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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Presentation Type:
Poster Presentation - Poster Presentation
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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Presentation Type:
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Subject Category: Outbreaks
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.
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