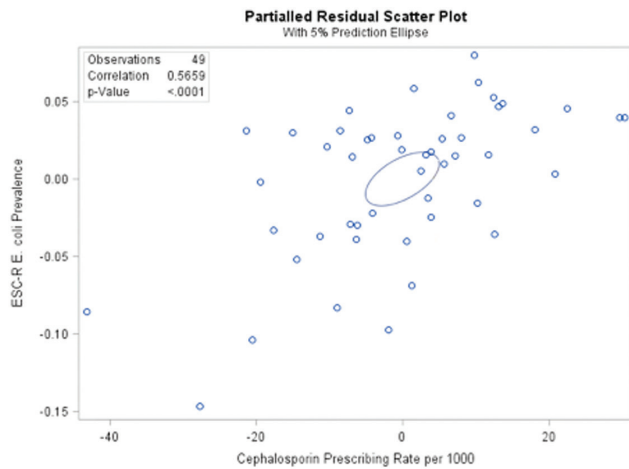**Background.** National surveillance is proposed to be part of a National Strategy to Combat Antibiotic Resistance (AR) in the United States; recent access of state-summary metrics around antibiotic use and antibiotic resistance allows an opportunity to evaluate variability in AR among healthcare-associated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

Methods. We utilized data from 2016 accessible in the CDCÓs 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.

Partialled Residual Scatter Plot
With 5% Prediction Ellipse

Observations 49
Correlation 0.5659
p-Value <.0001

(y-axis: ESC-R *E. coli* Prevalence; x-axis: Cephalosporin Prescribing Rate per 1000)

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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