Recurrent infection (CDI) is associated with significant morbidity, mortality and healthcare related costs. Up to 30% of CDI cases recur, resulting in 83,000 cases of recurrent CDI per year. Although agents for primary and secondary prophylaxis for CDI including the use of probiotics, antibiotics, fecal microbiota transplantations, and newer therapies such as bezlotoxumab have been reported, there is no consensus guidelines regarding their use. The purpose of this study was to assess physician practices regarding secondary prophylaxis for CDI.

Methods. This cross-sectional study using Qualtrics electronic survey (24 questions) assessed physician practice preferences. The survey was distributed through institutional emails and through the Infectious Disease Society of America "IDExchange" forum. Responses were collected and analyzed using descriptive statistics.

Results. A total of 246 surveys were completed. Physicians were surveyed from greater than 100 locations (see Figure 1). Most (229, 93%) of the physicians practiced in an inpatient setting. Respondent specialties were primarily infectious diseases (138, 56%) followed by internal medicine (74, 29%), Most physicians (173, 71%) use secondary prophylaxis for CDI prevention (see Figure 2). Vancomycin (121, 70%) and probiotics (114, 66%) were most commonly used for CDI secondary prophylaxis, (see Figure 3). Of 164 physicians who used secondary prophylaxis half of them (89, 54.2%), used prophylaxis only for patients with a history of recurrent CDI receiving antibiotics and about a third, (49, 29.9%) utilized it for patients with a history of recurrent CDI receiving antibiotics. ID physicians were more likely to prescribe secondary prophylaxis as compared with non-ID physicians (85% of 127 vs. 80% of 127, P = 0.052). The use of secondary prophylaxis was similar among private practice and academic physicians (84% of 39 vs. 80% of 157 respondents, P = 0.591).

Conclusion. The majority of the physicians who responded to this survey use secondary prophylaxis to prevent recurrent CDI, hence future CDI guidelines need to address the role of secondary prophylaxis in clinical practice.
Background. *Clostridium difficile* is the leading cause of healthcare-associated infection. As incidence rises, its epidemiology is also evolving. 20–50% of cases are now community-acquired; *C. difficile* cases arise from more diverse sources than previously thought. In this study, we investigated the diversity of *C. difficile* within a community hospital.

Methods. Stool samples were collected from symptomatic adults with a positive *C. difficile* PCR admitted to Duke Regional Hospital from July 2016 to July 2017. Healthcare-associated CDI was defined by any admission to a hospital, nursing or dialysis facility in the preceding 30 days. *C. difficile* was isolated by ethanol shock followed by plating on CDSA media. DNA was extracted using a chlex-based protocol. PCR ribotyping was conducted using the Bidet primers and agarose gel electrophoresis. A dendrogram was constructed in Bionumerics by the un-weighted pair-group method with the threshold for identical strains set at 95% similarity.

Results. *C. difficile* was successfully isolated from 85% of submitted specimens. For this pilot study, PCR ribotyping was performed on a convenience sample of 70 isolates. *C. difficile* exhibited substantial diversity: 47 distinct ribotypes were observed among 70 isolates (Figure 1). Fourteen clusters involving identical strain types were observed, totaling 35 isolates. Identical strain types suggestive of direct transmission were evenly split between hospital- (18 of 35, 51%) and community-acquired (17 of 35, 49%) cases. The median time between clustered cases was 50 days (range: 7 to 331 days). Thirty-five of 70 (50%) of all isolates exhibited entirely unique strain types.

Conclusion. *C. difficile* isolates in our community hospital exhibited tremendous genetic diversity. The high proportion of strains with entirely unique ribotypes suggests diverse sources of acquisition. These results are consistent with a growing body of literature in which 30–50% of *C. difficile* isolates are genetically distinct, even when direct transmission was suspected. We are currently expanding our survey to include a network of regional hospitals and clinics, with the goal of better characterizing *C. difficile*’s diverse and still poorly understood sources.

Figure 1. Dendrogram of *C. difficile* PCR ribotypes.

Disclosures. All authors: No reported disclosures.

498. Molecular Epidemiology of *C. difficile* Within a Community Hospital: A Pilot for a Regional Survey
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Session: 59. Healthcare Epidemiology: Updates in *C. difficile*
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Background. Hospitals may now be penalized for *Clostridium difficile* infection diagnosed after hospital day 3, which are classified as “hospital-onset” (HO) regardless of existence of true disease. Highly sensitive PCR-based testing has made this additionally problematic. As part of a *C. difficile* testing stewardship initiative, we sought to validate a *C. difficile* risk scoring tool using existing EHR data.

Methods. We conducted this study in a 2-hospital, >1,100-bed community-based academic healthcare system in northern Delaware. After piloting a paper-based Cdf risk scoring tool, intended for use after hospital day 3 to discourage testing in low-risk patients, we created a *C. difficile*-specific analytic application using the Health Catalyst clinical analytics platform over the existing data warehouse (Cerner). The scoring tool was modified from those in the literature and included patient age, body mass index and albumin (if available); prior hospitalization or long-term care facility stay (within 90 days); and receipt of any fluoroquinolone, cephalosporin or piperacillin/tazobactam (within 30 days). Only antibiotics received within our system were included. Using data from September 2015–April 2018, we calculated a receiver operating characteristic (ROC) curve for the risk score’s ability to predict a positive HO Cdf PCR. To increase specificity, we defined “true positive” *C. difficile* as +PCR tests occurring in patients with ≥3 diarrheal episodes and no laxative use during the 48h prior to testing, and either WBC >12 or temperature >38°C 24 hours before or after the +PCR.

Results. During the study period the health system had 150,554 inpatient encounters, of which 411 had positive PCR tests for HO *C. difficile* and 138 (33% of all PCR+) met our definition of “true positive.” The *C. difficile* risk stratification tool demonstrated an area under the ROC (AUC) of 0.77 (95% CI 0.75–0.79) to predict a +PCR test (Figure 1), with very similar results (AUC 0.76, 95% CI 0.73–0.80) if the outcome was “true positive” *C. difficile* (Figure 2).

Conclusion. Using readily available EHR data, we developed a *C. difficile* risk stratification tool that was able to predict *C. difficile* positivity with reasonable distinction, but did not differentiate colonization from true illness. The next step is to further refine the tool to better predict true *C. difficile* illness.

Figure 1.

Figure 2.

Disclosures. All authors: No reported disclosures.

499. Determining Risk of *Clostridium difficile* Using Electronic Health Record (EHR) Data
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Session: 59. Healthcare Epidemiology: Updates in *C. difficile*
Thursday, October 4, 2018: 12:30 PM

Background. *Clostridium difficile* infection diagnosed after hospital day 3, which are classified as “hospital-onset” (HO) regardless of existence of true disease. Highly sensitive PCR-based testing has made this additionally problematic. As part of a *C. difficile* testing stewardship initiative, we sought to validate a *C. difficile* risk scoring tool using existing EHR data.

Methods. We conducted this study in a 2-hospital, >1,100-bed community-based academic healthcare system in northern Delaware. After piloting a paper-based Cdf risk scoring tool, intended for use after hospital day 3 to discourage testing in low-risk patients, we created a *C. difficile*-specific analytic application using the Health Catalyst clinical analytics platform over the existing data warehouse (Cerner). The scoring tool was modified from those in the literature and included patient age, body mass index and albumin (if available); prior hospitalization or long-term care facility stay (within 90 days); and receipt of any fluoroquinolone, cephalosporin or piperacillin/tazobactam (within 30 days). Only antibiotics received within our system were included. Using data from September 2015–April 2018, we calculated a receiver operating characteristic (ROC) curve for the risk score’s ability to predict a positive HO Cdf PCR. To increase specificity, we defined “true positive” *C. difficile* as +PCR tests occurring in patients with ≥3 diarrheal episodes and no laxative use during the 48h prior to testing, and either WBC >12 or temperature >38°C 24 hours before or after the +PCR.

Results. During the study period the health system had 150,554 inpatient encounters, of which 411 had positive PCR tests for HO *C. difficile* and 138 (33% of all PCR+) met our definition of “true positive.” The *C. difficile* risk stratification tool demonstrated an area under the ROC (AUC) of 0.77 (95% CI 0.75–0.79) to predict a +PCR test (Figure 1), with very similar results (AUC 0.76, 95% CI 0.73–0.80) if the outcome was “true positive” *C. difficile* (Figure 2).

Conclusion. Using readily available EHR data, we developed a *C. difficile* risk stratification tool that was able to predict *C. difficile* positivity with reasonable distinction, but did not differentiate colonization from true illness. The next step is to further refine the tool to better predict true *C. difficile* illness.

Figure 1.

Figure 2.

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