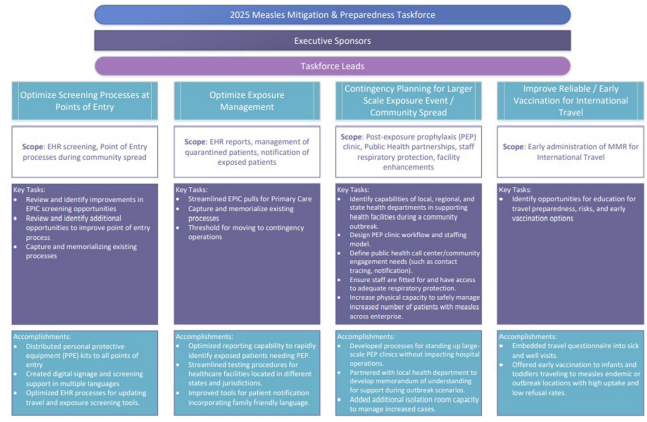
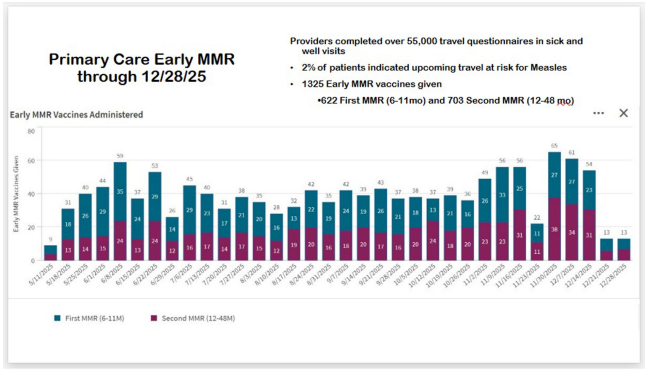
and result tracking. Optimize screening processes at points of entry (POE): Develop streamlined processes for reliable travel and exposure screening at all enterprise wide POEs. Contingency planning for larger scale exposure events/community spread: Develop post-exposure prophylaxis (PEP) delivery procedures to respond to large-scale community exposure events and establish partnerships with local public health (PH) departments. **Results:** Increase in vaccination for non-immune travelers in primary care: We built an EMR (electronic medical record) prompt into all child visits to screen for travel, which interfaced with vaccine clinical decision support to offer/administer vaccines. From May through 12/28/25 we administered 1325 early MMRs to travelling children (Figure 2). EMR-based report to identify exposed individuals and their immune status: This report allows all sites to rapidly identify patients needing PEP after exposure. We also developed processes for pre-emptive approval for large scale testing, result tracking, and high-volume patient notification. Optimization of Screening and POE with EMR upgrades, PPE kits: We are upgrading our EMR to better integrate travel & exposure screening. We developed additional resources including screening supports for non-English languages and PPE kits for immediate use at POE when patients screen positive. Development of PEP clinics and PH Collaboration: We developed processes to stand up PEP clinics at our hospitals to expedite large volume PEP administration. We worked with PH to outline roles, capabilities and resources for response to community outbreaks, optimized staff fit testing and developed drills across all care settings. **Conclusions:** Preparedness for highly contagious infectious diseases and emerging PH threats is critical. A taskforce approach provides a structured framework for collaboration and mobilization of resources. By utilizing an all-hazards lens, this framework is broadly applicable for vaccine preventable infections and other infectious threats.

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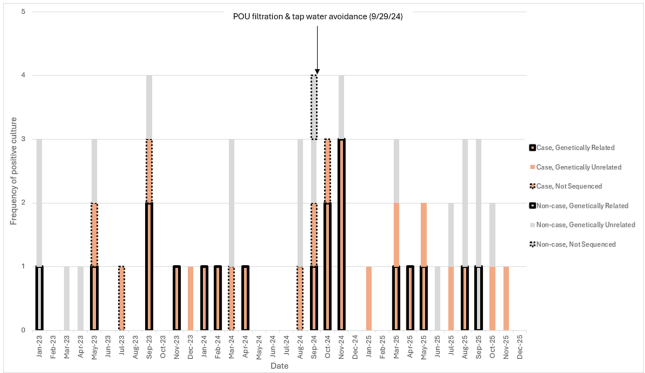

**Presentation Type:**
Oral Presentation
**Subject Category:** Outbreaks

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

Spencer Schrank[1], Alexander Sundermann[2], Ashley Ayres[3], Marissa Griffith[2], Kathleen Shutt[2], Kady Waggle[3], Lora Pless[2], Lee Harrison[2] and Graham Snyder[1]
[1]UPMC/University of Pittsburgh; [2]University of Pittsburgh and [3]UPMC

**Background:** Nontuberculous mycobacteria (NTM) are ubiquitously found throughout the environment, including healthcare facilities, and disproportionately affect immunocompromised hosts. We have a limited understanding of healthcare-associated transmission. Detailed outbreak investigations may yield insights into transmission risk. **Method:** An investigation of a Mycobacterium abscessus outbreak began after identifying a higher-than-expected frequency of infections among solid organ transplant recipients in September 2024. Cases were defined as individuals with a first-time positive M. abscessus culture from any anatomical site and a prior inpatient admission to our hospital. Our epidemiologic investigation included creating a case line list with potential exposures during the 90 days preceding microbiologic diagnosis, direct observations of patient care, a case-control study to identify potential point sources and transmission routes, and environmental cultures to test source/transmission hypotheses. Whole-genome sequencing (WGS) of case isolates was performed to confirm genetic relatedness (defined as ?10 single nucleotide variant difference). Prospective microbiologic surveillance was used to identify new cases. **Result:** Between May 2023 and the ongoing investigation through December 2025, 31 cases were identified. Twenty (65%) were solid organ transplant recipients, including 12 (60%) lung transplants (Figure 1, Table 1). Our epidemiologic investigation did not identify any other geographic, procedural, or point source exposures with commonality among <20% cases. The case-control study identified transplant status as a significant risk factor for transmission. We hypothesized transmission occurred through contaminated water exposure in inpatient rooms during routine care; environmental cultures demonstrated M. abscessus in potable water sources throughout the hospital (Figure 2). WGS identified 2 distinct clusters comprising 3 and 14 patients, with genetic relatedness to environmental M. abscessus isolates. Sequential flushing and chlorination of the facility-wide water system were performed without significant changes in the frequency of NTM isolation. To mitigate exposure risk, point-of-use filters were installed and tap water avoidance was enforced on units predominantly caring for patients with immunocompromising conditions. Following implementation of tap water avoidance, only 4 genetically related cases have been identified within 11 months of follow-up. **Conclusion:** Water exposure during routine patient care among susceptible hosts increases NTM risk. Eradication of NTM from aging plumbing systems is challenging; tap water avoidance combined with POU filtration appeared to have abated this outbreak. Infection prevention programs should consider routine monitoring of NTM infection rates, particularly

Figure 1. The incidence of *M. abscessus* positive cultures, by genetic relatedness and case definition, January 2023 – December 2025




‡The abstract titles in this supplement have been corrected since original publication. A notice detailing the changes has been published at https://doi.org/10.1017/ash.2026.10802.

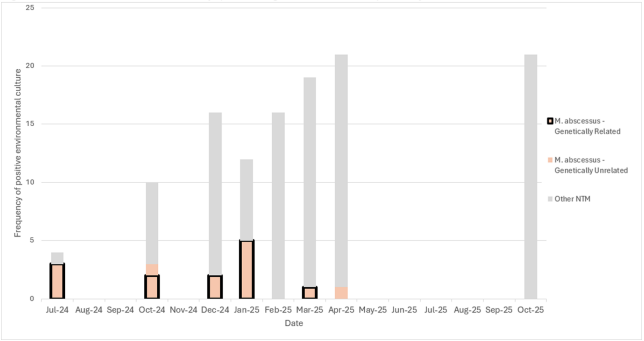


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Table 1. Clinical characteristics of outbreak cases

| Characteristic | Cases (n = 31) |
|---|---|
| Median age, y (IQR) | 63 (57-71) |
| Female, n (%) | 16 (52) |
| Solid organ transplant recipient, n (%) | 20 (65) |
| Lung | 12 (60) |
| Renal | 4 (20) |
| Small bowel | 2 (10) |
| Liver | 2 (10) |
| Treatment for *M. abscessus* infection, n (%) | 21 (68) |
| Death attributable to *M. abscessus* infection, n (%) | 3 (10) |

Figure 2. Positive NTM water culture results by species and genetic relatedness to patient *Mycobacterium abscessus* isolates




M. abscessus, to detect a higher-than-expected frequency. Routine water quality surveillance should include NTM cultures. Studies are needed to identify effective methods of NTM eradication from potable water supplies.

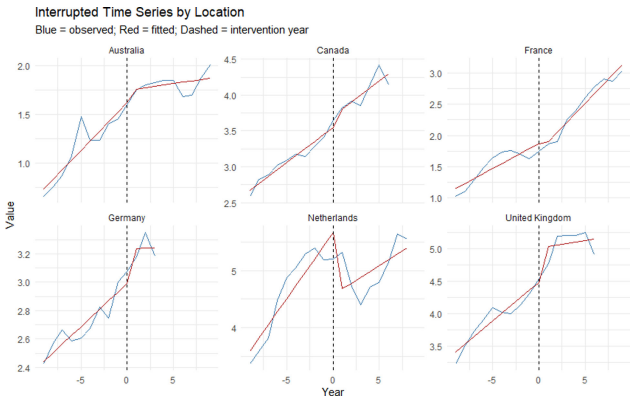
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doi:10.1017/ash.2026.10480

**Presentation Type:**
Oral Presentation
**Subject Category:** Public Health
**Do Laws Regulating Legionella Growth Reduce Legionella Mortality? Evidence from Six Countries**‡

Kevin Ikuta[1]
[1]Greater Los Angeles VA

**Background:** Legionella is the etiologic agent of Legionnaire's disease and Pontiac fever with an environmental niche in potable water systems. Globally, Legionella mortality is estimated to have increased fourfold since 1990. Several regulations have emerged to try and counteract this increase, with six countries (Netherlands, Germany, England, France, Australia, and Canada) enacting laws that target the growth of legionella from environmental samples for primary prevention. The effectiveness of these laws in mitigating legionella mortality has not been evaluated. We performed an interrupted time series analysis to evaluate the effect of laws with specific colony forming unit (CFU) thresholds on the legionella mortality rate in the country. **Methods:** We extracted legionella mortality rate estimates produced by the Global Burden of Disease project for the six countries with legionella laws with defined CFU thresholds for the ten years before the laws were enacted and ten years after the laws were enacted (or up to 2020). We then performed an interrupted time series analysis for these six countries. All analysis was performed in R version 4.5.2. **Results:** The median legionella mortality rate for the six countries included in analysis in the decade before laws were enacted was 2.86 deaths per 100,000 (IQR1.6-3.75). In the decade following law enactment the mortality rate was 3.35 legionella deaths per 100,000 (IQR 2.01-4.77). In the interrupted time series, there was an increase in legionella mortality of 0.17 deaths per 100,000 (95%CI 0.14 – 0.2) per year in the decade before CFU laws were introduced. The rate of increase did not statistically significantly change after law enactment with an annual increase of 0.102 per 100,000 (95%CI 0.03 – 0.17) persons. A country specific analysis found that the rate of annual increase in legionella mortality rates was statistically significantly lower following enactment of CFU specific laws in Germany, Netherlands, and the United Kingdom (Figure1). Discussion: We found that, collectively, laws including CFU thresholds had no significant effect on the rate of change in legionella mortality. However, at the individual country level, three countries did see a significant decrease in the rate of change in legionella mortality following enactment. One possible explanation for this heterogeneity is that several of these laws include additional mitigation measures and may confound the effect of the CFU based monitoring. Future studies should focus on these additional mitigation measures and compare legionella outcomes in countries with and without CFU thresholds in water safety laws.

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**Presentation Type:**
Oral Presentation
**Subject Category:** Public Health
**Connecting the Patients: Network Analysis of a Multi-facility Candidozyma auris Outbreak, Georgia, September 2024 – August 2025**‡

Michael Anderson[1], Benjamin Roberts[1], Dhondup Urg[1], Diane Yi[1], Shamta Warang[1], Lynn Reynolds, Sue Milligan[1], Karen Williams[1] and JoAnna Wagner[1]
[1]Georgia Department of Public Health

**Background:** Candidozyma auris is an emerging multidrug-resistant organism often associated with multi-facility outbreaks. We identified an outbreak in southeast Georgia spanning September 2024-August 2025. Although early response efforts focused on one long-term acute care hospital (LTACH) with extensive colonization, clinical cases were also identified in four acute care hospitals (ACHs), another LTACH, and one outpatient center within the public health district. Two ACH laboratories were only speciating Candida from blood cultures. We expanded the investigation to assess whether inter- and intra-facility transmission contributed to ongoing spread, to inform targeted testing, colonization screening, and infection control recommendations. **Method:** Colonization was detected in LTACH-A-LTACH-B via Polymerase Chain Reaction by Tennessee Laboratory Services, and clinical cases were identified via MALDI-TOF spectrometry at the Georgia Public Health Laboratory or clinical laboratories. Whole-genome sequencing (WGS) was conducted on 24 isolates. Clade data were analyzed alongside patient healthcare exposure histories to identify transmission clusters. Case data were managed in Excel, and healthcare exposure networks were visualized using visNetwork in RStudio. **Result:** C. auris cases were identified across 7 facilities, including ACH-A-ACH-D, LTACH-A-LTACH-B, and Outpatient-A. We identified 26 clinical and 62 screening cases. Clinical specimen sources included 31% blood, 27% wound, 23% urine, 15% respiratory, and 4% unknown. LTACH-A identified 3 clinical cases in Oct./Nov. 2024, leading to screening identifying 60 cases between 12/3/24-8/5/25. Of 60 screening cases in LTACH-A, 37% had prior exposure to ACH-A, 25% ACH-B, 17% ACH-C,

‡The abstract titles in this supplement have been corrected since original publication. A notice detailing the changes has been published at https://doi.org/10.1017/ash.2026.10802.



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