of in?house PCR (additional ?15%; -32% overall vs baseline) (Figure 1). Colonization detections increased when screening frequency changed from biweekly to weekly (5.3 to 13.8 per month; +160%) and then declined after in?house PCR (to 10.2 per month; -26%). These patterns were concordant with control?chart signals at the phase changes. **Conclusions:** Targeted, more frequent screening coupled with rapid in?house PCR was associated with fewer clinical C. auris cases and with higher detection of colonization, consistent with earlier identification and response. Because the clinical?case metric is less sensitive to testing intensity and speciation practices than colonization counts, it may better capture the impact of hospital interventions on transmission. Findings are limited by the single?center, retrospective design, potential confounding from concurrent infection?prevention measures, and use of monthly counts rather than rates; nonetheless, the phased approach provides actionable evidence to guide surveillance strategies during C. auris clusters.

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Presentation Type:
Poster Presentation
Subject Category: Outbreaks
Endoscopy-associated Salmonella Infections: Nearly Forgotten but Not Gone ‡

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Background: Contaminated endoscopes are a recognized source of nosocomial transmission of infection. Endoscope-associated Salmonella transmission was once common, however, as a result of stringent reprocessing guidelines, including high-level disinfection, a 2018 review indicated that no cases were reported since 1987. **Methods:** In July 2024, the Illinois Department of Public Health identified and notified the local health department (LHD) of a cluster of three Salmonella Enteritidis (SE) cases from the same jurisdiction that were related by whole genome sequencing (WGS). The LHD investigated the cluster, as well as other Salmonella cases that were pending WGS, to identify a common source. The investigation included case interviews, interviews of patients with a common exposure, medical record reviews, isolate serotyping and whole genome sequencing (WGS), scope culture, and site visits for Infection Control Assessment and Recommendations (ICAR). **Results:** Index case reported symptoms including fever, nausea, vomiting, and urgent diarrhea. Two weeks prior to symptom onset, the case-patient had an esophagogastroduodenoscopy (EGD) and colonoscopy at an outpatient gastroenterology and endoscopy center. 56 patients had EGDs performed with the same scope, 48 of whom were interviewed regarding gastrointestinal symptoms post procedure. Six patients reported experiencing symptoms following their procedure, five of whom were already included in the investigation. The sixth case tested positive for Salmonella Newport and was excluded. Seven total cases of Salmonella were identified as associated with this investigation with illness onset between May 3, 2024, and September 20, 2024. Six were confirmed to be SE and closely related (0 SNPs) by WGS; one specimen was not sent to the state lab for WGS. ICAR identified several opportunities for improvement however there was not a clear gap in the disinfection or other processes that were observed. Namely, the scope passed the facility's leak test. Scope culture was negative for Salmonella and other gram-negative organisms. The scope was sent to a third-party endoscope repair company; it did not pass their leak test, and the scope was refurbished. The facility planned to prospectively have all scopes inspected routinely. Staff was also retrained by the consultant company on reprocessing procedures. **Conclusion:** Scope-associated Salmonella transmission may be rare, but it is not entirely bygone. Cases may be under-reported if symptoms are attributed to the procedure itself or the underlying condition which prompted the procedure or are self-resolving and do not lead to diagnosis. Because scopes are complex in design and require fidelity to strict reprocessing, prospective maintenance routines, and re-training and auditing of reprocessing processes may be prudent.

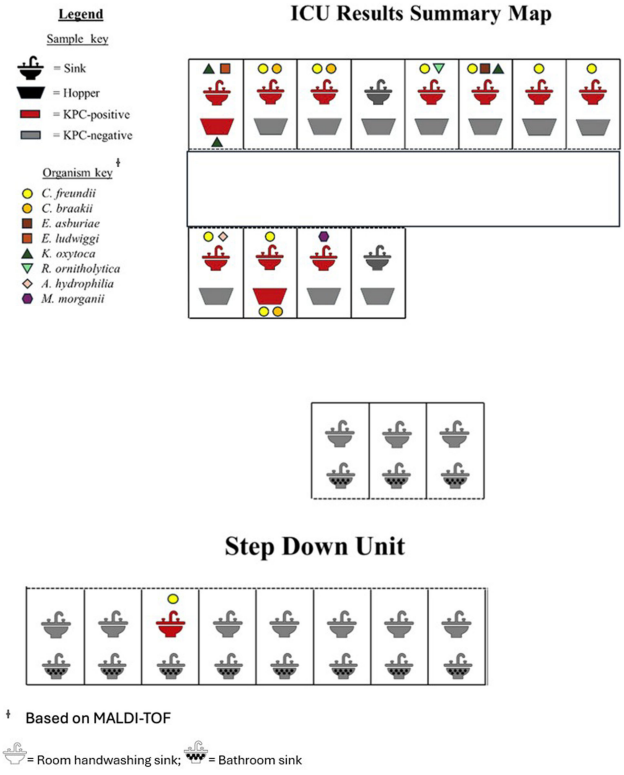
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Presentation Type:
Poster Presentation
Subject Category: Outbreaks
Prolonged KPC-CRE Outbreak with Horizontal Plasmid Transfer Associated with ICU Sink Drains‡

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Background: After CDC and local surveillance identified an increase in Klebsiella pneumoniae carbapenemase (KPC)-producing carbapenem-resistant Enterobacterales (KPC-CRE) caused by multiple organisms, an investigation was conducted at an acute care hospital. Cases clustered around an intensive care unit (ICU) and step-down unit (SDU), where wastewater plumbing was a suspected transmission source. Whole genome sequencing (WGS) was used to investigate this outbreak. **Methods:** A case was defined as detection of KPC-CRE or KPC (no organism cultured) from specimens collected at the hospital between 01/2019 to 10/2025. Clinical

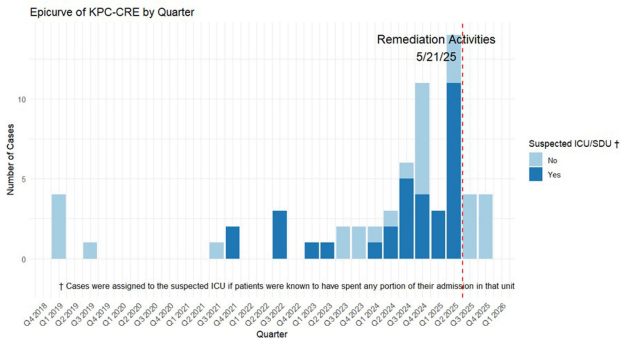
Fig. 1. Summary of Intensive Care Unit (ICU) and Step-Down Unit (SDU) Environmental Sampling for KPC + Target Organisms - May 2025.



‡The abstract titles in this supplement have been corrected since original publication. A notice detailing the changes has been published at https://doi.org/10.1017/ash.2026.10802.

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Fig. 2. Epi curve of KPC-CRE



cases were identified via carbapenemase testing of CRE isolates using PCR (Xpert Carba-R) or by multiplex PCR panels and screening cases through PCR with reflex to culture. ICU sink and hopper samples and SDU sink samples were tested using selective media, MALDI-TOF, and multiplex PCR for KPC-CRE detection. Isolates underwent short and long-read sequencing. **Result:** Overall, 64 cases (37 clinical; 27 screening), involving 54 patients, were identified; 28 patients had ICU/SDU admissions during their hospitalization. The 52 cases with an organism identified included seven species, of which the most common were Citrobacter (26), Klebsiella (14), and Raoultella (5); 24 harbored blaKPC-2 (37.5%), 18 blaKPC-4 (28.1%), 5 blaKPC-3 (7.8%), 1 blaKPC-160 (1.5%), and 16 were not subtyped (25%). Seventeen isolates from five species carried blaKPC-2 on a 42 kb IncP6 plasmid, while ten isolates from five species carried blaKPC-4 on a 69 kb plasmid with Col440I and IncM1 replicons. Environmental sampling in 05/2025 found KPC-CRE in 10/12 sinks and 2/12 hoppers in the ICU and 1/22 SDU sinks (fig1). KPC-CRE environmental isolates were closely genetically related to the Citrobacter, Klebsiella, and Roultella clinical isolates and harbored similar KPC-carrying plasmids. Infection prevention and control (IPC) rounding identified patient items within the sink splash zone, including placing bath-in-a-bag in the sink. In 05/2025, a campaign was initiated to remove items from the splash zone, switch to chlorhexidine wipes, and implement daily use of an EPA-registered, sodium dichloroisocyanurate-based biofilm drain disinfectant product. Starting 07/2025, pouring of lipids and total parenteral nutrition down drains was stopped. While repeat environmental sampling in 6/2025 also found KPC-CRE in sink drains, no additional cases were identified in the ICU or SDU following these remediation activities (fig2). **Conclusion:** ICU sinks served as a reservoir for KPC-CRE, with transmission to patients. KPC-CRE persisted in drains following initial drain disinfection measures; therefore, changes in sink and splash-zone IPC practices appear to be important for interrupting transmission.

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Characteristics of NDM-CRE clusters in the US: Using cluster size dispersion to estimate the probability of final cluster size‡

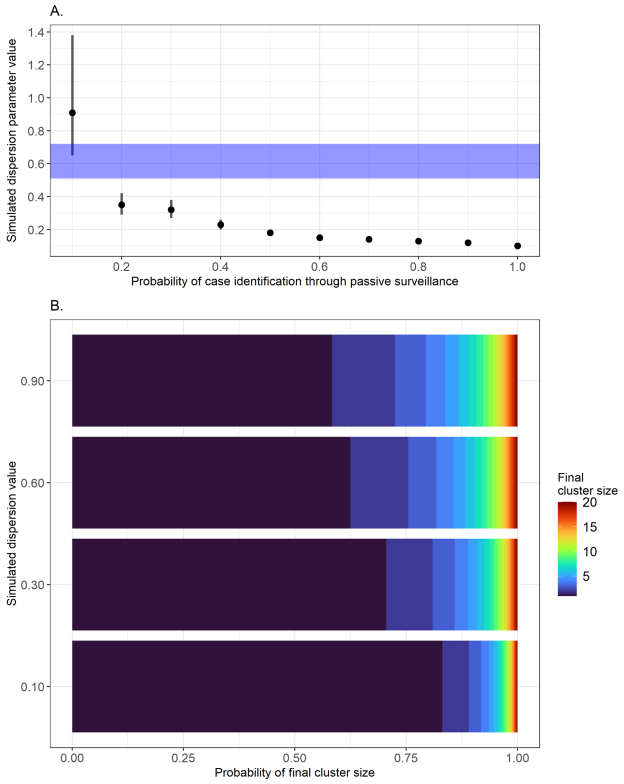
Velma Lopez[1], Ashley Styczynski[1], Richard Stanton[2] and Rachel Slayton[3]
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Introduction: Transmission of New Delhi metallo-beta-lactamase-producing carbapenem-resistant Enterobacterales (NDM-CRE) is stochastic in nature. Largescale NDM-CRE outbreaks have been observed throughout the world. Within the United States (US), the incidence of NDM-CRE infections increased by 5-fold between 2019 and 2023, highlighting concern for large outbreaks. Given this, estimating how large an NDM-CRE outbreak is likely to be (i.e., the probability of final cluster size) is a valuable first step in characterizing NDM-CRE transmission dynamics and informing outbreak response. **Methods:** The National Center for Biotechnology Information (NCBI) Pathogen Detection database is a global, public tool that identifies clusters of bacterial pathogen genomes based solely on genetic relatedness. We included all NDM-CRE genomes associated with a US cluster and uploaded between January 2009 and September 2025. Using cluster data, we estimated the dispersion parameter (k), which reflects transmission chain variance. Because we assume that NCBI does not capture all NDM-CRE cases in a cluster, we compared the estimated k values for the NDM-CRE clusters to simulated k values. Our simulations varied the probability of case identification and assumed the average number of new cases from each infection was 1.1 (based on literature; see Figure 1A). Using these simulated k values, we estimated the probability of final cluster size (see Figure 1B). **Results:** We included 1,104 clusters with a mean size of 5 genomes (standard deviation=20). The estimated k value was comparable to, but higher than, simulated k values, supporting our assumption that NCBI cluster data are incomplete (Figure 1A). Comparing the probability of the final cluster size between estimated k values, which were likely biased (<0.3), to simulated values k values <=0.3, final cluster sizes are most likely to have two cases and a low probability of clusters <=10 cases (Figure 1B). **Conclusions:** Unlike many other infectious diseases, NDM-CRE cluster dispersion values remain unknown, which is a critical gap. We estimated dispersion to show that US NDM-CRE clusters have a high probability of being small. However, additional analysis is needed since standardized NCBI cluster data may be subject to biological, technical, and sampling limitations and do not allow for assessing why US clusters were small. Strong infection prevention and control practices and assessment of patient travel history continue to be best practices for mitigating NDM-CRE outbreaks. Moreover, as the NDM-CRE epidemiology continues to evolve, monitoring US NDM-CRE clusters will provide insight into outbreak dynamics, including emergence of highly successful clones.

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Figure 1. A. Mean (shown as a point) and 95% confidence intervals (shown as a vertical bar) for simulated dispersion values across a range of case identification probabilities in a passive surveillance system. The blue band shows the estimated dispersion values for the NDM-CRE cluster data. B. The probability of final cluster size under different simulated k values.



‡The abstract titles in this supplement have been corrected since original publication. A notice detailing the changes has been published at https://doi.org/10.1017/ash.2026.10802.

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