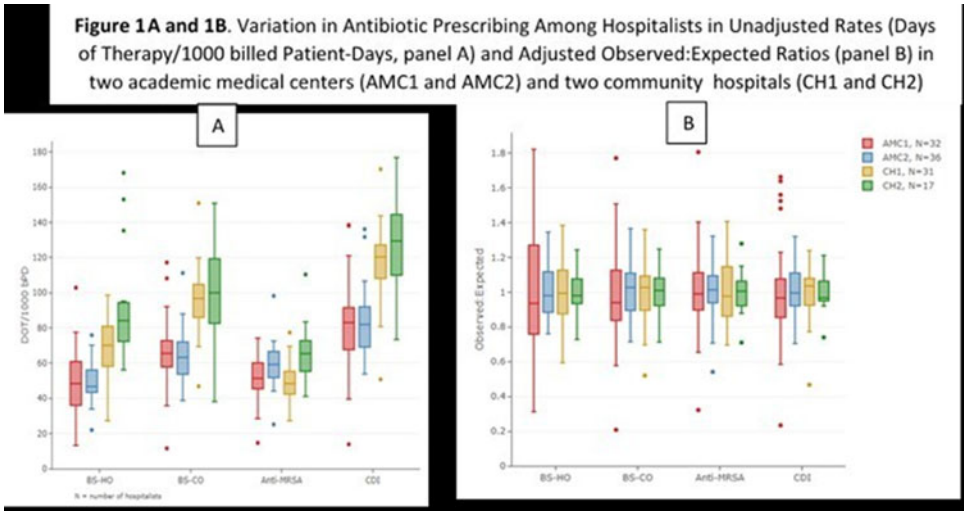

Fig. 1.

but we detected no significant differences in median O:E between hospitals (all antibiotic categories $P > .10$) (Fig. 1B). **Conclusions:** Adjusting for patient-level factors significantly reduced much of the variation in hospitalist-specific DOT per 1,000 bPD in some but not all hospitals, suggesting that unmeasured factors may drive antibiotic prescribing. This metric may represent a target for stewardship intervention, such as hospitalist-specific feedback of antibiotic prescribing practices.

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Presentation Type:
Oral Presentation

Whole-Genome Sequencing Reveals a Novel Subclade of Pansusceptible *Candida auris* in Ontario, Canada

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Background: *Candida auris* is an emerging pathogen that has recently disseminated globally and caused challenging outbreaks in healthcare facilities (HCFs), in part because it is commonly multidrug-resistant. *Candida auris* remains rare in Canada, with ~20 known cases to date. We describe the emergence of a novel subclade of *C. auris* in Ontario, Canada, using whole-genome sequencing (WGS). **Methods:** In Ontario, many HCFs submit yeast isolates from sterile sites requiring species-level characterization and antifungal susceptibility testing (AFST) to the provincial reference laboratory. Yeasts were identified using a combination of standard methods (morphology, API 20C, MALDI-ToF MS) including ITS2 sequencing. Sensititre YO9 panels were used for AFST. Genomic analysis of *C. auris* was performed using an Illumina HiSeq platform with at least 50× coverage; variants were called against the reference genome by using the previously published North Arizona SNP pipeline (NASP). Phylogenetic trees were produced by maximum parsimony method (MEGA7.0). **Results:** Between 2014 and 2018, yeast isolates from 5 different patients from 4 HCFs in the same region of Ontario were confirmed to be *C. auris* by ITS2 PCR and sequence analysis (Table 1). Based on interim CDC criteria for antifungal drug break points, all isolates were pansusceptible to common antifungals. WGS analysis demonstrated that the *C. auris* isolates were part of the South American clade (IV) and formed an isolated subclade that is well supported by bootstrap analysis, indicating clonal relationships among these isolates (Fig. 1). **Conclusions:** Although *C. auris* isolates are usually drug resistant, all 5 initial Ontario isolates were pansusceptible. WGS determined that these isolates clustered within clade IV and were clonal. This cluster of *C. auris* appears to represent a new subclade of the South American clade that has been transmitted among patients within a region of Ontario. *C. auris* may have been present in Ontario for some time, escaping earlier detection due to lack of screening programs in HCFs, historical challenges with microbiologic detection of *C. auris*, and the antifungal susceptibility of the circulating isolates. Investigations are underway to determine clinical features and epidemiologic relatedness among patients in this cluster.

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Disclosures: Susy Hota, Contracted Research - Finch Therapeutics

Doi:10.1017/ice.2020.542

Table 1. Summary of *Candida auris* isolates in Ontario, Canada 2014–2018

Year	Patient	Specimen	HCF	AFST profile	Clade
2014	1	Blood	A	Pansusceptible	IV
2014	2	Blood	B	Pansusceptible	IV
2014	3	Blood	A	Pansusceptible	IV
2015	4	Wound	C	Pansusceptible	IV
2017	5	Peritoneal fluid	D	Pansusceptible	IV

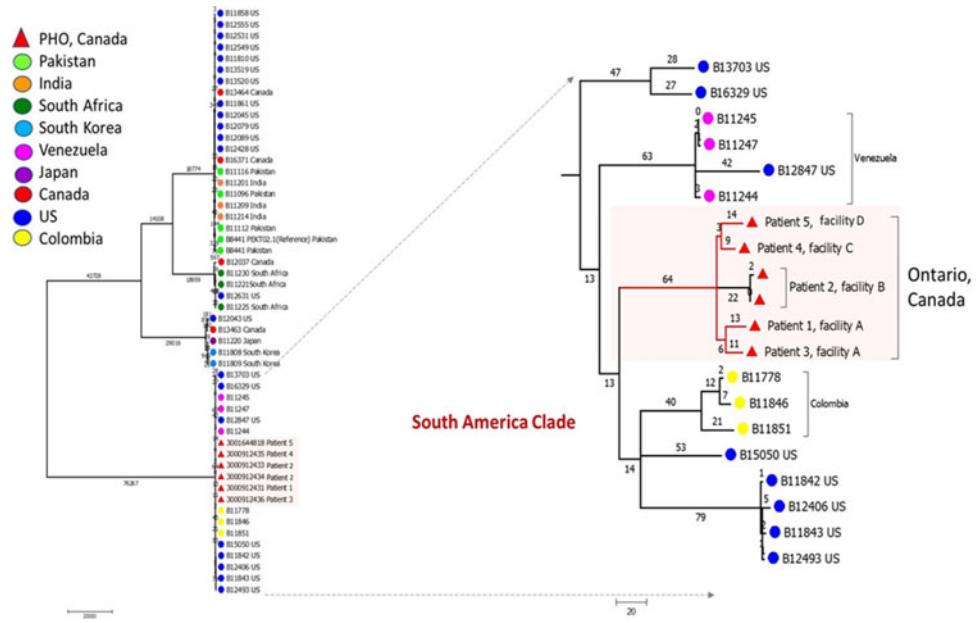

Fig. 1. Phylogenetic tree of *Candida auris* based on whole-genome sequencing

Presentation Type:
Top Rated Posters

Assessing the Efficacy and Unintended Consequences of Utilizing a Behavioral Approach to Reduce Inappropriate *Clostridioides difficile* Testing

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Background: Effective strategies to improve diagnostic stewardship around *C. difficile* infection (CDI) remain elusive. Electronic medical record-based solutions, such as 'hard' and 'soft' stops, have been associated with reductions in testing, but may not be sustainable due to alert fatigue. Additionally, data on the potential for undertesting, missed diagnoses, and the implications regarding patient harm or clusters of transmission are limited. In this study, we assessed the efficacy of a behavioral approach to diagnostic stewardship, while monitoring for unintended consequences. **Methods:** This quality improvement study was conducted January 2018–May 2019; baseline period: January–April 2018, implementation period: May–December 2018, sustainment period: January 2019–May 2019. First, we conducted an internal analysis and identified 3 barriers to appropriate testing: clinician's perceived risk of CDI, inconsistent definition of diarrhea, and lack of involvement of nurses in diagnostic stewardship. A multidisciplinary team to address these barriers was then convened. The team utilized the Bristol stool scale to improve the reliability of diarrhea description, and created a guideline-concordant testing algorithm with clinicians and nurses. The primary outcome was the number of tests ordered. The secondary outcomes were the proportion of inappropriate tests and the proportion of delayed tests. Delayed tests were defined as CDI-compatible diarrhea based on the algorithm where the test was sent >24 hours after symptom onset. **Results:** During the baseline period, we detected no significant change in number of tests ordered month to month, with 194.2 tests ordered per month on average. During the postimplementation period, the number of tests ordered decreased by ~4.5 each month between January 2018 and May 2019 ($P < .0001$). The proportion of inappropriate tests steadily decreased from 54% to 30% across the 3 study periods, and the number of delayed testing changed from 11% to 1% then increased to 20% in the sustainment period. There were no cases of toxic megacolon associated with delayed testing. **Conclusions:** The decision to test for CDI is complex. Interventions that address this issue as a simple 'right' and 'wrong' fail to address the root cause of CDI overdiagnosis, and they have no embedded mechanism to detect unintended consequences. Our study demonstrates that by taking a behavioral approach and addressing clinicians' safety concerns, we were able to sustain a significant reduction in testing. We could not determine the significance of the increase in delayed testing given the low numbers; however, further studies are needed to evaluate the safety of CDI reduction strategies through diagnostic stewardship only.

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