are likely looking at the tip of the iceberg when analyzing infected cases. It is difficult to ascribe causality to any one of these exposures without concomitant surveillance cultures of environment and personnel. Retrospective WGS is of limited value in infection control. We now have third generation sequencing with the MinION device to do real time sequencing with which we also validated some of our samples.

Disclosures. Atul Kothari, MD, Ansun Biopharma (Consultant)

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870. *Mycobacterium chimaera* Outbreak: Infection Control and Clinical Experiences in Edmonton, Alberta

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Session: P-41. HAI: Outbreaks

Background. *Mycobacterium chimaera* is responsible for a global outbreak due to contaminated heater-cooler units (HCUs) used in cardiothoracic surgery and has been associated with high mortality. Optimal treatment is not known. The objectives of this study were to describe the Infection Control strategies utilized by the University of Alberta hospital and Mazankowski Heart Institute (MAZ) prior to availability of new HCUs, and outline the clinical course of locally acquired *M. chimaera* infection.

Methods. We reviewed interventions undertaken to mitigate the risk of *M. chimaera* infection. Any MAZ patient with *M. chimaera* isolated at an anatomic site with a history of cardiothoracic surgery from 2012-present were identified. Charts were reviewed for patient and infection characteristics.

Results. All manufacturer's instructions for HCU cleaning-disinfection were followed. The MAZ was compliant with CDC recommendations for directing HCU ventilation exhaust away from the surgical field and to the use of filtered water. *M. chimaera* was isolated in 3/8 local HCUs. After decontamination procedure, 1 HCU grew *M. chimaera* but cleared after a second attempt. Smoke studies demonstrated aerosolization of HCU exhaust in October 2016 therefore the laminar air curtains were manipulated for increased flow in October and November 2016. By June 2017, HCUs were retro-fitted and in late 2017 all pre-2014 Sorin HCUs were replaced.

10 patients have been diagnosed with *M. chimaera* infection post-cardiothoracic surgery performed at the MAZ. None occurred after manipulation of the laminar air curtain. Mean patient age at time of cardiothoracic surgery was 62.3 years and 6 were male. All had implantation of prosthetic material. The most common culture-positive sites were blood in 9/10, urine in 5/10 and prosthetic material or surgical site in 3/10. 6/10 have died due to infection and mean life expectancy of those deceased from first positive culture is 123 days. An additional survivor has been transitioned to comfort care and lost to follow-up.

Conclusion. *M. chimaera* post cardiothoracic surgery has been challenging from an infection control perspective but the risk appears to have been mitigated through manipulation of the laminar air curtain. Locally, *M. chimaera* has been associated with significant (60%) mortality.

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

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871. Assessment of the Wide-resistant *Pseudomonas aeruginosa* Outbreak at a University Hospital in Brazil: Have We Lost This War?!

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Session: P-41. HAI: Outbreaks

Background. Resistance profile analysis in *Pseudomonas aeruginosa* isolates is extremely important to prevent its transmission and to detect outbreaks. Broadly resistant strains (BR) have a high mortality rate in invasive infections. By analyzing the clinical and microbiological characteristics of these infections, one can define more effective actions in a nosocomial outbreak setting in a university hospital in Brazil.

Methods. From January to September 2019, 13 patients from the oncohematology services and intensive care unit (ICU) followed by the stewardship program of a public university hospital in Brazil had *Pseudomonas aeruginosa* (PsA) BR infection. Resistant multidrug (MDR) was defined as resistant to three or more antimicrobial classes. Extensively resistant (XDR) was sensitive to a maximum of two antimicrobial classes. Resistant pandrug (PDR) has been defined as resistant to all antimicrobial classes. Bacterial samples were identified by the automated VITEK*2 system (BioMérieux). The resistance pattern was defined based on the CLSI-M100 2019 criteria. Colistin sensitivity was assessed by the colistin drop test (Pasteran et al., 2018). The modified carbapenemic inactivation method (mCIM) was performed by disk diffusion.

Results. The 13 strains of PsA were isolated from 84.6% (11/13) blood cultures and 15.4% (2/13) tracheal aspirates, being 76.9% (10/13) from the oncohematology unit and 23.1% (3/13) of the ICU. The resistance profile was 23.1% (3/13) strains PsA MDR, 61.5% (8/13) PsA XDR and 15.4% (2/13) strains resistant to all classes (PsA PDR). 69.2% (9/13) of the strains were mCIM positive, in which the therapeutic option was ceftazidime/avibactam in combination with polymyxin. Regarding the sites of infection and use of devices, 53.8% (7/13) of the patients developed the infection after the use of central venous catheter and/or mechanical ventilation. The mortality rate was 76.9% (10/13).

Conclusion. The investigation of the outbreak of *Pseudomonas aeruginosa* highlights the importance of infectious surveillance of this pathogen with this resistance

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profile, to better understand the causalities, minimize its damage and reduce potential recurrence of new outbreaks.

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

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872. Burden of Influenza Outbreaks in Long-Term Care Facilities in Philadelphia, 2012-2020

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Session: P-41. HAI: Outbreaks

Background. In the United States, influenza and other acute respiratory viruses contribute to a high burden of disease in long-term care facility (LTCF) residents. We aim to characterize the disease patterns and inter-seasonal variation of influenza virus outbreaks in LTCFs and identify institutional, environmental, and public health interventions associated with differences in outbreak outcomes and characteristics.

Methods. We conducted a retrospective, longitudinal study of influenza outbreaks in LTCFs reported to the Philadelphia Department of Public Health (PDPH) over eight consecutive seasons (November 2012 through March 2020). Characteristics of individual outbreaks, facilities, and infection control measures were reported in the PDPH Influenza Outbreak database, while quality measures and other facility-level data were extracted from the CMS Nursing Home Compare (NHC) database. Cases of influenza-like illness (ILI) in residents and staff were reported.

Results. 131 influenza outbreaks were reported among 56 facilities, leading to 1196 cases of ILI, 227 influenza-related hospitalizations and 20 deaths. The median number of facility residents affected per outbreak was 4 (range, 0-52), and the resident attack rate was 3.0% (IQR, 1.6-7.4). Facility staff were affected in 56 (43%) of outbreaks. A greater number of facility beds was associated with sites reporting 3 or more outbreaks compared to those that did not (180 vs 133 beds, p=0.019). Public health measures were associated with lower total attack rates for surveillance (1.9% vs 4.3%, p=0.0015), education (1.9% vs 5.1%, p=0.0004), visitation restrictions (1.8% vs 3.1%, p=0.049), and vaccination policies of staff and/or residents (1.6% vs 2.7%, p=0.047). Smaller outbreaks were associated with the implementation of droplet precautions (3 vs 6, p=0.0071), antiviral treatment and prophylaxis (3 vs 6, p=0.024), and admission restrictions (4 vs 7, p=0.015).

Conclusion. Larger facility size was associated with an increased frequency of outbreaks. Public health measures may reduce the size and severity of influenza outbreaks in LTCFs. These results emphasize the importance of ensuring consistent utilization of recommended infection prevention strategies.

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

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873. Clusters of Postpartum Group A *Streptococcus* (GAS) Infections on a Labor and Delivery (L&D) Unit June-October 2019

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Session: P-41. HAI: Outbreaks

Background. GAS can cause severe postpartum infections and may be transmitted from colonized healthcare workers (HCWs).

Methods. Two cases of GAS bacteremia following vaginal delivery were identified on the L&D unit June-July 2019 (Cluster 1), prompting a carrier-disseminator investigation. Two additional cases were identified September-October 2019 (Cluster 2), followed by an additional 3 cases late October 2019, all of whom delivered on the same night (Cluster 3).

All patients and HCWs were evaluated for GAS risk factors and screened for colonization via throat, vaginal and perirectal cultures. During Clusters 1 and 2, only HCWs with patient contact were screened, but this was expanded to the entire unit in October after Cluster 3 was identified. All GAS colonized HCWs were provided chemoprophylaxis and rescreened 7-10 days after treatment to ensure eradication. GAS isolates from patients and HCWs were analyzed by whole genome sequencing (WGS).

Results. During Cluster 1 a total of 43 HCWs were screened and HCWA was colonized at all three sites. In Cluster 2, nine HCWs were screened; HCWA was negative at that time but HCWB was colonized in the throat only. Patient 3 was confirmed to be community acquired by pulsed-field gel electrophoresis, patient 4 was closely related by WGS. A new policy was instituted that required all HCWs present at delivery to wear gowns, gloves, masks, eye protection, and to undergo infection prevention education and practice review. Following Cluster 3, all HCWs on the unit were screened (681

total). HCWA was again positive at all 3 sites and two additional HCWs were found to be colonized with the outbreak strain on throat swab only. Isolates from patients 1, 2, 4, 5, 6, 7 and the 4 HCWs were identified as subtype emm 28 and all closely related by WGS (figure 1). A household contact of HCWA was colonized with the outbreak strain as well.
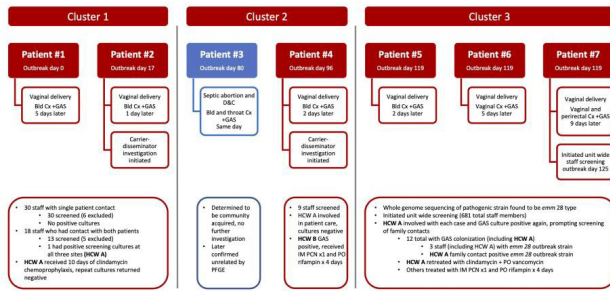
Figure 1

Figure 1

Conclusion. A carrier-disseminator investigation identified clusters of nosocomial postpartum GAS infections involving 6 patients, 4 HCWs and a HCW household contact that were highly related based on WGS. The outbreak strain of GAS was likely spread amongst HCWs via ping pong transmission on the unit. Transmission to patients was halted with implementation of strict infection prevention measures and mass screening and chemoprophylaxis of all colonized HCWs.

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874. Pseudo-outbreak of Adenovirus in Bronchoscopy Suite

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Session: P-41. HAI: Outbreaks

Background. Adenoviruses (Adv) are non-enveloped viruses that can survive for long periods on environmental surfaces. However, only 1 prior publication describes an adenovirus pseudo-outbreak associated with bronchoscopes. In 1/ 2020 infectious disease physicians noted a cluster of Adv PCR-positive bronchiolar lavage (BAL) samples, which prompted an outbreak investigation.

Methods. We reviewed medical charts, clinical microbiology, procedure logs, bronchoscope reprocessing logs, bronchoscope cleaning, and high-level disinfection (HLD) practices.

Results. On 1/28/20 an infectious diseases physician alerted infection prevention to a cluster of 5 lung transplant patients diagnosed with Adv positive BAL samples. Four out of the 5 patients had the bronchoscopy in the same bronchoscopy suite. We reviewed BAL results from all bronchoscopies performed in this suite from 11/1/19 to 1/24/20 and found a total of 10 patients with positive Adv PCR results. Eight out of the 10 patients had bronchoscopies with one of two bronchoscopes. Of all patients who had a bronchoscopy with the bronchoscope from 11/1/19 to 1/24/20 and had respiratory viral panel sent at that time, 6 of 11 (55%) who underwent procedure with Scope A and 4 of 24 (17%) who underwent procedure with Scope B had positive Adv PCR results. Sham BALs were performed on both bronchoscopes and testing for Adv was negative. However, on inspection by the manufacturer, one scope failed both wet and dry leak tests and had several physical defects. Following removal of both bronchoscopes from service we did not find any positive Adv samples from the bronchoscopy unit.

Conclusion. Previously, very few pseudo-outbreaks of Adv have been linked to bronchoscopes. We identified a pseudo-outbreak of Adv associated with 2 bronchoscopes in a hospital-based bronchoscopy suite that stopped once we removed the associated bronchoscopes from the procedural unit. Bronchoscopy-related pseudo-outbreaks occur despite standardized procedures for HLD. Bronchoscopy clinics, particularly those with a high volume of immunocompromised patients, should prospectively review BAL cultures to identify unusual pathogen trends. These trends may be a sign of damaged equipment that would otherwise go undetected.

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875. Pseudo-outbreak of *Clostridioides* (*Clostridium*) *difficile* amongst post-operative Oncology Patients

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Session: P-41. HAI: Outbreaks

Background. *Clostridioides difficile* infection rates are subject to infection prevention surveillance as a quality measure within the hospital setting. A large spike in *Clostridioides difficile* infections in post-operative patients, the majority of whom were

gastrointestinal surgery (GIS) patients, was noted within a six month period (June through November 2019) at our comprehensive cancer center. These patients had been housed in one of two inpatient units and there was appropriate concern that this represented a *C. difficile* outbreak possibly related some type of infection control breach.

Methods. In an effort to query case relatedness, whole genome sequencing was performed using Illumina MiSeq instrumentation and chemistry with Illumina Nextera XT library chemistry. Assembly and core genome multilocus sequence typing analysis were performed with Ridom SeqSphere+ software. Cases were classified as community or hospital acquired based on the National Healthcare Safety Network (NHSN) definitions.

Results. There were 23 samples submitted for possible whole genome sequencing (WGS). 5 samples were unable to be grown therefore WGS was not completed; 16 were found to be unrelated (51 or more allelic differences); 2 of the 18 isolates were found to be possibly related (7 to 50 allelic differences). There were no isolates found to be definitively related (zero to 6 allelic differences).

Conclusion. Given the overwhelming unrelatedness of the isolates via whole genome sequencing, this increase of *C. difficile* cases, identified by routine surveillance within two inpatient units, was determined to be representative of a pseudo-outbreak rather than an outbreak. This study has implications on public health reporting. National Healthcare Safety Network definitions are used to identify healthcare facility-onset *C. difficile* infection (CDI). The majority of cases in this study met the definition of healthcare facility-onset, and thus were reported as such, despite being genetically unrelated. This raises the concern that a significant percentage of *C. difficile* infections may be currently misclassified as hospital-associated and this may have negative, unfair consequences for hospitals, such as implications on reimbursement.

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877. Use of Statistical Process Control Charts for Early Detection of Healthcare Facility-Associated Nontuberculous Mycobacterial Outbreaks

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Session: P-41. HAI: Outbreaks

Background. Nontuberculous mycobacteria (NTM) are increasingly implicated in healthcare facility-associated (HCFA) outbreaks. However, systematic methods for NTM surveillance and outbreak detection are lacking and represent an emerging need. We examined how statistical process control (SPC) might perform in NTM outbreak detection.

Methods. SPC charts were optimized for surgical site infection surveillance and adapted to analyze 3 NTM outbreaks that occurred from 2013-2016 at a single hospital. The first 2 outbreaks occurred contemporaneously and consisted of pulmonary *Mycobacterium abscessus* complex (MABC) acquisition and cardiac surgery-associated extrapulmonary MABC infection, respectively. The third outbreak was a pseudo-outbreak of *Mycobacterium avium* complex (MAC) at a bronchoscopy suite.

We retrospectively analyzed monthly rates of unique patients who had: 1) positive respiratory cultures for MABC obtained on hospital day 3 or later; 2) positive non-respiratory cultures for MABC; and 3) positive bronchoalveolar lavage (BAL) cultures for MAC collected at the bronchoscopy suite. For each outbreak, we used these rates to construct a standardized moving average (MA) SPC chart with MA span of 3 months. Rolling baselines were estimated from average rates for months 7 through 12 prior to each monthly data point. SPC detection was indicated by the first data point above the upper control limit (UCL) of 3 standard deviations. Traditional surveillance detection was defined as the time of outbreak detection by routine infection control procedures.

Results. SPC detection occurred 5, 4, and 9 months prior to traditional surveillance outbreak detection for the three outbreaks, respectively (Figures 1 and 2). Prospective NTM surveillance using the MA chart potentially would have prevented an estimated 19 cases of pulmonary MABC, 9 cases of extrapulmonary MABC, and 80 cases of BAL MAC isolation (Table). No data points exceeded the UCL during 95 cumulative months of post-outbreak surveillance, suggesting low burden of false positive SPC signals.

Figure 1. Use of a moving average statistical process control (SPC) chart for early detection of hospital-associated outbreaks of pulmonary Mycobacterium abscessus complex (MABC) and cardiac surgery-associated extrapulmonary MABC infection. The pulmonary chart analyzes cases of hospital-onset respiratory isolation of MABC. The extrapulmonary chart analyzes cases of positive non-respiratory cultures for MABC. CL, center line; LCL, lower control limit; UCL, upper control limit.