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

	Multivariable		
	OR	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[1]; Javier Araujo-Meléndez, MD[2]; Pedro Torres-González, MD, MSc[2]; Mariana Mancilla-González, MD[2]; [1]Universidad Autónoma de San Luis Potosí, San Luis Potosi, San Luis Potosi, Mexico; [2]Hospital Central Dr. Ignacio Morones Prieto, San Luis Potosí, San Luis Potosi, Mexico

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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. Intrinsical 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 underecognized 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 IQR	 37 22.5	 32 27	1.0
Males Females	3 2	13 6	N/A
SOFA score Median IQR	 7.5 8	 3 6	0.02
Total MVD Median IQR	 4 3	 4 9	0.59
Total CVCD Median IQR	 4 3	 8 9	0.14

* 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.- *Klebsiella oxytoca, Enterococcus faecalis* 2.- *Candida utilis, Enterococcus faecalis*	Associated Death
2	M	19	Severe Traumatic Brain Injury	06/13/2018	1.- *Candida utilis* 2.- *Candida utilis*	Associated Death
3	M	52	Severe Traumatic Brain Injury	06/18/2018	1.- *Candida utilis* 2.- *Candida utilis*	Survived
4	F	45	Severe Pancreatitis	06/20/2018	1.- No growth 2.- *Candida utilis*	Associated Death
5	M	37	Pulmonary Abscess	06/20/2018	1.- *Candida utilis, Enterococcus gallinarum, Rahnella aquatilis* 2.- No growth	Associated Death

Table 3.- Unopened vials cultures*

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

* 18 more vials were cultured without growth

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

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

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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 subclade 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.

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

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

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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