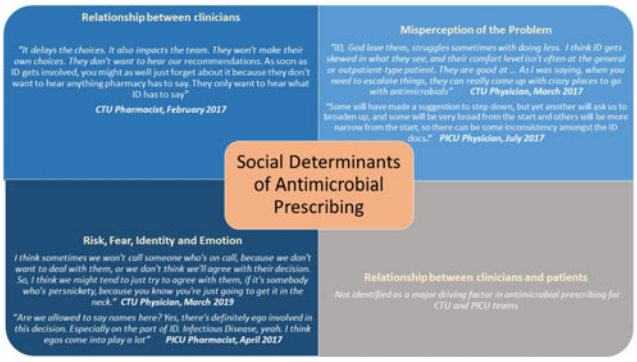

Fig. 1.

detrimental to antimicrobial prescribing decisions for CTU and PICU across 3 of the 4 SDAP domains (Fig. 1, qualitative research quotes). *Relationship between clinicians*: CTU physicians and pharmacists perceived ID involvement as negatively impacting the relationship of the team. Antimicrobial decisions were automatically defaulted to ID, whereas pharmacy involvement was disregarded and the decisions were delayed. *Risk, fear, and emotion*: These were experienced across all respondents' groups that identified ID specialists' egos and personalities as contrary to open collaborative discussion on antimicrobial decisions. *(Mis)perception of the problem*: ID physicians were identified as more conservative in their antimicrobial choices, leading to prolonged duration of treatment, broader choices, and longer hospitalizations. The CTU and pharmacy respondents felt that ID recommendations were inconsistent among physicians and deviated from guidelines with little justification. **Conclusions:** Although CTU and PICU teams tend to comply with ID prescribing recommendations and ID involvement with complicated cases, pharmacists, CTU physicians, and PICU physicians perceived ID consultations to negatively affect collaborative efforts for stewardship. These findings offer novel insights into how an ID service can improve its role to positively affect appropriate prescribing. CTU and PICU respondents called for a supportive and trusting relationship with the ID service as a major driver for behavioral change and enhanced stewardship.

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From Little Things Big Things Grow: The Development of an Auditing Program to Assess the Quality of Antimicrobial Prescribing

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Background: An important aspect of antimicrobial stewardship is the qualitative assessment of antimicrobial prescribing. Owing to lack of standardized tools and resources required to design, conduct and analyze qualitative audits, these assessments are rarely performed. **Objective:** We designed an audit tool that was appropriate for all Australian hospital types, suited to local user requirements and including an assessment of the appropriateness of antimicrobial prescribing. **Methods:** In 2011, a pilot survey was conducted in 32 Australian hospitals to assess the usability and generalizability of a qualitative audit tool. The tool was revised to reflect the respondents' feedback. A second study was performed in 2012 in 85 hospitals. In 2013, following further feedback and refinement, an online auditing tool, the Hospital National Antimicrobial Prescribing Survey (NAPS), was developed. Early audits demonstrated that surgical prophylaxis had the highest rates of inappropriate prescribing. In 2016, the Surgical NAPS was developed to further investigate reasons for this, and the NAPS program was further expanded to audit antimicrobial prescribing practices in Australian aged-care homes (ie, the Aged Care NAPS). **Results:** Between January 1, 2013, and November 12, 2019, 523 Australian public and private hospitals (53.8%) utilized the Hospital NAPS; 215 (22.1%) have utilized the Surgical NAPS; and 774 of Australian aged-care homes (29.0%) have utilized the Aged Care NAPS. National reporting has identified key target areas for quality improvement initiatives at both local and national levels. The following initiatives have been outlined in 14 public reports: improved documentation; prolonged antimicrobial prophylaxis; compliance with prescribing guidelines; appropriateness of prescribing; access to evidence-based guidelines; and improved microbiology sampling. **Conclusions:** By utilizing the Plan-Do-Study-Act cycle for healthcare improvement and by involving end users in the design and evaluation, we have created a practical and relevant auditing program to assess both quantitative and qualitative aspects of antimicrobial prescribing in a wide range of settings. This voluntary program is now endorsed by the National Strategy for Antimicrobial Resistance Surveillance, partners with the Antimicrobial Use and Resistance in Australian Surveillance System, and is utilized by facilities to meet mandatory national accreditation standard requirements. With the success of the NAPS program in Australia, it has now been implemented in New Zealand, Canada, Malaysia, Fiji, and Bhutan, with plans for other countries to implement the program soon. Current research is being conducted to expand the program to include audits for family physicians, veterinarians, and remote indigenous communities, and for antifungal use.

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Genomic analysis of Clostridioides difficile in two regions reveals a diversity of strains and limited transmission

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Background: The epidemic NAP1/027 *Clostridioides difficile* strain (MLST1, ST1) that emerged in the mid-2000 is on the decline. 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 potentially 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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Genomic Epidemiology of *Clostridioides difficile* Sequence Types 1 and 2 Across Three US Medical Centers

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Background: *Clostridioides difficile* is a toxin-producing bacterium that is the foremost cause of healthcare-associated diarrhea in the United States. Recent epidemiologic and genomic evidence indicates that divergent *C. difficile* strains have varying propensities for transmission within healthcare settings. We investigated whether and how these differences are reflected in the genomic epidemiology of 2 common *C. difficile* strains—sequence type (ST) 1 (analogous to Ribotype 027) and ST2 (associated with Ribotypes 014/020)—across 3 geographically distinct US medical centers. **Methods:** Between 2011 and 2017, a convenience sample of ST1 and ST2 *C. difficile* clinical isolates were collected from 3 US sites: The University of Michigan Medical Center, Texas Medical Center Hospitals, and Memorial Sloan Kettering Cancer Center. Isolates underwent whole-genome sequencing and *in silico* multilocus sequence typing to verify strain types. Sequences were mapped to ST1 and ST2 reference genomes and single nucleotide variants (SNVs) were identified, filtered, and used to construct pairwise SNV distance matrices. A range of pairwise SNV distance thresholds were applied to assess genetic linkages consistent with recent transmission within ST1 compared to within ST2. Proportions of genetically linked isolates were compared using χ^2 tests. **Results:** We identified 200 ST1 and 188 ST2 isolates across the 3 collection sites. Overall, ST2 was more genetically diverse than ST1 (pairwise SNV distance range, 0–156 SNVs and 0–78 SNVs, respectively). ST2 isolates displayed significantly less evidence of recent transmission: 10 ST2 isolates (5.3%) were within 2 SNVs of another isolate compared to 88 (44%) ST1 isolates ($P \leq .001$) (Fig. 1). As the SNV threshold increased to 5 and 10 SNVs, this trend was maintained (all $P < .001$). ST2 isolates were also more likely to be genetically linked to an isolate from a different collection site than ST1 isolates. Among isolates with genetic links to at least 1 other isolate at the 5 SNV and 10 SNV thresholds, 21 of 37 and 74 of 89 ST2 isolates (57%, 83%) were linked to an isolate from a different collection site, compared to 2 of 88 and 48 of 157 ST1 isolates (2% and 31%, respectively; both $P < .001$). **Conclusions:** Compared to *C. difficile* ST1 isolates, ST2 isolates displayed less evidence of recent healthcare transmission and were more likely to be genetically linked to isolates from divergent collection sites. Interpreting genetic linkages among *C. difficile* isolates requires an understanding of regional and strain-specific genetic diversity to avoid misattribution of genetic linkages to recent transmission.

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