

**Table 2:** Predictors of legionella infection in a multivariable regression model

	OR	Multivariable	
		95% CI	P-Value
Smoking (Current)	107.4	3.3 - 3459.94	<0.01**
Steroid Prior to Admission	28.5	2.45 - 331.42	<0.01**
Shower Documentation	21.5	1.29 - 365.51	0.03*
Number of showers prior to hyper-chlorination	1.05	0.11 - 9.78	0.04*
Days as In-patient	1.01	0.92 - 1.11	0.71

CI: Confidence Interval; OR: Odds Ratio; \*Significant at P = 0.05; \*\*Significant at P = 0.01

**Disclosures.** All authors: No reported disclosures.

**2452. Outbreak of Candidemia Associated With a Contaminated Intravenous (IV) Anesthetic in an Adult Intensive Care Unit (ICU) in San Luis Potosí, México.**

Carlos Portales-Castillo<sup>1</sup>; Javier Araujo-Meléndez, MD<sup>2</sup>; Pedro Torres-González, MD, MSc<sup>2</sup>; Mariana Mancilla-González, MD<sup>2</sup>; <sup>1</sup>Universidad Autónoma de San Luis Potosí, San Luis Potosí, Mexico; <sup>2</sup>Hospital Central Dr. Ignacio Morones Prieto, San Luis Potosí, San Luis Potosí, Mexico

**Session:** 257. HAI: Outbreaks

*Saturday, October 5, 2019: 12:15 PM*

**Background.** In June 2018, an unusual number of candidemia-associated sepsis cases were diagnosed in sedated patients hospitalized in the 12-bed adult ICU of a teaching hospital in Mexico. The pre-outbreak candidemia rate had been calculated at 0.66 cases/100 ICU admissions for the previous 3 years.

**Methods.** We performed a case-control and microbiological study designed to trace the source of the outbreak. Case definition included adult patients with systemic inflammatory response syndrome and *Candida* species isolated on BC (blood cultures). The rest of the patients in the ICU within the study period (6/12/2018–6/22/2018) were used as controls.

**Results.** A total of 5 cases and 19 controls were included in the study. Demographic and clinical characteristics were similar between groups, except for SOFA scores (Table 1). Differences in median SOFA scores between groups were statistically significant (7.5 in cases and 3 in controls (p = 0.02)). After review of common medications used between cases, propofol infusion use (5/5 in cases and 6/19 in controls) was calculated as the strongest risk factor for candidemia (OR 22.84 (p = 0.04)). In-use propofol infusions available at the time were stopped and sent for culture as were unopened vials stored in the pharmacy from the lot being used in the ICU. Intrinsic contamination with bacterial and fungal species related to the outbreak was identified (Table 3). Case fatality rate during the outbreak was 80% (4/5)

**Conclusion.** Lethal infections due to contaminated medications, including propofol, have been reported worldwide. Propofol is a potential source for infections given its lipophilic nature that promotes microbial growth. This likely remains an underrecognized problem that deserves awareness for early recognition. Epidemiological surveillance in our hospital prompted our case-control study and the subsequent implementation of effective control measures including rapid notification to hospital and national authorities (COFEPRIS), elimination of the identified contaminated lot, and increased promotion of both hand hygiene and adequate IV medication handling techniques among staff.

**Table 1.- Demographic Characteristics**

Variable	Cases (n=5)	Controls (n=19)	p value*
Age (Years)			
Median	37	32	1.0
IQR	22.5	27	
Males	3	13	N/A
Females	2	6	
SOFA score			
Median	7.5	3	0.02
IQR	8	6	
Total MVD			
Median	4	4	0.59
IQR	3	9	
Total CVCD			
Median	4	8	0.14
IQR	3	9	

\* Using Wilcoxon Signed Ranked Test

N/A = Not applicable. MVD = Mechanical Ventilation Days. CVCD: Central Venous Catheter Days

**Table 2.- Cases Characteristics**

Case	Sex	Age	Underlying Diagnosis	Date of Culture Result	Blood Culture Results	Outcome
1	F	33	Gunshot wound	06/12/2018	1- <i>Klebsiella oxytoca</i> , <i>Enterococcus faecalis</i> 2- <i>Candida utilis</i> , <i>Enterococcus faecalis</i>	Associated Death
2	M	19	Severe Traumatic Brain Injury	06/13/2018	1- <i>Candida utilis</i> 2- <i>Candida utilis</i>	Associated Death
3	M	52	Severe Traumatic Brain Injury	06/18/2018	1- <i>Candida utilis</i> 2- <i>Candida utilis</i>	Survived
4	F	45	Severe Pancreatitis	06/20/2018	1- No growth 2- <i>Candida utilis</i>	Associated Death
5	M	37	Pulmonary Abscess	06/20/2018	1- <i>Candida utilis</i> , <i>Enterococcus gallinarum</i> , <i>Rhizella aquatilis</i> 2- No growth	Associated Death

**Table 3.- Unopened vials cultures\***

Lot Number (Vials)	Culture Results
CV17127 (1)	<i>Candida utilis</i> , <i>E. gallinarum</i> , <i>R. aquatilis</i>
CV17127 (1)	<i>S. agalactiae</i> , <i>E. cloacae</i> , <i>K. oxytoca</i>

\* 18 more vials were cultured without growth

**Disclosures.** All authors: No reported disclosures.

**2453. Prolonged Local Epidemic of an XDR *P. aeruginosa* Subclone of High-Risk Clonal Complex 298**

Nathan B. Pincus, BS<sup>1</sup>; Kelly E. R. Bacht, MD PhD<sup>1</sup>; Egon A. Ozer, MD PhD<sup>1</sup>; Jonathan P. Allen, PhD<sup>1</sup>; Olivia N. Pura<sup>1</sup>; Francisco M. Marty, MD<sup>2</sup>; Alisha Pandit, BA<sup>3</sup>; John J. Mekalanos, PhD<sup>3</sup>; Alan R. Hauser, MD PhD<sup>1</sup>; <sup>1</sup>Northwestern University Feinberg School of Medicine, Chicago, Illinois; <sup>2</sup>Brigham and Women's Hospital, Boston, Massachusetts; <sup>3</sup>Harvard Medical School, Boston, Massachusetts

**Session:** 257. HAI: Outbreaks

*Saturday, October 5, 2019: 12:15 PM*

**Background.** Antimicrobial resistance (AMR) poses an increasing challenge to the treatment of the nosocomial pathogen *Pseudomonas aeruginosa*, with the majority of highly resistant infections caused by relatively few high-risk clones. We investigated the role of clonal complex 298 (CC298: ST298 and ST446) in multidrug-resistant (MDR) and extensively drug-resistant (XDR) infections at Northwestern Memorial Hospital (NMH).

**Methods.** We determined the AMR of 40 whole-genome sequenced CC298 isolates, including 30 from patients at NMH in Chicago (2000–2017), 7 from hospital environments (e.g., sinks) in Chicago (2017–2018), and 3 from patients at Brigham and Women's Hospital (BWH) in Boston (2015–2016). We used phylogenetics to assess the population structure of these isolates and 38 additional publicly available CC298 genomes. We interrogated the genomes of NMH CC298 isolates to uncover drivers of AMR.

**Results.** NMH CC298 isolates showed high rates of AMR, with 76.7% (23/30) MDR and 46.7% (14/30) XDR. Phylogenetic analysis revealed that 21/23 MDR (13/14 XDR) isolates from NMH formed a subclone of ST298, termed ST298\*, as of yet not seen elsewhere. A time-scaled phylogeny of ST298\* indicates a last common ancestor in 1980 (mean 1980.8, 95% HPD interval 1973.3–1987.4), with XDR ST298\* isolates seen between 2001 and 2017. Many ST298\* isolates, including all XDR isolates, harbored a large plasmid with an AMR class 1 integron. This plasmid is part of a family of large *Pseudomonas* genus plasmids. By comparing a plasmid-cured strain to its parent, we show that the plasmid imparts resistance to gentamicin and piperacillin-tazobactam. In the parental strain we detect T83I GyrA and S87L ParC substitutions known to cause fluoroquinolone resistance, showing that mutational resistance also contributes to the high AMR of ST298\*. Publicly available genomes and previous reports indicate that CC298 has caused infections worldwide with multiple instances of significant AMR.

**Conclusion.** The repeated isolation of XDR ST298\* *P. aeruginosa* at NMH over 16 years raises concern for the ability of this strain to persist in the healthcare environment. With this local epidemic and additional reports of MDR CC298 isolates around the world, we argue that CC298 should be considered a high-risk clone.

**Disclosures.** All authors: No reported disclosures.

**2454. A Cluster of Gram-Negative Bloodstream Infections in Connecticut Hemodialysis Patients Associated with Contaminated Wall Boxes and Priming Buckets**

Lauren Backman, RN, MHS<sup>1</sup>; Diane G. Dumigan, RN, BSN<sup>1</sup>; Adora Harizaj, MPH<sup>1</sup>; Marylee Oleksiw, RN, BSN<sup>1</sup>; Evelyn Carusillo, RN, MA<sup>1</sup>; Sue Malo, RN, MPH<sup>1</sup>; Acacia Ransom, RN<sup>1</sup>; Priti Patel, MD, MPH<sup>2</sup>; Duc Nguyen, MD<sup>2</sup>; Heather Moulton-Meissner, PhD<sup>2</sup>; John M. Boyce, MD<sup>3</sup>; <sup>1</sup>Connecticut Department of Public Health, Hartford, Connecticut; <sup>2</sup>Centers for Disease Control and Prevention, Atlanta, Georgia; <sup>3</sup>J.M. Boyce Consulting, LLC, Middletown, Connecticut

**Session:** 257. HAI: Outbreaks

*Saturday, October 5, 2019: 12:15 PM*

**Background.** Patients requiring maintenance hemodialysis (HD) are at increased risk of bloodstream infections. We investigated a cluster of infections due to unusual Gram-negative bacilli that affected patients undergoing HD at an outpatient unit with 19 stations (Clinic A).

**Methods.** A case was defined as a HD patient at Clinic A with >1 blood or urine culture positive for *Delftia acidovorans*, *Enterobacter absuriae*, or *Burkholderia cepacia* during the period February 1 – April 30, 2018. An investigation included review of patient records, facility policies, practice observation, environmental cultures, and

a 1:4 case-control study. Controls were patients without bloodstream infection (BSI) during the outbreak period.

**Results.** The cluster included 3 patients. Patient 1 had BSI due to *D. acidovorans* (2/08), *E. absuriae* (3/15) and *B. cepacia* (3/17). Patient 2 had BSI due to *D. acidovorans* (3/17 and 3/27) and *S. maltophilia* (4/5). Patient 3 had a urine culture positive for *D. acidovorans* and *S. maltophilia* (4/2). The case-control study showed that cases had been dialyzed more often than controls on the third shift ( $P < 0.0001$ ) and at station 2 ( $P < 0.0001$ ), where subsequently a wall box spent dialysate drain connection swab culture yielded *D. acidovorans*. *E. absuriae* was recovered from wall boxes and spent dialysate drain connection at two stations and from used prime buckets from two stations; one wall box culture grew *S. maltophilia*. *D. acidovorans* and *E. absuriae* patient isolates were not available for genomic analysis. Observations revealed that waste water was leaking onto the floor from several wall boxes, and that priming buckets were often rinsed with tap water after being disinfected with 1:100 bleach solution and not allowed to dry before reuse. Multiple deficiencies in hand hygiene and station disinfection were observed. No deficiencies in water treatment practices were identified. Multiple water cultures obtained in August were negative for the observed pathogens.

**Conclusion.** A cluster of unusual Gram-negative infections in outpatient HD patients was most likely due to exposures to contaminated wall boxes or priming buckets; poor hand hygiene and station disinfection can contribute to transmission to patients.

**Disclosures.** All authors: No reported disclosures.

#### 2455. Outbreak of carbapenemase-producing *Enterobacteriaceae* in cardiology units associated with contaminated water dispenser and sink drain in Korea

Jiwon Jung, MD<sup>1</sup>; Hye-Suk Choi, RN<sup>1</sup>; Jeong-Young Lee<sup>2</sup>; Min Jee Hong, RN<sup>1</sup>; Sun Hee Kwak, RN<sup>1</sup>; Heungsung Sung, PhD<sup>1</sup>; Mi-Na Kim, PhD<sup>1</sup>; Sung-Han Kim, MD<sup>1</sup>; <sup>1</sup>Asan Medical Center, Songpa-gu, Seoul-t'ukpyolsi, Republic of Korea; <sup>2</sup>Asam Medical Center, Songpa-gu, Seoul-t'ukpyolsi, Republic of Korea

**Session:** 257. HAI: Outbreaks

**Saturday, October 5, 2019: 12:15 PM**

**Background.** There is a growing concern about the importance of hospital water environment for the transmission of carbapenemase-producing *Enterobacteriaceae* (CPE). Herein, we report a large outbreak in cardiology units involving intensive care units (ICU) and wards at a tertiary care hospital.

**Methods.** During a CPE outbreak between July and December 2018, contact tracing and environmental sampling were performed. For outbreak control, we performed education to healthcare workers, hand hygiene enforcement, active surveillance test, preemptive isolation, chlorhexidine bathing for CPE positive patients, and deep terminal cleaning including UV and hydrogen peroxide non-touch disinfection. Patients with CPE were isolated at a single room with dedicated staffs, contact precaution was implemented, and when case patients were located in multi-patient room, we performed surveillance culture for exposed patients in the room.

**Results.** A total of 87 patients with CPE infection or colonization were identified at two cardiology ICUs and three cardiology wards. CPE from the first two index patients were identified from sputum culture suspecting pneumonia, and the remaining 85 patients were identified to harbor CPE through surveillance culture (exposed patients  $n = 22$ , active surveillance test  $n = 63$ ). Diverse organisms were identified; organisms with blaKPC ( $n = 13$ ), blaNDM-1 ( $n = 55$ ), blaVIM or blaIMP ( $n = 12$ ), blaOXA-48 ( $n = 3$ ), and co-producing organisms ( $n = 4$ ). We performed environmental culture; KPC-producing *Escherichia coli* was isolated from water dispenser in ICU and NDM-1 producing *Citrobacter freundii* and *Enterobacter cloacae* were isolated from sinks in the patient room. Outbreak ended after the removal of water dispenser and the replacement of sink drain with pouring bleach to the sink drain.

**Conclusion.** Water dispenser and sink drain were suspected for the possible reservoirs of CPE in this outbreak. Replacement of plumbing system and use of bleach for pouring to sink as well as the removal of water dispenser was needed to control outbreak. Investigation of water system is warranted for finding the source of CPE.

<b>Enterobacteriaceae (CPE) during outbreak</b>	144 ward	755 (13)
<b>Patient characteristics</b>	Acquisition from other units	14 (16)
Age, years, median (IQR)	CPE isolation within 2 days after admission	18 (21)
Male gender	Location of first positive CPE isolation	
Underlying disease or condition	CCU	15 (17)
Vascular heart disease	CSCU	18 (21)
Myocardial infarction or angina	133 ward	19 (22)
Heart failure	143 ward	16 (18)
Infective endocarditis	144 ward	9 (10)
Amyloma	Other ward	10 (11)
Acute aortic syndrome	Flora positive specimens	
Other underlying disease	Classical specimens (sputum)	2 (2)
End stage renal disease on hemodialysis	Surveillance culture specimens (stool or rectal swab)	81 (96)
ICU stay (> 2 days) before CPE isolation	Exposed patients	22 (25)
Underwent cardiac surgery before CPE isolation	Active surveillance test on admission	38 (44)
Days from admission to first positive CPE isolation, median (IQR)	Active surveillance test on discharge from ICU	5 (8)
	Weekly active surveillance test	20 (23)
	Infection	2 (2)
	Colonization	87 (96)
	Use of antibiotics before isolation of CPE within 1 month	49 (56)
	Carbapenem	6 (7)
	Piperacillin/tazobactam	10 (11)
	Cephalosporin	30 (34)
	Quinolone	10 (11)

Data are number (%) of patients, unless otherwise indicated.  
Abbreviation: IQR, interquartile range; ICU, intensive care unit; CCU, cardiac intensive care unit; CSCU, cardiac surgery intensive care unit; CV, cardiovascular; CS, cardiac surgery.

Table 2. Microbiologic results of 85 patients with carbapenemase-producing

<i>Enterobacteriaceae</i>	
Genotype and organism	Number (%)
<b>KPC producing organism</b>	<b>13 (15)</b>
<i>Escherichia coli</i>	9 (10)
<i>Klebsiella pneumoniae</i>	2 (2)
<i>E. coli</i> and <i>K. pneumoniae</i>	1 (1)
Xpert positive but not isolated on culture	1 (1)
<b>NDM-1 producing organism</b>	<b>55 (63)</b>
<i>Citrobacter freundii</i>	17 (20)
<i>Enterobacter cloacae</i>	5 (6)
<i>K. pneumoniae</i>	5 (6)
<i>E. coli</i>	5 (6)
Other <sup>a</sup>	10 (11)
Xpert positive but not isolated on culture	13 (15)
<b>Other MBL (VIM, IMP-1) producing organism</b>	<b>12 (14)</b>
<i>K. pneumoniae</i>	7 (8)
Other <sup>b</sup>	3 (3)
Xpert positive but not isolated on culture	2 (2)
<b>OXA-48 producing organism</b>	<b>3 (3)</b>
<i>E. coli</i> and <i>K. pneumoniae</i>	1 (1)
Xpert positive but not isolated on culture	2 (2)
<b>Co-producing (NDM-1 plus IMP, and NDM-1 plus VIM)</b>	<b>4 (5)</b>

Abbreviation: KPC, *Klebsiella pneumoniae* carbapenemase; NDM-1, New Delhi metallo-beta-lactamase 1; MBL, metallo-beta-lactamase; VIM, Verona integron-encoded metallo-beta-lactamase; IMP-1, imipenemase-1.

<sup>a</sup>*Klebsiella oxytoca* (n=1), *Klebsiella varicola* (n=1), *Citrobacter braakii* (n=1), *Enterobacter asburiae* (n=1), *E. kobei* (n=1), *E. cloacae* and *C. freundii* (n=1), *K. pneumoniae* and *E. coli* (n=3), *Raoultella ornithinolytica* and *C. freundii* (n=1)

<sup>b</sup>*R. ornithinolytica* (n=1), *K. oxytoca* (n=1), *C. freundii* (n=1)

Table 3. Results of environmental culture

Week	Location of environmental sampling	Number (%) of sampling of positive CPE results	Description of positive CPE results	
			Location	Organisms
33	ICU (Portable EKG machine, ultrasonography machine, computer keyboard and mouse of healthcare worker, sink U-trap and bowl, patient area, and water dispenser)	1/136 (0.7)	Water dispenser	KPC producing <i>Escherichia coli</i>
36	Water dispenser and sink around water dispenser at ward	0/19 (0)	-	-
37	Eight hand hygiene sinks (faucet, bowl, and U-trap) and toilet at ward	0/40 (0)	-	-
49	Ward (Computer keyboard, mouse, telephone, EKG machine, nursing cart, wheelchair, toilet, urinal, sink U-trap, bowl, and faucet, water dispenser, and patient area)	6/402 (1.5)	Toilet and urinal in the shared bathroom (n=3)	NDM-1 producing <i>Citrobacter freundii</i>
			Sink U-traps in the bathroom in patient room (n=3)	NDM-1 producing <i>Enterobacter cloacae</i> and <i>C. freundii</i>