our center recently expanded its intestinal and multivisceral transplant (IMVT) program, providing the opportunity to examine the epidemiology of CDI in this vulnerable population.

Methods. We conducted a retrospective study of all IMVT recipients between 2009 and 2018. CDI was defined as presence of diarrhea with a positive polymerase chain reaction (PCR) test for the toxin B gene. Early CDI constituted an episode of CDI within the first 6 months post-transplant. Data were collected on demographics, transplant characteristics, CDI episode, and outcomes.

Results. We identified 86 patients who underwent a total of 94 transplants: 60 (64%) isolated intestinal transplants, 21 (22%) intestine/liver/pancreas, 10 (11%) intestine/pancreas, two (2%) intestine/liver/pancreas/kidney, and one (1%) intestine/kidney transplant. All but three patients received perioperative metronidazole. Four patients (5%) had CDI prior to transplant, but none of them recurred in the first 6 months post-transplant. Five patients developed a total of seven mild-moderate episodes of early CDI (attack rate = 5.9%). Three patients (60%) with early CDI developed rejection, similar to the incidence (70%) in patients without CDI. Two patients with early CDI developed recurrence; both underwent intestinal re-transplantation. One-year mortality was similar among patients with and without early CDI (20% vs. 23%).

Conclusion. CDI is associated with allograft loss, rejection, and mortality in some SOT recipients. Although limited by sample size, we observed that early CDI was not associated with those outcomes in our population. Multicenter studies are merited to explore risk factors for CDI and associations with outcomes in IMVT.

Table 1. Stakeholders in daily conference calls related to ongoing contact investigation.

Stakeholders
Administrative Leadership
Adult Infectious Disease Staff
Pediatric Infectious Disease Staff
Occupational Health Representatives
Infection Control Nurses
Hospital Epidemiologist
Risk Management Representatives
Ombudsmen
Corporate Communications Representatives

Table 2. Rings of Exposure: Results of contact investigation for HCW with untreated LTBI at our institution.

HCW: Healthcare Worker; LTBI: Latent Tuberculosis Infection; PICU: Pediatric Intensive Care Unit

Ring of Exposure	Individuals Included	Number of Individuals
I	HCW's immediate family (husband)	1
IIa	PICU children directly cared for by HCW	13
IIb	PICU children on whom HCW charted	20
IIc	All other PICU children admitted during exposure period	230
III	PICU Visitors	
IV	PICU HCWs	

Table 3. Exposed children deemed "high-risk" and selected to receive prophylactic isoniazid.

PICU: Pediatric Intensive Care Unit; HCW: Healthcare Worker

Category
All children directly cared for by the HCW
All children admitted to the PICU under the age of 5 years
All children admitted to the PICU post-transplantation
All visitors to the PICU under the age of 5 years

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2402. Clinical Outcomes Associated with an Emerging Clostridioides difficile Ribotype 255 in Texas

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Background. PCR ribotyping of *Clostridioides difficile* strains is commonly used to describe the epidemiology of *C. difficile* infection (CDI). Certain ribotypes (RT) have been associated with more severe disease and clinical outcomes, such as RT 027, while others are considered less virulent, such as RT 014-020. Texas statewide surveillance identified the emergence of a rarely-described RT 255 beginning in 2015, which now represents the fifth most common ribotype across the state. Here we describe clinical outcomes associated with an emergent RT 255 in Texas.

Methods. A retrospective cohort study was conducted including patients from two tertiary care centers in Houston, Texas. Patients infected with *C. difficile* strains of either RT 255, 014-020, or 027 between 2016–18 were included. The primary outcome was disease severity as classified by the 2017 IDSA guidelines. Multivariable logistic regression analysis was done to control for other patient factors. Results were significant at $P < 0.05$, and all statistical analyses were completed using SPSS, version 25.

Results. A total of 150 patients were included (50 patients infected with each RT). Overall, 53% of the patients had severe or fulminant disease most commonly due to RT 027 (80%) followed by RT 014-020 (40%) and RT 255 (38%). Patients infected with RT 255 or 014-020 had a 75% relative reduction in the odds of severe disease compared with RT 027 after controlling for patient age and serum albumin level (OR, 0.25; 95% CI, 0.86–0.74; $P = 0.12$;). No differences were seen in the rates of 30- or 90-day recurrence between RTs.

Conclusion. Although RT 255 is becoming increasingly common across Texas, it does not appear to be associated with more severe disease when compared with other common ribotypes. Further studies are warranted to determine contributing factors for its increasing prevalence.

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2403. *Clostridium difficile* ribotypes and human microbiota differ in Taiwan and the United States with respect to diarrheal patients

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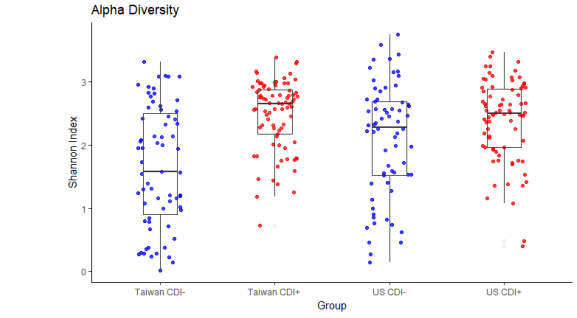
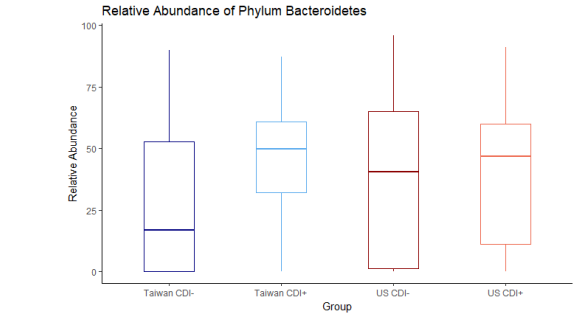
Background. *Clostridium difficile* infection (CDI) has high incidence in the United States, but less so in East Asian countries such as Taiwan. The reason for this is not understood, but microbial studies could reveal important epidemiologic insights. We hypothesized that the circulating strains of *C. difficile* and the gut microbiota differ between the United States and Taiwan.

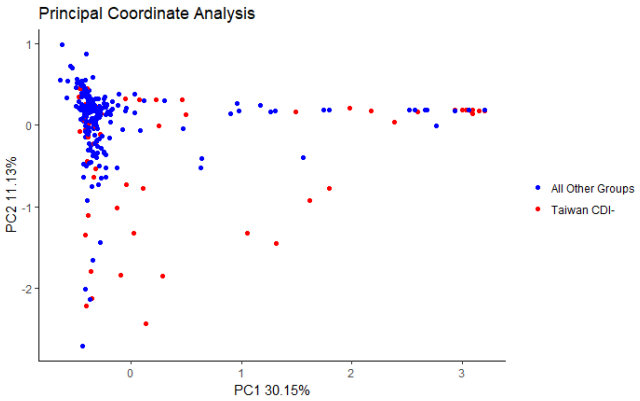
Methods. Patients with diarrhea ± CDI from the University of Michigan and Chang Gung Memorial Hospital were included. CDI was defined by + enzyme immunoassay for the glutamate dehydrogenase gene and toxins A/B, with reflex to *tcdB* gene PCR for discordants. *C. difficile* was isolated by anaerobic culture and characterized by PCR ribotype. The fecal microbiota was assessed by sequence analysis of 16S rRNA-encoding gene amplicons targeting the V4 region. Amplicon sequences were processed using the *mothur* bioinformatics pipeline, with an operational taxonomic unit (OTU) defined by < = 3% sequence homology. Analysis was performed via logistic regression, principal coordinates (PCoA), and ANOVA.

Results. Community diversity by Shannon index of CDI- patients was lower (Figure 1); this difference was greater in Taiwan ($P < .001$, OR = 3.9 per unit Shannon). Taiwanese CDI- patients had lower Bacteroidetes relative abundance (RA) (Figure 2). The Taiwanese CDI- group also differed on PCoA and ANOVA (Figure 3, $P < .001$). OTU1 (genus *Firmicutes*) was depleted in CDI+ patients ($P < .001$, OR = 0.69 per 10% RA increase). Circulating ribotypes (Table 1) differ between countries, with no epidemic strains (R027/R078) present in Taiwan ($P = .027$). R027 and 014/020 comprised > 50% of US isolates while > 50% of Taiwanese isolates were R002.

Conclusion. Taiwan and US CDI+ patients differ in dominant ribotypes. It is overall difficult to differentiate diarrheal CDI+ and CDI- patients by the microbiome. Taiwanese CDI- patients are outliers, and possible reasons (e.g., differential burden of parasitic infection; diet) require further study. The increased diversity and lower Bacteroidetes in CDI+ vs. CDI- diarrheal patients contrast with prior studies that instead compared with CDI- non-diarrheal patients. Circulating strains in Taiwan include no epidemic variants; whether this explains the differential incidence needs further study.







Top Ribotypes Taiwan (n=48)			Top Ribotypes US (n=80)	
Ribotype	**Count**		**Ribotype**	**Count**
F002	25 (52%)		F014-020	19 (24%)
F106	6 (13%)		F027	10 (13%)
F014-020	3 (6%)		F002	6 (8%)
F001	2 (4%)		F012	5 (6%)
FP435	2 (4%)		F015	5 (6%)
Other	10 (20%)		F106	5 (6%)
			F078-126	1 (1%)
			Other	51 (64%)

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2404. Molecular Epidemiology of Clostridioides difficile in the United States, 2017

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Background. In 2009, the Centers for Disease Control and Prevention (CDC) implemented *Clostridioides difficile* infection (CDI) surveillance through the Emerging Infections Program (EIP) to monitor the incidence and evolving epidemiology of CDI in the United States. Since 2012, ribotypes (RTs) 027, 106, 002, 014, and 020 have constituted the top five strain types among both US community- and healthcare-associated isolates. Here we describe the changes in molecular epidemiology of *C. difficile* isolates collected in the United States in 2017.

Methods. In 2017, CDI surveillance was conducted at 10 EIP sites (CA, CO, CT, GA, MD, MN, NM, NY, OR, and TN). A convenience sample of clinical laboratories across EIP sites submitted *C. difficile*-positive stool specimens to the MN Department of Health Public Health Laboratory and Hines VA Hospital (IL) for culture. Isolates were forwarded to CDC and characterized by capillary-based PCR-ribotyping and PCR detection of *tcdA*, *tcdB*, *cdtA*, *cdtB*, and deletions in *tcdC*.

Results. In 2017, 1,051 *C. difficile* isolates were submitted; the total number of isolates received from each site ranged from 11 to 286 with a median of 85.5. In total, 143 RTs were observed, with the majority of isolates harboring toxin genes *tcdA* and *tcdB* (95%) and a wild-type *tcdC* sequence (71%). Among 556 healthcare-associated isolates, RT 027 was the most prevalent and the top RT at 5 sites (CA, GA, MD, NM, TN). Ribotype 106 was the most prevalent among 495 community-associated CA isolates and the top RT at 6 sites (CO, CT, GA, MD, MN, TN). Ribotype 027 significantly decreased from 2012 to 2017 among both healthcare-associated (21% vs 15%; p = 0.02) and community-associated isolates (17% vs 6%; $P < 0.0001$). Among healthcare-associated isolates, RT 076, which was observed in 8 EIP sites, increased from 2% in 2016 to 5% in 2017 (p = 0.05) and replaced RT 020 as one of the top 5 healthcare-associated RTs in 2017.

Conclusion. Despite an overall decline since 2012, RT 027 remained the most prevalent RT among healthcare-associated isolates submitted in 2017. The increased frequency of RT 076 among healthcare-associated isolates submitted in 2017 highlights the evolving molecular epidemiology of *C. difficile* and the need for continued surveillance to monitor potential emerging strains.

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2405. Clinical Characteristics and Prognostic Factors for Extraintestinal Infection Caused by *Clostridium difficile*: An Analysis of 62 Consecutive Cases

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Background. Whereas Clostridium difficile enterocolitis has been well studied, data regarding extraintestinal *C. difficile* infection remain scarce and anecdotal. We investigated characteristics and prognostic factors in patients with extraintestinal *C. difficile* infection at a large university hospital over a recent 20-year period.

Methods. We conducted a retrospective cohort study of patients at a 2,700-bed tertiary care hospital from January 1997 through December 2018 whose extraintestinal clinical specimen revealed *C. difficile*. Gastrointestinal (GI) disruption was defined as compromised integrity of the GI tract by abdominal surgery, perforation, malignancy, or bleeding. Patients were divided into 3 groups: group A (GI disruption with malignancy, $n = 15$); group B (GI disruption without malignancy, $n = 23$); group C (No GI disruption or malignancy, $n = 24$). The main outcome was 30-day all-cause mortality.

Results. A total of 62 patients were enrolled, and the incidence of extraintestinal *C. difficile* infection was 2.81 per 100,000 admissions. Median age was 56 years and 36 (58.1%) of the patients were men. Seven patients (11.3%) had confirmed *C. difficile* enterocolitis, and 38 patients (61.3%) had a polymicrobial infection. *C. difficile*