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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Session: 257. HAI: Outbreaks
Saturday, October 5, 2019: 12:15 PM

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 March 2017 and March 2018. The in-room sink had prolonged hospitalizations 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 52. Environmental contamination 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 at DUMC in over 12 months.

Conclusion. We report an 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 or clinical cultures. 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 more effective cleaning strategies are needed to mitigate environment-to-patient transmission of CRO.

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

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Saturday, October 5, 2019: 12:15 PM

Background. E. coli is a leading cause of healthcare-associated infections. In a national surveillance collaboration, the Centers for Disease Control and Prevention, Atlanta, Georgia, collected E. coli isolates from 96 patients representing 26 STs (9 unique) were found. ST131 was the most common. We report the resistance patterns of 100 E. coli isolates from 96 patients representing 26 STs (9 unique) were found. We conducted a comprehensive search of isolates from 2013–2017 to determine if a pattern of E. coli resistance was evident.

Methods. NHSN isolate and antibiotic susceptibility testing data were collected from all E. coli associated with central line-associated bloodstream infections, catheter-associated urinary tract infections, ventilator-associated events, or surgical site infections. The pre vs. post-intervention periods. Thematic analysis of qualitative interviews with healthcare providers identified themes and barriers to implementation.

Results. Of 96,672 E. coli infections reported to NHSN, 13% were ESC-R/FQ-R, P < 0.001), 3.4 if ESC-R (P < 0.001), and 6.0 if ESC-R/FQ-R (P < 0.001). Using the national distribution of resistance combinations from NHSN, and assuming a minority (18.4% and 7.5%, respectively) were ST131, whereas of 38 ESC-R/FQ-S and 53 ESC-S/FQ-S isolates, ST131 was the majority (67.6% and 52.4%, respectively). The odds of an isolate being ST131 were 3.5 if ESC-R/FQ-R and 21 ESC-S/FQ-R laboratory isolates, the majority (67.6% and 52.4%, respectively). The odds of an isolate being ST131 were 3.5 if ESC-R/FQ-R and 21 ESC-S/FQ-R laboratory isolates, the majority (67.6% and 52.4%, respectively).

Conclusion. Molecular resistance patterns as generated from laboratory data to resistance signature data in reportable datasets may make national E. coli ST burden estimates possible. Further characterization of resistance combinations with strain type, infection rates, and clinical outcomes may inform targeted prevention strategies at the local/regional level.

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

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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 retroactively 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 CCFAP plates. Sequence types (STs) were generated by Sanger sequencing and MLST using standard protocols (pubmlst.org). C. difficile genes included adk, atpA, ddx, gylA, recA, sodA, tpi. MRSA genes included arc, arp, gprn, gnta, tpi, ypl. Staphylococcal protein A gene (spa) type was determined by spa typing.

Results. MLST assay (C. diff 33, M RSA 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. FT1 and ST2 (27, 20) were most common. 5 patients had 2–3 indentical STs over 2–180 days. Two HO-CD1 identified, 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) found. ST8/ spa 0008 (USA300) and ST5/ spa 002 (USA100) (44, 20) were more than 2016. 11 patients had 2–3 identical ST isolates over 2–367 days. Of 16 MRSA HAI identified, 1 transmission event (4 cases) was ruled out, 1 event (2 cases) lacked one strain and was unsolved.

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. MLST augmented surveillance was useful to rule-out hospital transmission events.

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

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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 Clostridiodiflixcidrio difflficidr infection (CDI) and a high burden of at least one of the following HAI's - 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. Over all, 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 not observed (CDI, 5.7 per 1000 patient-days; CLABSI, 0.88 per 1000 patient-days; CAUTI, 1.7 to 1.49 per 1000 catheter days; MRSA