fatality (8.3% vs. 3.5%; p < 0.01). Weekly staff testing and increased syndromic surveillance 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%), environmental cleaning (66.7% vs. 100%) and physical distancing (66.7% vs. 83.3%).

Conclusion. Integration of hospital with community congregate care homes was associated with improvements in resident outcomes during wave two of the pandemic. Further longitudinal support and evaluation is needed to ensure sustainability.

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

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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 contaminated water systems and sterile drug solutions which mainly occurs during manufacturing. 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 liquid inputs, intravenous administration solutions and commonly used drugs among patients including hydromorphone. Mass spectrometry (MALDI-TOF) was used for 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 identified. The global attack rate was 1.9%. 13/19 (58%) were women and 13/19 (68%) of the isolations 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 pathology, 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 7 patients with a diagnosis of SARS COV 2 and 6 patients with the use of corticosteroids. 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 of the isolates was from inward patients and 6/19 (32%) were from intensive care unit.

Conclusion. We confirmed an outbreak of R. picketti due to the contamination of two hydromorphone bags in Colombia. It is crucial to acknowledge the importance of infection control and surveillance during the COVID-19 pandemic as well as maintaining adequate quality control of medication production in order to avoid presenting this kind of outbreaks.

Figure 1. Corynebacterium striatum Respiratory Cultures January 2020-February 2021

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

Conclusion. Apparent transmission events can be resource intensive to investigate and manage. The application of rapid WGS allowed for early discontinuation of cluster investigations and conservation of resources.

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

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Session: P-43. HAi: Outbreaks

Background. Healthcare associated infections (HAIs) are a major contributor to patient 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 imperative to guide infection control. Whole genome sequencing of infecting pathogens paired with a single nucleotide polymorphism (SNP) analysis can provide high resolution closeness determination, yet these methods typically have long turnaround times. Here we examined the utility of the Oxford Nanopore Technologies (ONT) platform, a rapid sequencing technology, for whole genome sequencing based transmission analysis.

Methods. We developed a SNP calling pipeline called OR NT data, which exhibit higher sequencing error rates and can therefore be challenging for transmission