isolates did not have a common source, suggesting that *P. aeruginosa* gastrointestinal colonization may play a role in seeding these bacteremia infections.

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Verona Integron-Encoded Metallo-Beta-Lactamase (VIM)–Producing *Pseudomonas aeruginosa* Outbreak Associated with Acute Care

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Background: Contaminated healthcare facility plumbing is increasingly recognized as a source of carbapenemase-producing organisms (CPOs). In August 2019, the Tennessee State Public Health Laboratory identified Tennessee's twelfth VIM-producing carbapenem-resistant *Pseudomonas aeruginosa* (VIM-CRPA), from a patient in a long-term acute-care hospital. To determine a potential reservoir, the Tennessee Department of Health (TDH) reviewed healthcare exposures for all cases. Four cases (33%), including the most recent case and earliest from March 2018, had a history of admission to intensive care unit (ICU) room X at acute-care hospital A (ACH A), but the specimens were collected at other facilities. The Public Health Laboratory collaborated with ACH A to assess exposures, perform environmental sampling, and implement control measures. **Methods**: TDH conducted in-person infection prevention assessments with ACH A, including a review of the water management program. Initial recommendations included placing all patients admitted to room X on contact precautions, screening for CPO on room discharge, daily sink basin and counter cleaning, and other sink hygiene measures. TDH collected environmental and water samples from 5 ICU sinks (ie, the handwashing and bathroom sinks in room X and neighboring room Y [control] and 1 hallway sink) and assessed the presence of VIM-CRPA. Moreover, 5 patients and 4 environmental VIM-CRPA underwent whole-genome sequencing (WGS). **Results:** From February to June 2020, of 21 patients admitted to room X, 9 (43%) underwent discharge screening and 4 (44%) were colonized with VIM-CRPA. Average room X length of stay was longer for colonized patients (11.3 vs 4.8 days). Drain swabs from room X's bathroom and handwashing sinks grew VIM-CRPA; VIM-CRPA was not detected in tap water or other swab samples. VIM-CRPA from the environment and patients were sequence type 253 and varied by 0–13 single-nucleotide variants. ACH A replaced room X's sinks and external plumbing in July. Discharge screening and contact precautions for all patients were discontinued in November, 5 months following the last case and 12 consecutive negative patient discharge screens. Improved sink hygiene and mechanism testing for CRPA from clinical cultures continued, with no new cases identified. **Conclusions:** An ICU room with a persistently contaminated sink drain was a persistent reservoir of VIM-CRPA. The room X attack rate was high, with VIM-CRPA acquisition occurring in >40% of patients screened. The use of contaminated plumbing fixtures in ACH have the potential to facilitate transmission to patients but may be challenging to identify and remediate. All healthcare facilities should follow sink hygiene best practices.

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Successful Control of Human Parainfluenza Type 3 Outbreak in a Level IV Neonatal Intensive Care Unit

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Human parainfluenza (HPIV) is a common cause for upper respiratory tract illnesses (URTI) and lower respiratory tract illnesses (LRTI) in infants and young children. Here, we describe successful control of an HPIV type 3 (HPIV3) outbreak in a neonatal intensive care unit (NICU). NICU babies with new-onset clinical signs or symptoms of RTI and positive HPIV-3 nasopharyngeal specimen by respiratory pathogen panel (RPP) test on hospital day 14 or later were diagnosed with hospital-onset (HO) HPIV-3 infection. After 3 NICU babies were diagnosed with HO HPIV-3, an outbreak investigation was initiated on May 3, 2019, and continued for 2 incubation periods since the last identified case. Enhanced infection prevention measures were immediately implemented. All positive cases were placed in a cohort in a single pod of the NICU and were placed on contact precautions with droplet isolation precautions. Dedicated staffing and equipment were assigned. Environmental cleaning and disinfection with hospital-approved disinfectant wipes was performed daily. Visitors were restricted in the NICU. All employees entering the NICU underwent daily symptom screening for respiratory tract illness. All NICU babies were screened daily for respiratory tract illness with prompt isolation and RPP testing on positive screen. To determine the source of the HPIV3 outbreak, all HPIV3-positive specimens from the NICU and available temporally associated community-onset (CO) controls collected from non-NICU units were sent to the Centers for Disease Control and Prevention (CDC) for whole-genome sequencing (WGS) analysis. The first and last cases of HPIV-3 were diagnosed on May 1 and May 5, 2019, respectively. In total, 7 HO HPIV3 cases were reported: 1 in newborn nursery (NBN) and 6 in NICU. The case from the NBN was determined to be unrelated to the outbreak and the source was linked to a sick visitor. Of the 6 NICU babies, 5 had an LRTI and 1 had a URTI. Average time from admission to diagnosis was 71 days (range, 24–112). None had severe illnesses requiring intubation, and all had full recovery. No CO HPIV3

Figure 1: Maximum likelihood phylogenetic tree of HPIV3 WGS obtained from 6 hospital-onset cases (circles) and 3 community-onset controls (triangles). Dates in the strain names indicated specimens collecting dates. Bootstrap support values (1000 replicates) were plotted at internal branch nodes. Scale bar corresponds to nucleotide change per site.

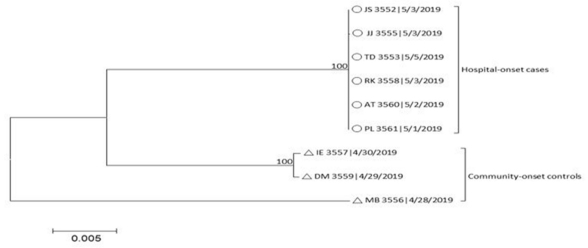

Figure 2: Epi Curve