Presentation Type:
Poster Presentation

A Continuously Active Antimicrobial Surface Coating Reduces Bioburden in a Healthcare Setting

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Background: It is well known that contaminated surfaces contribute to the transmission of pathogens in healthcare settings, necessitating the need for antimicrobial strategies beyond routine cleaning with momentary disinfectants. A recent publication demonstrated that application of a novel, continuously active antimicrobial surface coating in ICUs resulted in the reduction of healthcare-associated infections. **Objective:** We determined the general microbial bioburden and incidence of relevant pathogens present in patient rooms at 2 metropolitan hospitals before and after application of a continuously active antimicrobial surface coating. **Methods:** A continuously active antimicrobial surface coating was applied to patient rooms in intensive care units (ICUs) twice over an 18-month period and in non-ICUs twice over a 6-month study period. The environmental bioburden was assessed 8–16 weeks after each treatment. A 100-cm^2 area was swabbed from frequently touched areas in patient rooms: patient chair arm rest, bed rail, TV remote, and backsplash behind the sink. The total aerobic bacteria count was determined for each location by enumeration on tryptic soy agar (TSA); the geometric mean was used to compare bioburden before and after treatment. Each sample was also plated on selective agar for carbapenem-resistant Enterobacteriaceae (CRE), vancomycin-resistant enterococci (VRE), methicillin-resistant *Staphylococcus aureus* (MRSA), and *Clostridioides difficile* to determine whether pathogens were present. Pathogen incidence was calculated as the percentage of total sites positive for at least 1 of the 4 target organisms. **Results:** Before application of the antimicrobial coating, total aerobic bacteria counts in ICUs were >1,500 CFU/100 cm^2, and at least 30% of the sites were positive for a target pathogen (ie, CRE, VRE, MRSA or *C. difficile*). In non-ICUs, the bioburden before treatment was at least 500 CFU/100 cm^2, with >50% of sites being contaminated with a pathogen. After successive applications of the surface coating, total aerobic bacteria were reduced by >80% in the ICUs and >40% in the non-ICUs. Similarly, the incidence of pathogen-positive sites was reduced by at least 50% in both ICUs and non-ICUs. **Conclusions:** The use of a continuously active antimicrobial surface coating provides a significant ($P < .01$) and sustained reduction in aerobic bacteria while also reducing the occurrence of epidemiologically important pathogens on frequently touched surfaces in patient rooms. These findings support the use of novel antimicrobial technologies as an additional layer of protection against the transmission of potentially harmful bacteria from contaminated surfaces to patients.

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A Microbiome-Based Solution to Address Alarming Levels of Drug-Resistant Bacteria in the Newborn Infant Gut

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Background: Recent studies have focused on the early infant gut microbiome, indicating that antibiotic resistance genes (ARGs) can be acquired in early life and may have long-term sequelae. Limiting the spread of antimicrobial resistance without triggering the development of additional resistance mechanisms would be of immense clinical value. Here, we present 2 analyses that highlight the abundance of ARGs in preterm and term infants and a proof of concept for modulating the microbiome to promote early stabilization and reduction in ARGs in term infants. Methods: Large-scale metagenomic analysis was performed on 2,141 microbiome samples (90% from pre-term infants) from 10 countries; most were from the United States (87%) and were obtained from the Comprehensive Antibiotic Resistance Database (CARD). We assessed the abundance and specific types of ARGs present. In the second study, healthy, breastfed infants were fed *B. infantis* EVC001 for 3 weeks starting at postnatal day 7. Stool samples were collected at day 21 and were processed utilizing shotgun metagenomics. Selected antimicrobial-resistant bacterial species were isolated, sequenced, and tested for minimal inhibitory concentrations to clinically relevant antibiotics. Results: In the first study, globally, 417 distinct ARGs were identified. The most abundant gene among all samples was annotated as *msrE*, a plasmid gene known to confer resistance to macrolide-lincosamide-streptogramin B (MLSB) antibiotics. The remaining most-abundant ARGs were efflux-pump genes associated with multidrug resistance. No significant association in antimicrobial resistance was found when considering delivery mode or antibiotic treatment in the first month of life. In the second study, the EVC001-fed group showed a significant decrease (90%) in ARGs compared to controls ($P < .0001$). ARGs that differed significantly between groups were predicted to confer resistance to β-lactams, fluoroquinolones, or multiple drug classes. Minimal inhibitory concentration assays confirmed resistance phenotypes among isolates Notably, we found resistance to extended-spectrum β-lactamases among healthy, vaginally delivered breastfed infants who had never been exposed to antibiotics. **Conclusions:** In this study, we show that the term and preterm infant microbiome contains alarming levels of ARGs associated with clinically relevant antibiotics harbored by bacteria commonly responsible for nosocomial infections. Colonization of the breastfed infant gut by a single strain of *B. longum* subsp *infantis* had profound impacts on the fecal metagenome, including reduction in ARGs and reduction of potential pathogens. These findings highlight the importance of developing novel approaches to limit the spread of ARGs among clinically relevant bacteria and the relevance of an additional approach in the effort to solve AR globally.

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Accuracy of Infection Control Surveillance in Identifying Genomically Confirmed Cross Transmission Clusters

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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.

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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.

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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