Background: Infections with extended-spectrum β-lactamase–producing Enterobacteriaceae (ESBL-E) in nonoutbreak settings have not demonstrated the presence of dominant strains. Our objective was to determine the incidence, clinical characteristics, and genetic characteristics of ESBL-E infections among a group of Canadian children. **Methods:** From 2012 through 2017, patients aged ≤18 years with first-episode ESBL-E infections who presented at a pediatric center were reviewed. All clinical isolates were phenotypically identified in the laboratory as ESBL-producers. Demographic and clinical data were collected, including comorbid conditions, presence of devices, and previous antibacterial exposure. Community-associated infection was defined as a positive culture from a sterile site within the first 48 hours of hospital admission and no healthcare exposure during the preceding year. Isolates were sent to the Public Health Ontario Laboratory for whole-genome sequencing. Multilocus sequence typing was used to determine clonal relationship. **Results:** During the study period, 102 patients were identified with first-episode ESBL-E infection, and the proportion of ESBL-E isolates among all clinical isolates of *E. coli* and *Klebsiella* spp increased from 0.6% to 2.6% between 2012 and 2017, respectively ($P = .001$). The median age was 1 year (interquartile range, 0.8–5 years). Women comprised 66% of cases. No comorbid conditions were noted among 58 patients (57%), and 24% had previous antibiotic exposure, most frequently a cephalosporin (16%). ESBL-E was most frequently isolated in the urine (91%) and least frequently in the blood (2.2%) and was predominantly *Escherichia coli* (90%). Infection was most frequently diagnosed in the outpatient setting (61%); there were 11 healthcare-associated infections. Whole-genome sequencing of ESBL-E isolates revealed predominance of *bla*CTX-M-15 (63 isolates, 62%) and *bla*CTX-M-27 (16%) genes, and sequence type (ST) 131 (41%). Mutations conferring fluoroquinolone nonsusceptibility were noted among 62 isolates (61%), most frequently associated with ST131 (38 of 62 isolates, 61%) and among all 5 isolates with ST1193, an emerging multidrug-resistant *E. coli* clone. In addition, 15 patients had recurrence of ESBL-E infection at median of 113 days (IQR, 26–208); *bla*CTX-M-27 was found in 33% of recurrent infections compared to 12% of primary infections ($P = 0.045$). **Conclusions:** This study is the first in Canada to provide whole-genome sequencing data regarding ESBL-E in a pediatric population. The gene *bla*CTX-M-15 and ST131 clone were predominant. More than 60% of infections were community associated and demonstrated cross resistance to fluoroquinolones. With 76% of infections in antibiotic-naïve children, ESBL-E is a public health concern, and a One Health approach is critical to understanding the epidemiology and curbing the spread of multidrug-resistant Enterobacteriaceae.

Clinical Epidemiology and Risk Factors of *Candida auris* Bloodstream Infection in Trauma Patients
Omika Katoch, All India Institute of Medical Sciences, New Delhi; Vijeta Bajpai, JPN Apex trauma center, AIIMS, New Delhi; Surbhi Khurana, All India Institute of Medical Sciences, New Delhi; Sonal Katyal, All India Institute of Medical Sciences, New Delhi; Purva Mathur, All India Institute of Medical Sciences, New Delhi

Background: Candidiasis caused by *Candida auris* is one of the most serious hospital-acquired infection. Initially, *Candida auris* was reported to cause local infections; later, invasive candidasis was also reported in which the bloodstream, the central nervous system, kidneys, liver eyes, etc, are invaded. In this study, we evaluated the clinical epidemiology and risk factors in patients hospitalized to trauma center. **Methods:** This study was conducted at JPN Apex Trauma Centre of All India Institute of Medical Sciences, New Delhi, which is a 169-bed hospital. All patients who were identified to have candidemia due to *C. auris* over a period of 5 years from January 2012 to December 2016 were included. Blood samples were collected in BAC-T-Alert bottles (Bio Merieux, Durham, NC) and isolates were identified up to the species level by the VITEK 2 (version 8.01, BioMerieux). Conventional identification was performed by observing color development on CHROMagar (Becton Dickinson, Franklin Lakes, NJ). The demographic and clinical data of patients were collected from the hospital information system. **Results:** Over a period of 5 years, 20 patients admitted to our trauma hospital developed candidemia due to *Candida auris*. Among them, men were predominant (95%), and the mean (SD) age of the patients was 33 (+15) years. Among these patients, 80% were in hospitalized and 20% were follow-up patients. The median of the total length of stay in the hospital was 34 days (range, 7–122). All of the patients were on mechanical ventilation; 65% patients were catheterized and 75% patients had central line placed. Head injury was the major cause of trauma followed by abdomen, chest, and spine. The overall mortality rate was 40%. Most of the patients (65%) who developed *Candida auris* infection were immunocompromised. The different comorbidities present were hypertension (35%), diabetes (15%), renal disease (10%), and hepatitis C (5%). Broad-spectrum antibiotics were given: amoxicillin-clavulanate was given to 65% of patients; cefoperazone sulbactam was given to 30% of patients; chloroamphenicol, amicillin-sulbactam, or clindamycin was given to 10% of patients. Antifungal agents like fluconazole or caspofungin were given to 5% of patients. Major surgeries like cranioplasty were performed in 58% of patients. Pancreatectomy, laparotomy, and endoscopic necrosectomy were performed in 42% of patients. **Conclusions:** *Candida auris* is one of the dreaded and most commonly spread hospital-acquired fungal infections, especially in immunocompromised patients. Broad-spectrum antibiotics use, major surgery, and invasive devices were the most common risk factors for acquiring *Candida auris* infection.

Clinical Team Distribution and Antibiotic Use Patterns at a Tertiary-Care Academic Medical Center
Rebecca Choudhury, Vanderbilt University Medical Center; Ronald Beaulieu, Vanderbilt University Medical Center; Thomas Talbot, Vanderbilt University School of Medicine; George Nelson, Vanderbilt University School of Medicine

Background: As more US hospitals report antibiotic utilization to the CDC, standardized antimicrobial administration ratios (SAARs) derived from patient care unit-based antibiotic utilization data will increasingly be used to guide local antibiotic stewardship interventions. Location-based antibiotic utilization surveillance data are often utilized given the relative ease of

ascertainment. However, aggregating antibiotic use data on a unit basis may have variable effects depending on the number of clinical teams providing care. In this study, we examined antibiotic utilization from units at a tertiary-care hospital to illustrate the potential challenges of using unit-based antibiotic utilization to change individual prescribing. **Methods:** We used inpatient pharmacy antibiotic use administration records at an adult tertiary-care academic medical center over a 6-month period from January 2019 through June 2019 to describe the geographic footprints and AU of medical, surgical, and critical care teams. All teams accounting for at least 1 patient day present on each unit during the study period were included in the analysis, as were all teams prescribing at least 1 antibiotic day of therapy (DOT). **Results:** The study population consisted of 24 units: 6 ICUs (25%) and 18 non-ICUs (75%). Over the study period, the average numbers of teams caring for patients in ICU and non-ICU wards were 10.2 (range, 3.2–16.9) and 13.7 (range, 10.4–18.9), respectively. Units were divided into 3 categories by the number of teams, accounting for ≥70% of total patient days present (Fig. 1): "homogenous" (≤3), "pauciteam" (4–7 teams), and "heterogeneous" (>7 teams). In total, 12 (50%) units were "pauciteam"; 7 (29%) were "homogenous"; and 5 (21%) were "heterogeneous." Units could also be classified as "homogenous,"

Figure 1. Examples of ward types defined using patient days present

Fig. 1.

"pauciteam," or "heterogeneous" based on team-level antibiotic utilization or DOT for specific antibiotics. Different patterns emerged based on antibiotic restriction status. Classifying units based on vancomycin DOT (unrestricted) exhibited fewer "heterogeneous" units, whereas using meropenem DOT (restricted) revealed no "heterogeneous" units. Furthermore, the average number of units where individual clinical teams prescribed an antibiotic varied widely (range, 1.4–12.3 units per team). **Conclusions:** Unit-based antibiotic utilization data may encounter limitations in affecting prescriber behavior, particularly on units where a large number of clinical teams contribute to antibiotic utilization. Additionally, some services prescribing antibiotics across many hospital units may be minimally influenced by unit-level data. Team-based antibiotic utilization may allow for a more targeted metric to drive individual team prescribing.
Funding: None
Disclosures: None
Doi:10.1017/ice.2020.695

Presentation Type:
Poster Presentation
Clostridioides difficile **Testing Stewardship for Laxative Use Is Effective and Safe When Combined With Expert Clinical Input**
Francesca Torriani, UC San Diego Health; Frank Myers Robert El-Kareh; Minji Kang, University of California San Diego; Randy Taplitz; Shira Abeles, UCSD

Background: In January 2019, our large academic medical center implemented "hard stops" for ordering *Clostridiodes difficile* nucleic acid amplification testing (NAAT), and required a discussion with an infectious diseases physician if the order was placed in a clinical scenario not consistent with the 2017 IDSA/SHEA *C. difficile* infection (CDI) testing guidelines. Recently, some groups have expressed concerns that requiring the discontinuation of laxatives may delay the diagnosis of CDI and result in serious adverse outcomes. **Methods:** *C. difficile* testing stewardship interventions were performed at 2 hospitals within the same university health system to reduce inappropriate testing. In January 2019, a best practice advisory (BPA) was implemented to alert providers ordering *C. difficile* NAAT if patients had received laxatives within 24 hours, requiring a discussion with the ID physician to override the hard stop. We reviewed clinical outcomes of patients who had a BPA alert due to laxative use within the past 24 hours April 23 to October 23, 2019. **Results:** During the study period, there were 235 patients with a BPA because of laxative use within the past 24 hours. Moreover, 55 (23.4%) continued to experience diarrhea after the discontinuation of laxatives and were retested for CDI within 7 days. Only 8 tests returned positive, suggesting that, at most, 3.4% of cases had delayed diagnoses because of the hard stop. This finding is supported by the increase in the percentage of tests positive from 11.6% observed overall to 14.6% (8 of 55) after this intervention. There were no severe CDI cases (ICU admission, colectomy, or death) among patients who had delayed testing due to laxative use. **Conclusions:** In the setting of laxative use, *C. difficile* testing stewardship interventions with *C. difficile* NAAT using a hard-stop BPA are effective in reducing unnecessary testing and safe if they are used in combination with a real-time expert input of the risk of clinical disease.
Funding: None
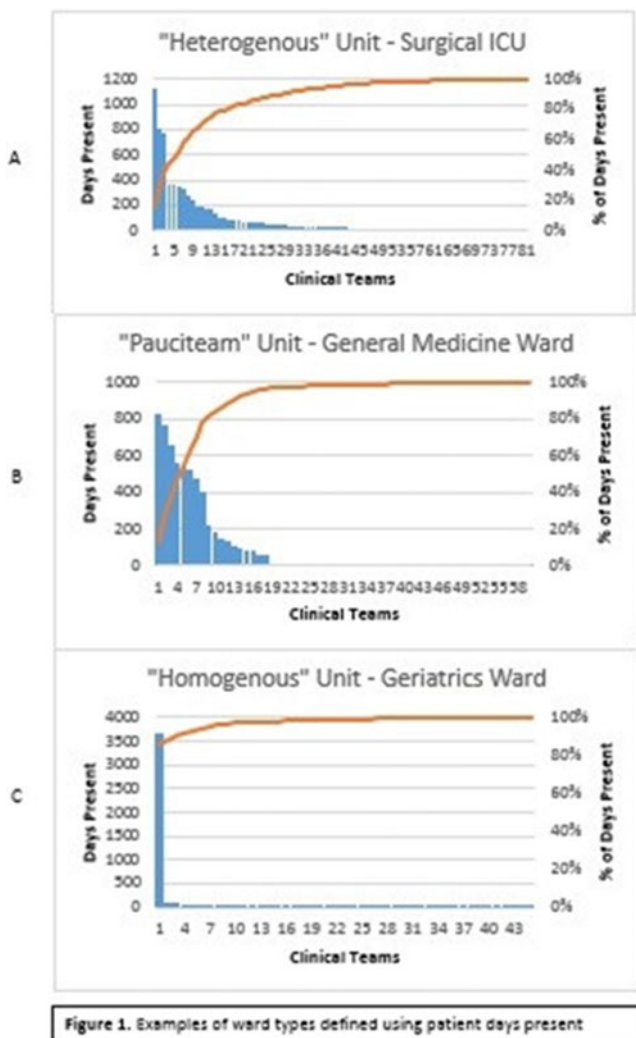**Disclosures:** None
Doi:10.1017/ice.2020.696