Bioinformatic prediction of multi-drug 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 outpatient antibiotic prescribing rates can explain much of the

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 Carbenapenem-Resistant Gram-Negative Bloodstream Infections (BSI) in U.S. Hospitals (2010–2015)

Bin Cai, MD, PhD1; Roger Echols, MD, FIDSA2; Deborah Rudin, MD3; Gareth Morgan, BA4 and Tsutae Nagata, MD, PhD, FFFP5; Shionogi Inc., Florham Park, New Jersey; ID3C, Easton, Connecticut

Session: 237. Healthcare Epidemiology: HAI Surveillance Saturday, October 6, 2018: 12:30 PM

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.

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

Rahul Batra, MD; Alex Natale, PhD2; Olga Tosas, PhD2; and Jonathan Edgeworth, PhD; MIRC, FRCPath, Centre for Clinical Infection and Diagnostics Research, Guy’s and St Thomas NHS Foundation Trust, London, United Kingdom

Session: 237. Healthcare Epidemiology: HAI Surveillance Saturday, October 6, 2018: 12:30 PM

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 from 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 four 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 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.

Disclosures. All authors: No reported disclosures.

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

Lubna Farooqi, MBBS1; Amina Faheem, MBBS, MPH2; Irene Armstrong, MD3; Emily Borgundvaag, MSc4; Brenda Coleman, PhD5; Karen Green, MSc, RN6; Kirit Javasinde, MSc7; Jennie Johnstone, MD, PhD8; Kevin Katz, MD, CM, MSc, FRCPC9; Philipp Kohler, MD10; Angel Li, MSc11; Roberto Melano, PhD12; Matthew Muller, MD, FRCPC, PhD13; Sarah Nanyan, PhD14; Samir Patel, PhD15; Aimie Paterson, MSc6; Susan Poutanen, MD, MIPHP16; Anu Rebappragada, PhD17; David Richardson, MD18; Alicia Sarabia, PhD19; Shofina Shaffzad, MD20

Affiliations. 1. University of Alberta, Edmonton, Alberta, Canada; 2. St. Michael’s Hospital, Toronto, Ontario, Canada; 3. University of British Columbia, Vancouver, British Columbia, Canada; 4. University of Manitoba, Winnipeg, Manitoba, Canada; 5. University of Alberta, Edmonton, Alberta, Canada; 6. University of Manitoba, Winnipeg, Manitoba, Canada; 7. University of Alberta, Edmonton, Alberta, Canada; 8. University of Alberta, Edmonton, Alberta, Canada; 9. University of Alberta, Edmonton, Alberta, Canada; 10. University of Alberta, Edmonton, Alberta, Canada; 11. University of Alberta, Edmonton, Alberta, Canada; 12. University of Alberta, Edmonton, Alberta, Canada; 13. University of Alberta, Edmonton, Alberta, Canada; 14. University of Alberta, Edmonton, Alberta, Canada; 15. University of Alberta, Edmonton, Alberta, Canada; 16. University of Alberta, Edmonton, Alberta, Canada; 17. University of Alberta, Edmonton, Alberta, Canada; 18. University of Alberta, Edmonton, Alberta, Canada; 19. University of Alberta, Edmonton, Alberta, Canada; 20. University of Alberta, Edmonton, Alberta, Canada

Session: 237. Healthcare Epidemiology: HAI Surveillance Saturday, October 6, 2018: 12:30 PM

Background. Carbanem-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 1.1 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.
Background. Carbenapenem-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/Toronto Peel Region, Canada. In households with ≥1 cohabiting household contact (HC), groin, rectal swabs and urine samples are submitted every 3 months for both HC and IC until the IC has three consecutive negative swab sets. Swabs/urines are incubated overnight in BHI, direct PCR for carbenapenem genes is performed; specimens positive for PCR are then cultured.

Results. Eighty-five households and 150 HC and 190 IC have been enrolled. Most common species/gene combinations in IC are: E. coli/NDM1 (33), E. coli/OXA48 (15), Klebsiella spp./NDM1 (11). HC's have a median of 8 swabs (range 2–14), 12 (8%) HC's 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 travelled outside Canada (OR 32, 95% CI 4–260), and more likely to have travelled (OR 11, 95% CI 1.2–78). IC 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.

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.

Disclosures. S. Poutanen, MERCK, Scientific Advisor, Speaker honorarium; COPAN, Speaking, but not part of a bureau, Travel reimbursement, Accelerate Diagnostics: Investigator, Research support; Bio-Rad: Investigator, Research support; bioMérieux: Investigator, Research support.

2166. Preparedness for Candida auris in Canadian Nosocomial Infection Surveillance Program (CNSIP) Hospitals, 2018
Fulbert Garcia Joles, MDP; Allison McGeer, MD, MSC; Amrita Bharat, PhD and Robyn Michelle, MHS; 1Infection Prevention and Control, Sinai Health System, Toronto, ON, Canada; 2Laboratory Medicine and Pathobiology, University of Toronto, Toronto, ON, Canada; 3Antimicrobial Resistance and Nosocomial Infections, National Microbiology Laboratory, Winnipeg, MB, Canada, 4Public Health Agency of Canada, Ottawa, ON, Canada

Session: 237. Healthcare Epidemiology: HA1 Surveillance Saturday, October 6, 2018: 12:30 PM

Background. C. auris is a rapidly emerging pathogen which is potentially multi-drug resistant, has caused large hospital outbreaks, and is difficult to identify in the routine microbiology laboratory. We surveyed CNSIP 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 MICRO and IPAC leads for all CNSIP sites in January 2018. Data were entered and analyzed in Excel.

Results. We received 32 IPAC surveys representing 58/66 (88%) CNSIP hospitals, and 27 MICRO surveys representing 27/32 (84%) CNSIP labs. Four of 58 (7%) hospitals have written a policy on C. auris screening of patients; and 42 (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 Biotype and 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 confirm that their current laboratory protocol would identify C. auris, if the isolate is from an SS, 17 (63%) if identified as being resistant to any antibiotic or if the isolate is from an IC, 3 (10%) if determined in 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 using known, 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 a over 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
Katharina Van Santen, MSHP1; Jonathan R. Edwards, MSc2 and Raymund Dantes, MD, MPH3; 1Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, Georgia, 2Department of Medicine, Emory University School of Medicine, Atlanta, Georgia, 3Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, GA; 4Department of Medicine, Emory University School of Medicine, Atlanta, GA; 5Department of Medicine, Emory University School of Medicine, Atlanta, GA

Poster Abstracts • OFID 2018:5 (Suppl 1) • 5639

Session: 237. Healthcare Epidemiology: HA1 Surveillance Saturday, October 6, 2018: 12:30 PM

Background. C. difficile is a complex organism with several pathotypes. Multiple studies have demonstrated that the geographical distribution of C. difficile pathotypes differs (1). This study sought to characterize the geographical distribution of C. difficile pathotypes in the United States (US) and evaluate temporal variation in its distribution.

Methods. Data were obtained from a longitudinal surveillance study (2011-2016) of C. difficile infections in community and hospital settings in the US (2). The US was divided into six regions (3). Over this time period, C. difficile infection strains were characterized using a panel of multiplex real-time polymerase chain reaction (PCR) assays (4). For this analysis, the C. difficile pathotype A and B were defined as the presence of the toxin B gene (tcdB) and the toxin A gene (tcdA), respectively. The C. difficile pathotype D was defined as the presence of the tcdB and the absence of the tcdA gene. The C. difficile pathotype E was defined as the presence of the tcdB and the tcdC gene. The C. difficile pathotype F was defined as the absence of the tcdB and tcdA gene. C. difficile pathotype G was defined as the absence of the tcdB and tcdC gene.

Results. A total of 11,369 C. difficile infections were characterized from 2011 to 2016. The most frequently isolated pathotype was C. difficile pathotype B (73.5%), followed by C. difficile pathotype D (7.2%), C. difficile pathotype E (5.9%), C. difficile pathotype F (11.8%), and C. difficile pathotype G (0.8%). There was a significant increase in the percentage of cases due to C. difficile pathotype B from 70.3% in 2011 to 74.7% in 2016 (P < 0.001). The percentage of cases due to C. difficile pathotype D was highest in the Midwest (10.4%) and lowest in the South (5.6%). The percentage of cases due to C. difficile pathotype E was highest in the Northeast (7.7%) and lowest in the West (3.4%). The percentage of cases due to C. difficile pathotype F was highest in the West (12.9%) and lowest in the Midwest (9.5%). The percentage of cases due to C. difficile pathotype G was highest in the South (0.9%) and lowest in the West (0.4%).

Conclusion. The geographical distribution of C. difficile pathotypes in the US has demonstrated significant temporal and regional variation. The increase in the percentage of cases due to C. difficile pathotype B from 2011 to 2016 suggests a changing epidemiology of C. difficile in the US.

Disclosures. All authors: No reported disclosures.