



Fig. 2.

IP-led interventions. We then showed 2 other HAIs, *Clostridium difficile* infection (CDI) and surgical site infections (SSIs), which did not meet our expected NHSN and institutional goals and were estimated to increase costs and potential mortalities in the upcoming year. We argued that proactive monies directed toward expanding our IP program and HAI mitigation efforts would cost a fraction of the impending healthcare expenditures as predicted by the model. **Conclusion:** By applying financial and mortality modeling, we helped our leadership perceive the concrete effect of IP-led interventions versus presenting abstract NHSN metrics. We also emphasized that without proactive leadership investment, we would continue to overspend healthcare dollars while not meeting our goals. This format of presentation gave us critical leverage to advocate for and successfully expand our IP department. Further SHEA-led cost-analysis modeling and education are needed to help IP departments promote their efforts in an effective manner.

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Presentation Type:

Top Rated Posters

Getting the Most Out of the ICAR Visit by Using a Scoring Report to Provide Feedback

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Background: The Centers for Disease Control and Prevention developed the Infection Control Assessment and Response (ICAR) tools to assist health departments in assessing infection

prevention practices and to guide quality improvement activities. ICAR tools are available for the following healthcare settings: acute care (including hospitals and long-term acute-care hospitals), outpatient, long-term care, and hemodialysis. The Virginia Healthcare-Associated Infections and Antimicrobial Resistance (HAI/AR) Program developed a scoring report that provides a quantitative measure for each infection control domain and summarizes strengths and opportunities for improvement. The scoring report aims to provide feedback to facility administration in a simple, user-friendly way to increase their engagement, prioritize follow-up actions for areas in need of improvement, and to analyze statewide data systematically to identify and address major defects. **Methods:** Scoring reports were developed for acute care, long-term care, and hemodialysis facilities. Each report includes 2 tables: infection control domains for gap assessment and direct observation of facility practices. The first table has rows for infection control assessment domains, and the second table summarizes direct observations conducted during the ICAR visit such as hand hygiene, point-of-care testing, and wound dressing change. Each row is stratified by the score, which is determined by responses to the ICAR tool, for each domain or observation, interpretation of the score, strengths, and opportunities for improvement. Stoplight colors with assigned percentages are used for score interpretation. ICAR visit results from 5 long-term care facilities (LTCFs) and 3 hemodialysis centers were entered into a REDCap database and analyzed. **Results:** Data from these visits elucidated consistent gaps in Infection Prevention and Control programs and defined what practices are most lacking. The low-performance areas in LTCFs included hand hygiene, personal protective equipment (PPE), environmental cleaning and disinfection, and antimicrobial stewardship. In hemodialysis centers, respiratory hygiene and cough etiquette, injection safety, and surveillance and disease

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.

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

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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.

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Impact of Roommates on MDRO Spread in Nursing Homes

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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