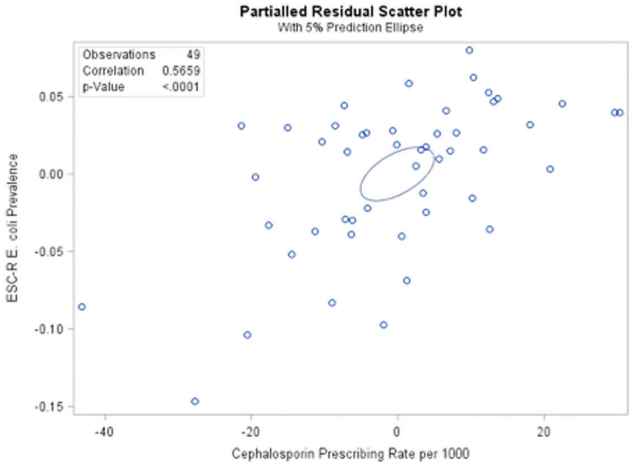
***Background.*** National surveillance is proposed to be part of a National Strategy to Combat Antibiotic Resistance (AR) in the United States; recent access of state-summary metrics around antibiotic use and antibiotic resistance allows an opportunity to evaluate variability in AR among healthcare-associated infections (HAIs) between U.S. states.

***Methods.*** We utilized data from 2016 accessible in the CDCÕs AR Patient Safety Atlas to create state-level values for the no. of HAIs (CLABSI, CAUTI, SSI) by select AR reported to NHSN, prescribing rates of outpatient antibiotics by class, and percentage of hospitals having full antibiotic stewardship programs. Other available data included 2016 CDC's Healthcare-Associated Infections Progress Report and U.S. Census Data. We correlated (Pearson's partial correlation coefficients) the state prevalence (% testing resistant) for multidrug-resistant *P. aeruginosa* (MDR-PA), extended-spectrum cephalosporin-resistant *E. coli* (ESC-*E. coli*), and methicillin-resistant *S. aureus* (MRSA) from HAIs with potential predictors; multivariate logistic regression was used to assess independence.

***Results.*** States prevalence of HAI AR varied and was explained in part by no. of skilled nursing facility bed days for MRSA ($P = 0.002$), % of population black for MRSA ($P < 0.001$) and ESC-*E. coli* ($P < 0.001$), % of population > 65 for ESC-*E. coli* ($P < 0.001$) and MDR-PA ($P < 0.001$), and no. of LTACHs for MDR-PA ($P = 0.01$). After adjusting for these, rates of outpatient fluoroquinolone (FQ) and cephalosporin prescribing (figure) were significant predictors of ESC-R *E. coli* HAIs (adjusted OR 1.02, $P < 0.001$ and 1.01, $P < 0.001$, respectively) and FQ rates for MRSA HAIs (aOR 1.01, $P = 0.004$); the MRSA correlation was slightly elevated in states with a higher population of African-Americans. Of note, % hospitals with inpatient stewardship did not explain geographic variability in any HAI AR studied.

***Conclusion.*** Outpatient antibiotic prescribing rates can explain much of the state-to-state variability in studied HAI-related AR even after adjusting for differences in age and healthcare facility composition. Stewardship across the spectrum of healthcare delivery is likely needed to improve patient safety in acute care hospitals.




***Disclosures.*** **All authors:** No reported disclosures.

**2163. Risk Factors for Carbapenem-Resistant Gram-Negative Bloodstream Infections (BSI) in U.S. Hospitals (2010–2015)**

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***Background.*** Carbapenem-resistant (CR) Gram-negative (GN) infections are associated with higher mortality and extended hospital stays. Time to effective antibiotic treatment is important for patient survival. Classifying the risk factors for CR GN BSI before identification and susceptibility results are known is critical; this study explores the risk factors associated with CR GN BSI in U.S. hospitals.

***Methods.*** BSI caused by 11 of the most common GN pathogens were identified from 181 acute care hospitals that contributed microbiology and susceptibility test data to the Premier Healthcare Database 2010–2015. We used univariate analyses to select potential risk factors and a multivariate logistic regression model to predict CR BSI with these risk factors.

***Results.*** Among 46,199 patients with GN BSI, 1,592 (3.6%) had CR pathogens. From univariate analyses, the significant factors ($P$-value <0.05) when comparing CR vs. carbapenem susceptible (CS) infections were age, race, gender, geographic location, admission source, Charlson Comorbidity Index, having BSI while in the ICU or after having stayed in the ICU, and index culture day. Adjusted odds ratios (OR) from multiple logistic regression are shown below.

| Effect | OR | 95% Confidence Limits | |
|---|---|---|---|
| Compared with 65-years-of-age (yoa) | | | |
| 18–54 | 2.3 | 2.0 | 2.6 |
| 55–64 | 1.6 | 1.4 | 1.9 |
| Male vs. female | 1.2 | 1.05 | 1.3 |
| Black vs. non-Black | 1.2 | 1.04 | 1.3 |
| Index culture >48 hours post-admission | 2.9 | 2.5 | 3.3 |
| Transferred vs. other admission source | 2.0 | 1.7 | 2.3 |
| Infection in/after ICU | 1.5 | 1.3 | 1.8 |
| Compared with New England | | | |
| East South Central | 1.9 | 1.4 | 2.7 |
| Middle Atlantic | 1.5 | 1.1 | 1.9 |
| Mountain | 3.1 | 2.2 | 4.2 |
| Pacific | 1.0 | 0.8 | 1.3 |
| South Atlantic | 0.8 | 0.6 | 1.05 |
| West North Central | 0.7 | 0.5 | 1.02 |
| West South Central | 0.8 | 0.6 | 1.05 |
| Myocardial infarction | 0.6 | 0.4 | 0.8 |
| Congestive heart failure | 1.2 | 1.1 | 1.4 |
| Peripheral vascular disease | 1.3 | 1.14 | 1.6 |
| Cerebrovascular disease | 0.6 | 0.4 | 0.8 |
| Dementia | 1.3 | 1.1 | 1.4 |
| Renal disease | 2.3 | 1.9 | 2.8 |
| Malignancy | 1.5 | 1.3 | 1.7 |

***Conclusion.*** Patients with CR GN BSIs were more likely to be of a younger age group, transferred from a health care facility, stayed in ICU, and had positive BSI culture more than 48 hours after admission. Risk of CR BSI increased for patients with congestive heart failure, peripheral vascular disease, dementia, renal disease, and any malignancy.

***Disclosures.*** **All authors:** No reported disclosures.

**2164. A Feasibility Study to Investigate the Spread of Antimicrobial Resistance in the Community Suggests Ongoing Dissemination Within Households**

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***Background.*** Despite the escalating level of concern regarding the spread of Carbapenem resistant and Extended spectrum β-lactamase (ESBL) producing Enterobacteriaceae (CR-E and ESBL-E), little is still known about their dissemination within households. In this small cohort study, four households were followed-up for 6 months, to track their carriage and spread after discharge.

***Methods.*** Inpatients at Guy's and St Thomas Hospital with confirmed diagnosis of CR- or ESBL-*Klebsiella pneumoniae* infection were approached for recruitment. Inclusion criteria were met only if each household member consented to participate. Each member was then asked to provide a stool sample, a hand swab and to complete a medical history questionnaire. Environmental samples were collected from three different common house areas. Baseline sampling was carried out before patient discharge and subsequently at 1, 2, 3, and 6 months. Colonisation was confirmed by isolation of resistant organisms onto chromogenic agar and organisms identified by Maldi-Tof. Resistance genes were detected by multiplex real-time PCR and resistance profile confirmed by standard susceptibility testing.

***Results.*** A total of 196 inpatients were screened, 58 (29.6%) met the inclusion criteria and 27 (13.7%) were approached. Of these, 6 households (3%) were included in the study. Among them, three were followed-up at all five time-points, one at for time points, while other two were lost to follow-up at T0 and T1, respectively. In three households, discharged patients remained colonised with ESBL-*K. pneumoniae* for all duration of the study. In these patients co-colonisation with ESBL-*E. coli* was also detected at one or more time points after discharge. In these three households, at least one of the other members resulted colonised with one of these two organisms at least at one time point. Furthermore, in three households, *K. pneumoniae* carrying the same resistance genes than inpatients was also isolated from the environment at T1 and at T2.

***Conclusion.*** This study illustrates the challenges, and suggests ongoing household dissemination of resistant bacteria following discharge from hospital. The dynamics of carriage and household dissemination remain to be elucidated.

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**2165. Risk Factors for CPE Colonization in Household Contacts of CPE Colonized/Infected Patients**

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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.

***Disclosures.*** **All authors:** No reported disclosures.

## 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.

***Disclosures.*** **All authors:** No reported disclosures.

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

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