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Case Report

A super-spreader of COVID-19 in Ningbo city in China

Jie Lin^a, Kun Yan^a, Jingfeng Zhang^{a,b}, Ting Cai^{a,b}, Jianjun Zheng^{a,b,*}

- a Hwa Mei Hospital, University of Chinese Academy of Sciences, China
- ^b Institute of Life and Health Industry, University of Chinese Academy of Sciences, China



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ABSTRACT

An outbreak of Coronavirus Disease 2019 (COVID-19) has spread rapidly. It is imperative to control the epidemic by understanding the epidemiological feature, preventative quarantine, and effective hygiene measures. In the present study, we report a case of super-spreader who transmitted the disease to over twenty-eight persons in Ningbo, Zhejiang. Identifying and isolated super-spreaders, understanding the reasons behind the efficient transmission ability are important for the control and management of the ongoing COVID-19 pandemic.

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Introduction

A novel coronavirus has resulted in an ongoing outbreak of viral pneumonia worldwide [1]. Superspreading events (SES), which are associated with both explosive growths early in an outbreak and sustained transmission in later stages challenge the prevention and control of the pandemic [2]. Understanding those SES is important for curbing the spread of the COVID-19 epidemic as well as future infectious disease outbreaks.

Case report

On January 29, a 64-year-old woman (Ms. S) in Ningbo was confirmed as a COVID-19 patient. She contacted with a person from Wuhan at a gathering on January 17 and felt a fever on January 19. Nevertheless, she joined a blessing ceremony in a temple held by a travel agency by a tour bus on January 19 (Figure S1 in Supplementary material). The blessing ceremony gathered 348 pilgrims and three tour buses were arranged to pick up the pilgrims. Coincidently, a 57-year-old woman in Cixi, a city 71.9 km from Ningbo, was confirmed as a COVID-19 patient also on January 29. She had no history of sojourning in Hubei and had not been exposed to confirmed COVID-19 cases. However, she drove to attend the blessing

ceremony on January 19 as well and contacted with Ms. S during the activity.

All members attended the blessing activity were found and isolated timely. Between January 29 and February 6, a total of twenty-five (included Ms. S) COVID-19 cases and one asymptomatic case related to the blessing ceremony were confirmed. Of note, twenty-five of them reported that have contacted with Ms. S and twenty-two (twenty-one COVID-19 cases and one asymptomatic cases) of them on the same tour bus with Ms. S (Fig. 1). All pilgrims attended the blessing ceremony without mask and all pilgrims except for Ms. S reported no history of epidemiological exposure and had no COVID-19 related symptoms. In addition, daughter and husband of Ms. S onset of illness on January 22 and were confirmed as COVID-19 on January 25 (The first nonimported case in Ningbo) and January 27, respectively. Besides, the infectious rate of her close contact is 32.99%, much higher than the average rate in Ningbo (6.15%) [3]. Given above information, we considered Ms. S as a super-spreader, who can infect 10 or more contacts. All seventy-seven patients infected by severe acute respiratory syndrome (SARS-CoV-2) virus involved in the present study were diagnosed by real-time reverse transcription polymerase chain reaction (RT-PCR) assay [4] according to treatment and diagnosis guidance published by National Health Commission [5]. And the attack rate is 7.47% (26/348) among the pilgrims.

As of February 12, accumulative total of 1257 related close contacts were monitored and isolated, and a total of seventy-seven persons (sixty-six COVID-19 cases and eleven asymptomatic cases) were confirmed to have been infected with the SARS-CoV-2 virus.

Abbreviations: COVID-19, coronavirus disease 2019; RT-PCR, reverse transcription-polymerase chain reaction; SARS-CoV-2, severe acute respiratory syndrome; SES, superspreading events.

^{*} Corresponding author at: Hwa Mei Hospital, University of Chinese Academy of Sciences, No. 41 Xibei Street, Haishu District, Ningbo, 315010 Zhejiang, China. E-mail address: zhengjianjun@ucas.ac.cn (J. Zheng).

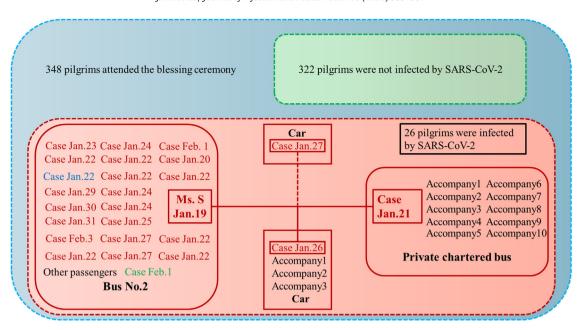


Fig. 1. A super-spreader event. Confirmed COVID-19 cases were presented as case plus onset time and highlighted in red; asymptomatic case was highlighted as green; red solid line indicated cases reported that contacted with Ms. S; confirmed COVID-19 case who did not attend the blessing activity was highlighted in blue.

Discussion

In the present case series, we reported a super-spreader who transmitted the SARS-CoV-2 virus to twenty-eight individuals and caused twenty-seven COVID-19 cases and an asymptomatic case. Furthermore, another forty-nine individuals were infected by the twenty-eight individuals (thirty-nine COVID-19 cases and ten asymptomatic cases). Fortunately, aggressive contact tracing and testing adopted by our government stopped the SES from further spreading [6]. This case arouses the concern regarding the reason behind the super-spreading ability and highlights the importance of identifying and quarantining any one in close contact with a confirmed COVID-19 patient as soon as possible.

Ms. S is a patient in moderate case, which is defined as with respiratory symptoms and pulmonary inflammatory lesion. To understand the reasons underlying the effective transmission ability, we summarized the SARS-CoV-2 viral load in sputum and throat swab samples from Ms. S during her thirty-five days (From January 27 to March 2) in our hospital (Fig. 2). Ct values are inversely correlated with viral RNA copy number, with Ct value of 30.76, 27.67 and 24.56 corresponding to a gene copy number of 1.5×10^4 , 1.5 \times 10⁵ and 1.5 \times 10⁶. The viral load in samples from Ms. S. was high and her virus shedding time was long (40 days, from January 19 to February 27). Additionally, all close contacts of Ms. S (From January 17 to January 27) were isolated and observed for fourteen days, and only her daughter, her husband and twenty-five pilgrims mentioned above including twenty-two pilgrims in the same tour bus with her was infected by SARS-CoV-2, indicating a closed and small space is necessary for high transmission efficiency. Besides, consistent with previous study, we observed a COVID-19 transmission within a family cluster by pre-symptomatic infectors in the SES, indicating the possibility of COVID-19 transmission before symptom onset [7]. Also, we observed a transmission carried by an asymptomatic case [8], and it is suggested that the infectiousness of an asymptomatic case is comparative to a symptomatic case [3]. However, the infectiousness of an asymptomatic case is still debatable.

Limitations of the present should be noted. Firstly, monitoring for genetic adaptation could help to determine whether transmissibility of SARS-CoV-2 is evolving and whether variants of the virus are more readily transmitted. However, neither data by wholegenome sequencing nor epidemiologic investigation was available. Secondly, host, pathogens, environmental, and behavioral features of superspreading event were mentioned in the present study. However, detailed information regarding each factor should be further explored. Lastly, despite great effort we have done, the confirmation of the index case is still controversial, more evidence should be added to determine the index case in the SES.

Conclusion

The current case and another previously published one during the SARS outbreak [9] suggest that a super-spreader may have the following features: (1) high viral load; (2) longer virus shedding time; (3) a super spreader may not be a severely ill patient, he/she may be active in social activities and have chances to contact many persons within a short period of time. On the other hand, finding out a super spreader may be difficult. Timely tracking each confirmed and suspected patient's recent activities, places visited, and events participated is important. For confirmed patients, timely isolation, without allowing them to attend any social activities, and continuous monitoring their virus load/virus shedding is also important.

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Ethical approval

This study was approved by Ethics Committee of our hospital.

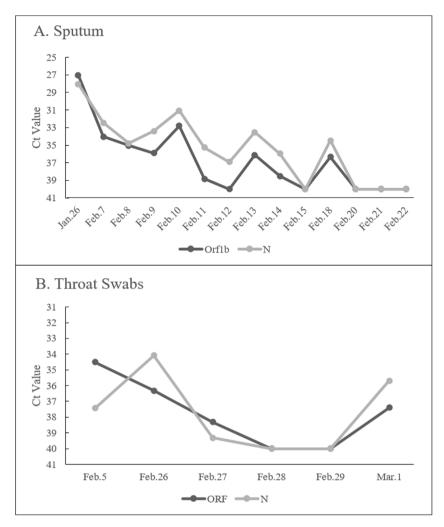


Fig. 2. Viral load detected in sputum and throat swabs from Ms. S. Negative samples are denoted with a Ct value of 40, which was the limit of detection.

Conflict of interest

None declared.

Author contributions

Jie Lin and Jianjun Zheng conceived the idea, Jie Lin drafted the paper. Kun Yan and Jingfeng Zhang collected the data. Ting Cai reviewed the paper. All authors read and approved the final manuscript.

Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.jiph.2020.05.023.

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