Conclusions: After initiation of the described action plan, no further transmission was identified in the ICU or INCU. Real-time observation and environmental culturing was critical in identifying the epidemiological link, and this finding speaks to the ability of this organism to persist on a surface for a substantial length of time. Fanny pack use for transport of patient-care supplies was identified as a high-risk practice due to the inability to be properly disinfected between rooms and limited laundering. Fanny packs are no longer permitted in clinical spaces at this facility.

Disclosures: None

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Outbreaks
Outbreak of *Stenotrophomonas maltophilia* infections in an intensive care unit—Alameda County, California, May–October 2022

Rebeca Elliott; Jeffrey Silvers; Axel Vazquez Deida; Paige Gable; Gillian McAllister; Alyssa Kent; Thomas Ewing; Janet Glowicz; Matthew Arduino; Heather Moulton-Meissner; Mir Noorbakhsh; Patricia Rodrigues; Munira Shemsu; Amit Chitnis; Hilary Metcalf; Barbara Allen; Suada Abdic; Alison Halpin; Kavita Trivedi; Amelia Keaton and Margarita Elsa Villarino

Background: *Stenotrophomonas maltophilia* is a gram-negative, biofilm-producing bacterium that is ubiquitous in water environments and often associated with healthcare-associated infections (HAIs). Outbreaks of *S. maltophilia* bloodstream infections are a rare event and raise the suspicion of a common source. We used whole-genome sequencing (WGS) for an investigation of a cluster of *S. maltophilia* HAIs at a single hospital. **Methods:** A patient was defined as an intensive care unit (ICU) patient with fever and *S. maltophilia* isolated from a culture and who was treated for an HAI from May to October 2022. The response to the cluster included an epidemiologic investigation, water infection control risk assessments (WICRA), and environmental sampling. We also conducted WGS to characterize and assess relatedness between clinical and environmental *S. maltophilia* isolates. **Results:** From May 5 to October 1, 2022, we identified 11 HAIs due to *S. maltophilia*: 9 bloodstream infections and 2 ventilator-associated pneumonia cases. The initial epidemiological investigation did not identify common medical products, procedures, or personnel as an exposure source. The WICRA identified several breaches that may have exposed patients to contaminated water from sink backsplashes in the ICU, computerized tomography (CT) rooms, and the emergency department. In the CT rooms, saline bags were sometimes used for multiple patients, as were single-use intravenous contrast solution bottles. No additional cases were identified once infection control breaches were mitigated by installing sink splashguards, disinfecting drains, dedicating sink use for handwashing, and adhering to single-patient use of pharmaceutical products in the CT rooms. Of 46 environmental water samples, 19 were culture-positive for *S. maltophilia*. Isolates available for WGS included 7 clinical isolates (6 blood and 1 respiratory) and 17 environmental isolates. Among the 24 isolates sequenced, 16 unique multilocus sequence types (MLSTs) were identified. The 6 blood isolates sequenced were highly related (ST239, 0–4 high-quality, single-nucleotide variants [hqSNV] over 98.99% core genome), suggesting a common source. Two clusters of related environmental isolates were identified; however, overall MLST and hqSNV analyses suggested no relatedness between clinical and environmental isolates. **Conclusions:** An ICU cluster of *S. maltophilia* bloodstream infections was likely associated with water contamination of room surfaces and use of single-use intravenous products for multiple patients in the setting of a national pharmaceutical product shortage. This investigation highlights the importance of strong surveillance and water infection control, including routine assessment of ancillary areas in which intravenous products are administered and interdisciplinary collaboration to properly mitigate nosocomial transmission.

Disclosures: None

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Subject Category: Outbreaks
Healthcare-associated *Stenotrophomonas maltophilia* infections in the United States, 2018–2022

Amelia Keaton; Lucy Fike; Kevin Spicer; Alexander Kallen and Kiran Perkins

Background: *Stenotrophomonas maltophilia* is an important cause of opportunistic healthcare-associated infections (HAIs) in critically ill patients and is difficult to treat due to intrinsic resistance to multiple antibiotic classes. During the COVID-19 pandemic, the CDC received anecdotal reports of increases in *S. maltophilia* respiratory infections. To further investigate these reports, we used a national electronic healthcare database to evaluate changes in *S. maltophilia* during the pandemic. **Methods:** Using the PINC-AI healthcare data (Premier Inc, Charlotte, NC) we identified all potential HAIs by calculating the total number of unique patients hospitalized during January 1, 2018, through December 31, 2021, who had any organism isolated on clinical culture obtained >3 days after admission. We calculated the proportion of patients with *S. maltophilia* detected in culture and stratified them by specimen source. To determine whether COVID-19 diagnosis influenced the proportion of patients diagnosed with *S. maltophilia* respiratory infections during the pandemic (January 1, 2020–December 31, 2021), we calculated the proportion of patients with *S. maltophilia* detected among those with any bacterial pathogen isolated from a respiratory culture >3 days after hospitalization. We stratified these results by presence or absence of concurrent COVID-19 diagnosis. Pearson χ^2 test was used to test for differences where appropriate. **Results:** Among hospitalized patients with any organism isolated from a clinical culture, the proportion with *S. maltophilia* detected was higher in 2021 (n = 2,554 of 118,029, 2.2%) than in 2018 (n = 2,063 of 155,624, 1.3%) p 3 days after hospital admission from 2018 to 2021. Most patient isolates were from respiratory specimens. A concurrent diagnosis of COVID-19 did not appear to increase the likelihood of respiratory *S. maltophilia* detection. The increases in *S. maltophilia* during the pandemic might be explained by challenges inherent to caring for increased numbers of higher-acuity patients during this time, including staffing shortages and changes to infection prevention practices. Additional exploration of these data, as well as data from other sources and from additional years, may help to elucidate this issue more fully.

Disclosures: None

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Subject Category: Outbreaks
Outbreak of *Burkholderia multivorans* among patients at two acute-care hospitals in California, August 2021–July 2022

Kiara McNamara; W. Wyatt Wilson; Dipesh Solanky; Sophie Jones; Elizabeth Ohlsen; J.B. Bertumen; Mark Beatty; Heather Moulton-Meissner; Paige Gable; John LiPuma; Grace Kang; Margaret Turner; Erin Epson; Kiran Perkin; Raymond Chinn and Jane Siegel

Background: *Burkholderia multivorans* are gram-negative bacteria typically found in water and soil. *B. multivorans* outbreaks among patients without cystic fibrosis have been associated with exposure to contaminated medical devices or nonsterile aqueous products. Acquisition can also occur from exposure to environmental reservoirs like sinks or other hospital water sources. We describe an outbreak of *B. multivorans* among hospitalized patients without cystic fibrosis at 2 hospitals within the same healthcare system in California (hospitals A and B) between August 2021 and July 2022. **Methods:** We defined confirmed case patients as patients without cystic fibrosis hospitalized at hospital A or hospital B between January 2020 to July 2022 with *B. multivorans* isolated from any body site matching the outbreak strain. We reviewed medical records to describe case patients and to identify common exposures. We evaluated infection control

practices and interviewed staff to detect exposures to nonsterile water. Select samples from water, ice, drains, and sink splash zone surfaces were collected and cultured for *B. multivorans* in March 2022 and July 2022 from both hospitals. Common aqueous products used among case patients were tested for *B. multivorans*. Genetic relatedness between clinical and environmental samples was determined using random amplified polymorphic DNA (RAPD) and repetitive extragenic palindromic polymerase chain reaction (Rep-PCR). **Results:** We identified 23 confirmed case patients; 20 (87%) of these were identified at an intensive care unit (ICU) in hospital A. *B. multivorans* was isolated from respiratory sources in 18 cases (78%). We observed medication preparation items, gloves, and patient care items stored within sink splash zones in ICU medication preparation rooms and patient rooms. Nonsterile water and ice were used for bed baths, swallow evaluations, and ice packs. *B. multivorans* was cultured from ice and water dispensed from an 11-year-old ice machine in the ICU at hospital A in March 2022 but no other water sources. Additional testing in July 2022 yielded *B. multivorans* from ice and a drain pan from a new ice machine in the same ICU location at hospital A. All products were negative. Clinical and environmental isolates were the same strain by RAPD and Rep-PCR. **Conclusions:** The use of nonsterile water and ice from a contaminated ice machine contributed to this outbreak. Water-related fixtures can serve as reservoirs for *Burkholderia*, posing infection risk to hospitalized and immunocompromised patients. During outbreaks of water-related organisms, such as *B. multivorans* , nonsterile water and ice use should be investigated as potential sources of transmission and other options should be considered, especially for critically ill patients.
Disclosures: None

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Subject Category: Outbreaks
New Delhi metallo-*β*-lactamase–producing *Escherichia coli* among dogs at an animal rescue facility—Wisconsin, 2022

Kiara McNamara; Caroline Habrun; W. Wyatt Wilson; Leslie Kollmann; G. Sean Stapleton; Richard Stanton; Katharine Benedict; Amanda Beaudoin; Paula Snippes; Melissa Anacker; Megin Nichols; Maroya Walters; Jordan Mason and Nikki Mueller

Background: New Delhi Metallo-β-lactamase (NDM)–producing *Escherichia coli* are highly resistant organisms that spread quickly. In the United States, organisms with *bla*NDM are rare and mostly associated with healthcare settings. However, in other countries, *bla*NDM can be relatively common and are found in community settings. State veterinary and public health partners detected NDM *E. coli* in a dog from Iran living at a Wisconsin animal rescue facility (ARF), where 40% of dogs had international origins. We investigated to determine spread among dog and human contacts and prevent further transmission. **Methods:** We screened dogs and humans at the ARF, a local veterinary clinic (clinic A), and ARF staff homes (homes A and B) for colonization with *bla*NDM. We reviewed veterinary records and conducted a case–control analysis to identify risk factors for *bla*NDM acquisition among dogs. We evaluated ARF infection control practices. Screening specimens that were positive for *bla*NDM were cultured. We conducted an analysis of short- and long-read whole-genome sequencing data to evaluate isolate relatedness. We compared NDM *E. coli* sequences from dogs to all NDM *E. coli* sequences from humans collected in Wisconsin and nearby states. **Results:** Screening identified *bla*NDM colonization in 27 (37%) of 73 ARF dogs and 4 (56%) of 7 dogs in home A, but not in ARF or staff in clinic A. Among ARF dogs with *bla*NDM, 20 (74%) 27 had international origins and 22 (81%) had ≥1 medical condition. Dogs sharing the same space (OR, 5.1; 95% CI, 1.8–14.7) were associated with *bla*NDM acquisition. We observed high animal density, soiled environments, and insufficient hand hygiene. ARF staff wore workwear and work shoes off site, including to home A. Sequencing identified 3 multilocus sequence types (STs) using the Achtman scheme among 27 isolates with *bla*NDM-5. Most isolates were ST361 (20 of 27, 74%) followed by ST167 (6 of 27, 22%) and ST1163 (1 of 27, 4%). Within-

MLST cluster variability was <1–3 high-quality single-nucleotide variant differences, each harboring a ST-specific plasmid with blaNDM-5. No NDM-*E. coli* sequences from humans appeared related. **Conclusions:** Investigation of a single isolate led to identification of widespread NDM-*E. coli* transmission among dogs at an ARF. There were multiple NDM *E. coli* introductions to the ARF, likely by dogs of international origin. Poor hygiene contributed to transmission among ARF dogs and to dogs outside the ARF. Transmission of *bla*NDM-5 at the ARF and offsite spread to home A demonstrate the potential for unrecognized community sources to disseminate NDM *E. coli* in community settings. Strategies and lessons learned from interventions to prevent antibiotic resistance in human healthcare settings may inform and support prevention in animal care.
Disclosures: None

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Importance of carbapenem-resistant Enterobacteriaceae screening to prevent transmission within an acute-care hospital

Meghan Hudziec; Sarah Totten; Larissa Pisney and Cara Faliano

Background: Carbapenem-resistant Enterobacteriaceae (CRE) present a serious public health risk because they are transmissible within the acute-care hospital setting, and they are associated with significant morbidity and mortality. Timely identification of CRE among hospitalized patients is essential to ensure that appropriate infection prevention measures are enforced to prevent transmission events. In 2022, 9 index CRE cases (5 Klebsiella pneumoniae carbapenemase (KPC)–producing and 4 New Delhi Metallo-β-lactamase (NDM)–producing cases) were identified within the University of Colorado Hospital (UCH) inpatient population. In response to index case identification, tracing was performed to identify patients with an epidemiologic link for targeted CRE screening to detect asymptomatic CRE carriage. **Methods:** In total, 645 patients were screened allowing for timely identification of CRE colonization within 6 patients (3-KPC; 1-OXA-48; 1-NDM; 1-KPC/OXA-48). Secondary case identification elicited additional evaluation of service team and mobile-device crossover between positive patients, as well as primary and ancillary treatment locations. **Results:** Investigations revealed 3 possible transmission events in 0.47% of the total screened population. Identification of secondary CRE cases prompted additional testing of exposed patients performed at 7-day intervals to capture a 21-day colonization period. In total, 95 additional patients were screened for CRE during secondary and tertiary CRE screening events. **Discussion:** Nursing staff collaboration and engagement were critical to achieving a high rate of compliance with CRE screening activities, not only collecting screening specimens but also providing explanation and reassurance to patients. Due to this partnership and diligence, UCH was able to achieve 77% compliance with initial CRE screening events. Secondary and tertiary CRE screening revealed testing compliance of 83% and 69%, respectively. To further reduce the risk of CRE transmission within hospitalized patients, UCH has implemented an enhanced cleaning process for high-risk patient rooms, which includes patients infected or asymptomatically colonized with CRE. This enhanced process is prompted based on CRE or infection status as documented in the electronic medical record (EMR), and it initiates a mandatory 2-phase cleaning process. Future plans include environmental testing audits to validate room decontamination and leveraging the EMR to capture pertinent healthcare and travel histories. Active engagement with public health partners will be pursued to enable molecular testing of high-risk touch points. **Conclusions:** Patient screening, enhanced decontamination, and monitoring activities are key elements to effectively prevent the spread of CRE within vulnerable patient populations and must be continuously evaluated for improvement opportunities.
Disclosures: None