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Poster Presentation

Developing a Public Health Model for Regional Infection Prevention Collaboration Among Healthcare Facility Networks

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Background: Antimicrobial resistance (AR), including *Clostridioides difficile* infection (CDI), can spread across the healthcare continuum when patients move between facilities. In 2015, the CDC recommended that healthcare facilities (HCFs) and local public health departments (LPH) coordinate their efforts to prevent the spread of AR and CDI. Accordingly, the California Department of Public Health (CDPH) Healthcare-Associated Infections (HAI) Program developed a model for implementing regionally based AR/CDI prevention collaboratives within HCF networks. **Methods:** The CDPH HAI Program began identifying regions in California with high AR/CDI incidence or risk for AR/CDI emergence using NHSN data. During 2015–2019, we organized AR/CDI prevention collaboratives in these regions. We recruited HCFs for participation by presenting at local professional organization meetings and engaging skilled nursing facility corporate leadership. HAI Program infection preventionists conducted onsite infection prevention assessments at each participating HCF. HAI Program and LPH staff convened quarterly in-person learning and discussion sessions focused on infection prevention and antimicrobial stewardship best practices. Participating HCFs committed to facility-tailored process improvement plans and conducted self-assessments to evaluate infection prevention practice changes at the conclusion of the collaborative. For CDI-focused collaboratives, we used data reported to CDPH via NHSN to assess changes in hospital- and community-onset CDI incidence among participating hospitals before and after the collaboratives. **Results:** Since 2015, 205 HCFs in 15 LPH jurisdictions have participated in 6 regional AR/CDI prevention collaboratives. Participating HCFs reported improved implementation of AR/CDI prevention strategies. For CDI-focused collaboratives, hospital-onset CDI incidence decreased by ~3% per month among participating hospitals. The collaboratives created forums for communication and relationship building, which previously did not exist among LPH and the HCF networks. We used our experience and feedback from partners to develop an HAI Program AR Prevention Collaborative Tool Kit to help LPHs and healthcare organizations develop and implement regional AR/CDI prevention collaboratives in other at-risk or high AR/CDI prevalence areas in California. The tool kit includes materials developed for each of our collaboratives, which may be adapted to meet local needs. **Conclusions:** Regionally coordinated AR/CDI prevention initiatives among LPHs and HCFs can contribute to increased AR awareness, improved AR prevention practices, and decreased AR/CDI incidence. The effectiveness of regional AR/CDI prevention collaboratives may be the result of concurrent efforts to improve AR prevention practices both within individual HCFs and across patient sharing networks.

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Development of a New High-Throughput Multilocus Sequence Typing Method to Monitor Causative Agents of Nosocomial Infections

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Background: Nosocomial infections cause 4%–56% mortality in newborns. Several epidemiological studies have shown that transmission of opportunistic pathogens from the sink to the patient, including *Pseudomonas aeruginosa*, *Stenotrophomonas maltophilia*, and *Serratia marcescens* are associated with nosocomial infections in neonatal intensive care units (NICUs). In this project, we aimed to develop fast, accurate, and high-throughput multilocus sequence typing assays (HiMLST-Illumina) to detect opportunistic pathogens to assess their distribution in the sink environment of NICUs and their transfer to patients. **Methods:** Genome sequences of *P. aeruginosa* (n = 45), *S. maltophilia* (n = 23) and *S. marcescens* (n = 34) strains were retrieved from public genome databases to build their pangenomes, using the open-source PGADB-builder server. The core genome was identified for each opportunistic pathogen and was searched for genes displaying the highest polymorphism. The minimal number of loci to include in a HiMLST-Illumina assay was determined by comparing topology of phylogenetic trees of concatenated loci based on genome similarity, computed as the average nucleotide identity (ANI) score. The primers used for HiMLST-Illumina schemes were designed *in silico* on a conserved domain and were tested on reference strains of each species. **Results:** Bioinformatics analyses showed that 3–4 loci (<300 base pairs per locus) distinguished strains with the same performances than ANI scores. The assays were tested using opportunistic pathogen isolates and environmental DNA originating from NICU sinks. The HiMLST-Illumina analysis of environmental DNA revealed the presence of at least 1 of the 3 studied opportunistic pathogens in 50% of sampled drains (n = 20). In a previous sampling, *P. aeruginosa* was isolated on selective culture media before and 48 hours after disinfection of a sink drain with chlorine. *S. marcescens* was also isolated from another sink 2 weeks after disinfection. Identification of the isolates was confirmed by HiMLST-Illumina analyses and will be typed to compare with clinical isolates. **Conclusions:** Initial *in silico* tests predict a high discriminating power of the HiMLST-Illumina method, suggesting that it would be possible to quickly identify strains of interest in a large number of samples. The power of this method is also in the possibility for molecular typing without a need for cultivation. Preliminary results suggest that sinks are readily colonized by opportunistic pathogens. This HiMLST-Illumina scheme will be applied in a 2-year intensive survey of NICUs in 3 hospitals in Montreal to evaluate the performance of new sink designs in limiting bioaerosol production and transmission of opportunistic pathogens to patients.

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