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Concise Communication

Nosocomial outbreak of SARS-CoV-2 delta variant among vaccinated healthcare workers and immunocompromised patients on a solid-organ transplant unit: Complexities of an epidemiologic and genomic investigation

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Abstract

In September 2021, a cluster of 6 patients with nosocomial coronavirus disease 2019 (COVID-19) were identified in a transplant unit. A visitor and 11 healthcare workers also tested positive for severe acute respiratory coronavirus virus 2 (SARS-CoV-2). Genomic sequencing identified 3 separate introductions of SARS-CoV-2 with related transmission among the identified patients and healthcare workers.

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Nosocomial outbreaks of coronavirus disease 2019 (COVID-19) are challenging to recognize and control.[1] Practices such as admission screening, universal masking, and visitation restrictions are used to minimize the risk of hospital transmission.[2] In September 2021, a COVID-19 outbreak occurred in a solid-organ transplant unit among patients and vaccinated healthcare workers (HCWs) despite strict infection control measures. We investigated this outbreak using contact tracing and whole-genome sequencing (WGS).

Methods

Our 718-bed academic hospital has a 48-bed solid-organ transplant unit with single-patient rooms. Standard practices included optional patient surgical masking, limitation of visitation to 2 visitors per patient, and surgical masking of HCWs and visitors was required. However, masks were not required for <5 HCWs present in nonclinical areas. Universal admission and preprocedure screening for severe acute respiratory coronavirus virus 2 (SARS-CoV-2) with a nasopharyngeal PCR assay was required. Nosocomial COVID-19 was defined as a positive SARS-CoV-2 test occurring ≥48 hours from admission with a negative admission test.[1]

After notification of a potential outbreak (day 0), contact tracing was conducted for patients and employees. All unit patients and HCWs working in the unit or the transplant service from outbreak day −1 to +1 were tested serially for SARS-CoV-2 by PCR. Potential exposures, test results, symptom onset date, sick contacts, prior positive SARS-CoV-2 test results, and vaccination status were collected from patients and HCWs. Positive SARS-CoV-2 samples with a cycle threshold (Ct) value <28 were subjected to WGS. A clade was defined as a group of samples with ≤4 single nucleotide polymorphism differences. WGS methodological details are provided in the Supplementary Material (online). Several unit-specific mitigation measures were implemented (Table 1).

Results

On outbreak day 0, 5 inpatients with positive SARS-CoV-2 tests were identified (Supplementary Fig. 1 online). On the same day, all 46 patients in the unit were tested with negative results. Serial SARS-CoV-2 testing identified 3 additional SARS-CoV-2–positive patients among 121 tests over 12 days. We excluded 2 of these patients (see Supplementary Material online). In total, 6 patients were associated with the outbreak.

The 6 SARS-CoV-2–positive patients had been hospitalized for at least 5 days (range, 5–30) and had had prior negative

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Table 1. Transplant Unit-Specific Mitigation Measures

Immediately transferred patients diagnosed with COVID-19 to a designated COVID-19 unit
Always closed patient doors to decrease airborne transmission
Added universal eye protection to universal masking
Limited visitors to 1 per patient with strict visitor screening for COVID-19 symptoms
Restricted HCWs from gathering without masks regardless of group size
Encouraged only essential HCWs to enter patient rooms
Ensured enhanced environmental cleaning was performed
Ensured air handling was functioning appropriately
Promptly tested and isolated symptomatic employees
Emphasized and enforced existing infection control policies (eg, patient and visitor masking)

Note. HCW, healthcare worker.

SARS-CoV-2 testing. Two patients had had liver transplants (see patient characteristics in Supplementary Table 1 online). Also, 3 patients were unvaccinated and 3 had completed 2 doses of mRNA vaccines >5 months prior. Of these 6 patients, 5 were symptomatic, but all had other concurrent conditions (eg, bloodstream infections). Half of the COVID-19 diagnoses were made incidentally as the result of preprocedural testing. Ultimately, 2 patients died; 1 of these patients died potentially due to COVID-19. The Ct values for SARS-CoV-2–positive cases are provided in Supplementary Table 2 (online).

Initial HCW testing (days 0–4) resulted in 9 positive and 164 negative SARS-CoV-2 tests. Employee health records over the prior month identified 2 additional positive HCWs with unit connections. A second round of HCW testing (days 7–11) detected no new cases (88 negative results and 24 requested tests not completed). All 11 SARS-CoV-2–positive HCWs had completed 2 doses of an mRNA vaccine, although >6 months had elapsed since the second dose. Of these 11 HCWs, 6 had mild symptoms. Also, 3 HCWs worked in administrative offices and 8 provided direct patient care.

We investigated patient visitation through patient and HCW interviews. Patient 2 had a visitor who tested positive for SARS-CoV-2 on day −4. Symptom onset, dates, and duration of exposure to this patient were unknown, but reportedly, they were compliant with masking policies and had been vaccinated. Visitors of other patients had noncompliance with masking policies, but none had known COVID-19.

Furthermore, WGS was performed for all 6 patients and for 6 of 11 HCWs (HCWs 1–6). Of the 5 nonsequenced samples (HCWs 7–11), 4 HCWs were asymptomatic with high Ct values (>28), and the Ct value for 1 of these HCWs was unavailable. WGS identified 3 clades (Supplementary Fig. 2 online), all of which were B.1.617.2 lineage [ie, the δ (delta) variant]. Patients 1–6 shared the same clade as HCWs 1–3 (clade 1). HCWs 4–6 (administrative personnel in a shared office) had 2 distinct clades (2 and 3), suggesting transmission between HCWs 5 and 6 (clade 3).

Epidemiologic tracing combined with WGS identified multiple virus introductions into the hospital environment (Fig. 1). Specifically, HCWs 4–6 had 2 separate introductions not involving patient care, and their strain was distinct from the outbreak strain. No clear index case could be identified. No further cases of patient spread were identified after outbreak mitigation (Table 1). The last SARS-CoV-2–positive test for an HCW occurred on day 7 of this outbreak.

Discussion

We identified a nosocomial outbreak of the SARS-CoV-2 δ (delta) variant in 6 patients and 8 vaccinated HCWs in a transplant unit. Other outbreaks in transplant units were reported in the prevaccination era.[3,4] Our transplant-unit outbreak was the first described during SARS-CoV-2 δ (delta) variant circulation. This outbreak was confirmed by WGS and included cases of vaccinated HCWs.

The source of the outbreak was difficult to define. We identified a temporal linkage between patient 2's visitor with COVID-19 diagnosed on day −4 and HCWs 1 and 8–10 between days −6 and −3. HCWs 8–10 had contact with the other 5 patients in that same time frame. Thus, HCWs 8–10 may have acquired SARS-CoV-2 from a patient or may have had community-onset COVID-19 and served as the index case. Possible airborne transmission may have occurred within this localized unit without negative-pressure isolation. Using WGS, we defined a separate outbreak among 3 office workers with unmasked exposures to each other.

This study had several limitations. Despite our best efforts, we could not discern a definite index case. This difficulty has been encountered by others investigating COVID-19 outbreaks[5] and was likely due to asymptomatic transmission and/or inherent limitations of contact tracing and WGS. Without dates of symptom onset for 5 asymptomatic HCWs with multiple exposures, we were unable to determine the timeline of transmission. Furthermore, ∼20% of HCWs did not complete the second round of testing. WGS was limited by specimen availability and viral load, making confirmation of outbreak involvement difficult for some cases. We also lacked information regarding visitor symptoms and exposure period, and we may have missed other visitor cases.

This outbreak has provided several lessons for the prevention of future COVID-19 outbreaks. First, this outbreak occurred despite high vaccination rates (100% of HCWs and 50% of patients), presumably due to waning vaccine-related immunity (all vaccinations had been received >5 months before the outbreak) and increased transmissibility of the SARS-CoV-2 δ (delta) variant.[7,8] We suspect that lapses occurred in infection control practices, specifically masking among patients and visitors as well as HCWs in nonpatient care areas. Our observations of HCW masking in clinical areas demonstrated excellent compliance, raising concern for transmission between masked HCWs and patients. Given these findings, booster vaccinations among HCWs and patients should be emphasized, and universal N95 use in all patient care areas should be considered when COVID-19 community transmission rates are high. Additionally, prompt isolation of even minimally symptomatic HCWs prevents further nosocomial spread.

Early recognition of outbreaks is essential to preventing spread, as has occurred in hospitals with less stringent infection control measures.[9] One difficulty in early identification is underlying disease processes that distract clinicians from considering nosocomial COVID-19. This report emphasizes vigilance with measures such as masking, universal admission testing, low threshold of testing of symptomatic inpatients, and vaccine boosters, especially with the more contagious SARS-CoV-2 o (omicron) variant and especially for immunocompromised patients. Traditional epidemiologic methods combined with WGS provide the best opportunity to understand the source and spread of these outbreaks.

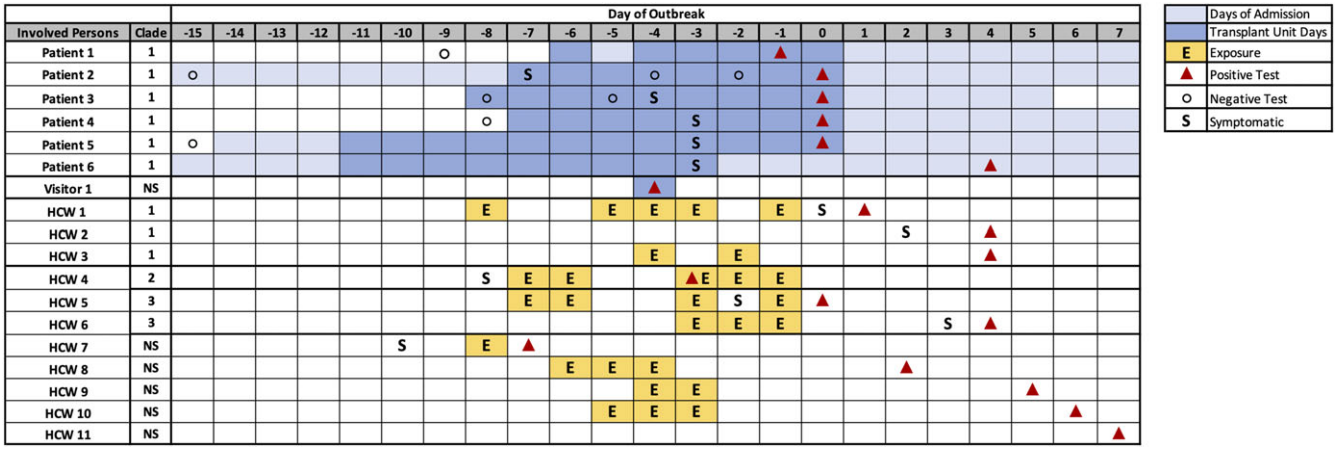

Fig. 1. Outbreak timeline. Timeline of outbreak among patients, a visitor, and healthcare workers (HCWs) with contact tracing and sequencing clades. Clades were determined by whole-genome sequencing. Clade 1 represents the solid-organ transplant unit outbreak. Clades 2 and 3 occurred in separate offices. Exposure was defined as any HCW self-reported contact with COVID-19 positive patient, >15 minutes with an unmasked COVID-19 positive HCW, or HCWs assigned to the same patient during the same shift based on nursing assignments (regardless of masking). No HCWs self-reported any unmasked exposure to patients. Note. NS: isolate not sequenced. Circle: negative SARS-CoV-2 PCR. Triangle: positive SARS-CoV-2 PCR. S: date of symptom onset.

Supplementary material. To view supplementary material for this article, please visit https://doi.org/10.1017/ice.2022.233.

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