

**Background:** Infections with extended-spectrum  $\beta$ -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  $\leq 18$  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.

**Funding:** None

**Disclosures:** None

Doi:10.1017/ice.2020.693

#### Presentation Type:

Poster Presentation

#### 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 candidiasis 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, ampicillin-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.

**Funding:** None

**Disclosures:** None

Doi:10.1017/ice.2020.694

#### Presentation Type:

Poster Presentation

#### 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