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Background: Infection prevention surveillance for cross transmission is often performed by manual review of microbiologic culture results to identify geotemporally related clusters. However, the sensitivity and specificity of this approach remains uncertain. Whole-genome sequencing (WGS) analysis can help provide a gold-standard for identifying cross-transmission events. **Objective:** We employed a published WGS program, the Philips IntelliSpace Epidemiology platform, to compare accuracy of two surveillance methods: (i.) a virtual infection practitioner (VIP) with perfect recall and automated analysis of antibiotic susceptibility testing (AST), sample collection timing, and patient location data and (ii) a novel clinical matching (CM) algorithm that provides cluster suggestions based on a nuanced weighted analysis of AST data, timing of sample collection, and shared location stays between patients. **Methods:** WGS was performed routinely on inpatient and emergency department isolates of *Enterobacter cloacae*, *Enterococcus faecium*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* at an academic medical center. Single-nucleotide variants (SNVs) were compared within core genome regions on a per-species basis to determine cross-transmission clusters. Moreover, one unique strain per patient was included within each analysis, and duplicates were excluded from the final results. **Results:** Between May 2018 and April 2019, clinical data from 121 patients were paired with WGS data from 28 *E. cloacae*, 21 *E. faecium*, 61 *K. pneumoniae*, and 46 *P. aeruginosa* isolates. Previously published SNV relatedness thresholds were applied to define genomically related isolates. Mapping of genomic relatedness defined clusters as follows: 4 patients in 2 *E. faecium* clusters and 2 patients in 1 *P. aeruginosa* cluster. The VIP method identified 12 potential clusters involving 28 patients, all of which were "pseudoclusters." Importantly, the CM method identified 7 clusters consisting of 27 patients, which included 1 true *E. faecium* cluster of 2 patients with genomically related isolates. **Conclusions:** In light of the WGS data, all of the potential clusters identified by the VIP were pseudoclusters, lacking sufficient genomic relatedness. In contrast, the CM method showed increased sensitivity and specificity: it decreased the percentage of pseudoclusters by 14% and it identified a related genomic cluster of *E. faecium*. These findings suggest that integrating clinical data analytics and WGS is likely to benefit institutions in limiting expenditure of resources on pseudoclusters. Therefore, WGS combined with more sophisticated surveillance approaches, over standard methods as modeled by the VIP, are needed to better identify and address true cross-transmission events.

Presentation Type:
Poster Presentation
Application of a Continuously Active Antimicrobial Surface Coating in Two Professional Sports Training Facilities

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Background: The role of surface contamination in infections is of interest in healthcare as well as other industries, especially where infections incur high cost. One such industry is professional sports, where infections pose significant risks to players and the organizations that employ them. Sports training facilities experience highly variable occupancy rates due to differing seasonal activities, presenting a measurement challenge because the relationship between occupancy and surface contamination is not well described. In a recent publication, a continuously active antimicrobial (CAA) surface coating demonstrated a reduction in bacterial bioburden in ICUs alongside a reduction in healthcare-associated infections (HAIs). **Objective:** We investigated the impact of a CAA surface coating on bioburden in 2 professional sports training facilities, despite changes in occupancy. **Methods:** A CAA surface coating was applied using an electrostatic sprayer to all surfaces in both facilities during a period of high-occupancy at facility A and during low occupancy at facility B. Surface cultures were taken using 3M Sponge-Sticks from lockers, gym equipment, and physiotherapy surfaces before treatment, 4–13 weeks after treatment at facility A and 4–23 weeks after treatment at facility B. Total aerobic bacteria counts were obtained by plating on tryptic soy agar, and geometric means of aerobic plate counts (APCs) were used to compare bioburden before and after treatment at both facilities and for an out-of-efficacy period at facility B (17–23 weeks). Occupancy rates were monitored as person days per week (pd/w) over the course of the study. **Results:** APC counts at facility A decreased 61% (585 CFU/100 cm^2 to 226 CFU/100 cm^2) from baseline to posttreatment, and occupancy remained constant (165 pd/w to 171 pd/w). At facility B, there was no significant change in APC (76 CFU/100 cm^2 to 80 CFU/100 cm^2), although occupancy increased >13,000% during the treatment period (3 pd/w to 386 pd/w). During the out-of-efficacy period at facility B, total bacteria increased 170% (217 CFU/100 cm^2) compared to the treatment period, and the occupancy remained relatively constant (344 pd/w). **Conclusions:** Levels of bioburden were significantly influenced by the application of the CAA surface coating, especially considering the variation in occupancy in both facilities before, during, and after the efficacy period. Facility A saw a significant reduction in bioburden during the treatment period ($P < .0001$), and a significant increase was observed at facility B during the out-of-efficacy period ($P < .0001$) despite constant occupancy rates, demonstrating the ability of the surface coating to reduce bioburden levels despite large changes in occupancy.

Presentation Type:
Poster Presentation
Comparative Antimicrobial Efficacy of Current Alcohol-Based Hand Rubs: Formulation, Dose, and Test Methods All Matter

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Background: Alcohol-based hand rubs (ABHRs) are the primary form of hand hygiene in healthcare settings globally. Many developed countries, and most US hospitals utilize wall-mounted ABHR dispensers throughout the facility. The