Presentation Type:
Poster Presentation
Subject Category: C. difficile
Emerging vancomycin and metronidazole resistance in Clostridioides difficile: Pilot Whole-Genome Sequencing analysis from a multicenter‡
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Background: Antimicrobial resistance in Clostridioides difficile threatens frontline therapies, particularly vancomycin and metronidazole. Rapid genomic screening can flag putative resistance mechanisms, informing infection prevention and stewardship. We present pilot WGS data focused on vancomycin- and metronidazole-associated determinants. Methods A multicenter collection included the University Hospital in Kraków and five long-term care facilities in Małopolska, in 2022-2023. Sixty-six C. difficile strains were sequenced (WGS, AVITI PE300) and analyzed bioinformatically (Genpax IDEM, version 2.6); eight originated from colonized individuals, the remainder from CDI cases. We extracted the prevalence of vancomycin-associated genes (vanR-Cd, vanS-Cd, vanT-Cd, vanG, vanZ1, and vanS-Cd_T369I variant) and the metronidazole-associated gene nimB-Cd. Results Markers linked to vancomycin resistance were frequent: vanR-Cd (93.9%), vanT-Cd (71.2%), vanS-Cd (63.6%), vanG (59.1%), vanZ1 (51.5%), and vanS-Cd_T369I (4.5%). The metronidazole resistance marker nimB-Cd occurred in 95.5% of isolates. Notably, only one strain lacked any vancomycin resistance gene, and this isolate was recovered from a patient with CDI. These pilot genomic findings suggest widespread carriage of loci associated with reduced susceptibility to vancomycin and metronidazole in our regional C. difficile population. Conclusions In this pilot dataset, C. difficile isolates frequently carry genomic elements associated with vancomycin and metronidazole resistance. However, the mere presence of these markers, such as nimB or genes under vanRS regulation, may not independently indicate phenotypic resistance without specific functional mutations or regulatory changes. Phenotypic confirmation remains essential to establish clinical relevance; standardized susceptibility testing and integration of genotypic–phenotypic correlations with clinical data will follow in the next phase. Until then, these preliminary WGS results should be interpreted with caution and primarily guide prioritization of surveillance and stewardship actions.

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Concordance between Emerging Infections Program and Centers for Medicare and Medicaid Services data for patients in Nashville, TN, 2022‡
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Background: As part of the Centers for Disease Control and Prevention's (CDC's) Emerging Infections Program (EIP), the Tennessee Department of Health (TDH) conducts surveillance on Clostridioides difficile infection (CDI) in a designated catchment area. As part of ongoing surveillance, select TDH staff have access to Centers for Medicare and Medicaid Services (CMS) patient-level data under a CDC-CMS data use agreement. The aim of this study was to assess the alignment between the most prevalent chronic conditions among CDI cases reported through EIP and those reported through CMS. **Methods:** We matched patients who were 65 years and older from 2022 EIP data with Medicare beneficiaries on date of birth, sex, county of residence, and ZIP code, and retained unique matches for our study. Comorbidities present in both the CMS 30 CCW Chronic Conditions list and in the CDI case report form were included. The most prevalent chronic conditions in each dataset were identified. We employed Cohen's Kappa to assess inter-rater reliability between chronic conditions reported through EIP chart abstractions and those reported via CMS claim submissions. A Cohen's Kappa greater than 0.4 indicates moderate or greater inter-rater reliability. Analysis was conducted using SAS Studio. **Results:** Of the 431 EIP CDI patients in 2022, 196 patients were 65 years or older and eligible for inclusion. 130 of these patients matched uniquely to a Medicare beneficiary ID on the demographics listed above (66.3%). The most prevalent chronic conditions identified among CDI patients were cardiovascular disease (CVD) (n=31), diabetes mellitus (n=26), chronic kidney disease (CKD) (n=21), and chronic pulmonary disease (CPD) (n=14). Diabetes mellitus diagnoses between the two datasets had the highest concordance with a Cohen's Kappa of 0.5226 (p<0.0001), followed by CKD at 0.3984 (p<0.0001), CPD at 0.2313 (p=0.0081), and CVD at 0.1371 (p=0.1162). **Conclusions:** Only diabetes mellitus diagnoses showed moderate concordance between EIP and CMS datasets. EIP processes utilize chart review to generate surveillance data, which is person-power intensive. This limited study indicates that comorbidity data for CDI patients may not be completely captured if surveillance was conducted through secondary analyses using CMS data rather than complete chart review by trained public health staff.

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Targeted Stewardship and Infection Prevention Interventions reduced Clostridioides difficile rates at a Veterans Affairs Hospital‡
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Background: Clostridioides difficile Infection (CDI) is one of the leading causes of hospital-acquired infections. The Veterans Health Administration launched a national CDI prevention initiative in 2012 that bundled core practices such as environmental cleaning, strict hand hygiene, and contact precautions. In contrast to prior studies which have noted a decline in CDI rates during the COVID-19 pandemic, rates of hospital-onset (HO)-CDI increased at our Veterans Administration Hospital, and we sought to address this issue with a multi-pronged approach. **Methods:** We assessed multi-modal approaches implemented to reduce HO-CDI rates at Veterans Affairs North Texas Health Care System (VANTHCS), a large, academic VA medical center from 2021 to 2025. This approach included laboratory changes to CDI testing, updates to infection prevention practices, and antimicrobial stewardship program (ASP) rounds for prospective audit and feedback for antibiotics (including those considered high-risk for CDI by the National Healthcare Safety Network). Our primary objective was to assess the impact of these interventions on the incidence of HO-CDI, comparing HO-CDI rates before (Q2 2020–Q4 2022) and after (Q2 2023–Q3 2025) their implementation. HO-CDI was defined as a LabID event collected from an inpatient location < 3 days after admission (i.e., on or after hospital day 4), and rates were reported as number of HO-CDI/10,000 bed days of care (BDOC). Cases were extracted from the Computerized Patient Record System. **Results:** In October 2021, VANTHCS switched from a standalone nucleic acid amplification test (NAAT) to a 2-step algorithm wherein an initial NAAT was reflexed to a toxin immunoassay if positive. The Infection Prevention and Control Program developed standard operating protocols for room cleaning and disinfection, and hand hygiene was reinforced. In February 2023, the facility ASP implemented thrice-weekly rounds.

‡The abstract titles in this supplement have been corrected since original publication. A notice detailing the changes has been published at https://doi.org/10.1017/ash.2026.10802.

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