

attack rate from children to household members was estimated to be only 0.5% (7). Reduced transmission from children in households was also reported in Switzerland and China and in educational settings in Australia (8–10).

This study is limited by its small sample size, which limits the ability to generalize its results. Moreover, we did not assess the patients' viral load, which could indirectly reflect the infectivity of the children, nor did we assess patient serology, which could further ascertain their infection status. Despite these limitations, our study provides information on SARS-CoV-2 transmission from children to guardians in isolation rooms. Additional assessments of the transmissibility of SARS-CoV-2 by children and the role of PPE in preventing infection could provide guidance during the ongoing pandemic. Nonetheless, our study adds to growing evidence that young children are less likely to contribute to the spread of COVID-19 among their adult guardians.

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Superspreading Event of SARS-CoV-2 Infection at a Bar, Ho Chi Minh City, Vietnam

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We report a superspreading event of severe acute respiratory syndrome coronavirus 2 infection initiated at a bar in Vietnam with evidence of symptomatic and asymptomatic transmission, based on ministry of health reports, patient interviews, and whole-genome sequence analysis. Crowds in enclosed indoor settings with poor ventilation may be considered at high risk for transmission.

Superspreading events occur when a few persons infect a larger number of secondary persons with whom they have contact (1,2). For severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), an R_0 of 2–3 with 6–8 secondary cases has been suggested to constitute a superspreading event (3).

Although SARS-CoV-2 is known to be transmitted through droplets and fomites, there has been growing

evidence of airborne transmission (4,5). Better understanding of specific settings in which superspreading events are facilitated remains critical to inform the development and implementation of control measures to avoid future waves of the pandemic (5).

On March 18, 2020, a 43-year old man, patient 1, sought treatment at the Hospital for Tropical Diseases in Ho Chi Minh City, Vietnam, for fever, cough, muscle aches, fatigue, and headache. A sample from a nasopharyngeal throat swab specimen taken at admission tested positive for SARS-CoV-2 by reverse transcription PCR.

During the 14 days before the onset of his symptoms on March 17, he had traveled to Thailand and within Vietnam, between Hanoi and Ho Chi Minh City. From 10:00 PM on March 14 until 2:30 AM of the next day, he participated in a St. Patrick's Day celebration at bar X in Ho Chi Minh City. The bar had 2 indoor areas for clients, an $\approx 300\text{-m}^2$ area downstairs and an $\approx 50\text{-m}^2$ area upstairs, with no mechanical ventilation. During open hours, the left and right entrances were typically kept closed to facilitate cooling with air conditioners that recycle indoor air; the middle entrance was kept open. The bar also has naturally ventilated outdoor spaces (Appendix, <https://wwwnc.cdc.gov/EID/article/27/1/20-3480-App1.pdf>). Patient 1 was inside the bar during the party.

After the confirmed diagnosis of COVID-19 in patient 1, we used contact tracing and testing to

Table. History of travel and patients and contacts of patients positive for severe acute respiratory syndrome coronavirus 2 in cluster associated with bar, Ho Chi Minh City, Vietnam, 2020*

Patient no.	Contact history and epidemiologic factors	Inside bar?	Travel history†	Occupation	Symptom onset	Diagnosed
Patients present at bar X for celebration on March 14–15, 2020						
1	Attended with patients 2, 3, and 4	Y	Y	Pilot	03/17	Mar 18
2	Attended with patients 1, 3, and 4; roommate of patient 3	UNK	Y	Teacher	Unavail.‡	Mar 22
3	Attended with patients 1, 2, and 4; roommate of patient 2	UNK	Y	Teacher	Unavail.	Mar 22
4	Attended with patients 1, 2, and 3	UNK	N	Teacher	Mar 21	Mar 22
5	Attendee; works at shoe company Y	UNK	N	Unavail.	Asympt.	Mar 23
6	Waiter at bar X; in close contact with patient 1	Y	N	Bar X waiter	Mar 16	Mar 23
7	Attendee	UNK	N	Unavail.	Unavail.	Mar 24
8	Attendee; friend of patient 7	UNK	N	Teacher	Unavail.	Mar 24
9	Attendee	UNK	N	Teacher	Mar 25	Mar 26
10	Attendee	UNK	N	Technician	Asympt.	Mar 26
11	Attended with patient 5	UNK	N	Unavail.	Unavail.	Mar 28
12	Attendee	UNK	N	Unavail.	Asympt.	04/02
13	Attended with patient 12	UNK	N	Unavail.	Mar 26	04/03
Contacts of patients present at bar X for celebration on March 14–15, 2020						
14	Contact of patients 5 and 19 as coworkers at shoe company Y	NA	N	Unavail.	Asympt.	Mar 25
15	Household contact of patient 10	NA	N	Unavail.	Asympt.	Apr 1
16	Household contact of patient 6	NA	N	Unavail.	Unavail.	Mar 27
17	Contact (driver) of patients 5 and 14	NA	N	Driver	Mar 27	Mar 30
18	Household contact of patient 14; also contact of patient 5 as a coworker at shoe company Y	NA	N	Unavail.	Asympt.	Mar 30
19	Contact of patients 5 and 14 as coworkers at shoe company Y	NA	N	Unavail.	Unavail.	Apr 6

*Asympt., asymptomatic; NA, Not applicable; unavail., unavailable; UNK, unknown.

†Traveled to an area with known local transmission in previous 14 d.

‡Because patient did not enroll in the clinical study, but asymptomatic at time of diagnosis.

detect 18 additional PCR-confirmed cases. Of these, 12 (patients 2–13) were at bar X during the evening of March 14; the other 6 (patients 14–19) were contacts (Table; Appendix Figure). Of the patients with confirmed cases attending the celebration, 4 were

in close contact with patient 1: patients 2–4 went to the celebration with patient 1 and patient 6 worked as a waiter in the bar. Patients 2 and 3, who were roommates, had traveled to Malaysia and returned to Vietnam, patient 2 on March 13 and patient 3 on

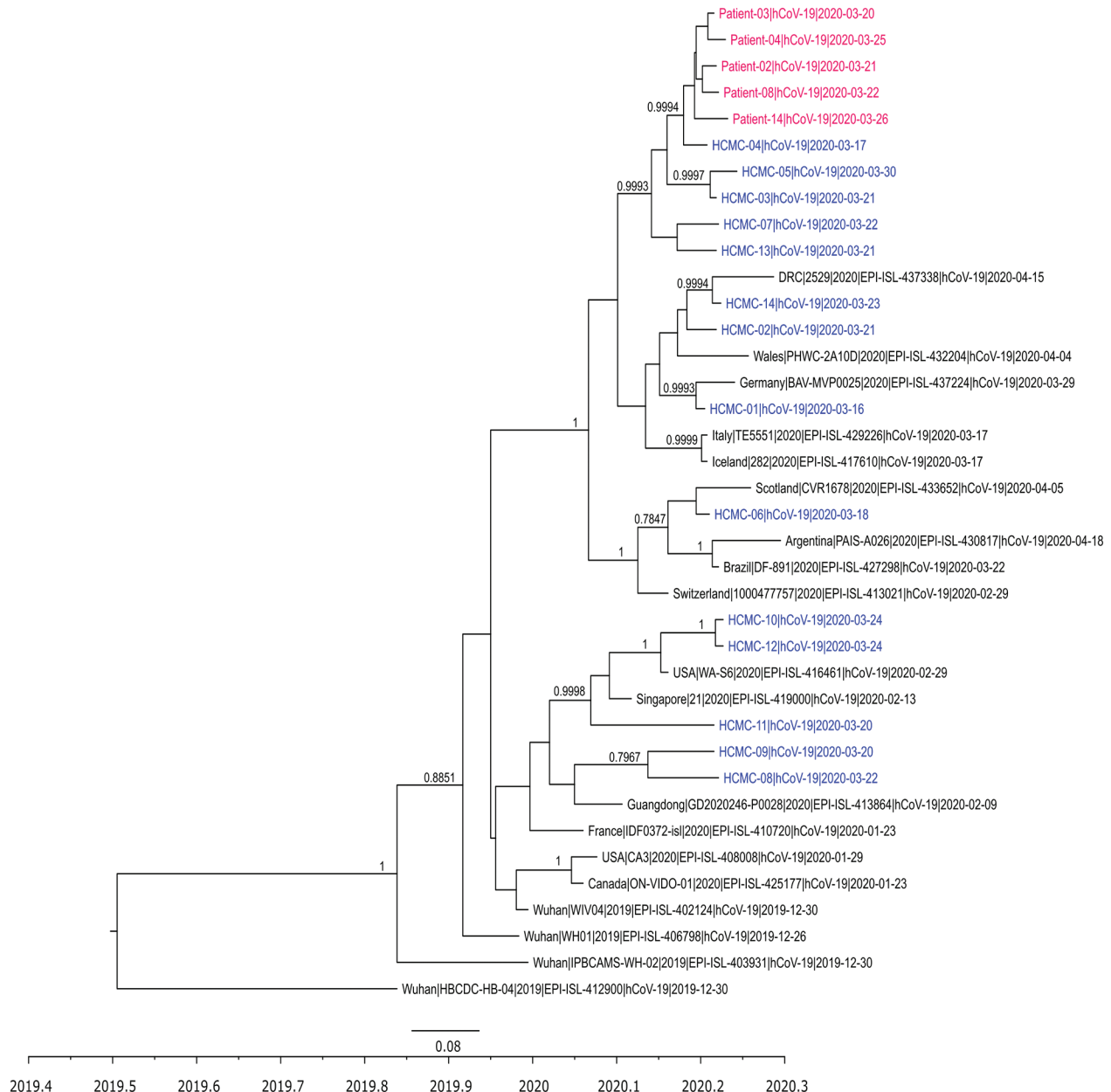


Figure. Time-scale phylogenetic tree illustrating the relatedness between whole-genome sequences of severe acute respiratory syndrome coronavirus 2 obtained from patients with confirmed cases of the cluster associated with a bar in Ho Chi Minh City, Vietnam, 2020, and reference sequences. Sequences from the cluster patients are in red; sequences from coronavirus disease patients in Ho Chi Minh City, not related to the cluster, are in blue. For those sequences, we obtained 21 genomes from the remaining 35 patients reported in Ho Chi Minh City as of April 24, 2020, for the purpose of the analysis; subsequently, we used 14 nonidentical sequences for the analysis. Representative sequences from patients not in Vietnam are in black. Posterior probabilities $\geq 75\%$ are indicated at all nodes. The analysis was carried out using BEAST version 1.8.3 (<https://beast.community>). For time-scale analysis, only 1 representative of sequences that were 100% identical to each other was included. Whole-genome sequences were generated using ARTIC primers version 3 (ARTIC Network, <https://artic.network/ncov-2019>).

March 6. The other patients, except for patient 1, had no recent history of travel outside of HCMC (Table).

By exploring the epidemiologic links discovered from in-depth interviews, we identified 3 possible transmission chains involving patients who attended the March 14 celebration (Table; Figure; Appendix Figure). Of these, 2 or 3 patients (patients 5, 10, and possibly 14) were asymptomatic but transmitted SARS-CoV-2 to their contacts (Table; Figure). None of the 19 patients with confirmed cases reported that they had respiratory signs or symptoms on March 14–15. However, in addition to patient 1, a total of 5 others developed mild respiratory symptoms (patient 4 on March 16, patient 6 on March 21, patient 9 on March 25, patient 13 on March 26, and patient 17 on March 27), suggesting an incubation period of 2–12 days. Follow-up data were available for 12 patients who participated in our clinical study (Appendix). Six remained asymptomatic during follow-up (Appendix Table 1).

A total of 11 whole-genome sequences of SARS-CoV-2 were obtained from the patients in the cluster. The obtained sequences were either 100% identical or different from each other by only 1–2 nt (Appendix Table 2). Phylogenetically, they clustered together tightly but were different from sequences obtained from other cases in Ho Chi Minh City during the same period.

As of September 15, 2020, only 30 cases of locally acquired infection had been reported in Ho Chi Minh City (6), but this cluster represents the only documented superspreading event (6,7). Together with data from previous reports (3,8,9), these data suggest that closed settings are facilitators of community transmission of SARS-CoV-2. The mechanism by which infected people without symptoms spread SARS-CoV-2 to others, especially in closed settings, warrants further research, including on transmission through aerosols, which has been suggested (4,10).

The high level of genome sequence similarity between the SARS-CoV-2 genomes obtained from the patients and the tight clustering on the phylogenetic tree strengthen the epidemiologic link between the PCR-confirmed cases from this cluster. Together with contact history, these data also support transmission chains involving asymptomatic carriers (patients 5 and 14) as the sources of the ongoing infection. However, the identity of the patient in the index case from the bar could not be confirmed, in part because in-depth interview data were available from only 8 of 13 patients with confirmed cases who consented to participate in the study. In conclusion, our results emphasize that persons in crowded indoor settings

with poor ventilation may be considered to be at high risk for SARS-CoV-2 transmission.

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Racial and Workplace Disparities in Seroprevalence of SARS-CoV-2, Baton Rouge, Louisiana, USA

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By using paired molecular and antibody testing for severe acute respiratory syndrome coronavirus 2 infection, we determined point prevalence and seroprevalence in Louisiana, USA, during the second phase of reopening. Infections were highly variable by race and ethnicity, work environment, and ZIP code. Census-weighted seroprevalence was 3.6%, and point prevalence was 3.0%.

We previously reported results from a seroprevalence study conducted in New Orleans, Louisiana, USA, which was hit hard early in the coronavirus

disease (COVID-19) pandemic (1). Baton Rouge is a large metropolitan area roughly 80 miles northwest of New Orleans; at the time of this study, it was in the second phase of reopening after a stay-at-home order. Although the seroprevalence in New Orleans (6.9%) (1) was similar to prevalence recorded in Spain (5%), São Paulo, Brazil (4.7%), and New York, USA (6.9%) (2,3; B.H. Tess, unpub. data, <https://doi.org/10.1101/2020.06.29.20142331>), Baton Rouge had only 3,427 more cases as of August 2, 2020 (17,093 cases), than New Orleans did by May 16, 2020 (13,666 cases) (4). This latest study estimated severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infections in the greater Baton Rouge area (Ascension, East Baton Rouge, Livingston, and West Baton Rouge Parishes), with additional information on potential workplace exposures.

The protocol was approved by the Ochsner institutional review board and was designed to enroll and test $\leq 2,500$ participants at 13 sites throughout Baton Rouge during July 15–31. Recruitment targeted a representative sample by using a method developed by Public Democracy (<https://www.publicdemocracy.io>) and described elsewhere (1,5). In contrast to the New Orleans study, in which persons tested were under a stay-at-home order, Baton Rouge was in phase 2 of reopening. A randomized subset of 500,000 Baton Rouge residents were targeted with digital ads for recruitment. Of those, 3,687 volunteers were recruited and restratified according to census designations; 2,309 were invited to participate, 2,179 enrolled and completed testing, and 2,138 were included in our final analysis. A total of 38 persons were excluded because they lived in ineligible ZIP codes, and 3 withdrew consent (Appendix Figure 1, <https://wwwnc.cdc.gov/EID/article/27/1/20-3808-App1.pdf>). All study materials were provided in English, Spanish, and Vietnamese. Participants were offered free transportation. Research staff verbally obtained consent from participants and electronically documented consent and survey responses. We then procured blood samples and nasopharyngeal swab specimens from participants.

We used US Food and Drug Administration Emergency Use Authorization–approved tests. Real-time reverse transcription PCR of nasopharyngeal swab specimens was performed by using the Abbott m2000 RealTime system (Abbott, <https://www.molecular.abbott>). Qualitative IgG blood tests were performed by using the ARCHITECT i2000SR (Abbott). The IgG test meets criteria established by the Centers for Disease Control and Prevention to yield high positive predictive value, which was validated by Ochsner Health laboratory and others (6,7). Study participants who tested positive on either or both tests were

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Appendix

The Study

Since the beginning of March 2020, a COVID-19 research program aimed at unraveling the natural history of SARS-CoV-2 infection has been conducted at the Hospital for Tropical Diseases (HTD) and at 1 of its 2 designated COVID-19 centers, Cu Chi Hospital in Ho Chi Minh City, Vietnam (1, 2). These are the largest COVID-19 treatment centers in the southern region, which has a population of >40 million people.

We tested patients admitted to HTD or Cu Chi Hospital using real-time reverse-transcriptase-PCR (rRT-PCR) to confirm SARS-CoV-2 infection. At enrollment, we collected nasopharyngeal throat swabs (NTS) from each participant, and combined them in 1 tube containing 1mL of viral transport medium. We also collected clinical and laboratory data, a travel history, and contact information from each study participant using a case record form developed by the International Severe Acute Respiratory and Emerging Infection Consortium (ISARIC, <https://isaric.tghn.org/>). The collected NTS sample was placed in storage at 4°C at the study sites within 4 hours and then transferred to the clinical laboratory at HTD for analysis. SARS-CoV-2 detection was carried out using WHO-recommended rRT-PCR assays (3).

The clinical studies received approvals from the Institutional Review Board of the HTD and the Oxford Tropical Research Ethics Committee of the University of Oxford. Additionally, we retrieved epidemiologic data from an official COVID-19 website of the Vietnamese Ministry of Health (4), and diagnostic results from the HTD database system.

COVID-19 Containment Approach in Vietnam

Since January 2020, various control measures, including isolation of confirmed cases, contact tracing, airport quarantine, and social distancing have been implemented in Vietnam with increasing stringency as the pandemic progressed worldwide (1). Accordingly, anyone known to have been in contact with a confirmed COVID-19 case or having traveled to Vietnam from a COVID-19-affected country, were isolated for ≥ 14 days at a designated isolation center.

From the second week of March 2020, all isolated persons were subject to serial SARS-CoV-2 NTS screening by rRT-PCR at least 2X (day 1 and day 14 of the quarantine) (1). A confirmed case was established if 2 independent RT-PCR assays (E gene and RdRP RT-PCR assays) were positive.

In response to escalation of COVID-19 cases in Vietnam, on April 1, 2020 the government issued Directive #16, requiring mass masking, was applied throughout Ho Chi Minh City. This directive was lifted on April 23, 2020.

Description of bar X

The bar has both indoor and outdoor spaces. The majority of the bar space, $\approx 350 \text{ m}^2$, is indoors. The ground floor has an indoor space $\approx 300 \text{ m}^2$ and outdoor spaces of $\approx 100 \text{ m}^2$ at the front with limited seating. At the back of the bar is a small outdoor smoking section of $\approx 20 \text{ m}^2$. The upstairs area is divided into an indoor area and a balcony. The former is $\approx 50 \text{ m}^2$, with a pool table, a small bar, and some seating; the latter is $\approx 20 \text{ m}^2$.

When the bar is open, the front is partly open, allowing some natural ventilation, but has air conditioners that recycle indoor air throughout. The other two entrances to the bar are kept closed to retain cool air. Except for some of the bar staff, none of the >200 participants was wearing masks on the night of the celebration.

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Appendix Table 1. Demographics and admission clinical and laboratory data of the study participants

Demographics	(N = 19)
Age in years, median (range)	33 (22–51)
Gender (female/male), n/n	9/10
Nationality	n (%)
Vietnamese	5 (26)
Others	14 (74)
Admission clinical and laboratory data	N = 12*
Days from confirmed diagnosis to enrolment, median (range)	2 (1–4)
Days from admission to enrolment, median (range)	1 (0–2)
Laboratory results	Median (range)/normal range
White-cell count ($\times 10^3/\mu\text{L}$)	5.5 (3.2–6.9)/(4–11)
Lymphocyte counts ($\times 10^3/\mu\text{L}$)	1.8 (0.5–2.6)/(1.5–4)
Hemoglobin (g/dl)	14.8 (10–17.3)/13–18
Hematocrit (%)	39.5 (29–43.4)/(37–52)
Platelet count (per μL)	243 (166–327)/(150–450)
Glucose (mg/liter)	89.7 (64–340)/(70–130)
Creatinine (mg/dl)	1.0 (0.9–1.5)/(0.5–1.2)
Aspartate aminotransferase (U/L)	24.2 (17–56.8)/(<40)
Alanine aminotransferase (U/L)	25.4 (11.5–44.9)/(<37)
Clinical signs/symptoms	n (%)
Fever,	3 (25)
Cough, n (%)	10 (33)
Rhinorrhea, n (%)	4 (33)
Fatigue, n (%)	2 (17)
Diarrhea, n (%)	0
Sore throat, n (%)	1 (8)
Muscle pain, n (%)	2 (17)
Headache, n (%)	2 (17)
Abdominal pain, n (%)	0
Lost sense of smell, n (%)	0
Baseline comorbidity, n (%)	4 (33)†

*Only available from patients participating in the aforementioned study

†Obesity (n = 2), diabetes without complication (n = 1), and kidney associated problem with 85% reduction of kidney function (n = 1)

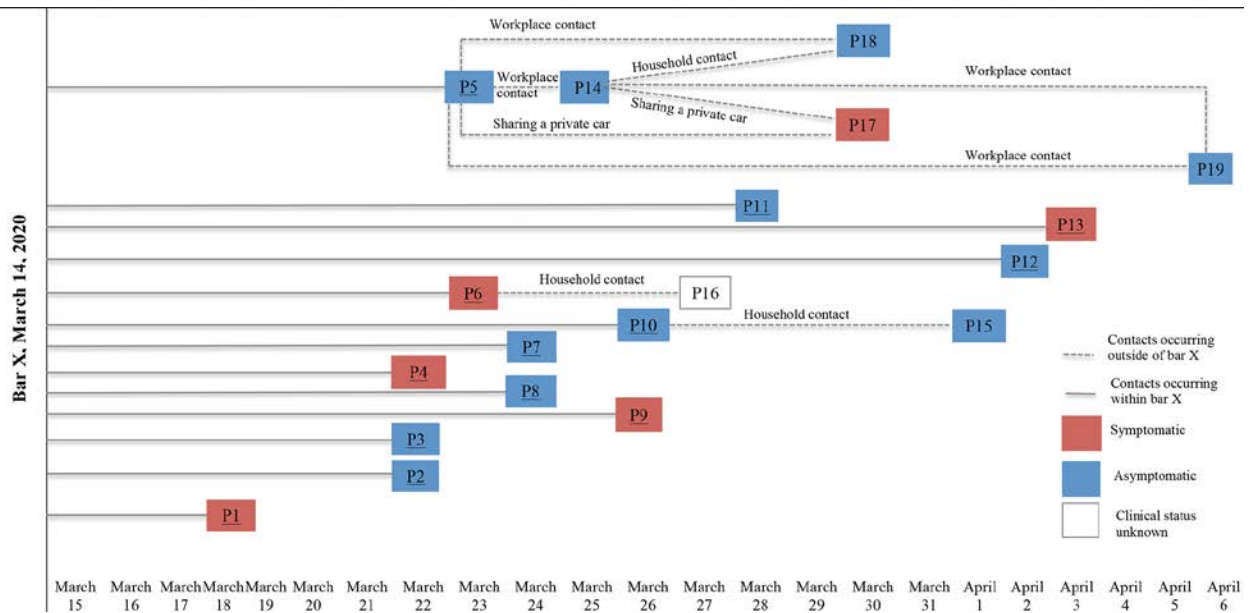
Appendix Table 2: The number of nucleotides different among the obtained genome sequences of the cluster

Patient*	17	18	5†	1†	16	3†	6†	14	4†	8†	2†
17	NA	0	0	0	0	0	0	1	1	1	1
18	0	NA	0	0	0	0	0	1	1	1	1
5†	0	0	NA	0	0	0	0	1	1	1	1
1†	0	0	0	NA	0	0	0	1	1	1	1
16	0	0	0	0	NA	0	0	1	1	1	1
3†	0	0	0	0	0	NA	0	1	1	1	1
6†	0	0	0	0	0	0	NA	1	1	1	1
14	1	1	1	1	1	1	1	NA	2	2	2
4†	1	1	1	1	1	1	1	2	NA	2	2
8†	1	1	1	1	1	1	1	2	2	NA	2
2†	1	1	1	1	1	1	1	2	2	2	NA

NA, not applicable

*Patient numbers correspond to those in Figure 1 and in the text

†Attended celebration on March 14, 2020



Appendix Figure. Illustration of timeline of the investigation and potential contacts occurring between SARS-CoV-2 positive cases. Details about travel history and contacts between cases, and types of workplace are shown in the Table in the main text. Dates shown are when a confirmed diagnosis was established. Patients 2, 3, 7, 8, 11, 16, and 19 did not consent to participate in the clinical study. Patients 2, 3, 7, 8, 11, 11, and 19 were asymptomatic at diagnosis. Patients in blue boxes were all asymptomatic during the course of quarantine. Clinical status of patient 16 was unknown. Patients from the initial bar cluster (1–13) are underlined.