

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