P = .0001). After the intervention, 299 patients had an override. Of these, samples from 218 patients (72.9%) were negative, 50 orders (16.7%) were cancelled, and 28 samples (9%) were positive. **Conclusions:** Diagnostic stewardship, utilizing an electronic hard stop, was effective in reducing inappropriate *C. difficile* testing in the setting of promotility agents without delaying diagnosis of HO-CDI. This strategy combined with standard best practices can significantly reduce HO-CDI rates.

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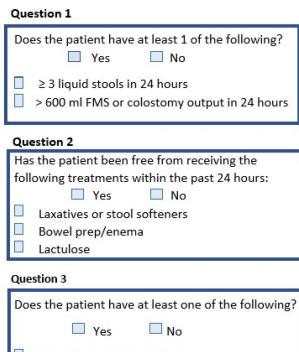
Disclosures: None

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Presentation Type: Poster Presentation - Poster Presentation Subject Category: C. difficile Prospective audit and feedback of Clostridioides difficile PCR at the time of ordering increases appropriateness of testing Daniel Tassone, Matthew Hitchcock, John Markley, Michael Stevens

Background: Over-testing for *Clostridioides difficile* infection outside acute diarrheal illness without a clear alternative cause can lead to inappropriate diagnosis and treatment with antibiotic therapy. Preanalytical interventions such as education, order restriction, and electronic order assistance are common but are limited in effectiveness. As an alternative

Step 2: Answer all 3 questions below:



- Yes No
 Fever > 100.4 in past 48 hours
 Abdominal pain/tenderness
 WBC 15,000 or < 4,000 within 48 hours
 Antibiotics within 30 days
 - Discharge from any healthcare facility within 30 days

Fig. 1.

approach, our antibiotic stewardship program (ASP) implemented prospective audit and feedback (PAF) on *C. difficile* PCR orders to reduce inappropriate testing.

Methods: The study was conducted at a 399-bed, tertiary-care, Veterans' Affairs Medical Center and included adult inpatients and outpatients for whom C. difficile PCR testing was ordered. In the preintervention period from June through September 2019, the ASP was alerted to C. difficile PCR tests and collected data but did not intervene. From October 2019 to January 2020, the ASP performed real-time PAF at the time of ordering. Appropriateness of testing was determined based on whether there was a negative result in the prior 7 days and a 3-step review of clinical factors (Fig. 1). When possible, a direct conversation took place with the ordering provider. If not possible, a general note delineating appropriate clinical criteria for testing was generated. No PAF was done outside standard hours. The ASP recommended cancelling tests deemed inappropriate. Monthly test rates during the pre- and postintervention periods were compared using the Student t test with $\alpha = .05$, and test appropriateness was compared using the χ^2 test. All analyses were conducted using Microsoft Excel software. Results: During the preintervention period, a total of 418 tests were ordered (104.5 per month). This number decreased to 276 (69 per month) during the intervention period. (p Conclusions: Direct PAF at the time of C. difficile PCR ordering may increase test appropriateness and is associated with a reduction in overall testing, primarily by reducing the number of tests that are considered not appropriate on clinical grounds. PAF is effective but requires significant time investment by ASP staff and may not be a sustainable intervention over time.

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Presentation Type:

Poster Presentation - Poster Presentation

Subject Category: C. difficile Evaluation of the genomic epidemiology and transmission of

Clostridioides difficile infection across a community

Brenda Tesini, Samantha Taffner, Trupti Hatwar, Steven Gill, Ghinwa Dumyati, Nicole Pecora

Background: Clostridioides difficile infection (CDI) is a major cause of morbidity and healthcare costs in the United States. The epidemiology of CDI has recently shifted, with healthcare-associated (HCA) CDI trending downward and community-associated (CA)-CDI becoming more prominent. The cause of this shift is not well understood but may be related to changing genomic epidemiology. We assessed C. difficile strains across a CDC Emerging Infections Program (EIP) site in Western New York, including strains from both HCA-CDI and CA-CDI cases to characterize predominating strains and putative transmission across epidemiological classifications and between index and recurrent cases. Methods: In total, 535 isolates of C. difficile were collected over a 6-month period in 2018 from the Monroe Country, New York, EIP site and were analyzed using whole-genome sequencing (WGS). Standard epidemiological definitions were used to classify cases as hospital onset (HO-CDI); community associated (CA-CDI); community onset, healthcare associated (CO-HCFA-CDI); or long-term care onset (LTCO-CDI). Recurrent cases were defined as those diagnosed within 8 weeks of an initial positive test. Multilocus sequence types (MLSTs) were assigned according to PUBMLST and single-nucleotide polymorphisms (SNPs) were determined using a modified CFSAN analytical pipeline. Cases resulting from putative transmission were defined as those separated by 0-1 core SNPs. Results: Of 535 isolates, 454 were from index and 81 were from recurrent cases. The index cases were comprised of CA-CDI (47.4%), CO-HCFA-CDI (24%), LTCO-CDI (8.1%), and HO-CDI (19.3%). Cases with recurrent disease mirrored the epidemiological distribution of the larger set. Common MLSTs included ST2 (12.3%), ST8 (10.5%), ST42 (7.9%), ST58 (4.9%), ST43 (4.5%), and ST11 (4.3%). The previously widespread epidemic strain,