

reporting had the lowest scores. Positive feedback on the scoring report was received from facilities and other state HAI programs. **Conclusion:** The Virginia HAI/AR Program developed a scoring report that engaged healthcare facility administration, including corporate leadership, by providing a composite score with interpretation. The report prioritized areas for improvement and guided public health follow-up visits. Common gaps in infection prevention practices were identified across facilities, and this information has been used to determine statewide training needs by facility type. The scoring report is an effective method to help allocate state resources and improve communication and engagement of healthcare facilities. Reports can be adapted for use in other jurisdictions.

Funding: None

Disclosures: None

Doi:10.1017/ice.2020.551

Presentation Type:

Top Rated Posters

Harnessing Next-Generation Sequence Technology to Elucidate Healthcare-Associated Infection Transmission Pathways

Paige Gable, Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention

Gillian McAllister, Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention; Erisa Sula, Oak Ridge Associated Universities, Oak Ridge, Tennessee; Danielle A. Rankin, Florida Department of Health, Orange County, Florida; Erin Breaker, Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention; Jonathan Daniels, Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention; Monica Y. Chan, Oak Ridge Associated Universities, Oak Ridge, Tennessee; Nychie Dotson, Florida Department of Health, Orange County, Florida; Maroya Walters, Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention; Alison Laufer Halpin, Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention

Background: Carbapenem-resistant Enterobacteriaceae (CRE) are multidrug-resistant bacteria that persist in healthcare environments, particularly in wastewater reservoirs where they can pose risks for patients. Healthcare-associated outbreaks of carbapenemase-producing (CP) CRE can be propagated via a single bacterial strain and/or mobile genetic element (MGEs) harboring a carbapenemase gene. Unlike chromosomally encoded carbapenemases, CP-MGEs can rapidly facilitate the spread of these carbapenemase genes across bacterial strains. From July 2017 to December 2018, the Florida Department of Health in Orange County investigated an outbreak of patients colonized with various bacterial genera of CP-CRE carrying the *Klebsiella pneumoniae* carbapenemase gene (*blaKPC*), indicating a potential MGE reservoir. WGS was performed to identify transmission pathways and linked cases, beyond what traditional testing provides. **Methods:** We selected a subset of *blaKPC*-harboring isolates for WGS on short- and long-read platforms (MiSeq, PacBio, MinION) to achieve high quality, complete genome and plasmid assemblies. Laboratory, clinical, and epidemiological data were combined to identify possible transmission events, common sources, and common MGEs. **Results:** Eleven clinical isolates from 5 genera (*Citrobacter*, *Enterobacter*, *Klebsiella*, *Morganella*, *Providencia*, and *Serratia*), and 10 environmental isolates collected from the pharmacy and medication room,

ICU, and patient rooms and comprising 4 genera (*Citrobacter*, *Enterobacter*, *Klebsiella*, and *Serratia*) underwent WGS. Although short-read WGS elucidated additional subsets of closely related strains, high genomic diversity was also observed within some species: *Citrobacter freundii*: 13,483 single-nucleotide variants (SNVs), 67% core genome; *Enterobacter* spp: 3–18,563 SNVs; 34%; and *K. pneumoniae*: 8–18,460 SNVs, 80%. Further analysis using long-read hybrid assemblies revealed 2 unique *blaKPC*-harboring plasmids. The first plasmid, pDHQP20145-KPC3 (50 kb), contained the *blaKPC-3* gene and was detected in both patient and environmental isolates across 3 of the 5 sequenced genera. The second plasmid, pDHQP201745-KPC2 (180 kb), contained the *blaKPC-2* gene, and was found across 2 CP-CRE genera isolated from both patients and the environment, including isolates from the medication room sink drain and a patient who received compounded oral medications. **Conclusion:** WGS identified 2 *blaKPC*-harboring plasmids, including pDHQP20145-KPC3, which was found across 3 genera of CP-CRE isolated from patients and the environment, supporting prolonged transmission of KPC-producing CRE in this facility, and a CP-MGE driving transmission. The rapid spread of emerging, potentially mobile, antimicrobial resistance has increased our need to further explore the genomic environment of promiscuous MGEs. WGS can contribute to infection control beyond traditional subtyping methods, such as pulsed-field gel electrophoresis (PFGE), as MGEs increasingly represent an important driver of transmission.

Funding: None

Disclosures: None

Doi:10.1017/ice.2020.552

Presentation Type:

Top Rated Posters

Impact of Roommates on MDRO Spread in Nursing Homes

Gabrielle M. Gussin, University of California, Irvine; Ken Kleinman, University of Massachusetts, Amherst; Raveena D. Singh, University of California, Irvine School of Medicine; Raheeb Saavedra, University of California Irvine School of Medicine; Lauren Heim, University of California, Irvine; Marlene Estevez, University of California, Irvine; Tabitha D. Catuna, University of California, Irvine; Eunjung Lee, University of California, Irvine; Avy Osalvo, University of California, Irvine; Kaye D. Evans, University of California Irvine Health; Julie A. Shimabukuro, University of California Irvine Health; James A. McKinnell, The Lundquist Institute at Harbor-UCLA Medical Center, Torrance, CA; Loren Miller, Harbor-UCLA Medical Center; Cassiana E. Bittencourt, University of California, Irvine; Ellena M. Peterson, University of California, Irvine; Susan Huang, University of California Irvine School of Medicine

Background: Addressing the high burden of multidrug-resistant organisms (MDROs) in nursing homes is a public health priority. High interfacility transmission may be attributed to inadequate infection prevention practices, shared living spaces, and frequent care needs. We assessed the contribution of roommates to the likelihood of MDRO carriage in nursing homes. **Methods:** We performed a secondary analysis of the SHIELD OC (Shared Healthcare Intervention to Eliminate Life-threatening Dissemination of MDROs in Orange County, CA) Project, a CDC-funded regional decolonization intervention to reduce

MDROs among 38 regional facilities (18 nursing homes, 3 long-term acute-care hospitals, and 17 hospitals). Decolonization in participating nursing homes involved routine chlorhexidine bathing plus nasal iodophor (Monday through Friday, twice daily every other week) from April 2017 through July 2019. MDRO point-prevalence assessments involving all residents at 16 nursing homes conducted at the end of the intervention period were used to determine whether having a roommate was associated with MDRO carriage. Nares, bilateral axilla/groin, and perirectal swabs were processed for methicillin-resistant *Staphylococcus aureus* (MRSA), vancomycin-resistant enterococcus (VRE), extended-spectrum β -lactamase (ESBL)-producing *Enterobacteriaceae*, and carbapenem-resistant *Enterobacteriaceae* (CRE). Generalized linear mixed models assessed the impact of maximum room occupancy on MDRO prevalence when clustering by room and hallway, and adjusting for the following factors: nursing home facility, age, gender, length-of-stay at time of swabbing, bedbound status, known MDRO history, and presence of urinary or gastrointestinal devices. CRE models were not run due to low counts. **Results:** During the intervention phase, 1,451 residents were sampled across 16 nursing homes. Overall MDRO prevalence was 49%. In multivariable models, we detected a significant increasing association of maximum room occupants and MDRO carriage for MRSA but not other MDROs. For MRSA, the adjusted odds ratios for quadruple-, triple-, and double-occupancy rooms were 3.5, 3.6, and 2.8, respectively, compared to residents in single rooms ($P = .013$). For VRE, these adjusted odds ratios were 0.3, 0.3, and 0.4, respectively, compared to residents in single rooms ($P = NS$). For ESBL, the adjusted odds ratios were 0.9, 1.1, and 1.5, respectively, compared to residents in single rooms ($P = nonsignificant$). **Conclusions:** Nursing home residents in shared rooms were more likely to harbor MRSA, suggesting MRSA transmission between roommates. Although decolonization was previously shown to reduce MDRO prevalence by 22% in SHIELD nursing homes, this strategy did not appear to prevent all MRSA transmission between roommates. Additional efforts involving high adherence hand hygiene, environmental cleaning, and judicious use of contact precautions are likely needed to reduce transmission between roommates in nursing homes.

Funding: None

Disclosures: Gabrielle M. Gussin, Stryker (Sage Products): Conducting studies in which contributed antiseptic product is provided to participating hospitals and nursing homes. Clorox: Conducting studies in which contributed antiseptic product is

provided to participating hospitals and nursing homes. Medline: Conducting studies in which contributed antiseptic product is provided to participating hospitals and nursing homes. Xtrium: Conducting studies in which contributed antiseptic product is provided to participating hospitals and nursing homes.

Doi:10.1017/ice.2020.553

Presentation Type:

Top Rated Posters

Incidence and Characteristics of Nosocomial Influenza at an Academic Medical Center

Ahmed Abdul Azim, Beth Israel Deaconess Medical Center; Gregory Schrank, University of Maryland Medical Center; Baevin Feaser, Beth Israel Deaconess Medical Center; Sharon Wright, Beth Israel Deaconess Medical Center

Background: Despite introduction of mandatory vaccination of healthcare workers (HCWs) in 2011, we continued to see occasional cases of nosocomial influenza. We sought to understand the characteristics of patients who acquired nosocomial influenza to better target prevention efforts. **Methods:** The study population was a retrospective cohort of all patients aged ≥ 18 years admitted to an academic medical center between September 2012 and August 2018. Patient data obtained included age, admission/discharge date, service line, influenza vaccination status on admission, and virus serotype. Nosocomial influenza was defined as positive polymerase chain reaction (PCR) or antigen testing for influenza A/B > 3 days after admission. Each influenza season, patients with nosocomial influenza or community-acquired influenza (CA-I) were censored after the positive test. Means with standard deviations are reported (SAS version 9.4). **Results:** Overall, 223,005 patient admissions occurred during the study period: 222,154 (99.6%) were without confirmed influenza infection, 788 (0.35%) had CA-I, and 63 (0.03%) had nosocomial influenza (Fig. 1). The mean age of patients without influenza infection was 57.6 ± 19.3 years compared to 66.5 ± 18.8 years for those with CA-I and 67.1 ± 13.5 with nosocomial influenza. Influenza A accounted for 630 cases (80%) of CA-I, and 58 cases (92%) of nosocomial influenza. Also, 31 (48%) with nosocomial influenza had been vaccinated against influenza prior to admission (Table 1). Most nosocomial influenza cases (78%) occurred on medicine and oncology units. **Conclusions:** Influenza A represented a larger percentage of nosocomial influenza compared to CA-I. The proportion of nosocomial influenza cases remained stable during

Table 1: Annual Incidence and Characteristics of Nosocomial Influenza Cases

	Total Admitted Influenza Cases in Season	Nosocomial Influenza Cases N (% of Total Admitted Cases)	Influenza A N (% of NI)	Influenza B N (% of NI)	Patients Vaccinated N (% of NI)
2012-2013	128	8 (6)	8 (100)	0 (0)	3 (38)
2013-2014	90	2 (2)	2 (100)	0 (0)	1 (50)
2014-2015	198	15 (8)	14 (93)	1 (7)	5 (33)
2015-2016	107	7 (7)	7 (100)	0 (0)	5 (71)
2016-2017	165	12 (7)	12 (100)	0 (0)	6 (50)
2017-2018	163	19 (12)	15 (79)	4 (21)	11 (58)
Total	851	63 (7)	58 (92)	5 (8)	31 (48)

NI=Nosocomial influenza

Fig. 1.