Infection Control & Hospital Epidemiology (2021), 1–4
doi:10.1017/ice.2021.471

Concise Communication

Hospital outbreak of the severe acute respiratory coronavirus virus 2 (SARS-CoV-2) delta variant in partially and fully vaccinated patients and healthcare workers in Toronto, Canada

Erica K. Susky MSc[1], Susy Hota MD, MSc[1,2,3], Irene E. Armstrong MD, MSc[4], Tony Mazzulli MD[5], Shaindel Kestenberg RN, MN[7], Leanne K. Casaubon MD, MSc[3,6], John Granton MD[3,7,8], Carly Rebelo MSc[1,2], Erika Bartels RN[4], Jeff Wrana PhD[9] and Alon Vaisman MD, MAS[1,2,3]

[1]Infection Prevention and Control Department, University Health Network, Toronto, Ontario, Canada, [2]Division of Infectious Diseases, University Health Network, Toronto, Ontario, Canada, [3]Department of Medicine, University of Toronto, Toronto, Ontario, Canada, [4]Toronto Public Heath, Toronto, Ontario, Canada, [5]Department of Microbiology, Mount Sinai Health System and University Health Network, Toronto, Ontario, Canada, [6]Division of Neurology, University Health Network, Toronto, Ontario, Canada, [7]Department of Health Services, University Health Network, Toronto, Ontario, Canada, [8]Division of Pulmonary and Critical Care, University Health Network, Toronto, Ontario, Canada and [9]Lunenfeld-Tanenbaum Research Institute Mount Sinai Hospital, Toronto, Ontario, Canada

Abstract

The severe acute respiratory coronavirus virus 2 (SARS-CoV-2) delta variant is highly transmissible, and current vaccines may have reduced effectiveness in preventing symptomatic infection. Using epidemiological and genomic analyses, we investigated an outbreak of the variant in an acute-care setting among partially and fully vaccinated individuals. Effective outbreak control was achieved using standard measures.

Keywords: COVID-19; outbreak; nosocomial transmission

(Received 30 July 2021; accepted 20 October 2021)

The delta variant of severe acute respiratory coronavirus virus 2 (SARS-CoV-2) continues to rapidly spread and, as of early October 2021, the variant was already responsible for >75% of all coronavirus disease 2019 (COVID-19) cases in Canada and the United States.[1] The rapid spread of the variant, secondary to its increased transmissibility compared to other variants, has also been coupled with a resurgence in hospitalization in regions where it predominates.[2] Currently, vaccines that are widely available are somewhat less effective against the variant; the most recent estimations indicate an ~20% reduction in protection against symptomatic disease after a single BioNTech-Pfizer BNT162b2 vaccine dose, for example.[3] Whether the variant poses increased risk of severe disease and mortality, particularly among vulnerable populations, remains unknown.

The delta variant is highly transmissible and current COVID-19 vaccines may be less protective; thus, hospitals continue to be susceptible to outbreaks. The effect the variant will have on transmission dynamics among vulnerable hospitalized patients who may or may not be fully vaccinated remains unknown. Whether current control measures (symptom screening, isolation of patients with high-risk exposures, physical distancing, surveillance testing, and universal masking of patients and staff) are effective in mitigating outbreaks also remains unknown. Here, we describe an outbreak due to the delta variant in an acute-care setting involving partially and fully vaccinated patients and healthcare workers (HCWs) along with the control measures necessary to curb transmission. The outbreak occurred at Toronto Western Hospital, Toronto, Canada, a tertiary-care hospital with 272 inpatient beds. The neurovascular unit has a maximum census of 31 beds in primarily multibed rooms, 10 of which are level-2 intensive care unit (ICU) beds.

Methods

During the study period, Toronto COVID-19 daily case rates ranged between 0.2 and 0.25 new cases per 100,000 people. Nearly all patients admitted to our facility during this time were tested for SARS-CoV-2 on admission, and all the patients included in our outbreak were tested on admission. Nosocomial cases of COVID-19 were defined as a positive SARS-CoV-2 polymerase chain reaction (PCR) test using nasopharyngeal swab detected ≥72 hours after admission. Confirmed epidemiological links were defined as any exposures between patients or HCWs during the period of infectivity. Outbreak control measures included SARS-CoV-2 PCR point-prevalence testing of all HCWs and of all patients every 3–5 days. Furthermore, HCWs were assigned to their units (ie, cohorted). Ambulation of patients was restricted, and strict adherence to patient masking within 2 m of others was strictly enforced. Droplet and contact precautions were observed for all patients, and daily cleaning of high-touch surfaces was enhanced. The unit was closed to new patient admissions and visitors.

PCR testing was performed using 1 of 4 platforms: BGI real-time fluorescent RT-PCR 2019 nCoV assay (BGI Gemonics, China), cobas SARS-CoV-2 assay (Roche Diagnostics, Basel, Switzerland), Seegene Allplex 2019 nCoV assay (Seegene, Seoul,

Author for correspondence: Dr Alon Vaisman, E-mail: alon.vaisman@uhn.ca
Cite this article: Susky EK, *et al.* (2021). Hospital outbreak of the severe acute respiratory coronavirus virus 2 (SARS-CoV-2) delta variant in partially and fully vaccinated patients and healthcare workers in Toronto, Canada. *Infection Control & Hospital Epidemiology*, https://doi.org/10.1017/ice.2021.471

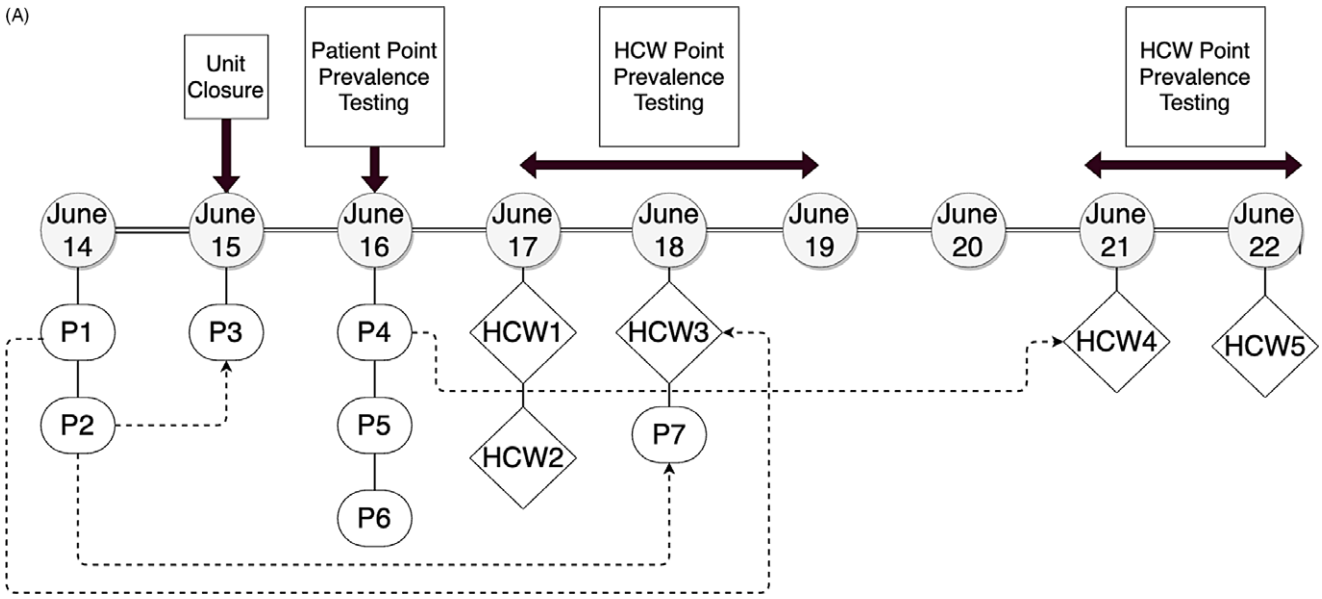

Fig. 1a. (A) Timeline of events pertaining to the outbreak. New cases are indicated below the corresponding date of testing. Patients (P) are identified in rounded rectangles; new healthcare worker (HCW) cases are identified in diamonds. Dotted lines represent suspected epidemiological links.

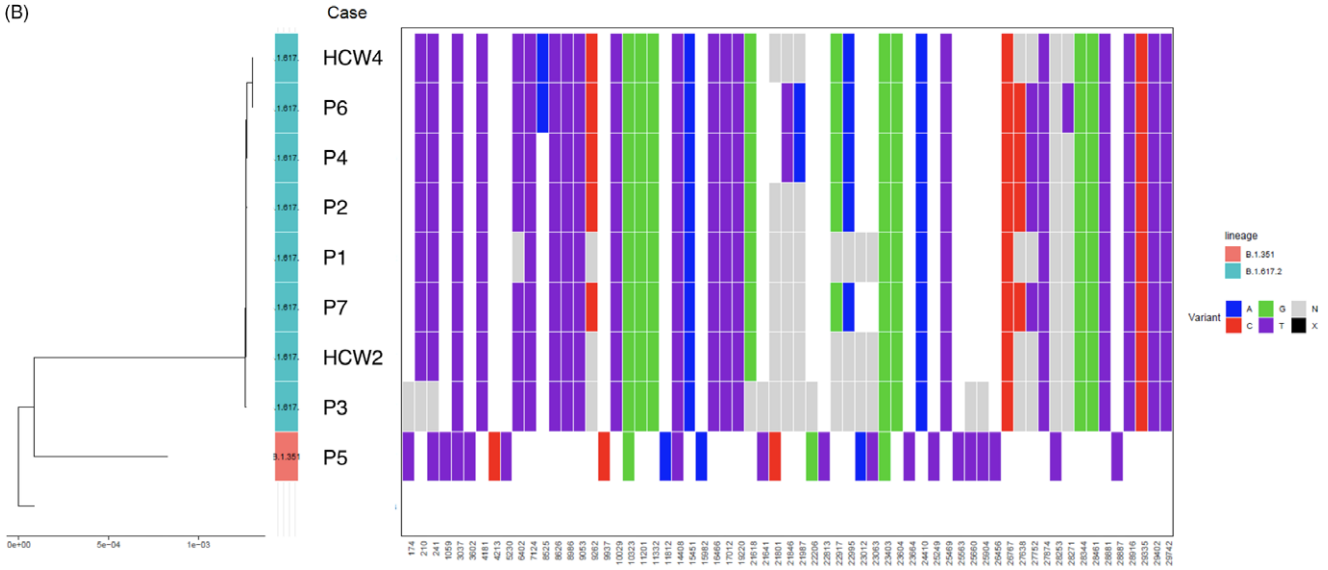

Fig. 1b. (B) SARS-CoV-2 whole-genome sequencing analysis and report for outbreak cases. Lineage assignment was determined using the phylogenetic assignment of the named global outbreak lineage (PANGOLIN) software tool Colors represent the detected amino acid at the position listed along the X axis. The phylogenetic tree on the left indicates the relatedness of the sequenced SARS-CoV-2 isolates for each patient. Isolates that differ by 0 mutations are considered "identical"; those that differ by 1–2 mutations are considered "nearly identical"; those that differ by 3 mutations are considered "similar"' and those that differ by >3 mutations are considered "different."

South Korea), and Luminex ARIES 2019-nCoV assay (Luminex, Austin, TX). Screening for variants of concern (VOCs) was conducted using the C19-SPAR-Seq platform, a multiplex RT-PCR method using primers corresponding to the RNA-dependent RNA polymerase, S-receptor–binding domain, envelope, nucleocapsid, and 2 regions of the spike gene.[4] Whole-genome sequencing (WGS) was conducted at the Hospital for Sick Children.

Results

During the outbreak, from June 15 to 22, 2021, COVID-19 cases were identified in 7 patients and 5 HCWs (Fig. 1A). Patient 1, admitted to hospital on June 7, developed fever upon transfer to the neurovascular unit on June 10. Although the fever was initially attributed to a urinary tract infection, the patient tested positive on June 14. The acquisition of SARS-CoV-2 infection was not attributable to the unit due to a symptom onset date prior to their transfer. A second patient tested positive on June 14, triggering a closure of the unit to new admissions and/or visitors 1 day after the first case was identified on June 15. Unit-wide point-patient prevalence screening of 22 patients was conducted on June 16, which identified 3 additional cases (patients 4, 5, and 6). Patients 3 and 7 were roommates of patient 2 during their period of infectivity (POI) and tested positive on June 15 and 18, respectively. Patient 2 was

Table 1. Line List of Patients (P) and Healthcare Workers (HCWs) Involved in the Outbreak

Identifier	Admission Date	Symptom Onset Date	Test Date	WGS	VOC Screen	Vaccination Status[a]	Symptom Status[b]
P1	07-Jun-21	10-Jun-21	14-Jun-01	Delta	N501Y+ E484K-	1 dose	Mild
P2	11-Jun-21	13-Jun-21	14-Jun-21	Delta	N501Y- E484K-	1 dose	Severe
P3	11-Jun-21	NA	15-Jun-21	Delta	N501Y- E484K-	2 doses	Asymptomatic
P4	18-May-21	14-Jun-21	16-Jun-21	Delta	N501Y- E484K-	2 doses	Mild
P5	20-May-21	15-Jun-21	16-Jun-21	Delta	N501Y- E484K-	1 dose	Mild
P6	13-Jun-21	17-Jun-21	16-Jun-21	Beta	N501Y+ E484K+	2 doses	Mild
P7	11-Jun-21	18-Jun-21	18-Jun-21	Delta	N501Y- E484K-	2 doses	Moderate
HCW1	NA	13-Jun-21	17-Jun-21	NA	501Y+ E484K-	2 doses	Mild
HCW2	NA	14-Jun-21	17-Jun-21	NA	NA	2 doses	Mild
HCW3	NA	17-Jun-21	18-Jun-21	Delta	N501Y- E484K-	2 doses	Mild
HCW4	NA	21-Jun-21	21-Jun-21	Delta	N501Y- E484K-	1 dose	Mild
HCW5	NA	NA	22-Jun-21	NA	N501Y- E484K-	2 doses	Asymptomatic

Note. WGS, whole-genome sequencing; VOC, variant of concern. The N501Y mutation is commonly found in the Alpha, Beta, and Gamma variants; the E484K mutation is commonly found in the β and γ variants.
[a]All vaccines were mRNA vaccines.
[b]Mild = cough, rhinorrhea, sore throat, no therapy required; moderate = requiring therapy but no ICU admission; severe = ICU admission.

considered a community case because symptom onset occurred only 48 hours into their admission.[5] None of the other patients had epidemiological links. Among the 7 patients, 4 patients (patients 1, 4, 5, and 6) developed mild symptoms. Of the remaining 3 patients, patient 3 was asymptomatic, patient 2 was readmitted to an intensive care unit at another hospital because their COVID-19 illness required supplemental oxygen but this patient was not intubated. Patient 7 developed pneumonia that required supplemental oxygen and treatment with dexamethasone but did not require ICU admission.

Point-prevalence testing of the staff working on the unit were performed from June 17 to 19 and again from June 21 to 22, yielding 3 positive results among 155 tests and 2 cases among 157 staff, respectively. Moreover, 3 HCWs were deemed to have had high-risk exposures to the SARS-CoV-2–positive staff, and none resulted in a transmission event. HCWs 3 and 4 had contact with SARS-CoV-2–positive patients P1 and P4, respectively, during their period of infectivity, but these HCWs were wearing eye protection and ASTM level III masks during these interactions. The remaining 3 HCWs did not have epidemiological links nor did they report exposures outside the workplace. All cases were fully vaccinated, with both doses of Pfizer-BioNTech vaccine >14 days before the outset of the outbreak except for patient 2 and HCW 4; they each had 1 dose of the Pfizer-BioNTech vaccine 14 days prior to infection. No HCW required hospitalization and 1 HCW was asymptomatic.

Of the 12 cases, 7 generated high-quality data (genome completeness >90%) with an additional 2 specimens providing adequate coverage for comparison (Fig. 1B). Overall, 8 specimens (6 patients and 2 HCWs) were consistent with the delta variant, and 1 specimen was a beta variant. All delta variant sequences were identical or nearly identical (with a 1 SNP difference). Patient 4, who was admitted on June 13 after a recent stay at a healthcare facility in South Africa, was initially considered part of the outbreak but was excluded when WGS confirmed the beta variant in this patient (Table 1). HCW 1 was excluded because they had a beta variant, which differed from the outbreak (delta) variant.

Discussion

This is the first publication of an outbreak in an acute-care setting involving the delta variant in partially or fully vaccinated individuals. Even full vaccination did not preclude infection or transmission of the delta variant in this setting, given the reduction in efficacy of vaccination against the delta variant.[6,7] Prior studies from skilled nursing facilities have demonstrated breakthrough SARS-CoV-2 infections in fully vaccinated individuals with non-delta variants; however, no transmission was demonstrated.[7,8] Another study involved a skilled nursing facility outbreak with SARS-CoV-2 infection in fully vaccinated residents and healthcare workers (26 and 20 cases, respectively) but with the SARS-CoV-2 R.1 lineage, which is not a VOC.[8] No prior studies describe outbreaks with the delta variant occurring in an acute-care setting.

Our outbreak study yielded several important findings. All HCW cases and most patient cases were mild to moderate in nature, with only 1 patient case requiring ICU admission. Despite vaccination, certain high-risk exposures (eg, patients sharing the same multibed room) or low-risk exposures (eg, HCWs

exposed to patients during their presymptomatic shedding) may result in transmission of the delta variant. Despite this risk, all conventional tools used for outbreak management were effective and managed to contain the outbreak at an early stage of detection including closing the unit to admissions, cohorting staff, and performing frequent testing surveillance on staff and patients. Finally, due to vaccination, falling case counts, and staff fatigue, timely recognition of COVID-19 symptoms among inpatients may become inconsistent; therefore, ongoing vigilance remains necessary for preventing future acute-care setting outbreaks.

Although vaccines are a critical tool, other measures (ie, universal masking, careful screening for COVID-19 symptoms and physical distancing), particularly in high-risk settings, will need to continue in acute-care settings because VOCs like the delta variant are becoming predominant circulating variants.[9]

Acknowledgments. The authors would like to acknowledge the contributions of Arlene Vasconcelos and Dr. Ivan Radovanovic in managing the outbreak. The authors would like to thank Dr. Aaron Campigotto for his work in completing the Whole Genome Sequencing.

Financial support. No financial support was provided relevant to this article.

Conflicts of interest. All authors report no conflicts of interest relevant to this article.

References

1. SARS-CoV-2 variant classifications and definitions. Centers for Disease Control and Prevention. https://www.cdc.gov/coronavirus/2019-ncov/science/about-epidemiology/studying-the-disease.html. Published 2020. Accessed July 11, 2021.
2. Sheikh A, McMenamin J, Taylor B, Robertson C. SARS-CoV-2 delta VOC in Scotland: demographics, risk of hospital admission, and vaccine effectiveness. *Lancet* 2021;397:2461–2462.
3. Lopez Bernal J, Andrews N, Gower C, *et al.* Effectiveness of COVID-19 vaccines against the B.1.617.2 (delta) variant. *N Engl J Med* 2021; 385:585–594.
4. Aynaud M-M, Hernandez JJ, Barutcu S, *et al.* A multiplexed, next-generation sequencing platform for high-throughput detection of SARS-CoV-2. *Nat Commun* 2021;12:1405.
5. Qin J, You C, Lin Q, Hu T, Yu S, Zhou X-H. Estimation of incubation period distribution of COVID-19 using disease onset forward time: a novel cross-sectional and forward follow-up study. *Sci Adv* 2020;6(33): eabc1202.
6. Keehner J, Horton LE, Binkin NJ, *et al.* Resurgence of SARS-CoV-2 infection in a highly vaccinated health system workforce. *N Engl J Med* 2021; 385:1330–1332.
7. Fowlkes A. Effectiveness of COVID-19 vaccines in preventing SARS-CoV-2 infection among frontline workers before and during B.1.617.2 (delta) variant predominance—eight US locations, December 2020–August 2021. *Morb Mortal Wkly Rep* 2021;70:1167–1169.
8. Teran RA, Walblay KA, Shane EL, *et al.* Postvaccination SARS-CoV-2 infections among skilled nursing facility residents and staff members—Chicago, Illinois, December 2020–March 2021. *Am J Transplant* 2021;21: 2290–2297.
9. Cavanaugh AM, Fortier S, Lewis P, *et al.* COVID-19 outbreak associated with a SARS-CoV-2 R.1 lineage variant in a skilled nursing facility after vaccination program—Kentucky, March 2021. *Morb Mortal Wkly Rep* 2021;70:639–643.
10. COVID Data Tracker. Centers for Disease Control and Prevention website. https://covid.cdc.gov/covid-data-tracker. Published 2020. Accessed September 29, 2021.