803. The Impact of Bundled Interventions to Decrease Transmission of Drug-Resistant *Pseudomonas aeruginosa* from Wastewater Drain Sites on a Hematologic Malignancy/Hematopoietic Stem Cell Transplant Unit

Laurie Fontana, D.O.1; Morgan Hakki, MD1; Richard Zhang, B.S. and B.A.1; William Messer, M.D., PhD1; Grace Walker-Stevenson, MPH Epidemiology Candidate 20211; Amy Laird, PhD1; Lynne Strasfeld, MSPH1; University of Minnesota, Minneapolis, Minnesota; 1Oregon Health and Science University, Portland, OR; 2University of Oregon, Corvallis, Oregon; 2Oregon Health and Science University-Portland State University; Portland, Oregon; 1Oregon Health & Science University, Portland, Oregon

Session: P-43. HAI: Outbreaks

**Background.** Wastewater drain (WWD) sites are an important reservoir for amplification, propagation and transmission of multidrug resistant organisms. We observed an increase in the incidence of carbapenem and fluoroquinolone non-susceptible (CP-NS and FQ-NS) *P. aeruginosa* bloodstream infections (BSI) among patients on our hematologic malignancies (HM) and hematopoietic cell transplant (HCT) unit. The incidence of CP NS/FQ NS *P. aeruginosa* BSI from 2012 through May 2021 is represented in Figure 1. We sought to determine the impact of low-cost, low-barrier interventions targeting WWD sites on the prevalence of patient and environmental *P. aeruginosa* colonization and incidence of BSI.

Figure 1. Incidence of *P. aeruginosa* BSI, 2012 through May 2021

**Results.** Characteristics of the pre- and post-intervention groups are presented in Table 1. Five of 27 (18.5%) and 1 of 26 (3.8%) patients in the pre- and post-intervention point prevalence survey, respectively, were confirmed to be colonized with *P. aeruginosa* (Figure 2), corresponding to a prevalence rate ratio of 0.21 (0.03,1.66). If the two indeterminate samples in the pre-intervention period were positive, the prevalence rate ratio would instead be 0.15 (0.02,1.12). The most frequent *P. aeruginosa* strains identified by WGS from the patients and environment were 111, 308 and 446. At least 87% of rooms were colonized with *P. aeruginosa* from at least one WWD site, from pre- and post-intervention periods (Table 2).

Table 1. Demographic and clinical characteristics of patients in each epoch. Results are given as percent (frequency) unless otherwise noted. Chi square test was used unless otherwise noted.

| Pre-Intervention Epoch | Post-Intervention Epoch | p-value |
|------------------------|-------------------------|---------|
| Male sex               |                         |         |
| Female                 | 48.1 (13)               | 63.5 (16) | 0.328 |
| Male                   | 51.9 (14)               | 36.5 (14) |         |
| Age, median (IQ*)      |                         |         |
| 63 (44,65)             | 60 (51,65)              | 0.605*  |
| Race                   |                         |         |
| Asian                  | 3.7 (1)                 | 3.8 (1)  |         |
| Other Pacific Islander | 3.7 (1)                 | 0.0 (0)  |         |
| White                  | 85.3 (23)               | 96.3 (23) |         |
| Declined to answer     | 7.4 (2)                 | 0.0 (0)  |         |
| Ethnicity              |                         |         |
| Hispanic               | 11.1 (3)                | 12.4 (4) | 1.000*  |
| Non-Hispanic           | 85.2 (23)               | 84.6 (22) |         |
| Declined to answer     | 3.7 (1)                 | 0.0 (0)  |         |
| Hematopoietic stem cell transplant (HCT) category | | |
| Allergic or CR-T cell transplant | 51.9 (14) | 46.2 (12) | 0.065* |
| Autologous transplant  | 22.2 (6)                | 38.1 (12) |         |
| Allogeneic or CR T-cell transplant | 27.1 (7) | 50.1 (13) |         |
| Central Venous Catheter (CVC) at time of death? | 96.3 (26) | 100 (26) | 1.000* |
| Hospital length of stay, days, median (IQR) | 22 (13,27) | 16.5 (7,28) | 0.493* |
| Time from admission to swab, days, median (IQR) | 8 (3,20) | 6.5 (4,15) | 0.953* |
| Unit hospital days prior to swab, median (IQR) | 19 (6,29) | 14 (3,18) | 0.587* |
| ICU admission during hospitalization in year prior to colonization in y? | 18.5 (5) | 19.2 (5) | 0.947 |
| Anti-Pseudomonas antitibiotics in 30 days? | 66.7 (18) | 65.4 (17) | 0.922 |
| Anti-Pseudomonas antitibiotics in 60 days? | 74.1 (20) | 73.1 (19) | 0.934 |

* Fisher's exact test was used.

Table 2. WWD site colonization, by phenotypic and WGS determination. Fisher’s exact test was used unless otherwise noted.

| Pre-Intervention Epoch, swabbed on 22 Jul 2019 | Post-Intervention Epoch (n=26) | p-value |
|---------------------------------------------|--------------------------------|---------|
| Colonized room (any site) - by phenotype    |                                 |         |
| Sample submitted for WGS                    | 100 (27/27)                     | 96.2 (25/26) |         |
| Colonized room (any site) - by genotype     | 85.2 (23/27)                    | 44.0 (11/25) |         |
| Location in Patient Room Colonized?         |                                 |         |
| Main sink drain                             | 92.6 (25)                       | 34.6 (9)  | <0.001* |
| Bathroom sink drain                         | 92.6 (25)                       | 88.5 (23) | 0.669   |
| Shower drain                                | 31.1 (3)                        | 0.0 (0)  | 0.236   |
| Toilet                                      | 18.5 (5)                        | 0.0 (0)  | 0.051   |
| Number of room locations colonized (out of four total) | | |
| Mean (SD)                                    | 2.35 (0.66)                     | 1.23 (0.51) | <0.01** |
| No locations                                | 0.0 (0)                         | 3.8 (1)   |         |
| One location                                | 11.1 (3)                        | 69.2 (18) |         |
| Two locations                               | 66.7 (18)                       | 26.9 (7)  |         |
| Three locations                             | 38.5 (5)                        | 0.0 (0)  |         |
| Four locations                              | 3.7 (1)                         | 0.0 (0)  |         |

* Welsh’s t-test was used.

**Conclusion.** *P. aeruginosa* WWD colonization on our HM/HCT unit may predispose patients to colonization and BSI. The prevalence of patient colonization decreased following implementation of the interventions, despite persistent environmental colonization. We will follow the incidence of *P. aeruginosa* BSI to determine the long-term impact of these interventions.

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

804. Infection Control and Clinical Support in Long-Term Care Homes During the COVID-19 Pandemic in North Toronto: A Quasi-Experimental Study

Maria M. Magaz, MD, MHS1; Jacly O’Brien, RN1; Victoria R. Williams, MPH2; Christina Chan, MA2; Adrienne Chan, MD, MPH3; Natasha Salt, BSc BAsC4; Jerome A. Leis, MD MSc FRCPC5; Sunnybrook Health Sciences Centre, Toronto, Ontario, Canada

Session: P-43. HAI: Outbreaks

**Background.** Wave one of the COVID-19 pandemic in Ontario, Canada, resulted in significant institutional outbreaks associated with high case fatality among older adults. Our hospital formally partnered with congregate care homes in north Toronto to support infection control and clinical management before wave two of the COVID-19 pandemic. Our aim was to evaluate the impact of this program on resident and healthcare worker (HCW) outcomes.

**Methods.** A multicentre quasi-experimental study was conducted comparing outcomes between wave one (March-June, 2020) and wave two (October-December, 2020) among 17 congregate care homes (4 long term care homes and 13 residential homes). During wave two, weekly meetings and 42 on-site visits were conducted along with on-site daily hospital presence for all COVID-19 outbreaks to support infection control and resident management. The primary outcomes included COVID-19 case fatality rate as well as overall resident fatality including COVID-19 and non-COVID-19 related causes. Secondary outcomes included healthcare worker COVID-19 infections, and infection control practices among homes with paired audits (n=6), including hand hygiene, use of personal protective equipment, environmental cleaning and physical distancing practices.

**Results.** Among 2203 residents during wave one and 2287 residents during wave two, there was reduction in COVID-19 case fatality rate (38.1% vs. 13.4%; p< 0.01), overall COVID-19-related fatality (2.3% vs. 1.0%; p< 0.01) and non-COVID-19 related...
fatality (8.3% vs. 3.5%; p < 0.01). Weekly staff testing and increased syndromic surveil-

lance was implemented during wave two. Among 2590 staff, there were 2.6% vs. 4.2% staff who tested positive for COVID-19 during wave one and two, respectively. Changes in infection control practice were observed in regard to directly observed hand hygiene (83.3% vs. 100%), use of personal protective equipment (16.7% vs. 83.3%), environ-

mental cleaning (66.7% vs. 100%) and physical distancing (66.7% vs. 83.3%).

**Conclusion.** Integration of hospital with community congregate care homes was asso-

ciated with improvements in resident outcomes during wave two of the pandemic. Further longitudinal support and evaluation is needed to ensure sustainability.

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

---

805. Outbreak of *Ralstonia pickettii* Bacteremia Caused by Contaminated Hydromorphone in a University Hospital in Bogota, Colombia

Shirley Vanessa Correa Forero, M.D; Ionne Tatiana Ordoñez Blanco, M. D.; Samuel Martinez-Vernaza, M.D.; Sandra Liliana. Valderrama-Beltrán, M.D., MSc.; Gloria Cortes, MSc.; Claudia Janneth Linares Miranda, Nurse; Angela Patricia Gonzalez Rubio, Nurse; Viviana Andrea Pinzon Garcia, pharmace-

utical chemistry 1; Hospital Universitario San Ignacio, Bogota, Distrito Capital de Bogota, Colombia; 2 Hospital Universitario San Ignacio - Pontificia Universidad Javeriana, Bogota, Distrito Capital de Bogota, Colombia.

Grupo de Investigación en Enfermedades Infecciosas HUI-PUJ

**Session:** P-43. HAI: Outbreaks

**Background.** *Ralstonia picketti* are aerobic non fermenter gram negative bacilli isolated in water and soil. It is related to nosocomial infection outbreaks and considered an opportunistic pathogen. There have been outbreaks reports due to con-

taminated water systems and sterile drug solutions which mainly occurs during manu-

facturing. We present the report of an outbreak of *R. picketti* bacteremia secondary to a contamination of hydromorphone vials.

**Methods.** In February 2021 an outbreak of *R. picketti* bacteremia was identified. All isolates were from blood cultures with slow growth, thus indicating the culturing of e-

liquid inputs, intravenous administration solutions and commonly used drugs among patients including hydromorphone. Mass spectrometry (MALDI-TOF) was used for the identification and antibiotic microdilution to determine sensitivity to antimicro-

bials of the isolates and clonality analysis of genetic relationships was carried out using the DICE coefficient, UPGMA algorithm.

**Results.** During the outbreak, 19 patients with *R. picketti* bacteremia were iden-

tified. The global attack rate was 1.9%. 13/19 (58%) were women and 13/19 (68%) of the isolates were from inward patients and 6/19 (32%) were from intensive care unit. Factors that could contribute to the appearance of the outbreak were underlying path-

ology, 2 patients with a diagnosis of diabetes mellitus, 10 patients with a diagnosis of arterial hypertension, 5 patients with obesity, 6 patients with heart disease, additionally 2 patients with a diagnosis of diabetes mellitus, 10 patients with a diagnosis of cardiovascular disease, 2 patients with a diagnosis of obstructive sleep apnea, 2 patients with a diagnosis of SARS COV 2 and 6 patients with the use of corticos-

teroids. The global attack rate was 1.9% and mortality was 31.5% (6 patients). *R. picketti* was identified from two batches of hydromorphone by MALDI-TOF and the clonality study concluded that the isolates analyzed, were clonal with a 100% similarity. The associated mortality rate was 5/29 (26.3%).

**Conclusion.** We confirmed an outbreak of *R. picketti* due to the contamination of two hydromorphone badges in Colombia. It is crucial to acknowledge the import-

ance of infection control and surveillance during the COVID-19 pandemic as well as of multidrug resistant pathogens which can lead to deadly nosocomial outbreaks. Current approaches to guide infection control. Whole genome sequencing of infecting pathogens are an important modality to guide infection control. Whole genome sequencing of infecting pathogens paired with a single nucleotide polymorphism (SNP) analysis can provide high resolution clonality determination, yet these methods typically have long turnaround times. Here we examined the utility of the Oxford Nanopore Technologies (ONT) platform, a rapid, cost-effective and high-resolution method to identify transmission events. A rapid, cost-effective and high-resolution method to identify transmission events is impor-

tant. Due to the scale of the outbreak, we have developed a novel SNP calling pipeline customized for ONT data, which allows for early detection of transmission events.

**Disclosures.** Virginia M. Pierce, MD, UpToDate, Inc. (Other Financial or Material Support, Author) and Mohammad Sater, PhD, Day Zero Diagnostics (Employee, Shareholder); Micah Huntsly, PhD, Day Zero Diagnostics (Employee, Shareholder) and Ian Herriott, BS, Day Zero Diagnostics (Employee, Shareholder) and Tim Farrell, MD, Day Zero Diagnostics, Inc. (Employee, Shareholder) and David C. Rosenberg, MD, Cepheid Diagnostics (Consultant) and Erica S. Shenoy, MD, PhD, Vertex Pharmaceuticals (Individual(s) Involved: Self); I gave a single lecture in 3/2020 for which I received financial compensation, Other Financial or Material Support.

**Abstracts • OFID 2021:8 (Suppl 1) • S497**

Panel showing single nucleotide polymorphism (SNP) differences between isolates for respective clusters.

**Conclusion.** Apparent transmission events can be resource intensive to investi-

gate and manage. The application of rapid WGS allowed for early discontinuation of cluster investigations and conservation of resources.

**Disclosures.** Virginia M. Pierce, MD, UpToDate, Inc. (Other Financial or Material Support, Author) and Mohammad Sater, PhD, Day Zero Diagnostics (Employee, Shareholder) and Miriam Huntley, PhD, Day Zero Diagnostics (Employee, Shareholder) and Ian Herriott, BS, Day Zero Diagnostics (Employee, Shareholder) and Tim Farrell, MD, Day Zero Diagnostics, Inc. (Employee, Shareholder) and David C. Rosenberg, MD, Cepheid Diagnostics (Consultant) and Erica S. Shenoy, MD, PhD, Vertex Pharmaceuticals (Individual(s) Involved: Self); I gave a single lecture in 3/2020 for which I received financial compensation, Other Financial or Material Support.

807. Same-day Transmission Analysis of Nosocomial Transmission Using Nanopore Whole Genome Sequencing

Mohammad Sater, PhD; Remy Schwab, MSc; Ian Herriott, BS; Tim Farrell, MS; Miriam Huntley, PhD; Day Zero Diagnostics, Boston, MA

**Session:** P-43. HAI: Outbreaks

**Background.** Healthcare associated infections (HAIS) are a major contributor to pa-

tient morbidity and mortality worldwide. HAIS are increasingly important due to the rise of multidrug resistant pathogens which can lead to deadly nosocomial outbreaks. Current methods for investigating transmissions are slow, costly, or have poor detection resolution. A rapid, cost-effective and high-resolution method to identify transmission events is im-

portant. Due to the scale of the outbreak, we have developed a novel SNP calling pipeline customized for ONT data, which exhibit higher sequencing error rates and can therefore be challenging for transmission.