

CoV-2) in wastewater remain unknown. In this study at skilled nursing facilities (SNFs), two wastewater concentration methods were evaluated for SARS-CoV-2 detection by droplet digital polymerase chain reaction (ddPCR): Electronegative membrane filtration (enMF) and Nanotrap® Magnetic Virus Particles (NP). SARS-CoV-2 case surveillance data from the SNFs was incorporated into this evaluation. **Methods:** Wastewater samples were collected weekly from manholes at three SNFs over 25 weeks in 2022. Samples were split and concentrated by both enMF and NP, then virus concentration was determined by ddPCR. We utilized a weekly questionnaire and each facility's National Healthcare Safety Network COVID-19 Report to identify the number of resident and healthcare personnel cases in each facility. Differences in the median SARS-CoV-2 concentration were compared across the enMF and NP methods using the Wilcoxon signed-rank test ($p=0.05$). Spearman's correlation (r) was used to evaluate the relationship between the SARS-CoV-2 concentration in wastewater and SARS-CoV-2 case counts. **Results:** For each facility separately, as well as overall, median virus concentration in wastewater from enMF was higher than that from NP (SNF A: 2.84 vs. 1.49 genome copies [gc]/100 mL; SNF B: 8.50 vs. 6.08 gc/100 mL; SNF C: 5.3 vs. 3.86 gc/100 mL; overall: 5.3 vs. 3.86 gc/100 mL). The Wilcoxon signed-rank test confirmed that the difference in median virus concentrations was statistically significant for SNF B ($p=0.001$) and overall ($p=0.001$). Spearman's correlation results showed overall higher correlations with enMF than with NP and a greater number of statistically significant results among subpopulations. For example: using enMF, the correlation among residents and healthcare personnel combined at SNF A was $r=0.86$ ($p<0.0001$), at SNF B was $r=0.50$ ($p<0.01$), and at SNF C was $r=0.59$ ($p<0.01$), whereas using NP, the correlation at SNF A was $r=0.54$ ($p<0.01$), SNF B was $r=0.46$ ($p=0.02$), and SNF C was $r=0.23$ ($p=0.26$). **Conclusions:** enMF yielded higher SARS-CoV-2 concentrations than NP and produced stronger correlations between wastewater signal and case counts, though both methods yielded acceptable results. enMF should be considered as an effective virus concentration method for healthcare facility-level WWS to strengthen and complement clinical methods of case detection.

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Clostridioides difficile Whole Genome Sequencing Does Not Support Transmission from Environmental Contamination by Prior Room Occupants

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Background: Candida auris, an emerging multidrug-resistant yeast, spreads rapidly in healthcare settings and is associated with difficult-to-control outbreaks. Prevalence has risen significantly in the Metro Detroit area, driven by interfacility transfers and inconsistent communication of colonization status. Patients can remain colonized for prolonged periods and shed the organism into the environment, where it persists for months. Active surveillance testing (AST) can support earlier detection and containment. We describe the implementation of a C. auris AST program across a multi-hospital health system. **Methods:** Screening for C. auris colonization can be either prevention-based or response-based. Response-based strategies, such as point prevalence surveys (PPS), are recommended by the Centers for Disease Control and Prevention when a new case is identified. Prevention-based AST is also recommended to detect cases early among high-risk groups. In April 2025, we launched a C. auris AST program across five hospitals in Southeast Michigan. Composite axilla-groin swabs were tested by real-time polymerase-chain reaction (PCR). High-risk patients were defined as those presenting from long-term acute care hospitals, skilled nursing facilities, subacute rehabilitation facilities, or inpatient rehabilitation centers who required ED admission or

Table. C. auris screening results

Metric	AST	PPS
Surveillance period	6 months	6 months
Patients screened	2710	1226
Tests performed	3044	1354
Positive results	37	22
Positivity rate	1.20%	1.60%

AST, active surveillance testing; PPS, point prevalence survey

transfer from another healthcare facility (including internal transfers) and had one or more of the following: indwelling devices (e.g., endotracheal or tracheostomy tubes), chronic or non-healing wounds, or colonization/infection with multidrug-resistant or carbapenem-resistant organisms. Upon order signing in the electronic health record, an alert prompted providers to order C. auris PCR and initiate contact precautions. Patients were retested upon readmission. PPS were also performed per state health department recommendations following identification of new cases. **Results:** During the 6-month surveillance period, 2,710 unique patients underwent AST, with 3,044 total tests completed. Of these tests, 969 (31%) were ordered in the emergency department at the time of admission. Overall, 37 patients (1.2%) screened positive for C. auris colonization (Table). During the same period, 1,354 tests were performed through 77 unit-based PPS, yielding 22 positive results (1.6%). **Conclusion:** Although AST was implemented as a prevention-based strategy, PPS remained necessary for identifying additional cases. Positivity rates were low across both approaches, yet each required substantial coordination, staff time, and laboratory resources. These findings highlight the need to balance the benefits of early detection with operational demands. Alternative approaches beyond widespread screening should be explored to optimize resource utilization while maintaining effective C. auris prevention and control.

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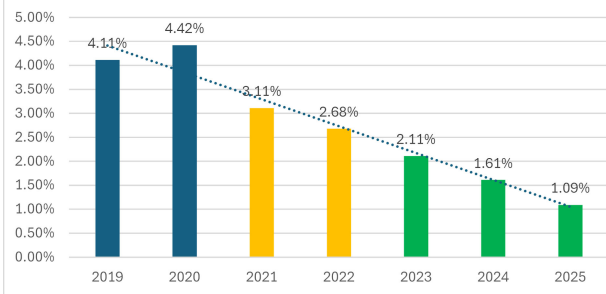
Mycobacterium abscessus associated with facility-wide water contamination: An outbreak investigation

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Background: Blood culture contamination (BCC) is a persistent problem in the hospital, contributing to unnecessary antibiotic exposure, excessive diagnostic testing, increased length of stay, and higher costs. For patients with suspected or confirmed sepsis, BCC has particularly serious implications, as early identification of the causative pathogen and prompt initiation of appropriate antimicrobial therapy are critical. National benchmarks define <3% contamination as acceptable, yet emerging evidence supports a more ambitious goal of <1%, particularly in high-risk populations such as patients with sepsis. **Methods:** Using a sequential practice change across three time periods: (1) no blood culture diversion device (2019–2020), (2) implementation of manual blood diversion device (BDD) #1 (2021–2022), and (3) automatic BDD#2 (2023–present), we have achieved a 74% reduction in BCC (Figure 1). In this project, we further evaluated the impact of this overall reduction on patients admitted with suspected or confirmed sepsis. **Results:** Data were extracted for adult patients admitted to the hospital who had a final discharge diagnosis of sepsis, regardless of their initial admission diagnosis. A total of 154 blood cultures were analyzed across the three time periods. During period 1 (2019 & 2020), 6/62 cultures were contaminated (9.7%). After implementation of manual BDD#1 (11/17/2021–2022), BCC decreased to 2/30 cultures (6.7%). After transition to automatic BDD#2 (1/20/2023–present), BCC further declined to 3/62 cultures (4.8%). One-way analysis of variance

Figure 1: Decrease in Overall Blood Culture Contamination Rates (2019-2025)



(ANOVA) demonstrated a statistically significant difference in BCC rates across the time periods, with post hoc comparisons showing a significantly lower contamination rate when using BDD#2 as compared with both no BDD and manual BDD#1. Additionally, manual BDD#1 was used in 48% (30/62) of the blood culture collections versus to 78% for automatic BDD#2, with staff feedback indicating greater ease of use with the automatic BDD#2 system. Conclusion Adoption of BDD was associated with a 50% (9.7-4.8%) reduction in BCC, with the lowest rates following implementation of automatic BDD#2. Compliance with BDD use was also highest with automatic BDD#2, and staff reported greater ease of use. These findings underscore the importance of optimizing BCC practices as a key component of sepsis management, antimicrobial stewardship, and patient safety efforts. Additional research is needed to identify strategies to further reduce BCC in sepsis patients, with particular attention to BDD usability, workflow integration, and process adherence during real-world use.

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How Clean is Clean? Mitigation Efforts of Ice/water Dispensers Linked to a *Mycobacterium chelonae* Outbreak at a Pediatric Hospital

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Background: We had a large-scale measles exposure event affecting 626 patients. Management of exposed patients was urgent, involving quarantine, post-exposure prophylaxis (PEP), and symptom monitoring on a case-by-case basis. Cases were initially tracked and managed using a combination of multiple spreadsheets amongst stakeholders as well as lists within the electronic health record (EHR). Using shared spreadsheets and lists created significant challenges with maintaining and editing multiple copies and updating workbooks simultaneously. **Methods:** Infection Prevention and Control (IPAC) worked with primary care personnel and EHR developers to create a shared registry that would prioritize communication and follow-up for exposed patients based on age and immunity. Patients are initially added to the shared registry within the EHR by reviewing non-registry reports and tagging patients, identified using exposure timeframes that overlapped with the index measles cases, in a manner that transferred them to the shared registry. From this registry, measles, mumps, and rubella vaccine status can be confirmed, immune status can be identified, and criteria for PEP assigned. High-risk patients are then contacted with recommendations from IPAC and primary care. Communication and follow-up are tracked directly within the shared registry to ensure appropriate patient management. The exposure management registry is further leveraged throughout the measles outbreak timeframe by

allowing real-time monitoring of patients that require additional precautions or guidance related to their exposure. **Result:** The shared registry enhanced documentation accuracy and transparency between stakeholders. It led to availability of real-time status of exposed patients for the duration of the measles outbreak timeframe. Overall, the registry enabled time-sensitive patient communication to all exposed patients and rapid identification of those who needed PEP. Communication could happen rapidly and seamlessly between care teams within the organization, and the necessary information could be shared quickly with public health authorities as required. **Conclusion:** Large scale exposures are a challenge to manage and ensure appropriate action and communication occurs. Errors can be prevented by having a single shared exposure management registry. A registry enables care teams to quickly identify and prioritize patients for measles follow-up, communication, PEP, and ongoing management across outbreak timeframes. This process reduces both time and operational burdens of exposure follow-up tracking outside of the EHR.

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Connecting the Patients: Network Analysis of a Multi-facility *Candidozyma auris* Outbreak, Georgia, September 2024 – August 2025

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Background: Central line-associated bloodstream infection (CLABSI) represents the most common and costly device-associated hospital-acquired infection in children. While prevention bundles are effective when reliably implemented, pediatric-specific risks often require strategies beyond standard bundles. Existing CLABSI risk models are insufficient for pediatric patients, remaining static during their hospital stay despite changing clinical conditions. Moreover, previously reported dashboards and predictive models generally do not incorporate data science principles to provide a daily prediction score, and they often exclude demographic factors beyond age and sex. The purpose of developing the CLABSI risk model was to leverage technology-driven strategies for identifying, intervening, and escalating care for high-risk pediatric patients in real time, thereby decreasing infection risk. **Methods:** Quality Improvement, Data Intelligence, and the interdisciplinary clinical team partnered to develop an evidence-based predictive model tailored to institutional risk factors. Using evidence and clinical expertise, an affinity diagram was created. Data from 61,068 inpatient central line days (January 2022- July 2024), sourced from electronic health records (EHR) and clinical surveillance software, formed the dataset. CLABSI was identified using NHSN surveillance definition. Patient risk factors from the infection date plus two days prior were evaluated. Exploratory data analysis was completed using RStudio integrated development environment to inform model development. Separate models were created for nontunneled lines and tunneled lines. Prediction models were developed using Python coding language and Databricks data intelligence platform. Under-sampling was used to account for uneven distribution between CLABSI and non-CLABSI cases. Logistic regression, random forest, and XGBoost models were created. Candidate models were compared using area under the curve (AUC), sensitivity, and specificity. **Result:** Using the XGBoost model for nontunneled line, the test AUC was 0.831, demonstrating strong discriminative power. This model achieved a sensitivity of 0.828, indicating its ability to correctly identify a high proportion of actual CLABSI cases, and a specificity of 0.751, reflecting its capacity to correctly identify non-CLABSI cases. Similarly, the tunneled line XGBoost model yielded an AUC of 0.845, showcasing excellent predictive performance. Its sensitivity was 0.833 and specificity was 0.668. In both models, the number of modifiable risks was the most significant factor (Tables 1-3). **Conclusion:** The CLABSI prediction model enables real-time identification and intervention to support proactive prevention,