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Session: 214. Host–pathogen Integration
Saturday, October 7, 2017: 8:30 AM

Background. Colonization with KPC-Kp precedes infection and represents a potential target for intervention. To identify microbial signatures associated with KPC-Kp acquisition, we conducted a prospective, longitudinal study of the fecal microbiota in LTACH patients at risk of acquiring KPC-Kp.

Methods. We collected admission and weekly rectal swab samples from patients admitted to one LTACH from May 2015 to May 2016. Patients were screened for KPC-Kp by PCR at each sampling time. KPC acquisition was confirmed by culture of KPC-Kp. To assess changes in the microbiota related to acquisition, we sequenced the 16S rRNA gene (V4 region) from collected rectal swabs. Diversity, intra-individual changes, and the relative abundance of the operational taxonomic unit (OTU) that contains KPC-Kp were compared in patients who were KPC-Kp negative upon admission and who had at least one additional swab sample collected.

Results. 318 patients (1247 samples) were eligible for analysis; 3.7 samples (mean) were collected per patient. Sixty-two patients (19.5%) acquired KPC-Kp (cases) and 256 patients remained negative for all carbapenem-resistant Enterobacteriaceae throughout their stay (controls). Median length of stay before KPC-Kp detection was 14.5 days. At time of KPC-Kp acquisition, levels of an Enterobacteriaceae OTU increased significantly compared with pre-acquisition samples and to samples from control patients (Wilcoxon test, $P < 0.0001$). Similarly, we observed a decrease in total diversity of the fecal microbiota at time of acquisition in cases ($P < 0.01$). Compared with controls, cases exhibited decreased intra-individual fecal microbiota similarity immediately prior to acquisition of KPC-Kp ($P < 0.01$). Comparison of microbial features at time of admission using random forest revealed a higher abundance of *Enterococcus* and *Escherichia* OTUs in controls vs cases.

Conclusion. We observed intra-individual changes in the fecal microbiota of case patients prior to acquisition of KPC-Kp. Compared with patients who did not acquire KPC-Kp, cases exhibited significant changes in microbiota diversity and increased abundance of potential KPC-Kp at acquisition. Our results suggest that shifts in the microbiota may precede colonization by KPC-Kp.

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1768. Reduction in the Prevalence of Healthcare-Associated Infections in U.S. Acute Care Hospitals, 2015 vs 2011

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**Session:** 215. National Trends in HAIs
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Background. A 2011 prevalence survey conducted by CDC and the Emerging Infections Program (EIP) showed that 1 in 25 hospital patients had ≥1 healthcare-associated infection (HAI). We repeated the survey in 2015 to assess changes in HAI prevalence.

Methods. In EIP sites (CA, CO, CT, GA, MD, MN, NM, NY, OR, TN) hospitals that participated in the 2011 survey were recruited for the 2015 survey. Hospitals selected 1 day from May–September 2015 on which a random patient sample was identified from the morning census. Trained EIP staff reviewed patient medical records using comparable methods and the same National Healthcare Safety Network HAI definitions used in 2011. Proportions of patients with HAIs were compared using chi-square tests; patient characteristics were compared using chi-square or median tests (OpenEpi 3.01, SAS 9.3).

Results. Data were available from 143 hospitals that participated in both surveys; data from 8954 patients in the 2011 survey were compared with preliminary data from 8833 patients in the 2015 survey. Patient characteristics such as median age, days from admission to survey, and critical care location were similar. Urinary catheter prevalence was lower in 2015 (1,589/8,833, 18.0%) compared with 2011 (2,052/8,954, 22.9%, $P < 0.0001$), as was central line prevalence (2015: 1,539/8,833, 17.4%, vs. 2011: 1,687/8,954, 18.8%, $P = 0.02$). The proportion of patients with HAIs was lower in 2015 (284/8,833, 3.2%, 95% confidence interval [CI] 2.9–3.6%) than in 2011 (362/8,954, 4.0%, 95% CI 3.7–4.5%, $P = 0.003$). Of 309 HAIs in 2015, pneumonia (PNEU) and *Clostridium difficile* infections (CDI) were most common (Figure); proportions of patients with PNEU and/or CDI were similar in 2015 (130/8833, 1.5%) and 2011 (133/8954, 1.5%, $P = 0.94$). A lower proportion of patients had surgical site (SSI) and/or urinary tract infections (UTI) in 2015 (77/8833, 0.9%) vs. 2011 (136/8954, 1.5%, $P < 0.001$).

Conclusion. HAI prevalence was significantly lower in 2015 compared with 2011. This is partially explained by fewer SSI and UTI, suggesting national efforts to prevent SSI, reduce catheter use and improve UTI diagnosis are succeeding. By contrast, there was no change in the prevalence of the most common HAIs in 2015, PNEU and CDI, indicating a need for increased prevention efforts in hospitals.

Figure: Prevalence and Distribution of HAIs, 2011 vs. 2015
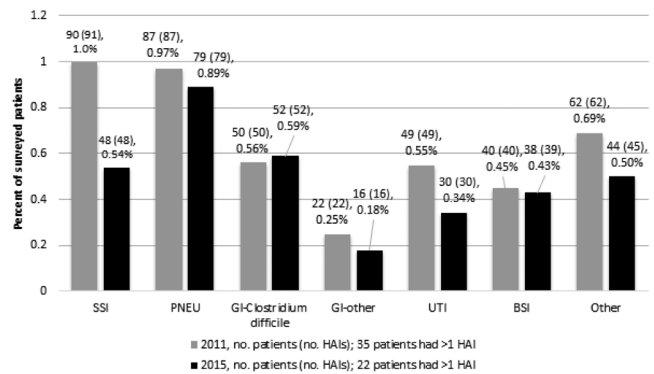
Disclosures. **All authors:** No reported disclosures.

1769. Assessing The Impact of The National Healthcare Safety Network's (NHSN's) New Baseline on Acute Care Hospital Standardized Infection Ratios (SIRs)

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Session: 215. National Trends in HAIs
Saturday, October 7, 2017: 8:30 AM

Background. To more accurately measure the progress of healthcare-associated infection (HAI) prevention efforts, the CDC's National Healthcare Safety Network (NHSN) surveillance system updated risk-adjustment models for computation of updated Standardized Infection Ratios (SIRs), the primary HAI summary measure by NHSN. This study sought to examine how the updated SIRs varied from the previous SIRs calculated using older baselines for acute care hospital HAIs.

Methods. We analyzed NHSN data for healthcare facility-onset laboratory-identified *Clostridium difficile* [CDI] and methicillin-resistant *Staphylococcus aureus* [MRSA] bacteremia reported in accordance with the CMS' inpatient quality reporting program requirement. The unit of analysis was CMS certification number (CCN) facility reporting in 2015. We compared overall distributions of CCN-level SIRs (CCN-SIRs) between new risk-adjustment models using a 2015 baseline (SIR_NEW) and old models using a 2011 baseline (SIR_OLD) and tested location shift (median away from null) of pairwise differences. We also examined the magnitude of shift in SIR from old to new baseline.

Results. For each HAI, the national pooled mean SIR of the new baseline was ~1.0. For CDI, the overall distributions of CCN SIR_NEW and CCN-SIR_OLD were different, and the median of pairwise difference was away from null with CCN-SIR_NEW slightly higher. For MRSA, the SIR differences were not significant. Most CCN-SIRs (83% for CDI, 93% for MRSA) remained in the same significance category across the old and new baselines ("worse," "better, 'not different from national benchmark'), and few CCN-SIRs were reclassified to a less favorable category. For 75% of