

**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

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**Presentation Type:**

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**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 Abdic; 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.

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**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  $\chi^2$  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 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.

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

Kiara McNamara; W. Wyatt Wilson; Dipesh Solanky; Sophie Jones; Elizabeth Ohlsen; J.B. Bertumen; Mark Beatty; Heather Moulton-Meissner; Paige Gable; John LiPuma; Grace Kang; Margaret Turner; Erin Epton; Kiran Perkin; Raymond Chinn and Jane Siegel

**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