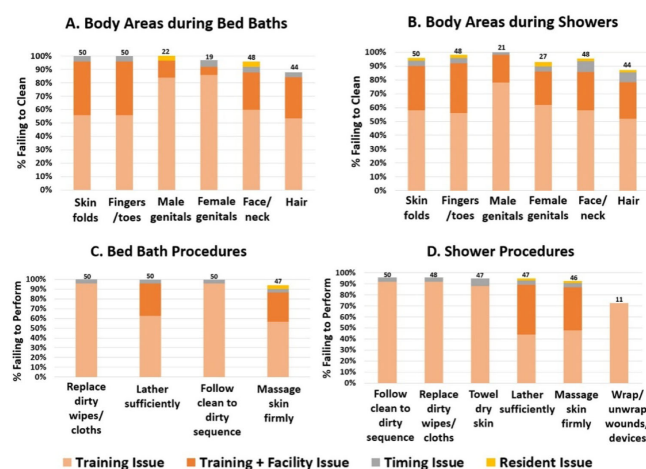## Frequency and Reasons for Failures during Bed Baths and Showers

* Values above bars reflect numerators out of 50 bed baths or 50 showers, except for "Male genitals," "Female genitals," and "Wrap/unwrap wounds/devices," which are out of the eligible population

showers separately. Reasons for failure were displayed graphically. **Results:** In total, 50 bed baths (NH range, 5–8) and 50 showers (NH range, 4–7) were observed across 8 NHs. Lapses in bathing quality and process were extremely common for both bed baths and showers (Fig.). Inadequate body cleansing occurred for all observed body sites (88%–100% failure for bed baths, 58%–100% failure for showers). Most body areas were either skipped or sprayed with water without soaping. Procedural failures were high for both bed baths and showers (insufficient lather: 100% for bed bath and 40% for shower) lack of firm massage for cleaning (94% for bed bath and 90% for shower), failure to change wipes or cloths when dirty (100% for bed bath and 96% for shower), failure to follow clean-to-dirty sequence (100% for bed bath and 96% shower). In addition, failing to wrap or unwrap devices (73%) and failing to towel dry (94%) were common after showering. Reasons for failure were largely based on training or facility shortcomings (eg, insufficient hot water, inflexible showerhead attachment). Also, 86% of residents complained of being cold. Timing constraints and resident combativeness or refusal were rare. Staff-to-staff bathing advice most commonly involved competing for the "better shower" and "bathing early to get hot water." **Conclusions:** Knowing how to appropriately bathe NH residents is not intuitive, and current training is brief and insufficient for high-quality resident care. Unacceptably high failures in proper bathing techniques in NHs necessitate re-evaluation of formal training and standardized practices to better cleanse residents. Moreover, common failures in facility processes for ensuring adequate water temperature and showerhead mobility for bathing or showering should be addressed.

Disclosures: None

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Long-term Care
Change to hospitalist providers had a minimal influence on overall antibiotic use in a VA long-term care setting
Taissa Bej; Brigid Wilson; Federico Perez and Robin Jump

Background: In long-term care settings, practice patterns among practitioners are stronger determinants of antibiotic use than resident characteristics. In July 2021, hospitalists from the acute medicine service replaced geriatricians and assumed the care of residents in a 110-bed community living center (CLC) at a large academic Veterans Affairs (VA) medical center. We assessed changes in antibiotic use associated with that change of practitioners to guide stewardship efforts. We hypothesized that

antibiotic use in the CLC would shift, reflecting the practice pattern of practitioners accustomed to treating patients in acute-care settings. **Methods:** We conducted a retrospective cohort study from July 1, 2020, through June 30, 2022, 1 year before and after the change of practitioners on July 1, 2021. We assessed resident characteristics and the following metrics of antibiotic use at monthly intervals: days of therapy (DOT) per 1,000 bed days of care (BDOC), antibiotic starts per 1,000 BDOC, and mean length of therapy (LOT) in days. We also compared the DOT per 1,000 BDOC for various antibiotics, in groups and individually. **Results:** In the years before and after the change of practitioners on July 1, 2021, the characteristics of CLC residents were comparable. Before and after July 1, 2021, monthly DOT per 1,000 BDOC (Fig. 1A), antibiotic starts per 1,000 BDOC, and mean LOT (Fig. 1B) were similar. After July 1, 2021, the use of fluoroquinolones decreased (14.31 vs 5.83 DOT per 1,000 BDOC; $P < .01$), and variations in anti-MRSA, narrow-spectrum, and broad-spectrum hospital agents were small, whereas the use of broad-spectrum community agents increased (29.42 vs 47.81 DOT per 1,000 BDOC; $P < .01$) (Fig. 2A). Within this group, there was increased use of doxycycline (7.42 vs 19.13 DOT per 1,000 BDOC; $P < .01$), ertapenem (2.03 vs 4.58 DOT per 1,000 BDOC; $P < .01$), and, modestly, azithromycin (0.40 vs 1.80 DOT per 1,000 BDOC) (Fig. 2B). **Conclusions:** The overall use of antibiotics, as measured by DOT, antibiotic starts, and LOT did not change after hospitalists assumed care of CLC residents. However, a notable decrease was observed in the use of fluoroquinolones, and an increase was observed in the use of doxycycline and ertapenem. Stewardship that is tailored to the type of provider and incorporates their practice patterns is needed to reinforce the prudent use of antibiotics. **Disclosures:** None
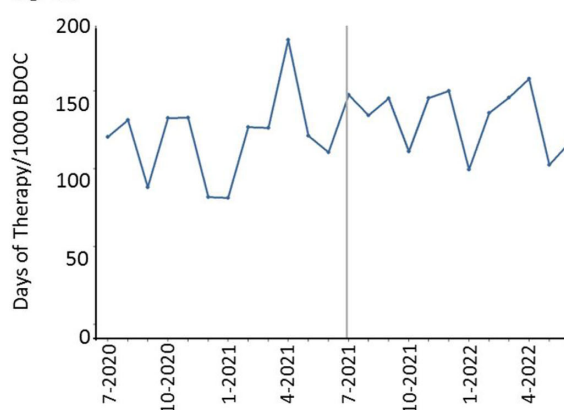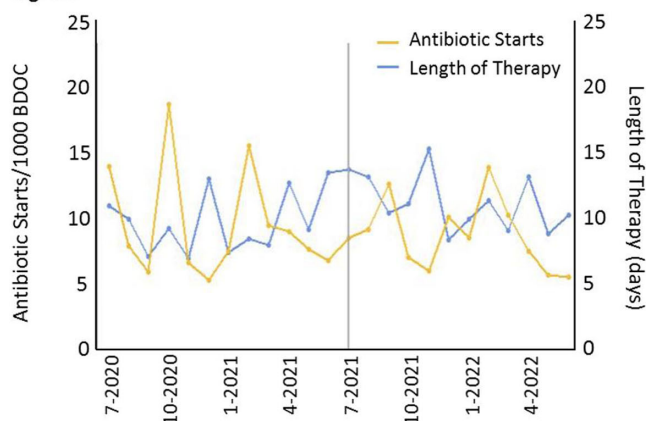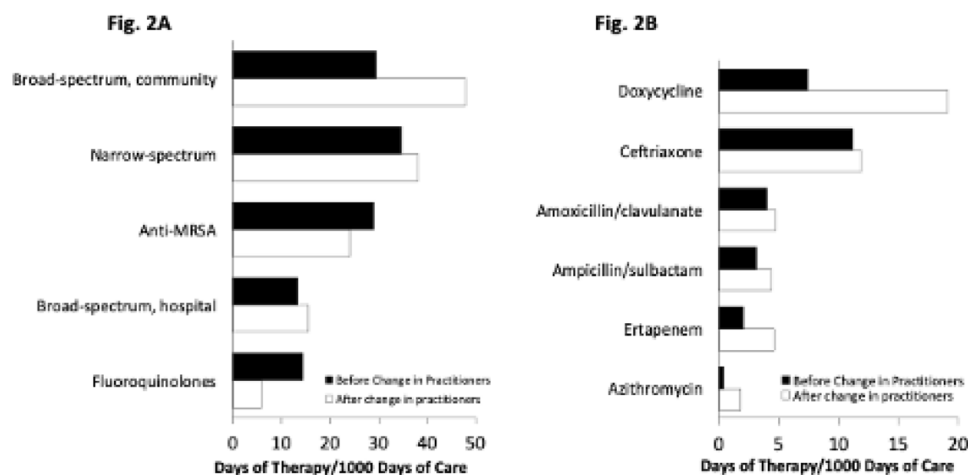
Fig. 1A

Fig. 1B

Fig. 2A

Fig. 2B

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: MDR GNR
Whole-genome sequencing of carbapenem-resistant Enterobacterales isolates and evaluation of hospital-acquired infections

Leama Ajaka; Shandra Day; Christina Liscynesky; Nora Colburn; Christine Sun; Michael Sovic; Preeti Pancholi; Joan-Miquel Balada-Llasat; Heather Smith and Shashanka Murthy

Background: Multidrug-resistant organisms (MDROs) are increasingly implicated in nosocomial outbreaks worldwide. We evaluated whole-genome sequencing (WGS) as an adjunctive epidemiological tool to identify infection clusters and MDRO transmission in the healthcare setting. **Methods:** Clinical isolates of carbapenem-resistant Enterobacterales (CRE) from July 1, 2021, to June 30, 2022, underwent Illumina WGS. Assembled genomes were taxonomically classified with GTDB-Tk software and were typed using multilocus sequence typing (MLST). Average nucleotide identity (ANI) was calculated between genomes. Numbers of differences among core single-nucleotide polymorphisms (SNPs) were calculated for pairs within taxonomic groups, and the data were evaluated in the context of patient dates and locations of care obtained from the electronic medical record. **Results:** In total, 39 CRE isolates underwent WGS (Fig. 1). *Klebsiella pneumoniae* represented the largest number of isolates (n = 18). Using MLST, 2 distinct groups of *K. pneumoniae* were identified (ST307 and ST258) with 5 and 4 isolates, respectively
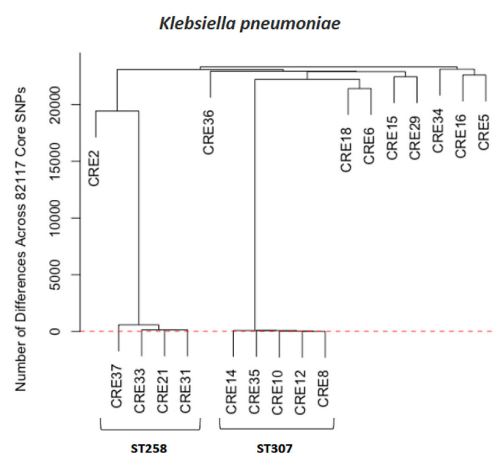

Klebsiella pneumoniae

Figure 2: Dendrogram for *Klebsiella pneumoniae* isolates using core SNPs. Red dotted line indicates 15 SNPs.

(Fig. 2). Within ST307, SNP differences ranged between 8 and 115. 3 isolates (CRE8, CRE10, and CRE12) were collected within 4 weeks of each other and had ≤26 pairwise SNP differences. Notably, CRE8 and CRE10 were located on the same unit at the same time and used the same MRI scanner on the same day. CRE35 had >95 SNP differences and was admitted 8 months prior to others in ST307 but had surgery in the same OR as CRE8. Within ST258, pairwise comparison of samples revealed 139–588 SNP differences. CRE21, CRE31, and CRE33 had SNP differences of ≤150. These patients were in the same hospital room (CRE33 and CRE21) and unit (CRE31 and CRE33), but they did not overlap temporally. CRE37 had >580 SNP differences, with no overlap in hospitalization dates or locations with other patients. **Conclusions:** Two closely related *K. pneumoniae* isolate populations were identified using WGS. Strong temporal and spatial commonalities were identified among isolates with few SNP differences. Isolate pairs with intermediate SNP differences shared spatial commonalities, suggesting possible indirect transmission between patients. No common exposures were identified for pairs with large numbers of SNP differences. WGS is an evolving tool to detect outbreak clonal populations of MDRO not identified through traditional epidemiologic techniques. WGS can provide insight into transmission patterns and the role of environmental contamination in propagating these nosocomial infections. More studies are needed to define the role and clinical significance of isolates with intermediate SNP differences in transmission of these pathogens between hosts and the healthcare environment.
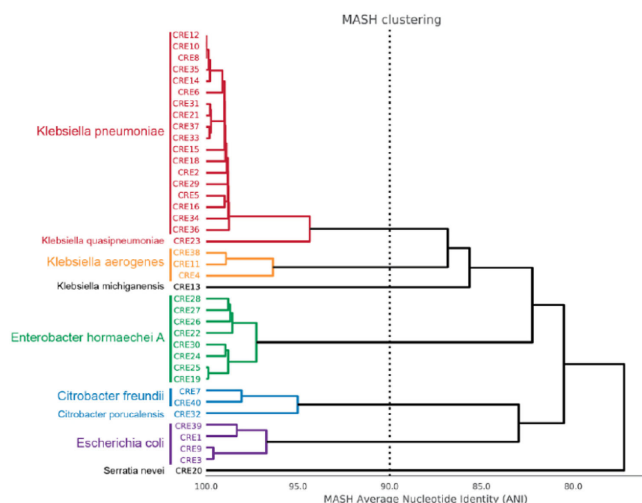
Disclosures: None

Figure 1: Primary dendrogram for all CRE genomes with taxonomy classification.