2466. What’s Lurking in the Drain? Serial transmission of NDM-1 Klebsiella pneumoniae to patients admitted 9 months apart to the same ICU room

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Background. We evaluated the role of an in-room sink in NDM-1 K. pneumoniae (NDMKP) transmission.

Methods. In October 2017, Infection Prevention (IP) initiated weekly point prevalence rectal screening cultures in 4 ICUs. In 3/2018, IP launched an epidemiologic and environmental investigation following identification of a patient with NDMKP rectal colonization. Environmental samples including swabs of biofilm from drain and water from p-traps were obtained from the in-room sink. Illumina whole-genome sequencing (WGS) was performed on all NDMKP patient and environmental isolates. Single nucleotide variants (SNVs) were identified against the reference Klebsiella pneumoniae strain MLST15 (NZ_CP022127), and isolates within 150 SNVs of each other were considered to be genomically related.

Results. Two patients were identified with NDMKP infection or colonization between October 2017 and March 2018. The index patient had prolonged hospitalization and developed NDMKP bacteraemia on hospital day (HD) 30. Approximately 9 months later, the second patient was admitted to the same ICU room that had been occupied by the index patient for 13 days and was identified to have NDMKP rectal colonization on HD 51. Sequence relatedness from the in-room sink of the ICU room grew NDMKP WGS demonstrated relatedness between NDMKP isolates from the 2 patients (112 SNV), the index patient and the sink (52 SNV), and the second patient and the sink (80 SNV). The in-room sink was replaced in 4/18 and no further cases of NDMKP infection or colonization have been identified during the intensive 12 months. The long duration of time between the index patient, secondary case, and sink culture may explain why WGS showed relatedness but not identical clones. Education around sink use, design, and environmental investigation following identification of a patient with NDMKP was helpful to rule-out hospital transmission.

Conclusions. NDM-1 K. pneumoniae transmission event possibly related to a contaminated in-room sink drain. Remarkably, 9 months elapsed between the index case and the second case, with no additional interim cases detected on weekly point prevalence screening for clinical cultures. The long duration of time between and the index patient, secondary case, and sink culture may explain why WGS showed relatedness but not identical clones. Education around sink use, design, and more effective cleaning strategies are needed to mitigate environment-to-patient transmission of CRO.

Disclosures. All authors: No reported disclosures.

2467. Infeffing Strain Type Attribution from Antibiotic Resistance Profiles among E. coli Causing Healthcare-Associated Infections in the United States, 2013–2017

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Session: 258. HAI: Surveillance - Molecular Epidemiology

Saturday, October 5, 2019: 12:15 PM

Background. E. coli is a leading cause of healthcare-associated infections (HAI), accounting for 40% of all bacterial HAIs in short-stay and long-term acute care hospitals, the Centers for Disease Control and Prevention (CDC) launched "States Targeting Reduction in Infections via Engagement" (STRIVE) - a national quality improvement program.

Methods. STRIVE consisted of a multimodal intervention implemented from November 2016 to May 2018 (Figure 1). Hospitals with excess Clostridioides difficile infection (CDI) and a high burden of at least one of the following HAIs - central line-associated bloodstream infection (CLABSI), catheter-associated urinary tract infection (CAUTI), or methicillin-resistant Staphylococcus aureus (MRSA) bloodstream infection were targeted. Monthly aggregate HAI and device utilization ratios - according to CDC National Healthcare Safety Network definitions - were measured during the pre vs. post-intervention periods. Thematic analysis of qualitative interviews with state partners was conducted to understand the influence of the intervention.

Results. Overall, 387 hospitals from 23 states and the District of Columbia participated. Changes in HAI rates and catheter utilization are illustrated in Figure 2. From pre- to post-intervention, substantial changes in HAI rates above temporal trends were observed (CDI, 5.7 per 1000 patient-days; CLABSI, 0.88 to 1.48 per 1000 days; CAUTI, 1.1 to 1.94 per 1000 catheter days; MRSA type, infection rates, and clinical outcomes may inform targeted prevention strategies at the local/regional level.

Disclosures. All authors: No reported disclosures.

2468. Is On-Demand Multilocus Sequence Typing of Methicillin-resistant Staphylococcus aureus (MRSA) and Clostridioides difficile Hospital Isolates Useful for Infection Control Practice?

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Session: 258. HAI: Surveillance - Molecular Epidemiology

Saturday, October 5, 2019: 12:15 PM

Background. MRSA and C. diff are important causes of hospital-onset (HO) or healthcare-associated infections (HAI). Molecular sequencing of bacterial pathogens is often used retrospectively during outbreak investigations to determine phylogenetic linkage. We evaluated the utility of on-demand multilocus sequence typing (MLST) in characterizing hospital transmission events.

Methods. Using VA or NHSN criteria, inpatients with MRSA-HAI or HO-C. difficile infection (HO-CDI) were identified by infection preventionists (IPs) for MLST (by time and location) during active hospital surveillance starting October 2016 or September 2017 (for C. difficile and MRSA, respectively) through March 2019. Vtek 2 identified MRSA from blood or other sources, and stool samples positive for C. difficile by Cepheid Xpert® C. difficile or FilmArray® Gastrointestinal (GI) Panel were collected and C. diff isolated on CCAFA plates. Sequence types (STs) were generated by Sanger sequencing and MLST using standard protocols (pubmlst.org). C. difficile genes included adk, ata, dta, dtxx, glx, gene, recA, sodA, tpi. MRSA genes included arce, argC, glp, gmk, pta, tpi, yqil. Staphylococcal protein A gene (spa) type was determined by spa typing.

Results. MLST assay (C. diff 33, MRSA 26) intervals ranged from 1–4 weeks based on IP request. 109 C. diff isolates from 105 patients representing 44 STs (10 unique) were found. ST1 and ST2 (27, 20) were most common. 5 patients had 2–3 identical STs over 21–180 days. 2 HO-CDI isolates, represented by 9 possible person-to-person transmissions events (33 cases) were ruled out; 3 events (9 cases) were ruled in; 14 events (21 cases) were not resolved due to missing samples or no growth. 100 MRSA isolates from 96 patients representing 26 STs (9 unique) were found. ST85/psa 0008 (USA300) and ST5/psa 0002 (USA100) (44, 29) were more similar. 100 MRSA transmission event (4 cases) was ruled out, 1 event (2 cases) lacked one strain and was unresolved.

Conclusion. Common MRSA and C. diff STs predominated among hospital isolates, yet significant heterogeneity was seen over a 2-year period and few true transmission events were documented. On-demand MLST augmented IP surveillance was useful to rule-out hospital transmission.

Disclosures. All authors: No reported disclosures.

2469. A National Intervention to Improve Infection Prevention Efforts in Hospitals with High Rates of Clostridioides difficile infection, Central Line-Associated Bloodstream Infection, Catheter-Associated Urinary Tract Infection and/or Methicillin-Resistant Staphylococcus aureus

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Session: 259. HAI: Surveillance, General

Saturday, October 5, 2019: 12:15 PM

Background. To strengthen state collaborative efforts and reduce common healthcare-associated infections (HAI) in short-stay and long-term acute care hospitals, the Centers for Disease Control and Prevention (CDC) launched “States Targeting Reduction in Infections via Engagement” (STRIVE) - a national quality improvement program.

Methods. STRIVE consisted of a multimodal intervention implemented from November 2016 to May 2018 (Figure 1). Hospitals with excess Clostridioides difficile infection (CDI) and a high burden of at least one of the following HAIs - central line-associated bloodstream infection (CLABSI), catheter-associated urinary tract infection (CAUTI), or methicillin-resistant Staphylococcus aureus (MRSA) bloodstream infection were targeted. Monthly aggregate HAI and device utilization ratios - according to CDC National Healthcare Safety Network definitions - were measured during the pre vs. post-intervention periods. Thematic analysis of qualitative interviews with state partners was conducted to understand the influence of the intervention.

Results. Overall, 387 hospitals from 23 states and the District of Columbia participated. Changes in HAI rates and catheter utilization are illustrated in Figure 2. From pre- to post-intervention, substantial changes in HAI rates above temporal trends were observed (CDI, 5.7 per 1000 patient-days; CLABSI, 0.88 to 1.48 per 1000 days; CAUTI, 1.1 to 1.94 per 1000 catheter days; MRSA...
bloodstream infection, 0.075 to 0.071 per 1,000 patient-days) Similarly, catheter utilization did not differ substantially between the pre- and post-intervention periods (24.05 to 22.07 central line days per 100 patient-days; 21.46 to 19.83 urinary catheter days per 100 patient-days). Qualitative analysis of 17 interviews with state partners showed that relationships among state partners and hospitals were strengthened, potentially facilitating collaboration on future infection prevention efforts.

**Conclusion.** Though HAI reductions were observed during STRIVE, these reductions were consistent with temporal trends. Hospitals struggling with high HAI rates may require additional novel approaches.

**Disclosures.** All authors: No reported disclosures.

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**2470. Readmission for Healthcare-Acquired Infections: Does Patient Disposition Matter?**

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**Session:** 259. HAI: Surveillance, General

**Saturday, October 5, 2019: 12:15 PM**

**Background.** Although common and preventable, healthcare-acquired infections (HAI) are associated with high risk for hospital readmission. This risk may increase when follow-up care is not provided. However, whether infection-related readmissions are more common in older adults discharged from the hospital to a skilled nursing facility (SNF) vs. home or home healthcare is unknown.

**Methods.** We used 2013–14 national discharge data and logistic regression models to retrospectively examine the relationship of discharge disposition (home, SNF, home healthcare) with unplanned readmission for the same HAI observed at the index admission, among Medicare beneficiaries 65, controlling for patient sociodemographics, comorbidity score, and length of stay during index hospitalization.

**Results.** Of 318,134 index admissions involving HAI treatment, 158,682 (50%) were discharged to a SNF, 76,523 (24%) to home, and 82,929 (26%) to home healthcare. Overall, 7,867 (2.5%) of index admissions involving treatment for an HAI resulted in a linked HAI readmission. HAI readmissions were more common for *Clostridium difficile* infections (4.0%) and urinary tract infections (UTI, 2.3%) than for ventilator-acquired pneumonia (1.4%) or surgical site infections (1.1%) (P < 0.001). Being discharged home or to home healthcare, compared with a SNF, was associated with increased odds (OR: 1.63, P < 0.001 for each) of HAI readmission. This was equivalent to a 1.2% lower risk of a linked HAI readmission for those discharged to a SNF compared with home or home healthcare. This risk difference was observed to increase with greater patient comorbidity scores.

**Conclusion.** We conclude that *Clostridium difficile* and UTIs result in higher risk for readmission than other HAIs. Patients discharged to nursing facilities are protected from readmission. Further research into identifying modifiable mechanisms for HAI readmission, in order to improve post-hospital care of infection at home, is needed.

**Disclosures.** All authors: No reported disclosures.