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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