2. Leong KWC, et al. Emergence of vancomycin-resistant *Enterococcus faecium* at an Australian Hospital: a whole genome sequencing analysis. *Sci Rep.* 2018:8(1):6274.

3. de Been M, et al. Core genome multilocus sequence typing scheme for high-resolution typing of *Enterococcus faecium*. J Clin Microbiol. 2015:53(12):3788–97.

Disclosures. All authors: No reported disclosures.

1256. New Acquisitions of ET-12 *Burkholderia cenocepacia* in Adults With Cystic Fibrosis: Role of Whole Genome Sequencing in Outbreak Investigation

Fibrosis: Kole of Whole Verbine Sequencing in Outbreat Investigation Ana C. Blanchard, MDCM, FRCPC¹; Manal Tadros, MBBS, MSc. PhD²; Lin Tang, ICP³; Matthew Muller, MD, FRCPC, PhD⁴; Theodore Spilker, BSc⁵; Valerie Waters, MD, MSc, FRCPC¹; John Lipuma, MD⁶ and Elizabeth Tullis, MD, FRCPC⁷; ¹Pediatric Infectious Diseases, The Hospital for Sick Children, Toronto, ON, Canada, ²Laboratory Medicine, St Michael's Hospital, Toronto, ON, Canada, ³Infection Control, St Michael's Hospital, Toronto, ON, Canada, ⁴Infectious Diseases, St Michael's Hospital, Toronto, ON, Canada, ⁵Department of Pediatrics and Communicable Diseases, University of Michigan, Ann Arbor, Michigan, ⁶University of Michigan, Ann Arbor, Michigan, ⁷Respiratory Medicine, St Michael's Hospital, Toronto, ON, Canada

Session: 139. Healthcare Epidemiology: Outbreaks Friday, October 5, 2018: 12:30 PM

Background. Transmission of *Burkholderia cenocepacia* ET-12 strain (ET-12Bc) can cause epidemics in the cystic fibrosis (CF) population. The Toronto Adult CF center currently follows 500 patients; 20% have infection with *B. cepacia* complex (BCC), including 48 patients infected with ET-12Bc. The center adheres to the 2013 infection prevention and control guidelines and patients are also segregated by clinics. Despite this, there have been 11 new acquisitions of ET-12Bc since 2008. The objective of this study was to describe the investigation of an ET-12Bc outbreak in CF patients, using whole-genome sequencing (WGS).

Methods. Investigations included multilocus sequence typing (MLST) and WGS of 34 isolates (11 new ET-12Bc acquisitions, 18 isolates of known ET-12Bc patients (including all patients with hospital admissions that overlapped with new acquisitions), four isolates from CF patients in the USA and the J2315 reference strain). Each of the seven MLST alleles from ET12Bc strain J2315 was downloaded from PubMLST and used to "Blast" each of the 16 WGS databases. WGS was done using 150 bp paired-end runs on an Illumina HiSeq4000. Single nucleotide polymorphisms (SNPs) between the newly sequenced strains and J2315 were profiled.

Results. Ten patients had a hospital admission within the 2 months preceding their first ET-12Bc positive sputum culture, except for one in whom ET-12Bc was detected 12 months following hospital admission. In all isolates, the seven alleles (*atpD*, *gltB*, *gyrB*, *recA*, *lepA*, *phaC* and *trpB*) matched 100% to sequence type 28 and clonal complex 31, and were identical to J2315. WGS SNP analysis confirmed that transmission occurred from known cases on the unit in 10/11 (90.9%) patients. To date, 8/11 patients with new acquisitions have died (median survival of 95 days).

Conclusion. Our investigations found epidemiological evidence suggestive of ET-12Bc transmission on the CF unit, which was confirmed by MLST and WGS SNP analysis. Compared with MLST, WGS SNP analysis had better discriminatory power and was well correlated with the identified epidemiological links between patients. Recognition of ET-12Bc transmission with associated high mortality rates has led to a change in our hospital policy. ET-12Bc positive patients will no longer be cared for on the same unit as ET-12Bc negative patients with CF.

Disclosures. All authors: No reported disclosures.

1257. Assessing Risk Factors for an Outbreak of *Burkholderia cenocepacia* in Noncystic Fibrosis (CF) Patients

Alexandra Hill-Ricciuti, MPH¹; William Greendyke, MD^{2,3}; Matthew Oberhardt, PhD³; Fann Wu, PhD⁵; Daniel Green, MD⁵; Susan Whittier, PhD⁵; Elaine Larson, RN PhD⁶; Lisa Saiman, MD, MPH^{1,2} and E. Yoko Furuya, MD, MS^{7,8}; Prediatrics, Columbia University Medical Center, New York, New York, ²Infection Prevention and Control, NewYork-Presbyterian Hospital, New York, New York, ³Department of Medicine, Columbia University Medical Center, New York, New York, ⁴Value Institute, NewYork-Presbyterian Hospital, New York, New York, ⁵Pathology, Columbia University Medical Center, New York, New York, ⁶School of Nursing, Columbia University, New York, New York, ⁷Medicine, Columbia University Medical Center, New York, New York

Session: 139. Healthcare Epidemiology: Outbreaks Friday, October 5, 2018: 12:30 PM

Friday, October 5, 2018: 12:50 FM

Background. Burkholderia spp. have been associated with outbreaks of healthcare-associated infections in non-CF patients, mostly attributable to point sources of contaminated solutions or medications. Fewer non-point source outbreaks have been described.

Methods. We conducted a matched case:control (1:3) study to assess risk factors for *B. cenocepacia* during an outbreak that occurred in 2017 in a 738-bed university-affiliated hospital involving patients hospitalized on several ICUs and non-ICUs. Clinical isolates identified as *B. cepacia* complex were speciated using sequencing of the *recA* allele and genotyped by pulsed field gel electrophoresis (PFGE). Case subjects were patients with a positive culture for the *B. cenocepacia* outbreak strain (PFGE pattern 17-A, *recA* 365) from June 1–December 31, 2017. Control subjects had negative respiratory cultures for *Burkholderia* spp. within 10 days of respective cases'. Potential risk factors including procedures, devices, and medications (previously linked to point source outbreaks) were examined. A 5-day exposure window was studied for procedures and devices as this was the shortest interval noted between a case subject's negative and first positive culture. Exact conditional logistic regression was used to analyze risk factors; Mann–Whitney U and Fisher's exact tests were used to compare demographic and clinic characteristics of case and control subjects.

Results. Seventeen cases (all with positive respiratory tract cultures) and 41 unitmatched controls were studied. Case and control subjects had similar demographic characteristics, illness severity, and comorbidities. No point source was identified. Only exposure to invasive mechanical ventilation was associated with case status (OR: 10.5, $[CI_{95}, 1.9, \infty)$, P = 0.0083). Cases had longer hospital lengths of stay (52 vs. 33 days, P = 0.02) than controls, but similar in-hospital mortality (24% vs.12%, P = 0.43).

Conclusion. These findings suggest that suboptimal infection prevention and control practices related to respiratory interventions, including cleaning and disinfection of ventilators, may have contributed to the outbreak. Reinforcement of best practices helped reduce transmission of the outbreak clone.

Disclosures. All authors: No reported disclosures.

1258. The Eyes Have It: Investigating a Cluster of Non-lactose Fermenting Gram-Negative Bacilli From Donor Corneal Rim Tissue

Christopher Olson, BS, MLT(ASCP)M, CIC¹; Kathleen Schomer, RN, BSN, CIC¹; Iarissa Pisney, MD² and Michelle Barron, MD³; ¹Infection Prevention and Control, University of Colorado Hospital, Aurora, Colorado, ²Medicine, Infectious Disease, University of Colorado School of Medicine, Aurora, Colorado, ³Internal Medicine/ Infectious Diseases, University of Colorado Denver, Aurora, Colorado

Session: 139. Healthcare Epidemiology: Outbreaks

Friday, October 5, 2018: 12:30 PM

Background. Following corneal transplant, donor corneal rim tissue are sometimes cultured to help predict the risk of post-keratoplasty endophthalmitis. In July 2016, the Infection Control (IC) team was notified by the microbiology laboratory of three donor corneal rim cultures growing non-lactose fermenting (NLF) Gramnegative bacilli, which was unusual for this type of specimen. The IC team initiated an epidemiological outbreak investigation to determine the source of the NLF Gramnegative bacilli.

Methods. A 12-month retrospective review of donor corneal rim cultures was performed from July 2015 to July 2016, with continual prospective monitoring of donor corneal rim cultures. The protocols used to prepare corneal donor tissues were reviewed. The standard protocol included flooding the tissue with povidone iodine followed by rinsing with a sterile saline solution and then placement in a sterile container with Opitsol GS (a preservative solution with gentamycin and streptomycin). The sterile saline rinse that was normally used for processing had been on back order and had been replaced with an alternative brand from March 2016 to July 2016. Unopened bottles of the alternative brand of sterile saline fluid and Optisol GS were sent to an outside laboratory for bacterial culture and remaining product was temporarily quarantined.

Results. Microbiology review revealed seven donor corneal rim cultures positive for NLF Gram-negative bacilli from May to July 2016. Organisms isolated from the donor corneal rim tissue included *Achromobacter xylosoxidans* (4), *Burkholderia cepacia* (3), *Stenotrophomonas maltophilia* (2), and *Elizabethkingia meningoseptica* (1). Sterility cultures of Opitsol GS demonstrated no growth. Sterility cultures of the sterile saline rinse grew Gram-positive and -negative bacteria from all samples. A FDA MedWatch was submitted in July 2016, and on September 6, 2016 an FDA recall notice was published. The quarantined saline was permanently removed. No clinical infections associated with the positive donor corneal rim cultures were identified.

Conclusion. Microbiologists are the front line for IC surveillance. Close partnership between the IC team and the microbiology laboratory can help identify potential outbreaks by alerting them of the growth of atypical organisms or clusters. *Disclosures.* All authors: No reported disclosures.

1259. The Local Hospital Milieu and Healthcare-Associated VRE Acquisition

Margaret Zhou, MD¹; Jianhua Li, MD²; Hojjat Salmasian, MD, PhD³; Philip Zachariah, MD, MS⁴; Yu-Xiao Yang, MD⁵ and Daniel Freedberg, MD, MS⁶; ¹Department of Medicine, Columbia University Medical Center, New York, New York, ²Biomedical Informatics, New York Presbyterian Hospital, New York, New York, ³Data Science and Evaluation, Brigham and Women's Hospital, Boston, Massachusetts, ⁴Department of Pediatrics, Columbia University Medical Center, New York, New York, ⁵Division of Gastroenterology, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, ⁶Division of Digestive and Liver Diseases, Columbia University Medical Center, New York

Session: 139. Healthcare Epidemiology: Outbreaks

Friday, October 5, 2018: 12:30 PM

Background. The relationship between the local hospital environment and VRE acquisition is not fully understood. The objective of this study was to identify risk factors for healthcare-associated VRE acquisition related to the local hospital milieu.

Methods. This retrospective cohort study included patients admitted to six ICUs at an academic medical center from January 1, 2012 to December 31, 2016 with negative rectal VRE cultures on admission. VRE acquisition was defined as a positive subsequent surveillance swab performed at any time after the initial negative surveillance swab during the index hospitalization. VRE colonization pressure was defined to encapsulate the circulating VRE burden during the at-risk patient's ICU stay (patient-days of VRE exposure based on concurrently colonized patients on the unit, divided by time at risk). VRE importation pressure was defined to encapsulate the VRE burden at the time of ICU admission (patient-days of VRE exposure on the unit during the preceding 30 days, divided by total patient-days). Multivariable Cox proportional hazards modeling was used, with patients followed until VRE acquisition, death, or for up to 30 days.

Results. There were 161 patients who acquired VRE among 8,485 patients with negative VRE cultures upon admission, including 1,131 patients who had repeat VRE cultures during the index hospitalization. On univariate analysis, patients with VRE acquisition were more likely to have received vancomycin, have had a neighboring patient who received vancomycin, have high VRE importation pressure, or have high VRE colonization pressure. On multivariable analysis, among these factors only high VRE colonization pressure was an independent predictor of VRE acquisition (aHR 1.79, 95% CI 1.19-2.70).

Conclusion. VRE colonization pressure was the most important risk factor for healthcare-associated VRE acquisition in this ICU population, regardless of VRE importation pressure or local use of vancomycin. Interventions seeking to reduce healthcare-associated VRE acquisition may wish to focus on ways to minimize transmission of VRE between patients with known VRE and the local hospital environment. **Disclosures.** All authors: No reported disclosures.

1260. Decreasing Hospital Acquired Blood Stream Infections Through Self-Investigation by Hospital Wards

Pnina Shitrit, MD^{1,2}; Michal Chowers, MD³; Beatriz Gerber, MA RN¹ Hanni Lederman, MA RN¹ and Mira Maram, MD⁴; ¹Infection Control Unit, Meir Medical Center, Kfar Saba, Israel, ²Medicine, Sackler Medical School, Tel-Aviv University, Tel-Aviv, Israel, ³Medicine, Sackler Faculty of Medicine, Tel-Aviv University, Tel-Aviv, Israel, ⁴Medical Management, Meir medical center, Kfar Saba, Israel

Session: 139. Healthcare Epidemiology: Outbreaks

Friday, October 5, 2018: 12:30 PM

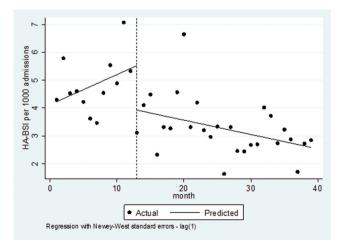
Background. Data on the incidence of hospital-wide acquired bloodstream infection (BSI) and the best ways to reduce it are lacking. Our aim was to increase hospital-wide awareness and decrease incidence of hospital-acquired (HA)-BSI through self-investigation.

Methods. Meir Medical Center is a 740-bed hospital. Beginning in January 2016, reports of HA-BSI events were sent daily to the wards with requests to investigate the source of infection, and preventability using a structured questionnaire. The infection control staff gave immediate feedback to the wards regarding their investigation. A summary of the results was sent to all wards and to hospital management quarterly. Interrupted time series analysis was used to compare the monthly rate of HA-BSI before and after the intervention. We estimated the number of cases prevented by the intervention by applying the HA-BSI rate in 2015 to the number of admissions in 2016–2017 and comparing the observed number of cases to the expected if the rate had not changed.

Results. In 2016, 64% of HA-BSI underwent investigation by the wards; this increased to 78% in 2017. As illustrated in the figure, before the intervention, the HA-BSI rate per 1,000 admissions increased by 0.11 per month (not significant P = 0.15). In the first month of the intervention, the HA-BSI rate decreased significantly by 0.43 (P = 0.04, 95% CI: -0.84 to -0.02). The HA-BSI rate continued to decrease (relative to the pre-intervention period) by 0.045 per month (P = 0.05, 95% CI: -0.09 to 0.00). During these 3 years, there was no significant change in the rate of community-acquired BSI (8.46, 8,88, 8,58, P for trend = 0.83) or in the rate of blood cultures drawn. During the intervention, the rate of HA-BSI decreased in both ICU units and in non-ICU wards. The number of HA-BSI caused by Enterobacteriaceae decreased from 170 in 2015 to 116 in 2017. S. aureus decreased from 51 to 30 and Candida from 11 to 0. The most common sources of BSI were urinary tract infection (31.4%) and central line associated BSI (16.4%). All-cause 30-day mortality for patients with HA-BSI was 30%. We estimated that in 2016-2017, 200 cases of HA-BSI and 60 deaths were prevented.

Conclusion. Increase awareness to HA BSI through self-investigation by the wards led to hospital-wide significant reduction in HA-BSI.

Figure 1.



Disclosures. M. Chowers, GSK: Grant Investigator, Research grant

1261. Utility of a Multiplex Molecular Gastrointestinal Panel in Rapid Identification and Control of a Norovirus Outbreak in a Pediatric Tertiary Care Center

<u>Jeannette L. Comeau</u>, MD, MSc^{1,2,3}; Allana M. Ivany, BScN, RN, CIC³; Terry Romeo, MLT⁴; Bridget S. Maxwell, BN, RN, CIC³; Natalie Nymark, BScN, RN, MN³; Belinda MacKinnon, BSc, MLT⁴; Erin Doon, MLT⁴ and Tim Mailman, MD^{1,2,5}; ¹Department of Pediatrics, Division of Infectious Diseases, IWK Health Centre, Halifax, NS, Canada, ²Dalhousie University, Halifax, NS, Canada, ³Infection Prevention and Control, IWK Health Centre, Halifax, NS, Canada, ⁴Microbiology Laboratory, IWK Health Centre, Halifax, NS, Canada, ⁵Department of Microbiology and Immunology, IWK Health Centre, Halifax, NS, Canada

Session: 139. Healthcare Epidemiology: Outbreaks

Friday, October 5, 2018: 12:30 PM

Background. Norovirus is one of the most common viral pathogens implicated in gastroenteritis outbreaks in community and healthcare settings. The virus' short incubation period and high attack rate allow its rapid spread through inpatient wards to patients (Patients), staff and visitors. Early identification and appropriate implementation of infection prevention and control measures is essential to interrupt transmission.

Methods. The IWK Health Centre is a 250-bed tertiary care Pediatric and Women's hospital serving the Maritime Provinces, Canada. We describe a norovirus outbreak in our Pediatric Medical Unit, a 24-bed, single room ward with individual bathrooms for patients and families. Hospital-acquired norovirus definition: Patients admitted \geq 48 hours with lab-confirmed norovirus AND \geq 1 of: (1) acute onset diarrhea (no noninfectious cause) or (2) $\geq\!\!2$ of: nausea, vomiting, abdominal pain, fever, or headache. In 2017 the FilmArray Gastrointestinal (GI) Panel was introduced in the Clinical Microbiology Laboratory as part of a prospective post-implementation study. Since then, stool samples sent for viral, bacterial, or parasitic testing are evaluated by PCR. The panel tests for 22 GI analytes, including five viruses, with a 2-hour turnaround time. Previously, in-house stool viral testing was limited to adeno- and rotavirus antigen. Patient characteristics were collected and analyzed for this study.

Results. Patients 1, 2, and 3 had new onset diarrhea and emesis; Pt 1 on day 0, and Patients 2 and 3 on day 1. Patient 3's parents (likely source) had had diarrhea and emesis on days 3 and 2, and used the ward kitchen. Two care-givers of Patient 2, and 1 medical resident developed diarrhea and emesis over days 0 to 2. The outbreak was declared over on day 7. Patients 1, 2, and 3 all tested positive for norovirus in stool on day 1. On days 2-3, six other patients with diarrhea tested norovirus negative. All symptomatic patients were immediately placed on contact precautions, room/ward cleaning frequency increased and proper hand hygiene was reinforced. Common areas (playroom/kitchen) were closed until the outbreak was over. All patients with loose stool were tested during the outbreak.

FilmArrayGI panel enabled same-day identification of norovirus in Conclusion. this single-ward outbreak and permitted real-time identification of the termination of the outbreak.

Disclosures. All authors: No reported disclosures.

1262. Investigation and Mitigation of a Multi-Species Outbreak of Invasive Fungal Infections on Two Oncology Wards

Kirk Huslage, MSPH, BSN, RN, CIC^{1,2}; Matthew Stiegel, Ph.D³; Erica Lobaugh-Jin, BSN, RN, CIC¹; Amy Hnat, BSN, RN¹; Nancy Striitholt, BSN, RN, CIC¹; Sarah S. Lewis, MD MPH^{1,2}; Arthur W. Baker, MD, MPH^{2,4}; Wayne R. Thomann, DrPH³ and Becky Smith, MD^{1,2}; ¹Infection Prevention and Hospital Epidemiology, Duke University Medical Center, Durham, North Carolina, ²Duke Center for Antimicrobial Stewardship and Infection Prevention, Durham, North Carolina, ³Occupational and Environmental Safety Office, Duke University Medical Center, Durham, North Carolina, ⁴Division of Infectious Diseases, Duke University School of Medicine, Durham, North Carolina

Session: 139. Healthcare Epidemiology: Outbreaks Friday, October 5, 2018: 12:30 PM

Background. We investigated an increase in hospital-acquired invasive fungal infections (HA-IFI) among patients admitted to adjacent hematopoietic stem cell transplant (HSCT) and hematologic malignancy (HM) wards in the setting of a large construction project adjacent to the hospital.

Methods. We defined cases of HA-IFI as HSCT or HM patients who met criteria for probable or proven IFI with suspected inpatient acquisition. We hypothesized that outside construction increased internal particle/spore counts despite preconstruction prevention efforts. The environmental investigation included an evaluation of storage/ distribution of supplies, air handler inspections, air particulate counts, and bioaerosol sampling of airborne fungal spores.

Results. From October 2017 to January 2018, 11 cases of probable/proven HA-IFI occurred (Figure 1). Infections caused by multiple pathogens (Figure 2) ranged from pneumonia and sinusitis to disseminated disease. Bioaerosol sampling and particulate counts were taken from unit corridors and rooms on both wards. Fungal species identified via bioaerosol sampling were primarily Penicillium and Cladosporium species, with rare Aspergillus identified. Geometric mean particulate counts of 1 µm aerodynamic size were reduced by 88% and 75% on the HM and HSCT wards, respectively (Figure 3). Interventions on these units occurred from January to February 2018 and included: limiting the frequency of outdoor air exchanges on air handler units, reinforcing seals around entrance doors, adjusting room pressurizations to be positive or neutral on HM ward (HSCT ward is already a positive pressure environment), eliminating cardboard associated with supplies, and requiring N95 respirators for HSCT patients when off unit. After implementing these environmental control measures, we have not identified additional cases of HA-IFI on these wards.