

in the VAD population. Further studies are reasonable and warranted.

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Poster Presentation

Evaluation of the bioMérieux EPISEQ-CS Software for wgMLST-Based Bacterial Strain Typing

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Background: Whole-genome sequencing (WGS) is becoming the method of choice for outbreak analysis of microbial pathogens. However, the main challenge with WGS for microbial strain typing is the conversion of raw sequencing data to actionable results for epidemiology and surveillance analysis. We evaluated the bioMérieux EPISEQ-CS, a cloud-based WGS data analysis software for outbreak detection to compare the results for 4 groups of different species previously characterized by strain typing and commonly isolated in hospital-acquired infections. **Methods:** In total, 30 methicillin-resistant *Staphylococcus aureus* (MRSA), 15 *Clostridioides difficile* (CDIFF), 17 *Pseudomonas aeruginosa* (PSA), and 10 *Acinetobacter baumannii* (ACB) isolates were included in this study. All isolates had been previously characterized by rep-PCR using the DiversiLab system (bioMérieux, France) and saved at -70°C . Before testing, samples were thawed and plated, and DNA extraction was performed on the QIACube (Qiagen, Hilden, Germany) using the DNEasy Ultra Clean Microbial kit extraction protocol. DNA libraries were prepared using the Nextera DNA Flex Kit and sequenced on the Illumina iSeq100 platform according to manufacturer's recommendations (Illumina, San Diego, CA). Generated sequences were uploaded into EPISEQ-CS, and wgMLST-based analysis was performed. We compared clusters generated by the DiversiLab system and EPISEQ-CS. **Results:** DiversiLab identified 9 MRSA clusters among 30 isolates. EPISEQ-CS reclassified 14 of 30 isolates into 5 MRSA clusters and the remaining 16 isolates were unrelated. DiversiLab identified 2 CDIFF clusters among 15 isolates. EPISEQ-CS reclassified 3 isolates into 1 CDIFF cluster and determined the remaining 12 to be unrelated. DiversiLab identified 5 PSA clusters among 17 isolates, whereas EPISEQ-CS reclassified all 17 isolates as unrelated. DiversiLab identified 2 ACB clusters among 10 isolates, whereas EPISEQ-CS reclassified 2 ACB isolates into 1 cluster and determined 8 to be unrelated. Analysis using Simpson's diversity index (D) suggested that the EPISEQ-CS showed increased diversity when compared to DiversiLab clustering across all bacterial species analyzed in this study. **Conclusions:** EPISEQ-CS enabled a comprehensive wgMLST analysis, including quality control and comparative epidemiological analysis, thereby providing a more reliable method for bacterial strain typing. As WGS becomes more affordable and applicable to routine epidemiological surveillance, EPISEQ-CS provides an informative tool in the monitoring of hospital-acquired infections.

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Evolution and Associated Factors of Hand Hygiene Compliance in the Surgical Areas of a Tertiary-Care Hospital

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Background: Hand hygiene (HH) is the most important measure for preventing healthcare-associated infections. The objective is to gain insight into the evolution of the degree of compliance with recommendations (DCR) on HH and its associated factors in the surgical areas of a tertiary-care hospital. **Methods:** This observational, cross-sectional study, was repeated over time, with direct observation of the DCR on HH during the daily activity of health-care workers in surgical areas: general surgery, urology, vascular surgery, traumatology, neurosurgery, thoracic surgery, heart surgery, pediatric surgery, otorhinolaryngology, gynecology and obstetrics, ophthalmology. Over 14 years (from 2005 to 2018), 15,946 HH opportunities were registered, together with different additional variables (age, sex, professional position, surgical area ...). The χ^2 test was used to study the association and the crude, and adjusted odds ratios were used to quantify its magnitude. **Results:** The DCR on HH in surgical areas was 49.7% (95% CI, 48.9%–50.5%), and in the group of nonsurgical areas it was

53.4% (95% CI, 53.1%–54.1%). The area with the highest degree of compliance was urology (56.7%; 95% CI, 53.9%–59.6%), and the area with the lowest degree of compliance was traumatology (43.3%; 95% CI, 40.4%–46.2%). Some associated factors were the indications “after an activity has been performed” (58.6%; aOR, 2.7; 95% CI, 2.5–2.9) and the availability of pocket-size alcohol-based disinfectant (63.8%; aOR, 2.4; 95% CI, 2.2–2.5). **Conclusions:** The DCR on HH in surgical areas is lower than in other hospital areas, and there is still some margin for improvement. We have identified some modifiable factors that have an independent association with HH compliance in surgical areas. Focusing on them will increase compliance with HH with the ultimate goal of reducing healthcare-associated infections.

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Evolution of Healthcare-Associated Infections and Antibiotic Resistance Programs in US Health Departments, 2009–2018

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Background: Domestically, the integration of public health into healthcare-associated infection (HAI) and antibiotic resistance (AR) prevention activities represents a major development. We describe CDC **Funding:** of public health HAI/AR programs through the Epidemiology and Laboratory Capacity (ELC) cooperative agreement to improve local capacity to prevent HAIs and detect and contain the spread of AR threats. **Methods:** We reviewed ELC budget reports and program documents to summarize the evolution of funded activities and programs from 2009 to 2018. **Results:** In 2009, 51 programs (49 states, 2 cities and territories) received US\$35.8 million through the American Recovery and Reinvestment Act for an initial 28-month period. These funds supported each jurisdiction to establish an HAI coordinator and a multidisciplinary HAI advisory group, coordinate and report HAI prevention efforts, conduct surveillance and report HAI data, and maintain an HAI plan; ~27 programs were also funded to coordinate multicenter HAI prevention collaboratives among acute-care hospitals. Through 2011, 188 state or local HAI/AR program positions were at least partially funded by the CDC. From 2011 to 2015, investments from the Affordable Care Act (~US\$10–11 million annually) were used to maintain the HAI/AR programs, with some expansion of program goals related to non-acute-care settings and antibiotic stewardship. In 2015, following the Ebola outbreak in West Africa, supplemental ELC funds were awarded to 61 programs (50 states, 11 cities and territories) totaling US\$85 million over 36 months. These awards marked an expansion of HAI/AR program activities to develop healthcare provider inventories, to conduct data-driven education and training, and to perform onsite infection control assessments in healthcare facilities. In 2016, through its AR Solutions Initiative, CDC invested US\$57.3 million in **Funding:** to 57 programs (50 states, 7 cities and territories), expanding laboratory capacities for AR threat detection (via the AR Laboratory Network) and epidemiologic activities to rapidly contain novel and targeted

multidrug-resistant organisms. As of 2018, >500 state or local HAI/AR program positions were at least partially funded by the CDC. **Conclusions:** State and local HAI/AR programs have grown substantially over the 10 years of their existence, as reflected in major increases in funding, staffing, scope, and partnerships. CDC investments and guidance have supported the development of HAI/AR epidemiology prevention and response capacity.

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Exploring the Potential Limitations of Using Medicare Data to Study the Spread of Infections from Hospital Transfers

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Background: Patient sharing between hospitals has long been known to be a contributor to the regional transmission of hospital-acquired infections. This inter-healthcare-facility connectedness suggests that regional, as opposed to local, control and surveillance strategies should be favored. However, the absence of easily and universally accessible patient transfer data hampers researchers and public health agencies who wish to build accurate network models of interfacility transmissions. Medicare data offer only a biased subsample of the full patient transfer network, but because it is widely available, this data source has historically been used for inference and simulation studies. **Objective:** The purpose of this study was to determine whether Medicare data could successfully be recalibrated to more closely resemble 100% inpatient capture data. **Methods:** We used data from the Healthcare Cost and Utilization Project (HCUP) to construct 100% capture and Medicare-only patient sharing networks among hospitals in Iowa, Wisconsin, and Nebraska. We used matrix decomposition techniques on the Medicare-only networks along with hospital characteristics from the American Hospital Association (AHA) data for feature construction in a truncated Poisson regression model, and we used Monte Carlo integration to obtain predicted values. These predicted values served as calibrated Medicare-only networks. We split the patient transfer data into training and testing sets and computed the mean squared prediction error (MSPE) for the testing data. We also built an individual based model (IBM) using HCUP and AHA data to perform epidemic simulations that depended on a matrix of patient transfer rates between hospitals. We then compared epicurves from these IBMs resulting from 100% capture networks, Medicare-only networks, and our calibrated networks. **Results:** Our calibrated networks reduced the MSPE with respect to Medicare-only networks by 84%, 47%, and 88% for Iowa, Wisconsin, and Nebraska, respectively. Although the epicurves from Medicare-only networks differed considerably from that from 100% capture networks, our calibrated networks retained high fidelity to the curves obtained from 100% capture networks. **Conclusions:** Medicare-only networks greatly underestimate the number of patients transferred between hospitals. Our approach allows us to use Medicare data to estimate networks when 100% inpatient capture is unavailable.

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