

Fig. 1.

required guidelines, policies, and the appropriate COVID-19 case definitions. 67% of the facilities had updated supply inventories for past week. Only 50% of the facilities had adequate supplies of N95 masks. The assessment revealed that 52% of healthcare facilities had trained their healthcare workforce; morticians were the least trained (only 17% of facilities). Moreover, 41% of the facilities had clear work plans for monitoring healthcare workers exposures to COVID-19, but only 33% of the facilities had policies on the management of infected healthcare workers. **Conclusions:** The findings provided critical information for stakeholders at all levels to be used for policy decisions, to prioritize key intervention areas in leadership and governance of facility IPC programs, for guideline development, and for capacity building and targeted investment in IPC to improve COVID-19 facility preparedness.

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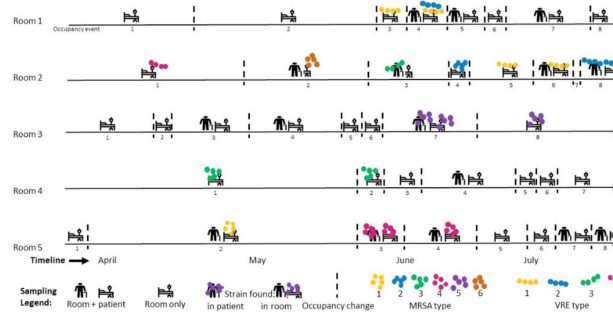
Subject Category: Long-Term Care

Diversity and persistence of MRSA and VRE in nursing homes: Environmental screening and whole-genome sequencing

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Background: Transmission of methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant *Enterococcus* (VRE) is of special concern among frail patients in nursing homes. To understand environmental contamination patterns in this setting, we screened a suitable section of a nursing home over time and assessed MRSA and VRE prevalence in patients and their rooms. We were especially interested in assessing whether MRSA and VRE strains persist in rooms during changes of occupancy after patient discharge. **Methods:** We conducted a prospective cohort study of MRSA and VRE colonization and contamination among successive patients in a cluster of 9 single-occupancy rooms. Using flocked swabs, 5 high-touch surfaces were screened 3 times a week for 34 weeks. Patients were also screened (ie, nares, groin, and hands), if they agreed to participate. Whole-genome sequencing was performed on 67 nonredundant MRSA and VRE strains. Single-nucleotide polymorphism heatmaps and similarity trees were generated to evaluate strain diversity and persistence the facility. **Results:** Overall, 146 distinct occupancy events were captured during the study (16.5 average per room; range, 11–22), with 387 study visits and 4,670 total swabs collected. All rooms were contaminated with VRE, and 8 of 9 were contaminated with MRSA at least once during the study period. New contamination of a room with MRSA or VRE was observed in 43 (23%) of 185 opportunities, with potential persistence during occupancy changes in 25 (32.9%) of 76 opportunities. Sequencing of 67 nonredundant isolates identified at least 6 enterococcal clades and 10 MRSA clades (6 USA100 and 4 USA300), indicating a high degree of

Figure. Schematic diagram exemplifying MRSA and VRE strain type persistence and diversity in five of the study rooms over a partial (four-month) time span. Only MRSA and VRE strains typed using whole genome sequencing are shown.



diversity and probably multiple introductions in the facility during the study time. In 3 separate cases, whole-genome sequencing confirmed persistence of a specific MRSA strain during a change of room occupancy, including 1 case of a MRSA strain persisting in a clean room before admission of the next patient. For VRE, 2 cases of persistence during room occupancy changes were confirmed, along with 6 cases of possible persistence (contamination across noncontiguous room occupancy events). **Conclusions:** Active surveillance screening and a recurring evaluation of terminal cleaning procedures should be considered due to high levels of circulation and persistence of MRSA and VRE in the nursing home setting.

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Characteristics of patients positive for COVID-19 and multidrug-resistant organisms in Tennessee, 2020–2021

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Background: Multidrug-resistant organisms (MDROs) are a global threat. To track and contain the spread, the Tennessee Department of Health (TDH) performs targeted surveillance of carbapenemase-producing and pan-nonsusceptible organisms. When these MDROs are identified, TDH conducts a containment response and collects epidemiological data, which includes risk factors such as indwelling devices and previous hospitalizations. The impact of the COVID-19 pandemic on these MDROs is not well understood. Therefore, we have described the characteristics of cases positive for both COVID-19 and select MDROs. **Methods:** MDRO investigation data from January 1, 2020–September 30, 2021 were matched with all COVID-19 case data from the TDH statewide surveillance system, National Electronic Disease Surveillance System Base System. MDRO-positive date was defined as the specimen collection date; COVID-19 case date was first defined as the date of symptom onset and if missing, then diagnosis date, and investigation creation date, respectively. Descriptive statistics and Fisher exact tests were calculated using SAS version 9.4 software. **Results:** Among 336 MDRO cases, 50 had a reported SARS-CoV-2-positive result. MDRO types were Enterobacterales (CRE) ($n = 31$), *Acinetobacter* spp (CRA) ($n = 18$), and *Pseudomonas aeruginosa* ($n = 1$). Of these 50 cases, 20 were MDRO-positive before and 30 days after the COVID-19 case date, respectively. Of the 18 CRA cases, 16 (89%), were positive after the COVID-19 case date, compared to 13 (42%) among 31 CRE cases ($P < .01$). Also, 35 patients (70%) had a record of hospitalization, and 22 (63%) had their MDRO specimen collected after the COVID-19 case date ($P = .37$). Of these 22 patients, 4 had their MDRO specimen collected during their COVID-19 hospitalization, with an average duration from admission to MDRO collection date of 17 days (range, 4–36).