To address the gap in antimicrobial prescribing decision-making, we developed an auditing tool that could be tailored to the needs of different healthcare settings. **Objective:** To create a user-friendly auditing tool that enhances collaborative decision-making and improves antimicrobial prescribing. **Methods and Results:** An auditing tool was developed and tested across healthcare settings, evaluating its impact on prescribing practices.

**Main Findings:**
- The tool effectively improved communication and decision-making among healthcare providers.
- Prescribing practices were aligned more closely with guidelines and evidence-based recommendations.
- Patient outcomes and healthcare costs were positively impacted.

**Conclusion:** The tool has the potential to significantly improve antimicrobial prescribing practices, enhance patient care, and reduce healthcare costs. Further research is needed to evaluate its long-term effectiveness in diverse settings.

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**Disclosures:** None.

**References:**
Background: The epidemic NAP1/027 *Clostridioides difficile* strain (MLST1, ST1) that emerged in the mid-2000s is on the rise. The current distribution of *C. difficile* strain types and their transmission dynamics are poorly defined. We performed whole-genome sequencing (WGS) of *C. difficile* isolates in 2 regions to identify the predominant multilocus sequence types (MLSTs) in community- and healthcare-associated cases and potential transmission between cases using whole-genome single-nucleotide polymorphism (SNP) analysis. Methods: Isolates were collected through the CDC Emerging Infections Program population-based surveillance for *C. difficile* infections (CDI) for 3 months between 2016 and 2017 in 5 Minnesota counties and 1 New York county. Isolates were limited to incident cases (CDI in a county resident with no positive *C. difficile* test in the preceding 8 weeks). Cases were classified as healthcare associated (HA-CDI) or community associated (CA-CDI) based on healthcare exposures as previously described. WGS was performed on an Illumina MiSeq. The CFSAN (FDA) pipeline was used to compute whole-genome SNPs, SPAdes was used for assembly, and MLST was assigned according to www.pubmlst.org. Results: Of 431 isolates, 269 originated from New York and 162 from Minnesota; 203 cases were classified as CA-CDI and 221 as HA-CDI. The proportion of CA-CDI cases was higher in Minnesota than in New York: 62% vs 38%. The predominant MLSTs across both sites were ST42 (9%), ST8 (8%), and ST2 (8%). MLSTs more frequently encountered in HA-CDI than CA-CDI included ST1 (note that this ST includes PCR Ribotype 027; 76% HA-CDI), ST53 (84% HA-CDI), and ST43 (80% HA-CDI). In contrast, ST110 (63% CA-CDI) and ST3 (67% CA-CDI) were more commonly isolated from CA-CDI cases. ST1 accounted for 7.6% of circulating strains and was more common in New York than Minnesota (10% vs 3%) and was concentrated among New York HA-CDI cases. Also, 412 isolates (1 per patient) were included in the final whole-genome SNP analysis. Of these, only 12 pairs were separated by 0–3 SNPs, indicating potential transmission, and most involved HA-CDI cases. ST1, ST17, and ST46 accounted for 8 of 12 pairs, with ST17 and ST46 forming small clusters. Conclusions: This analysis provides a snapshot of the current genomic epidemiology of *C. difficile* across 2 geographically and epidemiologically distinct regions of the United States and supports other studies suggesting that the role of direct transmission in the spread of CDI may be limited.

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