

Presentation Type:

Poster Presentation - Oral Presentation

Subject Category: Molecular Epidemiology

Research and implementation of a whole-genome sequencing surveillance system for outbreak detection

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Background: Traditional infection prevention (IP) methods for outbreak detection often rely on geotemporal clustering confined to single locations. We recently developed the Enhanced Detection System for Healthcare-Associated Transmission (EDS-HAT), which combines whole-genome sequencing (WGS) surveillance and machine learning of the electronic health record (EHR). Our retrospective research findings show potential transmissions averted and cost savings using EDS-HAT in real time. Here, we describe the process and initial findings from EDS-HAT real-time implementation. **Methods:** Real-time whole-genome sequencing surveillance began on November 1, 2021. Patient cultures positive for select bacterial pathogens who were hospitalized for ≥ 3 days or had a recent healthcare exposure in the prior 30-days were collected. Isolates were deemed genetically related if ≤ 15 single-nucleotide polymorphisms (SNPs) were identified for all organisms except *Clostridioides difficile* (≤ 2 SNPs). Clusters were manually investigated by both research and IP teams, and interventions were performed by the IP team. Data on collection, analysis, notification, and intervention dates were gathered. **Results:** As of January 11, 2022, 413 isolates had undergone whole-genome sequencing. Among them, 18 unique patient isolates were genetically related to ≥ 1 other isolate, comprising 7 clusters (range, 2–6 patients). Notable findings include a *Pseudomonas aeruginosa* cluster possibly related to a shared bronchoscope, a pseudo-outbreak of *Serratia marcescens* related to autopsy blood culture practice, and a cluster of vancomycin-resistant *Enterococcus faecium* on a shared transplant unit. Only 1 cluster of 2 isolates of *Klebsiella pneumoniae* had no known possible transmission routes. The median turnaround time from patient’s culture date to IP notification was 19 days (range, 13–28), with noted delays over the winter holiday. **Conclusions:** Real-time WGS can identify small clusters including potentially interruptible transmission routes. Rapid turnaround time, coordination between clinical and genomic laboratories, and a robust IP team are key factors in implementing a WGS surveillance program. Real-time WGS surveillance has the potential to reduce costs for hospitals, improve patient safety, and save lives.

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Table 1. Isolates sequenced and clusters detected

Organism	Isolates Sequenced	Clusters	Unique Patient Isolates Related
<i>Acinetobacter baumannii</i>	10	0	0
<i>Burkholderia cepaciae</i>	1	0	0
<i>Citrobacter freundii</i>	4	0	0
<i>Clostridioides difficile</i>	46	0	0
<i>Enterobacter</i> species	4	0	0
<i>Escherichia coli</i>	27	0	0
<i>Klebsiella oxytoca</i>	4	0	0
<i>Klebsiella pneumoniae</i>	27	2	5
Methicillin-resistant <i>Staphylococcus aureus</i>	42	0	0
<i>Proteus mirabilis</i>	33	0	0
<i>Providencia</i> species	4	0	0
<i>Pseudomonas aeruginosa</i>	119	3	6
<i>Pseudomonas</i> species (not <i>aeruginosa</i>)	4	0	0
<i>Serratia marcescens</i>	40	1	5
<i>Stenotrophomonas maltophilia</i>	30	0	0
Vancomycin-resistant <i>Enterococcus faecium</i>	18	1	2
Total	413	7	18

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Monitoring disparities in healthcare-associated infection surveillance: A SHEA Research Network (SRN) Survey

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Background: Inequities are seen in many health-related outcomes, and systemic and structural factors result in inequitable care based on social determinants of health (SDOH). However, whether disparities exist specifically in healthcare-associated infections (HAIs) based on these factors has not been well described. Furthermore, there are no national standards on whether information related to equity and SDOH should be included in HAI surveillance and how such information could be used. **Methods:** We surveyed US members of the SHEA Research Network (SRN), a consortium of healthcare facilities with leaders interested in healthcare epidemiology and infection prevention, via an online REDCap survey from October to December 2021. **Results:** Of the 68 eligible US SRN facilities, 28 (41%) responded. Among them, 27 institutions provide direct patient care and were analyzed. Of these 27 facilities, 8 (30%) collected data regarding variables related to equity including language for care, race or ethnicity, insurance status, and other. Of these facilities, 38% are collecting but not otherwise using this information; other facilities use this information for a variety of reporting and intervention purposes (Fig. 2). Only 3 facilities (11%) analyzed whether disparities exist in any HAI rates. The most common barrier to collecting SDOH information is that facilities have not considered doing this work (Fig. 3). Of the 15 facilities not yet undertaking such work, 10 (67%) were interested in doing so. Specific recommendations about how to operationalize such collection are needed (Table 1). **Conclusions:** Most institutions in this sample are not collecting data that would allow for assessment of disparities in the rates of HAIs; however, there is interest in doing so. A minority of early adopter facilities are assessing whether disparities exist and are designing interventions. National guidance can play a key role in standardizing the collection of this

Figure 1. Are Facilities Collecting or Analyzing SDOH Data?

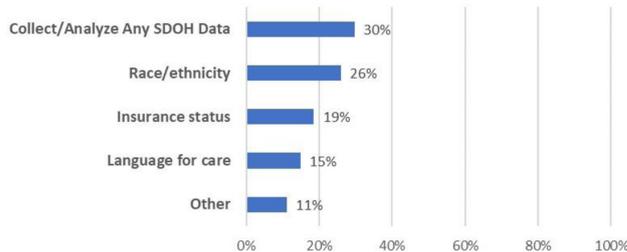


Figure 2. When Facilities Collect SDOH Data for HAIs, How is It Used?

