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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Presentation Type:
Oral Presentation
Subject Category: Outbreaks
Verona Integron-Encoded Metallo-Beta-Lactamase (VIM)–Producing *Pseudomonas aeruginosa* Outbreak Associated with Acute Care
Allison Chan; Alicia Shugart; Albert Burks; Christina Moore; Paige Gable; Heather Moulton-Meissner; Gillian McAllister; Alison Halpin; Maroya Walters; Amelia Keaton; Kelley Tobey; Katie Thure; Sarah Schmedes; Paige Gable; Henrietta Hardin and Adrian Lawsin

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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Disclosures: None

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Presentation Type:
Oral Presentation
Subject Category: Outbreaks
Successful Control of Human Parainfluenza Type 3 Outbreak in a Level IV Neonatal Intensive Care Unit
Bhagyashri Navalkele; Sheila Fletcher; Sanjosa Martin; Regina Galloway and April Palmer

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.

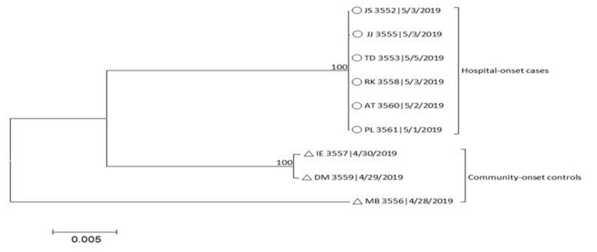
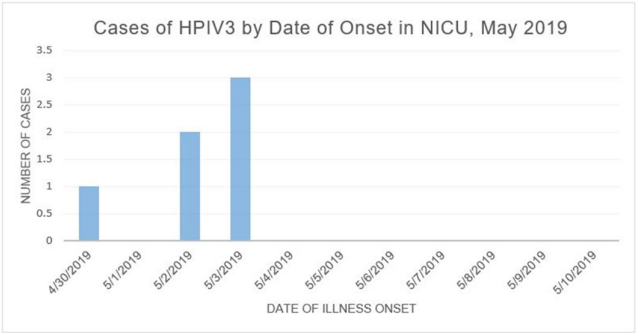


Figure 2: Epi Curve



cases were reported from the NICU during the investigation. A maximum likelihood phylogenetic tree of HPIV3 WGS (Figure 1) showed that sequences from the 6 HO cases clustered together separately from the 3 CO controls, suggesting a single source of transmission, and 3 CO cases were not related to the HO cases or source of the outbreak. Early diagnosis and isolation of respiratory tract viral infections is important to prevent an outbreak. Successful control of outbreak in NICU requires prompt implementation of infection prevention measures with focus on symptom screening, cohorting, and disinfection practices.

Funding: No

Disclosures: None

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Oral Presentation
Subject Category: Pediatrics

Results of a Multicenter Diagnostic Stewardship Collaborative to Optimize Blood Culture Use in Critically Ill Children

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Group Name: Bright STAR Authorship Group

Background: Blood cultures are fundamental in the diagnosis and treatment of sepsis. Culture practices vary widely, and overuse can lead to false-positive results and unnecessary antibiotics. Our objective was to describe the implementation of a multisite quality improvement collaborative to reduce unnecessary blood cultures in pediatric intensive care unit (PICU) patients, and its 18-month impact on blood culture rates and safety metrics. **Methods:** In 2018, 14 PICUs joined the Blood Culture Improvement Guidelines and Diagnostic Stewardship for Antibiotic Reduction in Critically Ill Children (Bright STAR) Collaborative, designed to understand and improve blood culture practices in critically ill children. Guided by a centralized multidisciplinary study team, sites first reviewed existing evidence for safe reduction of unnecessary blood cultures and assessed local practices and barriers to change. Subsequently, local champions developed and implemented clinical decision-support tools informed by local patient needs to guide new blood-culture practices. The coordinating study team facilitated regular evaluations and discussions of project progress through monthly phone calls, site visits if requested by sites or the study team, and collaborative-wide teleconferences. The study team collected monthly blood culture rates and monitored for possible delays in obtaining blood cultures using a standardized review process as a safety balancing metric. We compared 24 months of baseline data to 18 months of postimplementation using a Poisson regression model accounting for the site-specific patient days and correlation of culture use within a site over time. **Results:** Across the 14 sites, before implementation, 41,768 blood cultures were collected over 259,701 PICU patient days. The mean preimplementation site-specific blood culture rate was 15.7 cultures per 100 patient days (rate range, 9.6–48.2 cultures per 100 patient days). After implementation, 22,397 blood cultures were collected over 208,171 PICU patient days. The mean postimplementation rate was 10.4 cultures per 100 patient days (rate range, 4.7–28.3 cultures per 100 patient days), which was 33.6% lower than the preimplementation (relative rate 0.66; 95% CI, 0.65–0.68 p <0.01). In 18 months post-implementation, sites reviewed 793 positive blood cultures, and identified only one suspected delay in culture collection possibly attributable to the site's blood culture reduction program. **Conclusions:** Multidisciplinary quality improvement teams safely facilitated a 33.6% average reduction in blood culture use in critically ill children at 14 hospitals. Future collaborative work will determine the impact of blood culture diagnostic stewardship on antibiotic use and other important patient safety outcomes.

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Oral Presentation
Subject Category: Pediatrics

Association of Antibiotic Duration and Outcomes among NICU Infants with Invasive *Staphylococcus aureus* Infections

Areej Bukhari; Ibukunoluwa Akinboyo; Kanecia Zimmerman; Danny Benjamin; Veeral Tolia and Rachel Greenberg

Background: *Staphylococcus aureus* is the second-leading cause of late-onset sepsis among infants in US neonatal intensive care units (NICUs). Management of *S. aureus* bacteremia and meningitis in infants varies widely due to the lack of standardized guidelines. We examined the association between initial antibiotic duration and recurrent *S. aureus* infection or death among NICU infants with *S. aureus* bacteremia and/or meningitis. **Methods:** We conducted a retrospective cohort study of infants in Pediatrix Medical Group NICUs from 1997 to 2018 with first episode of *S. aureus* bacteremia and/or meningitis, identified as having at least 1 blood or cerebrospinal fluid (CSF) culture growing only *S. aureus* at any point during their NICU stay. Excluded infants were those not started on antistaphylococcal therapy within 2 days of positive culture, those with had endocarditis or osteomyelitis, or those who died or were discharged during or up to 1 day after antibiotic cessation. Antibiotic cessation was defined as last day of antibiotic given if followed by at least 3 days without antibiotics. Multivariable logistic regression was used to analyze the association between antibiotic duration categorized as <14 or ≥14 days) and recurrent SA infection (within 12 weeks of antibiotic cessation, prior to hospital discharge), or death (within 7 days of antibiotic cessation and at discharge). **Results:** Of 4,086 infants included, 3,991 (98%) had *S. aureus* bacteremia only and 95 (2%) had meningitis ± bacteremia. Of those with bacteremia only, 2,017 (50.5%), and 17 (18%) of those with meningitis received <14 days antibiotics (Figure 1). Longer antibiotic duration was associated with lower gestational age, methicillin-resistance, severe illness and bacteremia duration of ≥4 days (Table 1).

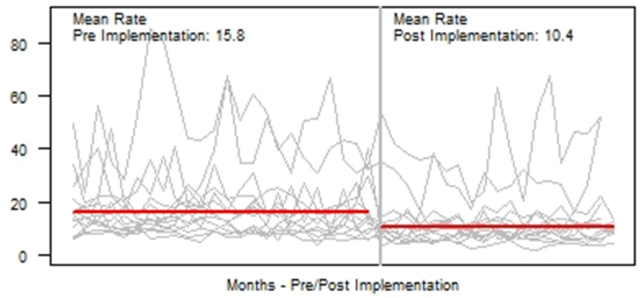
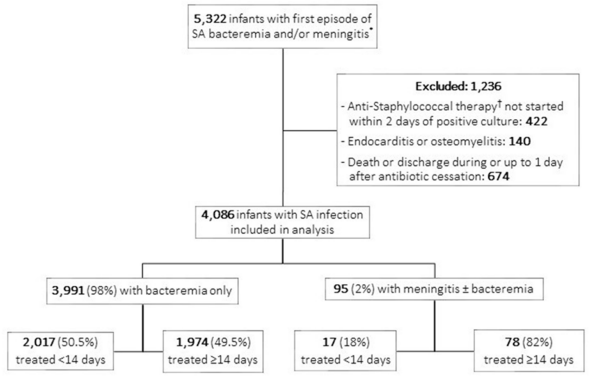


Figure 1.

Figure 1. Flow diagram of NICU infants with *Staphylococcus aureus* (SA) bacteremia and/or meningitis included in the study.



*Defined as at least one blood or cerebrospinal fluid (CSF) culture growing only *Staphylococcus aureus* at any point during NICU stay.

†Anti-Staphylococcal therapy broadly defined as MRSA-active agents (vancomycin, linezolid, clindamycin or trimethoprim-sulfamethoxazole) for infants with MRSA infection or MSSA-active agents (nafcillin, oxacillin, piperacillin-tazobactam, cloxicillin, dicloxicillin, ticarcillin-clavulanate, ampicillin-sulbactam, methicillin, or MRSA-active agents) for infants with MSSA infection.