Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Outbreaks
A single-center experience with microbiologic surveillance of LivaNova 3T heater-cooler devices (HCDs)
Scott Curry; Yosra Alkabab; Danny Nixon; Susan Dorman and Cassandra Salgado

Background: The global outbreak of *Mycobacterium chimaera* infections associated with HCDs resulted in new maintenance recommendations. Since 2018, HCDs have been disinfected according to instructions for use (IFU), including twice-monthly bleach disinfection and monitoring hydrogen peroxide (H_2O_2) to maintain a minimum daily concentration of 100 ppm. In February 2020, the IFU added the recommendation to perform microbiologic surveillance of HCD tank water to ensure effectiveness of disinfection to levels of <1 colony forming unit per milliliter (CFU/mL) of nontuberculous mycobacterium (NTM). We report our experience with this microbiologic surveillance as well as that of culturing the HCD environment to investigate modes of transmission. **Methods:** In 2022, we began culturing tank water in 10 HCDs for NTM. For a subset of 6 HCDs, quantitative NTM culturing of tank water before and after bleach disinfection was done. After initial results indicated widespread-contamination of HCDs with *M. chimaera*, we performed fill water cultures from 5 sinks in 4 HCD maintenance rooms. We also conducted 20 two-hour NTM settle-plate cultures of a cardiac operating room (OR) at different sites both inside (n = 7) and outside (n = 3) the OR: 10 with the HCD (located outside the OR) turned off (controls) and 10 with HCD turned on (exposure). A paired *t* test was used to evaluate differences in mean recovery of NTM in tank water samples. **Results:** Cultures from 7 (70%) of 10 HCDs were positive, with a mean of 13.6 CFU/mL *M. chimaera* (Table 1). There was no significant difference between the 10 pairs of pre- and postdisinfection NTM cultures done according to the IFU from 6 HCDs: mean predisinfection cultures (15.5 CFU/mL) versus mean postdisinfection cultures (12 CFU/mL) ($P = .90$) (Table 2). For fill water, 1 of 7 sink samples in 1 of 4 rooms was positive for *M. chimaera* (<1 CFU/mL) from a specimen from a fresh 0.2-µm filter that had been stored in the fill-sink splash zone. OR settle-plate cultures showed 0 (0%) of 10 control sites and 1 (10 %) of 10 exposure sites inside the OR positive for NTM, with a single CFU of *M. avium–intracellulare* complex. **Conclusions:** Our data cannot clearly refute either of 2 possible scenarios for HCD contamination: cross contamination during device maintenance versus at the point of manufacture. Despite the IFU guidance or disinfection being implemented, disinfection procedures failed to suppress NTM contamination, and tank water within most HCDs was contaminated with *M. chimaera* regardless of age or whether it was deep cleaned or upgraded with an aerosol containment device.

Table 1: Summary of all non-tuberculous mycobacterium cultures performed on heater-cooler devices (HCDs) at the Medical University of South Carolina from April to November 2022. All organisms recovered in HCD cultures were identified as *M. chimaera*.

Heater cooler device	Manufacture Date	Deep-cleaned by manufacturer / Aerosol containment upgrade (date completed)	NTM-positive samples +/total (%)	Mean CFU/ml	Notes
A	Oct 2010	Yes / Yes (2019-01-30)	0/1 (0%)	0	2
B	Dec 2012	Yes / Yes (2019-06-12)	4/5 (80%)	16	
C	Aug 2013	Yes / Yes (2020-03-12)	4/4 (100%)	19	
D	2019	N/A	1/1 (100%)	14	2
E	2018-11-15	N/A	3/4 (75%)	30	
F	2019-09-12	N/A	0/1 (0%)	0	2
G	2021-07-09	N/A	7/7 (100%)	25	
H	2021-07-12	N/A	4/4 (100%)	3	
I	2021-07-13	N/A	6/7 (86%)	2	
J	2022-06-02	N/A	0/2 (0%)	0	3

1 Four units were not cultured and are not shown on the table
2 Non-IFU samples only from standby / broken units
3 Sampled before placed into service on the first occasion
HCD; Heater cooler Device, CFU; colony forming unit

Table 2. Results of quantitative non-tuberculous mycobacterium (NTM) cultures performed per HCD IFU from 450 mL tank water before and after bleach disinfection procedures from seven HCDs sampled on 10 dates. Of note, all recovered organisms were identified as *M. chimaera*.

Heater cooler device	Device age (years) at sampling	Sample date	Pre-disinfection NTM-positive (CFU/ml)	Post-disinfection NTM-positive (CFU/ml)
H	0.9	2022-05-23	7	0.5
B	9.5	2022-05-24	20	60
G	0.9	2022-05-25	3	34
C	8.8	2022-05-25	36	36
I	0.9	2022-05-25	4	4
E	3.6	2022-06-06	18	3
I	0.9	2022-06-08	2	1
C	8.9	2022-06-20	4	1
B	9.6	2022-06-21	1	1
G	1.0	2022-06-21	60	5

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s91
doi:10.1017/ash.2023.356

Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Outbreaks
Aeromonas nosocomial cluster: Investigation review of possible modes of transmission
Anjali Bisht; Hannah Gray; JR Caldera; Shangxin Yang and Dan Uslan

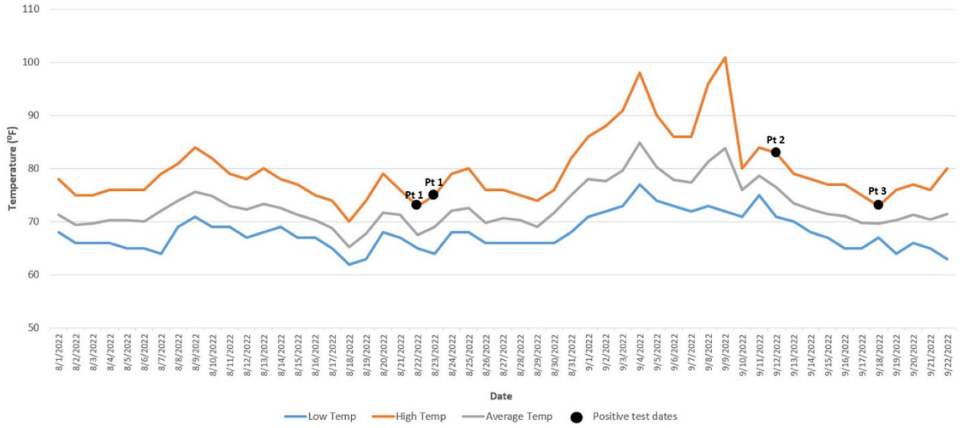
Background: *Aeromonas* is a gram-negative rod known to be present in water, sewage and soil which may cause infections especially in immunocompromised hosts. Cases of *Aeromonas* gastroenteritis have been associated with warmer weather. In total, 3 patients with extensively drug resistant (XDR) Aeromonas were identified at our facility between August and September 2022 on 2 intensive care units (ICUs). Our infection prevention, microbiology, and facility teams investigated these cases to determine whether a common source could be the mode of transmission. **Methods:** To first determine whether patients' *Aeromonas* specimens were related, whole-genome sequencing (WGS) of the clinical isolates from 3 patients was performed using the Illumina DNA Prep Kit and Illumina MiSeq. Sequencing analysis was performed using CLC Genomics Workbench for de novo assembly, single-nucleotide polymorphisms (SNP) calling, and tree generation, Geneious Prime for reference-based assembly, annotation, and quality assessment, KmerFinder for reference identification, and the Comprehensive Antibiotic Resistance Database for resistance gene detection via protein homology. Chart review revealed that patients occupied multiple rooms between 2 ICUs (Fig. 1). Because water is a known source of *Aeromonas*, facility records were reviewed for water intrusion events. This analysis identified several cases in the affected patient and surrounding rooms. Sinks and faucets from 10 rooms were swabbed followed by direct plating on blood, MacConkey agar, and *Aeromonas*-selective cefsulodin-Irgasan-novobiocin (CIN) agar plates. Lastly, the city temperatures before and after positive cases were reviewed to identify whether any correlation could be shown between temperature and timing of infection. **Results:** WGS analysis revealed that the 3 *Aeromonas* isolates (all identified as *A. hydrophila*) were not directly related (minimum distance, 934 SNPs) and harbored between 4 and 19 unique antimicrobial resistance genes, including co-occurring

Map of patient rooms, environmental sampling locations and results

Room No.	Source	Isolate	Colony Morphology	MALDI ID
4418	Sink	NFB 1	Small, round	S. maltophilia
		NFB 2	Large, spready	Pseudomonas aeruginosa
		NFB 3	Pink, spready	Pseudomonas veronii

Room No.	Source	Isolate	Colony Morphology	MALDI ID
8456	Faucet	NFB 1	Small, round	S. maltophilia

Temperature and timing of *Aeromonas* cultures



carbapenemases VIM-2 and KPC-3 in 1 isolate and OXA-232 in another. Of the 20 environmental samples, few gram-negative nonfermenting bacteria and no *Aeromonas* isolates were detected (Fig. 1). Elevated city did loosely proceed patient cases of *Aeromonas*, suggesting a possible role of higher temperature, which may have promoted the growth of *Aeromonas* during the periods of the 3 cases and thus may contribute to the nosocomial infections (Fig. 2). **Conclusions:** Although our investigation did not reveal a definitive cause for the *Aeromonas* cases, it did show the importance prompt identification and investigation can have on mitigating the spread of a cluster. Our facility has not identified any additional nosocomial cases. Monitoring water intrusion events and plans for remediation continue to be a priority.

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s91–s92
doi:10.1017/ash.2023.357

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

Polyclonal *Burkholderia cepacia* complex outbreak caused by contaminated chlorhexidine gluconate solution

Christel Valdez; Cybele Abad; Karl Evans Henson; Mark Carascal and Raul Destura

Background: *Burkholderia cepacia* complex is an opportunistic environmental pathogen that has been linked to nosocomial outbreaks. We describe an outbreak of bacteremia caused by *Burkholderia cenocepacia* from a contaminated chlorhexidine gluconate solution. **Methods:** The hospital infection control team carried out an outbreak investigation on February 21, 2021, when 3 adult hemodialysis patients developed *B. cenocepacia* bacteremia. Patient demographics and clinical profile were reviewed retrospectively. Potential sources of infection were identified,

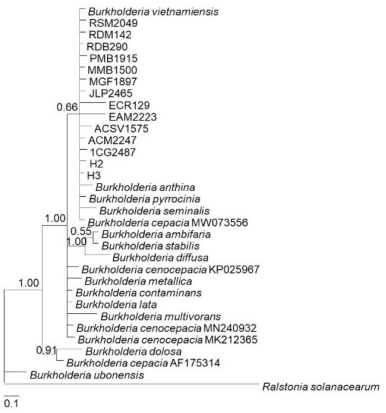


Figure 1. Bayesian inference tree of the sample sequences based on 563 nucleotides of the 16S rRNA gene and two majority consensus trees. The tree is rooted on the bacteria *Ralstonia solanacearum*. Numbers on nodes represent posterior probabilities.