

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 healthcare 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