Training on Infection Control And Prevention with Healthcare workers (Nurses)

Training on Infection Control And Prevention with Healthcare workers (Doctors)

Results. A total of 1562 HCW's participated in the training: 804 doctors, 445 nurses and 313 support staff in 26 training sessions. Majority of the participants (85%) did not receive any formal training earlier on infection control and often provided incorrect responses on basic IPC during interactive session. None of the hospitals had an IPC committee. After the training, we found a significant increase from 0% at baseline to 24% ($p < 0.001$) in hand hygiene including 43% ($p < 0.001$) and 45% ($p < 0.001$) in mask and gloves use respectively. All respondents (n=84) from the qualitative assessment, reported the training as highly effective which reinforce their learning in action in the hospitals. Participants from all three groups urged to arrange refresher training more frequently and in small groups to uphold the practices.

Conclusion. This pilot program demonstrated HCWs lack basic IPC principals and tailored IPC training sessions can significantly improve HCWs IPC practice. Formation of active IPC committee could enable arranging periodic refresher and in-service training updates for HCWs with the reallocation of resources to adopt regular IPC practices.

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

867. The Scope of a Weekly Infection Control Team Rounding in an Acute-care Teaching Hospital

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Session: P-40. HAI: Occupational Infection Prevention

Background. Activities of infection control and prevention are diverse and complicated. Regular and well-organized inspection of infection control is essential element of infection control program. The aim of study was to identify strong points and limitations of weekly infection control rounding (ICTR) in an acute care hospital.

Methods. We conducted weekly ICTR to improve the compliance of infection control in the real field at a 734-bed academic hospital in Republic of Korea. The monitoring team consists of five infection prevention practitioners and four infectious diseases physicians. Total 85 practices of infection control and prevention belonging to the respective category among 9 categories were observed. The result of the rounding are categorized well maintained, improvement is needed, long-term support such as space or manpower is needed, not applicable and could not observed. We investigated retrospectively the functional coverage of a weekly ICTR from January to December 2018.

Results. During the study period, weekly ICTR were performed total 47 times in 37 departments. ICTR visited median 7 times [interquartile range (IQR) 6-7 times] per department. When visiting a department, ICTR observed median 16 practices (IQR 12-22). During the monitoring period, we could observe 7511 practices in total. Of those results, Most of the practices (74.8%) were able to be monitored properly by ICTR, while some of the practices were not applicable (21.3%) or difficult to observe through ICTR (3.9%)(Table 1). The most common practices among the difficult-to-observe group belong to strategies to prevent catheter-related or surgical site infection and pneumonia (13%, 68/538), safety injection practices (8%, 65/758), linen and laundry management (7%, 33/496), followed by strategies to prevent occupationally-acquired infection (6%, 37/578).

Table 1.

Table 1. Results of infection control team rounding

Categories of practices	A (%)	B (%)	C (%)	D (%)	E (%)	Total
Hand hygiene	936 (93.6)	46 (4.6)	0	0	18 (1.8)	1000
Safety injection practice	664 (75.0)	28 (3.2)	1 (0.1)	127 (14.4)	65 (7.3)	885
Isolation	391 (57.5)	12 (1.8)	0 (0)	262 (38.5)	15 (2.2)	680
Strategies to prevent occupationally acquired infection	506 (80.6)	35 (5.6)	0	0	37 (5.9)	628
Practice to prevent catheter-related (central, urine catheter) or surgical site infections and pneumonia	451 (48.6)	19 (2.0)	0 (0)	390 (42.0)	68 (7.3)	928
Decontamination, disinfection, and sterilization	1349 (69.6)	128 (6.6)	12 (0.6)	388 (20.0)	61 (3.1)	1938
Linen and laundry	451 (78.7)	33 (5.8)	6 (1.0)	77 (13.4)	6 (1.0)	573
Environmental prevention of infection	403 (68.1)	24 (4.1)	0	142 (24.0)	23 (3.9)	592
Maintain negative/positive pressure	57 (25.0)	6 (2.6)	0	165 (72.4)	0	228
Total	5208 (69.9)	331 (4.4)	19 (0.3)	1601 (21.5)	293 (3.9)	7452

A: "well maintained", B: "improvement is needed", C: "long-term support such as space or manpower is needed", D: "not applicable" and E: "could not be observed."

Conclusion. ICTR has strength in regular visits to each department. However, additional observation is necessary, especially for prevention of cathether-related infection and surgical site infection.

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

868. Investigations of Healthcare-Associated *Elizabethkingia* Infections – United States, 2013-2019

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Session: P-41. HAI: Outbreaks

Background. *Elizabethkingia* (EK) are non-motile gram-negative rods found in soil and water and are an emerging cause of healthcare-associated infections (HAIs). We describe Centers for Disease Control and Prevention (CDC) consultations for healthcare-associated EK infections and outbreaks.

Methods. CDC maintains records of consultations with state or local health departments related to HAI outbreaks and infection control breaches. We reviewed consultations involving EK species as the primary pathogen of concern January 1, 2013 to December 31, 2019 and summarized data on healthcare settings, infection types, laboratory analysis, and control measures.

Results. We identified 9 consultations among 8 states involving 73 patient infections. Long-term acute-care hospitals (LTACHs) accounted for 4 consultations and 32 (43%) infections, and skilled nursing facilities with ventilated patients (VSNFs) accounted for 2 consultations and 31 (42%) infections. Other settings included an acute care hospital, an assisted living facility, and an outpatient ear, nose, and throat clinic.

Culture sites included the respiratory tract (n=7 consultations), blood (n=4), and sinus tract (n=1), and *E. anophelis* was the most commonly identified species. Six consultations utilized whole genome sequencing (WGS); 4 identified closely related isolates from different patients and 2 also identified closely related environmental and patient isolates.

Mitigation measures included efforts to reduce EK in facility water systems, such as the development of water management plans, consulting water management specialists, flushing water outlets, and monitoring water quality, as well as efforts to minimize patient exposure such as cleaning of shower facilities and equipment, storage of respiratory therapy supplies away from water sources, and use of splash guards on sinks.

Conclusion. EK is an important emerging pathogen that causes HAI outbreaks, particularly among chronically ventilated patients. LTACHs and VSNFs accounted for the majority of EK consultations and patient infections. Robust water management plans and infection control practices to minimize patient exposure to contaminated water in these settings are important measures to reduce infection risk among vulnerable patients.

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

869. Outbreak of Vancomycin Resistant Enterococcus faecium (VREfm) in a Hematology Unit Identified Through Whole Genome Sequencing

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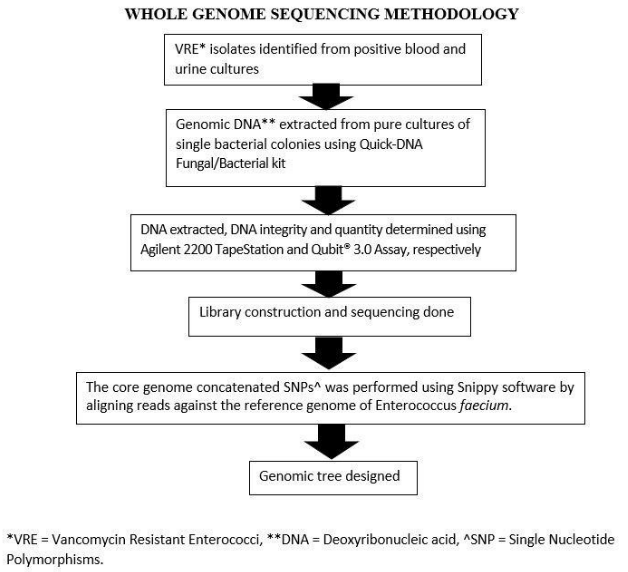
Session: P-41. HAI: Outbreaks

Background. VREfm is a major cause of Hospital Acquired Infection in the United States. We analyzed all the VREfm infections that occurred in our institution between 2018 and 2019 using Whole Genome Sequencing (WGS) to understand epidemiological relationship between previously unidentified clusters. In this study we describe a cluster in our hematology oncology unit.

Methods. A total of 109 discrete VREfm isolates from 66 patients were analyzed. VREfm isolates used in this study were identified from positive blood and urine cultures. Genomic deoxyribonucleic acid (DNA) was extracted from pure cultures. The purity and integrity of extracted DNA were determined using appropriate assays. Library construction and sequencing were conducted and Multi Locust Sequence Typing (MLST) obtained (image 1). Phylogenomic tree was plotted using the Interactive Tree of Life (image 2).

Image 1 - methods



WHOLE GENOME SEQUENCING METHODOLOGY

VRE* isolates identified from positive blood and urine cultures

Genomic DNA** extracted from pure cultures of single bacterial colonies using Quick-DNA Fungal/Bacterial kit

DNA extracted, DNA integrity and quantity determined using Agilent 2200 TapeStation and Qubit® 3.0 Assay, respectively

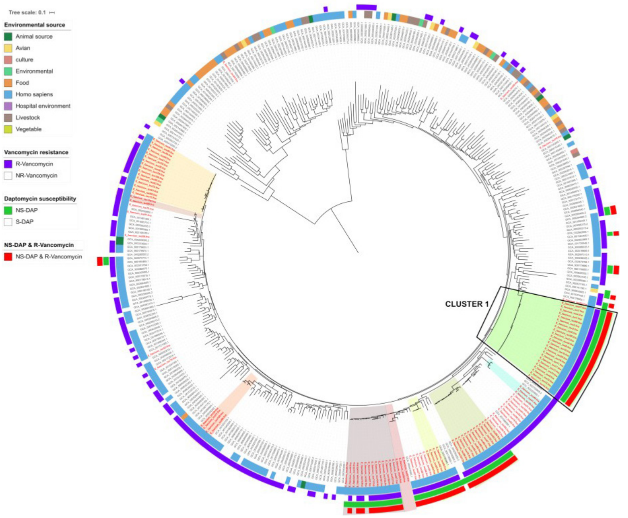
Library construction and sequencing done

The core genome concatenated SNPs^ was performed using Snippy software by aligning reads against the reference genome of Enterococcus *faecium*.

Genomic tree designed

*VRE = Vancomycin Resistant Enterococci, **DNA = Deoxyribonucleic acid, ^SNP = Single Nucleotide Polymorphisms.

Image 2 - Tree of Life



Results. Total of 7 clusters were identified. Here we describe one cluster (image 3) with the highest genetic similarity which showed maximum difference of 5 Single Nucleotide Polymorphisms (zero between patient 1 and 2, image 4). The cluster is composed of 24 clinical strains of VREfm from 6 patients, over a 9 month time period (Image 5). All patients had hematologic malignancies; 4/6 patients had received recent chemotherapy and 5/6 patients were neutropenic. 4 patients were admitted in a single unit (labelled E7), 1 patient was on a sister unit (labelled F7); and 1 patient was in the cancer infusion center. All patients had central venous access placed by radiology at the time of diagnosis of infection and had visited our outpatient infusion center multiple times during this time frame.

Image 3 - Close look at cluster 1

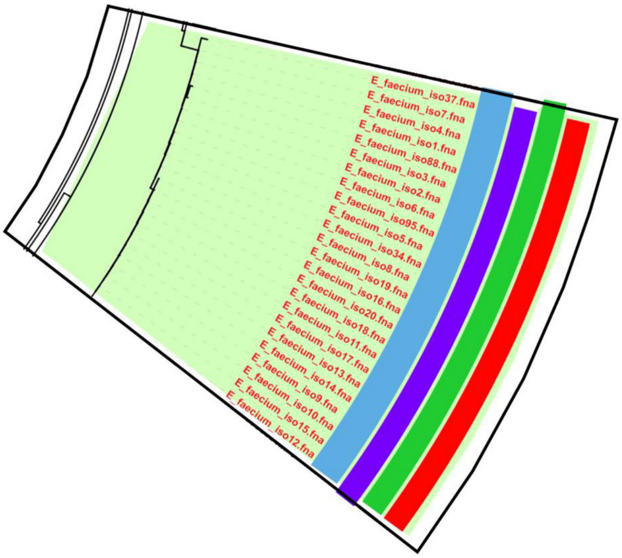


Image 4 - Dendrogram of 106 isolates performed with coreSNP(Single Nucleotide Polymorphisms) pairwise distances. • Dendogram shows different patients (same color for isolates that belong to the same patient) and the patient numbers. • Besides the patient number, the number of largest number SNPS that separate those isolates is shown. • Branches represent the number of coreSNPs that differ strains from that branch. As you see isolates from cluster 1 differ in a maximum of 5 SNPs but isolates of patient 1 and patient 2 differ in 0 SNPs between them. Cluster 1 is represented by a green square.

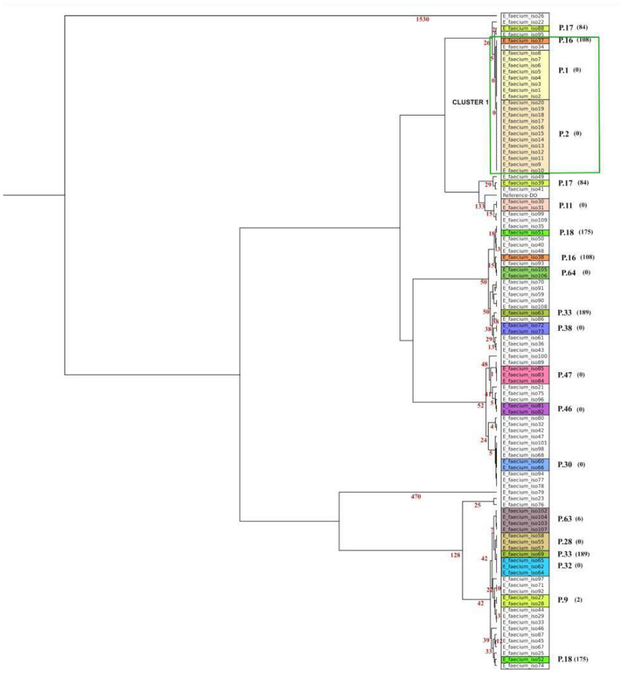
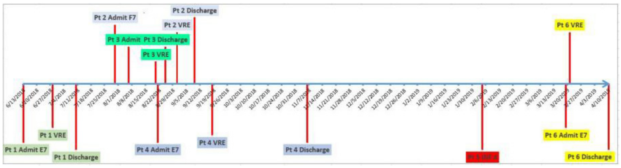


Image 5 - Time period of infections



Conclusion. The prolonged period in our cluster argues in favor of an environmental niche in the hospital unit. We are unable to elucidate pattern of transmission in a cluster of infections without knowing patient colonization of VREfm; because we 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)

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

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

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

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

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