Use of whole-genome sequencing to investigate a cluster of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections in emergency department personnel

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Abstract

Several recent reports have raised concern that infected coworkers may be an important source of severe acute respiratory coronavirus virus 2 (SARS-CoV-2) acquisition by healthcare personnel. In a suspected outbreak among emergency department personnel, sequencing of SARS-CoV-2 confirmed transmission among coworkers. The suspected 6-person outbreak included 2 distinct transmission clusters and 1 unrelated infection.

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Healthcare personnel are at risk of acquiring severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) at work and in the community.1 In healthcare facilities, strategies such as universal masking and preadmission screening have reduced the risk of acquiring SARS-CoV-2 from patients.2 However, recent reports have highlighted the potential for infected personnel to transmit SARS-CoV-2 to coworkers despite universal masking.3–5 Exposures to infected coworkers often occur in settings such as nursing stations and breakrooms.4, 5 In our facility, many personnel diagnosed with coronavirus disease 2019 (COVID-19) denied higher-risk exposures but worked on the same ward as infected coworkers with the potential for multiple brief interactions and shared fomites.4

Although transmission of SARS-CoV-2 among coworkers is often suspected, there is uncertainty regarding the actual source(s) of acquisition, particularly in the setting of widespread community transmission. SARS-CoV-2 sequencing studies are needed to provide more definitive evidence regarding personnel as a source of transmission.6 In this study, we performed full genome sequencing of SARS-CoV-2 to investigate a cluster of COVID-19 infections among emergency department personnel.

Methods

Study setting

The Cleveland VA Medical Center’s emergency department has a central open work area with closely spaced computer stations shared by nurses, physician’s assistants, and other ancillary staff; physicians have a separate work room. A break room is shared by all staff. During the study period, personnel providing care for patients with suspected or known COVID-19 wore gloves, gown, a respirator, and face shield. Medical procedure face masks were worn during care of other patients and in shared work areas or breakrooms. Testing for SARS-CoV-2 was performed using commercial reverse-transcriptase polymerase chain reaction (RT-PCR) assays.

Contact tracing investigation

The study protocol was approved by the Cleveland VA Medical Center’s Institutional Review Board. Six employees in the emergency department were diagnosed with COVID-19 infection between July 8 and July 25, 2020, including 2 registered nurses (RNs), 1 nursing assistant (NA), 2 medical technologists (MTs), and 1 physician’s assistant (PA). The infection control department conducted contact tracing in accordance with Centers for Disease Control and Prevention (CDC) recommendations.1 Surveillance nasopharyngeal swab testing was recommended for all emergency department personnel.
**SARS-CoV-2 sequencing and data analysis**

We sequenced SARS-CoV-2 from 6 symptomatic personnel and 2 control COVID-19 patients seen in the emergency department during the outbreak period. For 1 control patient, 4 specimens collected over 23 days were sequenced to assess sequence variation within a single infection and to serve as a reference for between-infection comparisons. Sequences were aligned to a reference COVID-19 sequence (NCBI accession no. NC_045512.2) using Bowtie2. Variant positions were defined as any genomic position that had an alternate allele frequency >50% in any of the sequenced samples and were determined using samtools and mpileup. Variant positions were assigned to a transmission cluster if they had ≤2 base differences based on their variant positions. The consensus sequences for each strain were classified into 3 different commonly referenced clade classification systems using Nextstrain (nextstrain.org) and Pangolin (github.com/cov-lineages/pangolin). A detailed description of the next-generation sequencing methods and a table showing base differences from the reference genome are included as supplementary material (online).

**Results**

**Contact tracing investigation**

All 6 employees with COVID-19 reported that brief interactions within 2 m (6 feet) of coworkers were common and unavoidable in shared work areas and the break room. None of the employees reported 15 minutes of continuous close contact with an infected coworker in work areas or in the break room, but 3 reported cumulative close contact of 15 minutes or more during a 24-hour period in work areas. None of the employees reported higher-risk community exposures. During the outbreak period, 31 patients with COVID-19 were seen in the emergency department.

In response to the outbreak, infection prevention staff reinforced face mask and eye protection compliance, increased spacing of computer workstations, and encouraged social distancing and avoidance of shared meals. Of 103 asymptomatic emergency department personnel, 96 (93%) underwent surveillance testing and 3 (3%) tested positive, including 1 environmental services employee, 1 nursing assistant, and 1 registered nurse. No additional symptomatic COVID-19 cases were identified among personnel.
2020, and June 26, 2020, varied by 1 to 2 allelic differences at nucleotides 8146 and 24776.

**Discussion**

Recent reports have raised concern that infected coworkers may be an important source of SARS-CoV-2 acquisition by healthcare personnel. However, in the setting of widespread community transmission, sequencing of SARS-CoV-2 is essential as an adjunct to contact tracing to confirm transmission among personnel. In the current investigation, sequencing confirmed transmission of SARS-CoV-2 among emergency department personnel but demonstrated that the suspected 6-person outbreak included 2 distinct transmission clusters and 1 unrelated infection. Our results suggest that SARS-CoV-2 variants initially acquired in the community were subsequently spread among hospital personnel.

Our findings provide support for CDC recommendations to encourage physical distancing among personnel to minimize the risk for SARS-CoV-2 transmission. Emergency departments are high-risk work areas because personnel often share open work spaces and break rooms in a busy environment where it can be difficult to maintain social distancing. In our facility, the outbreak resolved after efforts were made to reinforce face mask and eye protection compliance, to increase spacing of workstations, and to encourage the avoidance of shared meals and breaks.

Our study has some limitations. We only sequenced SARS-CoV-2 from symptomatic personnel and from 2 patients during the initial investigation. However, we subsequently sequenced 75 SARS-CoV-2 samples collected from 75 patients and employees between May 1, 2020, and November 12, 2020, in our facility. No B.1.240 lineage SARS-CoV-2 was detected before or during the emergency department outbreak, and only 4 of 50 (8%) SARS-CoV-2 sequenced after the outbreak were B.1.240 lineage. Therefore, although we cannot exclude exposures to patients or asymptomatic personnel as a source of transmission, the B.1.240 lineage was not a common source of infections in our facility. The sequencing analysis identified 2 distinct clusters within the B.1.240 lineage with 3–4 allelic differences. We cannot exclude the possibility that all the B.1.240 variants were related with allelic differences due to mutations.

**Supplementary material.** To view supplementary material for this article, please visit https://doi.org/10.1017/ice.2021.208

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