Methods. We conducted a national retrospective study of Veterans with a first CDI between 2010 and 2014, defined as a positive *C. difficile* toxin(s) and no episode in the year prior. Those treated with guideline recommended CDI treatment were included (10–14 days of PO or IV metronidazole, PO or PR vancomycin, or fidaxomicin). The exposure of interest was any non-CDI antibiotic use during CDI treatment; and the outcome was all cause death within 30 days of the end of CDI treatment. Inverse probability of treatment weighted Cox proportional hazards models were used to estimate the effect of concomitant antibiotic use on time to mortality. Weights were derived from propensity score modeling of the probability of exposure to antibiotics during CDI treatment as a function of potential confounders. Sensitivity analyses by antibiotic class were conducted.

Results. Of the 9,517 patients included in the study cohort, mean age was 65.3 years (±SD 14.6), 92.5% ($n = 8,802$) were male, and 75.03% ($n = 7,141$) were white. Half were exposed to non-CDI antibiotics during CDI treatment (51.8%, $n = 4,925$) and 8.9% ($n = 849$) died. In unadjusted and adjusted analyses, concomitant antibiotic use was associated with death (HR 5.74, 95% CI 4.75–6.93; aHR 2.39, 95% CI 2.07–2.75). Advanced generation cephalosporin (aHR 2.36, 95% CI 2.05–2.71), β-lactam/β-lactamase inhibitor combinations (aHR 1.45, 95% CI 1.16–1.82), and clindamycin (aHR 1.95, 95% CI 1.26–3.02) were associated with death, while fluoroquinolone use was not (aHR 0.97, 95% CI 0.84–1.12)

Conclusion. Among our national cohort, concomitant antibiotic use was common during CDI treatment. Any concomitant antibiotic use increased the risk of death; however, results suggest risk might vary by antibiotic class. Results support continued efforts in the reduction of unnecessary antibiotic use during CDI treatment, and future studies into which antibiotics may have the least risk of death when treatment is necessary.

Disclosures. **H. Appaneal**, Merck: Grant Investigator, Research support. **A. Caffrey**, Pfizer: Investigator, Research support. Merck: Investigator, Research support. The Medicines Company: Investigator, Research support. **K. LaPlante**, Merck: Grant Investigator, Research grant. Pfizer Pharmaceuticals: Grant Investigator, Research grant. Allergan: Scientific Advisor, Honorarium. Ocean Spray Cranberries, Inc.: Grant Investigator and Scientific Advisor, Honorarium. Achaogen, Inc.: Scientific Advisor, Honorarium. Zavante Therapeutics, Inc.: Scientific Advisor, Honorarium.

471. Prevalence and Characteristics of *Clostridioides difficile* Infection in Bangladesh

Amelia K. Sofjan, PharmD[1]; M. Jahangir Alam, PhD[1]; M. Aminul Islam, PhD[2] and Kevin W. Garey, PharmD, MS[3]; [1]University of Houston College of Pharmacy, Houston, Texas, [2]The International Centre for Diarrhoeal Disease Research, Dhaka, Bangladesh, [3]Pptr, University of Houston College of Pharmacy, Houston, Texas

Session: 59. Healthcare Epidemiology: Updates in *C. difficile*
Thursday, October 4, 2018: 12:30 PM

Background. The estimated prevalence of *Clostridioides difficile* infection (CDI) in several South Asian countries is 10.5%, similar to that in North America and Europe. However, the epidemiology of CDI in Bangladesh is unknown. We aimed to assess the prevalence of CDI and assess hospital environmental contamination of toxigenic *C. difficile* in Bangladesh.

Methods. This was a prospective observational cohort study at two large tertiary care centers in Dhaka, Bangladesh, conducted from January 2017 to December 2017. Stool samples were collected from hospitalized adults with diarrhea (≥3 loose stools in a 24-hour period) and antimicrobial exposure within the past 30 days. Hospital environmental samples were collected by swabbing surfaces of common areas in the hospital. All samples underwent toxigenic culture. *C. difficile* isolates were tested for toxins A and B and PCR-ribotyped.

Results. Of 204 stool samples collected, 16 (7.8%) were positive for toxigenic *C. difficile*. Patients with CDI shared a room with significantly more patients (Table 1). Of 392 environmental samples, 48 (12.2%) were positive for toxigenic *C. difficile,* which was more common in patient care vs. nonpatient care areas (14.4% vs. 7.8%, $P = 0.057$). Twelve clinical stool isolates and 42 environmental isolates were ribotyped. Ribotypes identified in stool isolates were F017 (50%), FP053-163 (17%), FP435 (17%), F106 (8%), and F014-020 (8%). With the exception of FP435, these were also the most common ribotypes in environmental isolates: F017 (24%), FP053-163 (12%), F106 (26%), and F014-020 (10%).

Conclusion. For the first time, we report the prevalence of CDI and ribotypes in at risk patients in Bangladesh. Rates and ribotypes are similar to other resource-rich or resource-limited countries.

Table 1: Demographic Data for All Stool Samples

Variable	No toxigenic *C. difficile* ($n = 188$)	Toxigenic *C. difficile* ($n = 16$)	P
Female sex, n (%)	77 (41)	9 (56)	0.234
Age, years, median (IQR)	46 (32–58)	39 (25–53)	0.212
Hospital A, n (%)	149 (79)	13 (81)	>0.99
Length of prior hospital stay, days, median (IQR)	13 (7–23)	14 (8–32)	0.798
Duration of previous antibiotics, days, median (IQR)	10 (7–17)	12 (6–20)	0.687
Number of patients in the same room, median (IQR)	13 (7–19)	19 (14–20)	0.009

Disclosures. **K. W. Garey**, Merck & Co.: Grant Investigator, Grant recipient.

472. Prevalence, Risk Factors, and Outcome of Postoperative *Clostridium difficile* Infection After Orthopedic Surgery

Dong Youn Kim, MD[1]; Yu-Mi Lee, MD[1]; Young Jin Kim, MD[2]; Misuk Lee, MD[1]; Hee-Joo Lee, MD[2] and Ki-Ho Park, MD[1]; [1]Division of Infectious Diseases, Department of Internal Medicine, Kyung Hee University Hospital, Kyung Hee University School of Medicine, Seoul, Korea, Republic of (South), [2]Department of Laboratory Medicine, Kyung Hee University Hospital, Kyung Hee University School of Medicine, Seoul, Korea, Republic of (South)

Session: 59. Healthcare Epidemiology: Updates in *C. difficile*
Thursday, October 4, 2018: 12:30 PM

Background. The patients undergoing orthopedic surgery may have many risk factors of *Clostridium difficile* infection (CDI), including increased age, multiple underlying comorbidities, the use of perioperative antibiotics, and prolonged length of stay. The aim of this study was to identify prevalence, risk factor, and outcome of postoperative CDI in patients who underwent orthopedic surgery.

Methods. We performed a retrospective cohort study including all patients aged ≥18 years who underwent orthopedic surgery from January 2016 through December 2017 in a tertiary care hospital in Seoul, South Korea.

Results. During the study period, 7,369 episodes of orthopedic surgery were identified. The prevalence of *C. difficile* infection was 7.7 cases per 1,000 surgical procedures (95% confidence interval, 6.0–10.0). The risk of CDI was the highest among patients who underwent spine surgery (33.8 cases per 1,000 surgical procedures), followed by hip/femur surgery (12.4), knee (3.8), and extremity (3.2). The risk of CDI increased according to the increase in duration of proton pump inhibitor: 0.1% (no use), 0.3% (1–7 days), and 2.7% (>7 days, $P < 0.001$). The independent risk factors associated with postoperative CDI were age (odds ratio [OR] per 1-year increase, 1.04; $P < 0.001$), Charlson comorbidity index score (OR per 1-point increase, 1.26; $P < 0.001$), duration of proton pump inhibitor (OR per 1-day increase, 1.02; $P < 0.001$), and operation time (OR per 1-hour increase, 1.30; $P = 0.003$). Of 6,724 episodes of surgical procedure for which patients received exclusively perioperative antibacterial prophylaxis, 22 episodes of postoperative CDI occurred (3.2 cases per 1,000 surgical procedures). Among this subgroup, the risk of CDI increased according to increase in duration of antibacterial prophylaxis: 0% (<24 hour), 0.28% (1–7 days), and 1.27 (>7 days; $P < 0.001$). After adjusting confounding factors, duration of perioperative antibacterial prophylaxis remained a significant risk factor for postoperative CDI (OR per 1-day increase, 1.11; $P < 0.001$). Patients with CDI had a higher rate of postoperative mortality (10.5% vs. 0.6%; $P < 0.001$) and an increased length of hospital stay (mean 42 vs. 10 days; $P < 0.001$).

Conclusion. Judicious use of proton pump inhibitor and avoiding of extension of prophylactic antibiotics can reduce postoperative CDI after orthopedic surgery.

Disclosures. All authors: No reported disclosures.

473. Molecular Typing of *Clostridium difficile*: Concordance Between PCR-Ribotyping and Multilocus Sequence Typing (MLST)

Xiong Wang, DVM, PhD[1]; Stacy Holzbauer, DVM, MPH[1]; Kelly Pung, BS[1]; Maria Bye, MPH[1]; Michelle Adamczyk, BS[2]; Ashley Lyn Paulick, BS[2]; Nicholas Vlachos, MS[2]; Alice Guh, MD, MPH[2]; Alison S. Laufer-Halpin, PhD[2]; Maria S. Karlsson, PhD[2]; Dave Boxrud, MSc[1] and the Emerging Infections Program CDI Workgroup; [1]Minnesota Department of Health, Saint Paul, Minnesota, [2]Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, Georgia

Session: 59. Healthcare Epidemiology: Updates in *C. difficile*
Thursday, October 4, 2018: 12:30 PM

Background. *Clostridium difficile* infection (CDI) incidence has increased dramatically in the past decade, making CDI one of the most common causes of infectious diarrhea and an urgent public health threat. Understanding the biological features and spread of *C. difficile* strains can help target control efforts. PCR-ribotyping, the current method of choice for *C. difficile* typing, remains subjective and challenging for interlaboratory comparisons. Multilocus sequence typing (MLST), based on the alleles of seven housekeeping genes, represents a more robust tool that would enhance interlaboratory reproducibility. However, a comprehensive translation system to ribotyping is a prerequisite. Here, we describe the concordance between MLST and PCR-ribotyping.

Methods. The Centers for Disease Control and Prevention's (CDC) Emerging Infections Program (EIP) conducts CDI surveillance in 10 US sites. *C. difficile* isolates cultured from a subset of cases underwent capillary-based PCR-ribotyping at CDC. A representative sample, selected from the top 30 ribotypes (RTs), underwent whole genome sequencing (WGS) at Minnesota Department of Health. An additional subset of isolates, representing the top 10 RTs, underwent WGS at CDC. At both laboratories, the Illumina MiSeq platform was used to obtain 250 bp paired-end sequencing reads. MLST analyses were done using the pubMLST *C. difficile* scheme.

Results. A total of 479 *C. difficile* isolates, including at least 10 isolates for each RT, were analyzed by WGS. Among the 30 RTs represented, 35 different MLST sequence types (STs) were identified. Twenty-two of the RTs (including 027) were each associated with a single unique ST, while 8 RTs (020, 014, 015, 076, 046, 153–251, A27, and 075) presented more genetic diversity with single-locus or double-locus variants, resulting in multiple STs within one ribotype. There were two instances of two different RTs sharing the same ST.

Conclusion. Multilocus sequence typing and PCR-Ribotyping showed comparable discriminatory abilities. However, the ST is not always predictive of the RT and vice versa. This represents the first step toward a transition to using WGS for standard *C. difficile* typing.

Disclosures. All authors: No reported disclosures.