

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

Presentation Type:

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Subject Category: Other

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?

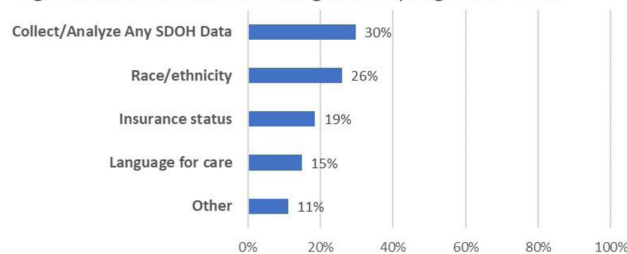


Figure 2. When Facilities Collect SDOH Data for HAIs, How is It Used?

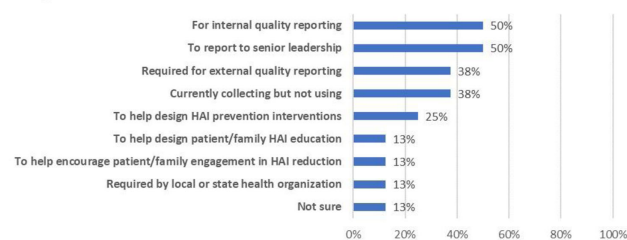
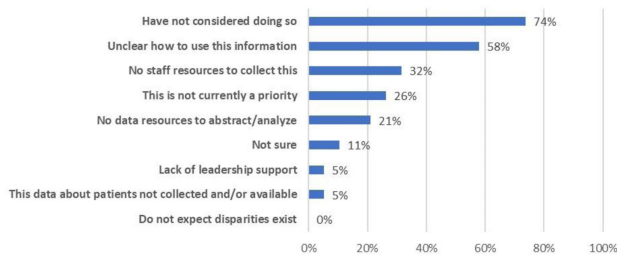


Figure 3. Reasons Why Facilities Do Not Collect SDOH Data for HAIs



information and translating early findings to identify and subsequently improve disparities within HAIs.

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A SARS-CoV-2 outbreak due to vaccine breakthrough in an acute-care hospital

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Background: The δ (delta) variant has spread rapidly worldwide and has become the predominant strain of SARS-CoV-2. We analyzed an outbreak caused by a vaccine breakthrough infection in a hospital with an active infection control program where 91.9% of healthcare workers were vaccinated. **Methods:** We investigated a SARS-CoV-2 outbreak between September 9 and October 2, 2021, in a referral teaching hospital in Korea. We retrospectively collected data on demographics, vaccination history, transmission, and clinical features of confirmed COVID-19 in patients, healthcare workers, and caregivers. **Results:** During the outbreak, 94 individuals tested positive for SARS-CoV-2 using reverse transcription-polymerase chain reaction (rtPCR) testing. Testing identified infections in 61 health care workers, 18 patients, and 15 caregivers, and 70 (74.5%) of 94 cases were vaccine breakthrough infections. We detected 3 superspreading events: in the hospital staff cafeteria and offices (n = 47 cases, 50%), the 8th floor of the main building (n = 22 cases, 23.4%), and the 7th floor in the maternal and child healthcare center (n = 12 cases, 12.8%). These superspreading events accounted for 81 (86.2%) of 94 transmissions (Fig. 1, 2). The median interval between completion of vaccination and COVID-19 infection was 117 days (range, 18–187). There was no significant difference in the mean Ct value of the RdRp/ORF1ab gene between fully vaccinated individuals (mean 20.87, SD±6.28) and unvaccinated individuals (mean 19.94, SD±5.37, P = .52) at the time of diagnosis. Among healthcare

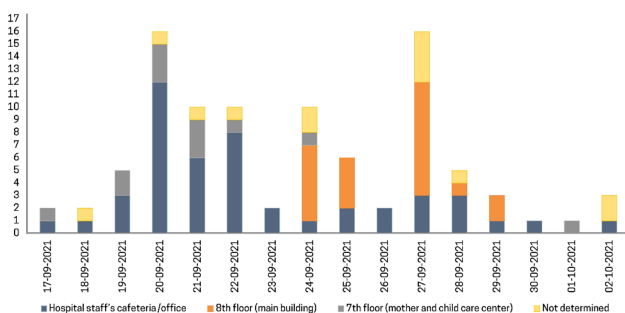


Fig. 1.

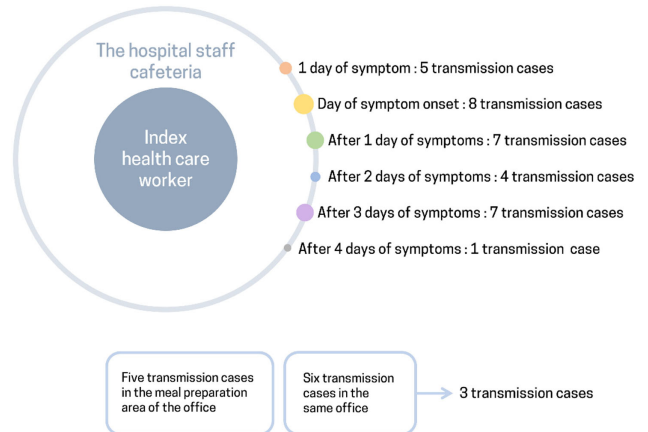


Fig. 2.

Table 1. Clinical course and outcome of the study participants

	Health care workers (n=61)	Patients (n=18)	Caregivers (n=15)	P value
Place of isolation				<0.001
Community treatment center	52 (85.2)	0	9 (60.0)	
Hospital	6 (9.8)	18 (100.0)	6 (40.0)	
Home	3 (4.9)	0	0	
Duration of hospitalization/isolation, days	9 (8-10)	13 (9-19)	9 (6-11)	0.01
Clinical course				<0.001
Not hospitalized, no limitations of activities	53 (86.9)	0	9 (60.0)	
Not hospitalized, limitation of activities	1 (1.6)	0	0	
Hospitalized, not requiring supplemental oxygen	6 (9.8)	7 (36.8)	6 (40.0)	
Hospitalized, requiring any supplemental oxygen	1 (1.6)	6 (33.3)	0	
Hospitalized, requiring noninvasive ventilation or HFNC	0	1 (5.6)	0	
Hospitalized, receiving invasive MV or ECMO	0	0	0	
In hospital mortality	0	4 (22.2)	0	0.001

^aHFNC: high-flow nasal cannula; MV: mechanical ventilation; ECMO: extracorporeal membrane oxygenation.

workers and caregivers, only 1 required oxygen supplementation. In contrast, among 18 patients, there were 4 fatal cases (22.2%), 3 of whom were unvaccinated (Table 1). **Conclusions:** Superspreading infection among fully vaccinated individuals occurred in an acute-care hospital while the δ (delta) variant was dominant. Given the potential for severe complications, as this outbreak demonstrated, preventive measures including adequate ventilation should be emphasized to minimize transmission in hospitals.

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Subject Category: Outbreaks

Nosocomial outbreak of δ (delta) variant SARS-CoV-2 on a liver transplant unit: A complex epidemiologic and genomic investigation

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Background: In late September 2021, a cluster of patients with nosocomial COVID-19 was identified on a liver transplant unit at University of Nebraska Medical Center. **Methods:** The outbreak investigation included contact tracing via patient chart and employee health record reviews and serial prevalence testing for SARS-CoV-2 among potentially exposed patients and healthcare workers (HCWs). Routine admission and preprocedural screening for SARS-CoV-2 was performed, and involved patients had negative admission screening results with positive SARS-CoV-2 tests >5 days from admission. Mitigation strategies involved reinforcement of patient care and visitation procedures. Whole-genome sequencing of positive SARS-CoV-2 specimens was conducted. **Results:** The potential outbreak cluster included 6 patients in the same quadrant of the liver transplant unit, 1 visitor, and 11 healthcare workers (Fig. 1). Moreover,