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Background. Carbapenemase-producing Enterobacteriaceae (CPE) are a global threat. Risk of transmission of CPE in households remains poorly understood

Methods. Population-based surveillance for CPE colonization/infection is conducted in Toronto/Peel Region, Canada. In households with ≥1 consenting household contact (HC), groin, rectal swabs and urine samples are submitted every 3 months for both IC and HC until the IC has three consecutive negative swab sets. Swabs/urines are incubated overnight in BHI, direct PCR for carbapenemase genes is performed; specimens positive for PCR are then cultured.

Results. Eighty-five households and 150 HC have been enrolled. Most common species/gene combinations in IC are: *E. coli*/NDM (33), *E. coli*/OXA48 (15), *Klebsiella spp.*/NDM (11). HCs have a median of eight swabs (range 2–14). 12 (8%) HCs were colonized with CPE (median 1.5 pos samples, range 1–8). IC and HC had same gene in 11(92%) cases, and same species/gene in seven (58%) cases. NDM+OXA48 ICs were more likely to have CPE colonized HC, see table. CPE colonized HC were older, more likely to be the IC's spouse (OR 32, 95% CI 4–260), and more likely to have travelled outside Canada (OR 9.7, 95% CI 1.2–78).

Conclusion. HC colonization with CPE is uncommon, but not rare, and may be associated with either household transmission, or co-exposure of HC and IC via travel. Spouses are most often colonized.

Characteristic	CPE Positive *N* = 12	CPE Negative *N* = 138	*P*-Value
Gender (*n*, % male)	3 (25%)	53 (38%)	0.27
Median age (range)	70y(24-89)	42y (4-98)	0.005
Chronic illness	6 (50%)	35 (25%)	0.08
Relationship to IC			
Spouse	11(92%)	35 (25%)	<0.0001
Child	1 (8%)	41 (30%)	
Other	0	62 (45%)	
Hospitalization (last year)			
Outside Canada	0	2 (2%)	0.84
In Canada	0	12 (9%)	0.35
Travel outside Canada (last year)	11 (92%)	73 (54%)	0.01
to Indian subcontinent	8 (67%)	47 (35%)	0.03
Receipt antibiotics (6 mos)	1 (8%)	10 (7%)	0.61
Contact with IC			
Regular skin-skin contact	5 (42%)	68 (50%)	0.76
Share washroom	11 (92%)	97 (72%)	0.18
Share towels	7 (58%)	61 (47%)	0.37
IC organism			
E. coli	6/12(50%)	46/73 (63%)	0.59
Klebsiella spp.	4 (33%)	18 (25%)	
IC gene			
NDM	3 (25%)	43 (59%)	<0.001
OXA-48	4 (33%)	18 (24%)	
NDM and OXA-48	5 (42%)	2 (3%)	
KPC	0	7 (10%)	
Other	0	3 (4%)	
IC colonization			
>3 months	7/11(64%)	32/61(52%)	0.72
>6 months	6/10(60%)	23/53(43%)	0.49

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2166. Preparedness for *Candida auris* in Canadian Nosocomial Infection Surveillance Program (CNISP) Hospitals, 2018

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Background. *C. auris* is a rapidly emerging pathogen which is potentially multidrug resistant, has caused large hospital outbreaks, and is difficult to identify in the routine microbiology laboratory. We surveyed CNISP sites to evaluate infection prevention and control (IPAC) and microbiology laboratory (MICRO) preparedness.

Methods. An electronic survey with five IPAC and 12 MICRO questions was sent out to IPAC and MICRO leads for all CNISP sites in January 2018. Data were entered and analyzed in Excel.

Results. We received 32 IPAC surveys representing 58/66 (88%) CNISP hospitals, and 27 MICRO surveys representing 27/32 (84%) CNISP labs. Four of 58 (7%) hospitals have a written policy for *C. auris* screening of patients; and 22 (38%) recommend screening; most commonly: roommates of any patient colonized/infected with any *C. auris* ($n = 7$), room/wardmates (RWM) of patients colonized/infected with any *C. auris* ($n = 7$) or RWM of patients with MDR *C. auris* ($n = 3$). Without resource limitations, 50 (86%) hospitals would screen RWM of *C. auris* patients and 34 (59%) would screen patients previously hospitalized in the Indian subcontinent. Overall, 13/27 (48%) labs identify all clinically significant *Candida* spp. to the species level and 13 identify sterile site (SS) isolates. Twenty-two (81%) labs use MALDI-TOF for identification: 10 Bruker Biotyper and 12 VitekMS. 26 (96%) labs refer non-identified species and commonly misidentified yeast from SS for definitive identification. Twenty-three (85%) labs perform antifungal susceptibility testing for all *Candida* from blood and CSF. Twenty-two (81%) labs are confident that their current laboratory protocol would identify *C. auris* if the isolate is from an SS, 17 (63%) if identified as being resistant to at least 1 antifungal and 20 (74%) if the isolate is from a non-SS culture and is identified to the species level. Four (15%) labs have a protocol for *C. auris*colonization detection. Four labs have identified six *C. auris* isolates: two reported retrospective identification of three fluconazole susceptible *C. auris*; and two reported one resistant and two MDR isolates identified prospectively in 2017/2018.

Conclusion. MDR *C. auris* have been identified in Canada. Gaps remain in ensuring reliable identification of *C. auris*, particularly from non-SS, and most IPAC CNISP teams and MICRO do not yet have protocols for identification of *C. auris*colonization.

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2167. Predicting Carbapenem-Resistant *Enterobacteriaceae* (CRE) Carriage on Admission using Updated Statewide Hospital Discharge Data

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Background. We previously built a patient-level prediction model to assess an individual's risk of Carbapenem-resistant *Enterobacteriaceae* (CRE) carriage upon hospital admission based on the following factors: past hospital visits (short- and long-term acute care (STACHs and LTACHs)), endoscopic procedures, infection-related diagnosis codes, and patient age and sex. Our model discriminated CRE cases relatively well (*c*-statistic = 0.86). In the hopes of operationalizing our results, we evaluated the distribution of predicted probabilities on an updated dataset using existing model parameters.

Methods. We used Illinois Hospital discharge data (CYs 2015–2016) with ICD-10 diagnosis and procedure codes to establish baseline exposure history (2015) and to generate predicted probabilities (2016). We calculated the number of hospital visits and the average number of hospital days in the past year (STACH and LTACH). We identified infection-related diagnosis codes using prior knowledge, and included procedure codes for endoscopic retrograde cholangiopancreatography (ERCP). We then used the model parameters from our previous work to generate predicted probabilities corresponding to each hospital visit.

Results. Our study year (2016) included 1,229,158 visits by 816,500 unique adult patients. Sixty-two percent of patients had no inpatient visits in the previous year. Among those with a prior hospitalization, the median STACH length of stay was 4 days (IQR: 2–6). Three thousand five hundred and sixty-six patients (0.4%) had previous LTACH exposure upon admission, with a median length of stay of 25 days (IQR: 13–40). Thirty-two percent of hospital visits had an infection-related diagnosis code, and 0.5% had an ERCP procedure code. Of the more than 1.2 million visits, our model predicted 10,614 visits associated with a CRE risk of over 1%, 946 visits of over 10%, and 96 visits by 63 unique patients with over a 50% risk. On average, highest risk patients were exposed to (median) 15 (7–97) STACH, 104 LTACH (37–174) days; 83% had infection codes.

Conclusion. Using a large, de-identified statewide dataset, we were able to identify a small number of extremely high-risk individuals. Selective screening of these individuals upon admission could prove to be a valuable way to identify CRE-colonized patients in order to take proper precautions.

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2168. Regional Variation in Community-Onset and Hospital-Identified *Clostridium difficile* Infection, 2017

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