Presentation Type:
Oral Presentation
Subject Category: Outbreaks
***Mycobacterium abscessus* Surgical Site Infections Due to Modular Cooler-Heater Units in Cardiac Surgery**
Ahmed Abdul Azim; Sharon Wright; Bryan Connors; Patrick Gordon and Preeti Mehrotra

Background: In the spring of 2020, we identified 3 patients with organ-space surgical site infections (SSIs) secondary to *Mycobacterium abscessus* (Table 1). All 3 patients underwent cardiac surgery in the same operating room (OR) during which the CardioQuip Modular Cooler-Heaters (MCHs) were used. We describe key aspects of our cluster investigation, which ultimately led to release of a national safety alert by the Food and Drug Administration (FDA). **Methods:** For environmental cultures, we obtained samples from 9 MCHs in circulation; 2 scrub sink samples; ice from the OR ice machine; water samples from sinks in the cardiovascular critical care unit, and water samples from floors above the cardiac ORs. All samples were sent for molecular genotyping. For pathway studies, an external environmental engineering team was consulted who conducted smoke pathway tests in 3 different ORs. The team also conducted a particle generator experiment, simulating the set-up of a cardiac bypass surgery case. To assess disinfection practices, we reviewed the manufacturer instructions for use (IFU) protocol of the MCHs and audited our own policies and procedures to ensure compliance. **Results:** For environmental cultures, molecular typing from 5 of 9 MCHs and all 3 patient SSI isolates returned positive for the identical hybrid species *M. abscessus bolleti*. All other samples with mycobacterial growth returned with different species. For pathway studies, the particle-generator experiment demonstrated particle movement from the MCH to the sterile field with facilities-guidelines–compliant OR ventilation and despite MCH manufacturing design. For disinfection practices, despite compliance with the stated IFU, and in consultation with experts, we implemented disinfection of associated Quick-connect devices (otherwise not stated in the IFU), and we also initiated a precleaning step prior to disinfection. **Conclusions:** Our investigation concluded that 3 patients developed SSIs with *Mycobacterium abscessus* that was aerosolized from the CardioQuip MCH. This finding led to the national FDA safety report alerting providers to risks associated with the device and the need for continued vigilance around disinfection. In addition, we implemented other control measures including placement of MCHs outside all ORs; creation of a separate MCH fleet for non-OR use; and use of modified disinfection protocols. To date, no additional cases have been identified.

Table 1: Timeline of Cardiac Surgery Surgical Site Infections

	Surgery	Date of surgery	Date of SSI
Patient A	CABG	2/12/2020	4/22/2020
Patient B	CABG	3/20/2020	5/17/2020
Patient C	Aortic dissection repair	3/24/2020	5/9/2020

CABG: Coronary artery bypass graft; SSI: Surgical site infection

Funding: No
Disclosures: None
Antimicrobial Stewardship & Healthcare Epidemiology 2021;1(Suppl. S1):s25
doi:10.1017/ash.2021.45

Presentation Type:
Oral Presentation
Subject Category: Outbreaks
Outbreak of *Pseudomonas aeruginosa* Bacteremia Infections among Stem-Cell Transplant Patients Related to Change in Prophylaxis
Kerrie VerLee; Chau Nguyen; Russell Lampen; Jim Codman and Tunisia Peters

Background: *Pseudomonas aeruginosa* outbreaks can originate from various sources and can cause severe complications in posttransplant patients.

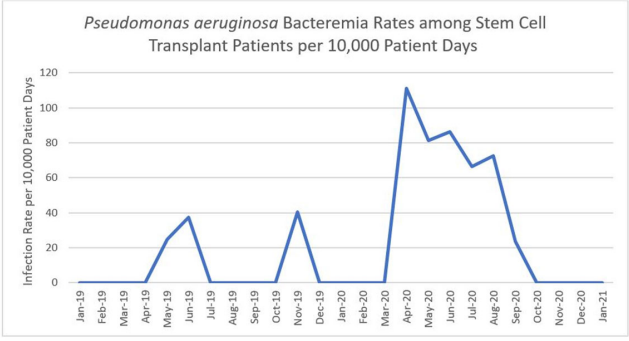

Figure 1. *Pseudomonas aeruginosa* bacteremia rates among stem cell transplant patients per 10,000 patient days.

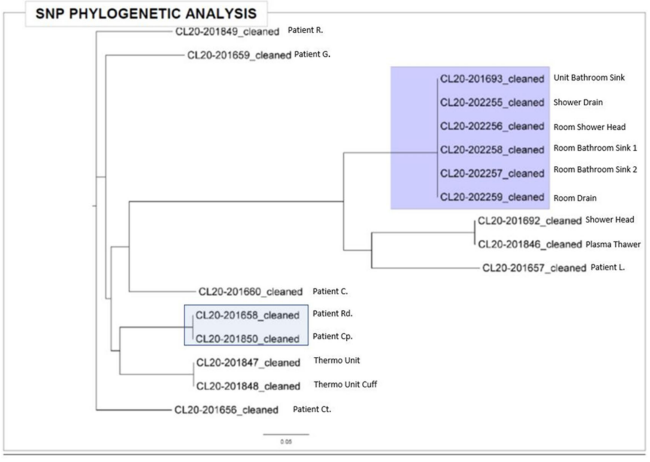

Figure 2. Whole-genome sequencing results, November 2020.

Antibiotic prophylaxis can decrease posttransplant infections; however, consideration must be given to *P. aeruginosa* coverage as we outline an outbreak among the stem-cell transplant (SCT) population. **Methods:** A multidisciplinary outbreak investigation was conducted to evaluate sources of contamination and changes in clinical processes. Positive blood cultures from SCT patients and environmental isolates were analyzed using whole-genome sequencing (WGS). Incidence density rates for *P. aeruginosa* blood cultures from January 2019 through October 2020 were calculated per 10,000 patient days and stratified by unit, specimen, and transplant type. Statistical analysis was calculated with significance at $p < 0.05$. **Results:** A cluster of 8 SCT patients was identified between May and September 2020. Moreover, 10 environmental samples were positive for *P. aeruginosa* including drains, water sources prior to the point-of-use (POU) filter and blood-bank thaw machines. Phylogenetic analysis revealed 1 cluster of 2 patients who shared the same room, 5 patients with unique *P. aeruginosa* isolates, and 2 separate clusters of environmental isolates with relatedness only to each other. Review of clinical processes showed a change from fluoroquinolone prophylaxis to cephalosporin in the spring of 2020. Also, 5 *P. aeruginosa* bacteremia infections occurred prior to June (11.78 cases per 10,000 patient days). During the period of cephalosporin use, 8 infections were identified (58.27 cases per 10,000 patient days) (P = .006). Following the restart of fluoroquinolone, zero infections have occurred to date, as of January 28, 2021. **Conclusions:** Discontinuation of fluoroquinolone prophylaxis was associated with *P. aeruginosa* bacteremia infections in SCT patients. Use of fluoroquinolone prophylaxis in SCT patients is protective from *P. aeruginosa* bacteremia infections. There have been no further infections in the following 3 months after the change back to the use of fluoroquinolone. Additionally, WGS showed that most patient

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

Funding: No
Disclosures: None
Antimicrobial Stewardship & Healthcare Epidemiology 2021;1(Suppl. S1):s25–s26
doi:10.1017/ash.2021.46

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.

Funding: No
Disclosures: None
Antimicrobial Stewardship & Healthcare Epidemiology 2021;1(Suppl. S1):s26
doi:10.1017/ash.2021.47

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.

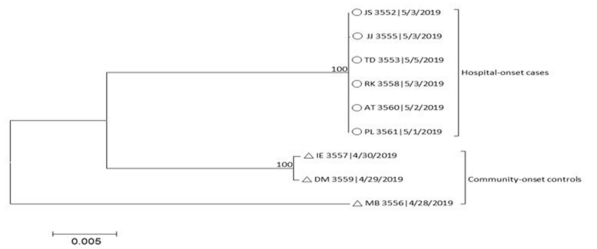

Figure 2: Epi Curve