Presentation Type:
Poster Presentation

Use of a Biological Tracer to Investigate Microbial Aerosols Generated by Heater-Cooler Units

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Background: A multinational outbreak of *Mycobacterium chimaera* endocarditis following cardiac surgery has been attributed to the use of heater-cooler units (HCUs) during cardiopulmonary bypass. It is hypothesized that mycobacteria can be transmitted to the surgical site via the aerosolization of contaminated water from within the unit. In the United Kingdom, *M. chimaera* infections have been linked to 1 specific make and model of HCU, which was shown to generate microbial aerosols when circulating water. The manufacturer has since modified this HCU and claims that the dispersal of aerosols has now been prevented. *M. chimaera* is a common contaminant of HCUs, regardless of make, model, and manufacturer. To help inform local decision making, hospitals require evidence that this modified HCU and/or alternative heater-cooler systems can reduce the risk of mycobacterial infection by incorporating design features that prevent the generation of microbial aerosols external to the device. The time required to culture *M. chimaera* means investigations focusing on naturally or artificially contaminated HCUs are problematic. Instead, specialist aerobiological techniques incorporating a nonpathogenic, aerostable, biological tracer (*Bacillus atrophaeus*) were used to investigate microbial aerosols generated and released from brand-new and 'upgraded' HCUs. **Methods:** 4 HCUs (A–D), supplied directly by the manufacturers, were filled with filtered tap water, and high numbers of *B. atrophaeus* (10^9 CFU/L) were added to the tanks. High-volume cyclone samplers were used to sample the air when each HCU was switched off and during different operational phases. Samplers were operated for 5 minutes and the collecting fluid cultured for *B. atrophaeus*. The number of colonies was converted to CFU per cubic meter of air. **Results:** Under controlled experimental conditions, HCU-A released a small but significant level of aerosol during operational phases (eg, cooling) that resulted in increased pressure within the tank. The filler flap was identified as the principal area of aerosol release. The circulation of water within HCU-B and HCU-C was shown to generate an aerosol but, when connected to an 'aerosol collection set,' this aerosol was not released. However, it is essential that effective and sufficient vacuum is maintained. There was no aerosol release from HCU-D. **Conclusions:** A specialist in aerobiology using a biological tracer can determine the level of aerosol released from an HCU and its location. However, transmission of *M. chimaera* could occur via aerosolization of contaminated water, but it is not the only possible route of infection. The efficacy of recommended decontamination procedures must also be assured.

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Use of Health Information Exchange Improved the Identification of Healthcare-Associated Group A *Streptococcus* Infections

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Background: Healthcare-associated group A *Streptococcus* (GAS) infections can cause severe morbidity and death. Invasive GAS is a reportable condition in the 5-county metropolitan area of Denver, Colorado. Prior to August 2018, methodology to identify long-term care facility (LTCF) residency among reported GAS cases was accomplished by reviewing addresses reported electronically, and identification of postsurgical cases and outbreaks relied on reporting by healthcare facilities. We evaluated whether the use of a health information exchange (HIE) to identify healthcare exposures improved our ability to detect and rapidly respond to these events. **Methods**: In August 2018, we implemented a review of health records available in the HIE accessible by the Colorado Department of Public Health and Environment for all incoming reports of GAS for selected healthcare exposures: LTCF residency, surgery, delivery, wound care, and other relevant exposures. We defined an LTCF-related case as GAS in a current or recent resident (ie, in the 14 days prior to the positive culture) of an LTCF. Postpartum and postsurgical cases were defined as GAS isolated from a sterile site or wound during the inpatient stay or within 7 days of discharge following a delivery or surgical procedure. Outbreaks in each of these settings were defined as 2 or more cases within a 3-month period. We compared the number of cases and outbreaks identified in each category during a 1-year period before and after implementation of the use of the HIE in the case ascertainment process. **Results:** During August 2017 through July 2018, prior to implementation of the HIE process, we detected 45 LTCF cases and conducted outbreak investigations in 9 facilities. Moreover, 1 postsurgical case and 1 postpartum outbreak were reported by healthcare facilities; none were detected via surveillance. During August 2018 through July 2019, after the implementation of HIE process, we identified 70 LTCF cases and conducted outbreak investigations in 13 LTCFs. We detected 5 postsurgical cases and 3 postpartum cases, which resulted in 2 outbreak investigations. **Conclusions:** Enhanced GAS surveillance through use of a HIE resulted in detection of more healthcare-associated GAS infections and outbreaks. Timely identification of healthcare-associated GAS infections can allow for prompt response to outbreaks and promotion of proper infection control practices to prevent further cases. Jurisdictions in which GAS is a reportable condition should consider the use of HIEs as part of routine surveillance to identify GAS outbreaks in high-risk settings. HIEs should be made available to public health agencies for case ascertainment and outbreak identification.

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Use of Varying Single-Nucleotide Polymorphism Thresholds to Identify Strong Epidemiologic Links Among Patients with Methicillin-Resistant *Staphylococcus aureus* (MRSA)

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Background: Whole-genome sequencing (WGS) has a high discriminatory power in confirming outbreaks. Outbreak investigation models that categorize the possibility of an outbreak based on the degree of genetic relatedness of isolates are highly dependent on the single-nucleotide polymorphism (SNP) threshold used. **Methods:** NYU Langone Medical center is a 725-bed academic center that has implemented WGS of methicillin-resistant *Staphylococcus aureus* (MRSA) isolates since 2016. Patients admitted to a medical or intensive care unit were screened on admission and transfer. The first surveillance and clinical MRSA isolate during each hospitalization was sequenced. We conducted a retrospective analysis to identify strong epidemiologic links among patients involved in genetically related clusters. We used different SNP thresholds to define genetic relatedness to identify the optimal threshold that should prompt an outbreak investigation. We considered strong hospital epidemiologic links sharing the same room or unit or having resided in the same room or unit within 7 days. A pairwise analysis was conducted to compare the epidemiologic links among patients involved in genetically related clusters. **Results:** Among 1,070 isolates, our analysis focused on 777 belonging to USA100 and USA300 clones. For USA100 isolates, we identified 8, 14, and 20 clusters comprising of 16, 29, and 42 patients when the threshold for genetic relatedness was set at 20, 40, and 60 SNP differences, respectively. Patients identified in a cluster yielded a strong hospital epidemiologic link in 62.5%, 87.5%, and 91.7% of cases (Fig. 1). For USA300 isolates, SNP differences of 10, 20, and 30 were used, identifying 20, 34, and 40 clusters of 43, 79, and 127 patients. The expansion of the threshold from 10 to 30 resulted in a decrease of the percentage of pairwise analyses with a strong hospital epidemiologic link from 57.7% to 13.6% by increasing 13-fold the number of analyses that were conducted to identify only 3 times more cases with strong epidemiologic links (Fig. 2). **Conclusions:** The results of our study indicate that SNPs thresholds determined by intrapatient variability of MRSA isolates might need to be tailored to the individual setting to guide infection control interventions because optimal thresholds might vary depending on characteristics of the population, MRSA isolates, and screening practices. Establishing conservative thresholds might allow the identification and quantification over time of the locations (eg, rooms or units) where transmission is occurring as well as the investigation of the clusters without strong epidemiologic links that might be valuable in elucidating unrecognized routes of transmission.

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Figure 1. USA100 isolates **A.** Number of pairwise comparisons that yielded a shared room, shared unit (not room), shared room within 7 days or shared unit (not room) within 7 days between genetically related cases when the single nucleotide polymorphisms (SNPs) cutoff for defining relatedness was set at 20, 40 and 60. **B.** Percentage of pairwise comparisons that yielded any strong hospital epidemiologic link when the SNPs cutoff for defining relatedness was set at 20, 40 and 60.

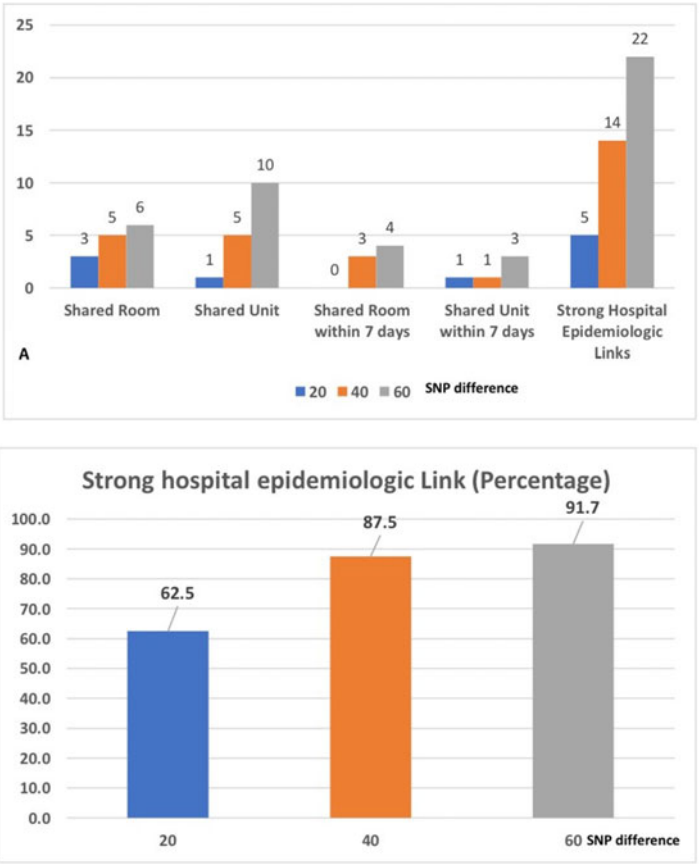

Fig. 1.