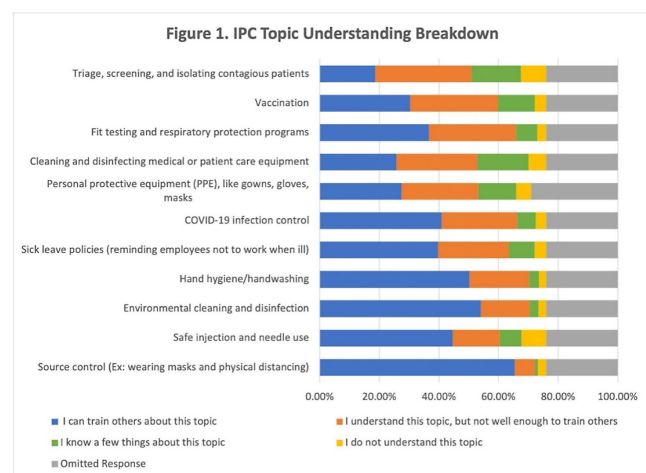




relating to triage and isolation of contagious patients and fit testing of respiratory protection devices. For these topics, 3,208 HCP (66.21%) and 3,657 HCP (75.48%) HCP, respectively, did not understand the topic well enough to teach others (Fig. 1). The highest number of HCP ($n = 2,512$, 39.36%) requested additional training in methods on how to educate others about IPC topics (ie, “train the trainer”). Surveyed respondents most frequently used personal computers for job trainings in both work and at-home settings ($n = 4,603$, 72.12%) and 3,437 HCP (53.85%) were open to either in-person or remote formats for job education. The CDC and OHA were the most frequented and trusted IPC sources among surveyed HCP: 4,124 HCP (64.62%) and 3,584 HCP (56.16%), respectively. **Conclusions:** IPC is a critical topic in HCP training across all healthcare facility types and employee roles. Effective educational planning includes understanding the learners’ knowledge needs and preferred methods of learning. Our learning needs assessment identified important IPC knowledge gaps and will help ensure that our training courses will be offered in effective educational formats for Oregon’s diverse HCP. Future training will include appropriate triage of potentially infectious patients, respiratory fit testing, and general IPC “train the trainer” sessions. Additionally, we will offer both in-person and remote options.

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s87–s88

doi:10.1017/ash.2023.348

Presentation Type:

Poster Presentation - Poster Presentation

Subject Category: Other

Environmental factors associated with invasive mold infections at a tertiary-care hospital

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Background: Invasive mold infections (IMIs) in hospitalized patients can result in significant morbidity and mortality. Environmental factors, such as hospital construction and negative air-pressure rooms (NAPRs), have been associated with hospital-acquired IMI. Increased utilization of NAPRs during the COVID-19 pandemic created a unique opportunity to examine the impact of NAPRs on IMI risk. **Methods:** From 2018 to present, a new pavilion was being constructed adjacent to our hospital. The Theradoc platform was used to identify positive mold cultures among adult patients hospitalized at our institution between March 1, 2017, and October 15, 2022. We performed a retrospective chart review of 262 mold isolates to determine patient demographics, timing of IMI, and their relationship to hospital construction and exposure to NAPR. IMI incidence was compared across 3 observation periods: (A) before hospital construction; (B) during hospital construction alone; and (C) during hospital

construction and NAPR enhancement during the COVID-19 surge. Hospital-acquired IMI was defined as an infection that occurred >72 hours after admission. A REDCap database was created for data storage and R software was used for data analysis. **Results:** Of the 262 mold isolates identified, 61 cases were classified as IMI, of which 29 were hospital-acquired IMI. The mean age of IMI patients was 51.8 years, and 55.2% were male. Among them, 20.7% were exposed to NAPR during admission; 65.5% were immunocompromised; and 2 patients were diagnosed with COVID-19. The all-cause mortality rate among hospital-acquired IMI cases was 79.3% (23 of 29). Also, 82.8% of hospital-acquired IMI cases were respiratory in nature, with 83.3% of these cases due to *Aspergillus* spp. Yearly rates of hospital-acquired IMI were 3.0 before construction versus 5.6 during construction (periods B and C). Yearly rates of hospital-acquired IMI, respiratory IMI, and invasive pulmonary aspergillosis by period were as follows: Period A had 3 hospital-acquired IMI cases per year, 2 hospital-acquired respiratory IMI cases per year, and 3 hospital-acquired invasive pulmonary aspergillosis cases per year. Period B had 4.5 hospital-acquired IMI cases per year, 3.5 hospital-acquired respiratory IMI cases per year, and 3.0 hospital-acquired invasive pulmonary aspergillosis cases per year. Period C had 6.5 hospital-acquired IMI cases per year, 5.4 hospital-acquired respiratory IMI cases per year, and 5.0 hospital-acquired invasive pulmonary aspergillosis cases per year. **Conclusions:** Hospital-acquired IMI was associated with a high mortality. Our data demonstrate a >2-fold increase in yearly incidence of hospital-acquired IMI before construction compared with during construction in association with increased implementation of NAPR. We have now reversed the trend in NAPR at our hospital’s designated COVID-19 units.

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s88

doi:10.1017/ash.2023.349

Presentation Type:

Poster Presentation - Poster Presentation

Subject Category: Outbreaks

Fanny pack transmission of carbapenem-resistant *Acinetobacter baumannii*

Amber DelleFave; Juliana Mandarano and Nayef El-Daher

Background: Carbapenem-resistant *Acinetobacter baumannii* (CRAB) is a gram-negative coccobacillus that has garnered notoriety as a formidable cause of nosocomial infection with significant mortality. This organism poses a significant threat due to its multitude of resistance mechanisms and ability to endure within the environment. In the summer of 2022, a 350-bed acute-care hospital identified an outbreak of CRAB among critically ill patients in the intensive care unit (ICU) and intensive nursing care unit (INCU). Here, we report actions taken to contain the outbreak and to identify a common environmental source. **Methods:** In total, 7 nosocomial CRAB infection cases were identified by the infection prevention team between July and September 2022. A multidisciplinary team reviewed the cases using relevant medical history and available microbial susceptibilities. Clinical culture sites include 1 PICC tip, 1 urine sample, 1 peritoneal fluid samples, 5 wounds, and 1 sputum sample. Of 7 infections, 6 met the criteria for hospital onset, with an average time to infection from admission of 61 days. We quickly initiated universal contact precautions in the ICU and INCU for 6 weeks, enhanced daily cleaning of high-touch surfaces, provided staff and visitor education, conducted adenosine triphosphate (ATP) testing, collected observations, and performed selective environmental culturing based on observations. **Results:** In total, 71 environmental specimens were collected for culture. All were negative with the exception of 1 isolate obtained from the fanny pack of a wound-care nurse that was positive for CRAB. Also, 4 available patient isolates and the environmental isolate were sent to New York State Department of Health Wadsworth Center (NYSDOH Wadsworth) for genome sequencing, and relation to the same cluster was confirmed. Of 7 isolates, 6 were confirmed to express the *bla*OXA-23 resistance mechanism (1 was not available for testing). Subsequently, chart review identified that a wound-care nurse had had contact with all 7 patients within 30 days of their infections.

Conclusions: After initiation of the described action plan, no further transmission was identified in the ICU or INCU. Real-time observation and environmental culturing was critical in identifying the epidemiological link, and this finding speaks to the ability of this organism to persist on a surface for a substantial length of time. Fanny pack use for transport of patient-care supplies was identified as a high-risk practice due to the inability to be properly disinfected between rooms and limited laundering. Fanny packs are no longer permitted in clinical spaces at this facility.

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s88–s89

doi:10.1017/ash.2023.350

Presentation Type:

Poster Presentation - Poster Presentation

Subject Category: Outbreaks

Outbreak of *Stenotrophomonas maltophilia* infections in an intensive care unit—Alameda County, California, May–October 2022

Rebecca Elliott; Jeffrey Silvers; Axel Vazquez Deida; Paige Gable; Gillian McAllister; Alyssa Kent; Thomas Ewing; Janet Glowicz; Matthew Arduino; Heather Moulton-Meissner; Mir Noorbakhsh; Patricia Rodrigues; Munira Shemsu; Amit Chitnis; Hilary Metcalf; Barbara Allen; Suada Abdi; Alison Halpin; Kavita Trivedi; Amelia Keaton and Margarita Elsa Villarino

Background: *Stenotrophomonas maltophilia* is a gram-negative, biofilm-producing bacterium that is ubiquitous in water environments and often associated with healthcare-associated infections (HAIs). Outbreaks of *S. maltophilia* bloodstream infections are a rare event and raise the suspicion of a common source. We used whole-genome sequencing (WGS) for an investigation of a cluster of *S. maltophilia* HAIs at a single hospital.

Methods: A patient was defined as an intensive care unit (ICU) patient with fever and *S. maltophilia* isolated from a culture and who was treated for an HAI from May to October 2022. The response to the cluster included an epidemiologic investigation, water infection control risk assessments (WICRA), and environmental sampling. We also conducted WGS to characterize and assess relatedness between clinical and environmental *S. maltophilia* isolates. **Results:** From May 5 to October 1, 2022, we identified 11 HAIs due to *S. maltophilia*: 9 bloodstream infections and 2 ventilator-associated pneumonia cases. The initial epidemiological investigation did not identify common medical products, procedures, or personnel as an exposure source. The WICRA identified several breaches that may have exposed patients to contaminated water from sink backsplashes in the ICU, computerized tomography (CT) rooms, and the emergency department. In the CT rooms, saline bags were sometimes used for multiple patients, as were single-use intravenous contrast solution bottles. No additional cases were identified once infection control breaches were mitigated by installing sink splashguards, disinfecting drains, dedicating sink use for handwashing, and adhering to single-patient use of pharmaceutical products in the CT rooms. Of 46 environmental water samples, 19 were culture-positive for *S. maltophilia*. Isolates available for WGS included 7 clinical isolates (6 blood and 1 respiratory) and 17 environmental isolates. Among the 24 isolates sequenced, 16 unique multilocus sequence types (MLSTs) were identified. The 6 blood isolates sequenced were highly related (ST239, 0–4 high-quality, single-nucleotide variants [hqSNV] over 98.99% core genome), suggesting a common source. Two clusters of related environmental isolates were identified; however, overall MLST and hqSNV analyses suggested no relatedness between clinical and environmental isolates. **Conclusions:** An ICU cluster of *S. maltophilia* bloodstream infections was likely associated with water contamination of room surfaces and use of single-use intravenous products for multiple patients in the setting of a national pharmaceutical product shortage. This investigation highlights the importance of strong surveillance and water infection control, including routine assessment of ancillary areas in which intravenous products are administered and interdisciplinary collaboration to properly mitigate nosocomial transmission.

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s89

doi:10.1017/ash.2023.351

Presentation Type:

Poster Presentation - Poster Presentation

Subject Category: Outbreaks

Healthcare-associated *Stenotrophomonas maltophilia* infections in the United States, 2018–2022

Amelia Keaton; Lucy Fike; Kevin Spicer; Alexander Kallen and Kiran Perkins

Background: *Stenotrophomonas maltophilia* is an important cause of opportunistic healthcare-associated infections (HAIs) in critically ill patients and is difficult to treat due to intrinsic resistance to multiple antibiotic classes. During the COVID-19 pandemic, the CDC received anecdotal reports of increases in *S. maltophilia* respiratory infections. To further investigate these reports, we used a national electronic healthcare database to evaluate changes in *S. maltophilia* during the pandemic. **Methods:** Using the PINC-AI healthcare data (Premier Inc, Charlotte, NC) we identified all potential HAIs by calculating the total number of unique patients hospitalized during January 1, 2018, through December 31, 2021, who had any organism isolated on clinical culture obtained >3 days after admission. We calculated the proportion of patients with *S. maltophilia* detected in culture and stratified them by specimen source. To determine whether COVID-19 diagnosis influenced the proportion of patients diagnosed with *S. maltophilia* respiratory infections during the pandemic (January 1, 2020–December 31, 2021), we calculated the proportion of patients with *S. maltophilia* detected among those with any bacterial pathogen isolated from a respiratory culture >3 days after hospitalization. We stratified these results by presence or absence of concurrent COVID-19 diagnosis. Pearson χ^2 test was used to test for differences where appropriate. **Results:** Among hospitalized patients with any organism isolated from a clinical culture, the proportion with *S. maltophilia* detected was higher in 2021 ($n = 2,554$ of 118,029, 2.2%) than in 2018 ($n = 2,063$ of 155,624, 1.3%) $p < 0.001$ 3 days after hospital admission from 2018 to 2021. Most patient isolates were from respiratory specimens. A concurrent diagnosis of COVID-19 did not appear to increase the likelihood of respiratory *S. maltophilia* detection. The increases in *S. maltophilia* during the pandemic might be explained by challenges inherent to caring for increased numbers of higher-acuity patients during this time, including staffing shortages and changes to infection prevention practices. Additional exploration of these data, as well as data from other sources and from additional years, may help to elucidate this issue more fully.

Disclosures: None

Antimicrobial Stewardship & Healthcare Epidemiology 2023;3(Suppl. S2):s89

doi:10.1017/ash.2023.352

Presentation Type:

Poster Presentation - Poster Presentation

Subject Category: Outbreaks

Outbreak of *Burkholderia multivorans* among patients at two acute-care hospitals in California, August 2021–July 2022

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Background: *Burkholderia multivorans* are gram-negative bacteria typically found in water and soil. *B. multivorans* outbreaks among patients without cystic fibrosis have been associated with exposure to contaminated medical devices or nonsterile aqueous products. Acquisition can also occur from exposure to environmental reservoirs like sinks or other hospital water sources. We describe an outbreak of *B. multivorans* among hospitalized patients without cystic fibrosis at 2 hospitals within the same healthcare system in California (hospitals A and B) between August 2021 and July 2022. **Methods:** We defined confirmed case patients as patients without cystic fibrosis hospitalized at hospital A or hospital B between January 2020 to July 2022 with *B. multivorans* isolated from any body site matching the outbreak strain. We reviewed medical records to describe case patients and to identify common exposures. We evaluated infection control