Familial cluster of SARS-CoV-2 infection associated with a railway journey

Shaofu Qiu, PhD[1,*], HONGBO Liu, PhD[1,*], Peng Li, PhD[1,*], Hongjun Jia, MD[2,*], Xinying Du, PhD[1,*], Hongbo Liu, MD[1], Hui Wang, MS[1], Mingjuan Yang, MD[1], Ligui Wang, PhD[1] and Hongbin Song, PhD[1]

Running title: SARS-CoV-2 infection associated with a journey

[*] These authors contributed equally to this article.

Author affiliation:

[1] Chinese PLA Center for Disease Control and Prevention, Beijing, China

[2] The Fifth Medical Center of PLA General Hospital, Beijing, China

Corresponding author：

Hongbin Song, Chinese PLA Center for Disease Control and Prevention, No. 20 Dongda Street, Fengtai District, Beijing 100071, China.

Email: hongbinsong@263.net.

Keywords: Familial cluster; SARS-CoV-2; COVID-19; railway journey; Beijing

TO THE EDITOR

A novel coronavirus named SARS-CoV-2 has caused an ongoing outbreak of viral pneumonia in China and other regions worldwide[1]. There is evidence of person-to-person transmission[2,3]. Here, we report a familial cluster of SARS-CoV-2 infection, in which the initial patient probably acquired the infection on a railway journey.

On January 28, 2020, a family of four patients were admitted to a tertiary hospital in Beijing due to their respiratory symptoms and Wuhan travel history (Figure 1). Patient 4 (the younger son) had been living in Wuhan since August 2019. Patient 2 (the father) traveled to Wuhan on January 4, 2020, and Patient 1 (the mother) and Patient 3 (the elder son) went to Wuhan on January 18, 2020. On January 20, they were driven to the Wuhan railway station by a relative, and they took approximately 4 h to return to Beijing by train without masks. Once they arrived in Beijing, they drove their own car back home and were isolated at home until Patient 1 developed respiratory symptoms on January 23. She was admitted to the tertiary hospital on Jan 25, and confirmed as positive for SARS-CoV-2 by real-time reverse transcriptase polymerase chain reaction (RT-PCR) assays on Jan 26, 2020. As close contacts, her family members including her husband (patient 2) and two sons (patient 3-4) developed dry cough or fever on Jan 27 and were admitted to the same hospital on Jan 28, who were confirmed as positive for SARS-CoV-2 by RT-PCR on Jan 29, 2020. Whole-genome sequencing analysis revealed that the genomes sequenced from these four patients clustered together, with other SARS-CoV-2 genomes (Figure S1).

During their stay in Wuhan, they stayed at home and were only in contact with eight

relatives. They denied a history of contact with confirmed or suspected COVID-19 patients, wild animals, or visits to markets. As of March 24, their relatives did not have any respiratory symptoms and tested negative for SARS-CoV-2 by RT-PCR. During the railway journal, the Patient 1 recalled a passenger without a mask behind her coughed a few times on the train. Therefore, the most likely scenario of transmission is that Patient 1 first acquired the infection during the railway journey and then transmitted the virus to other family members. To our knowledge, this is the first report to provide an example of a familial cluster of SARS-CoV-2 infection probably associated with a railway journey. Transmission of SARS could occur on an aircraft[4], and a taxi driver in Thailand has been infected with SARS-CoV-2, potentially from Chinese tourists[5]. Our study highlights the risk of SARS-CoV-2 transmission during a railway journey. Vehicles, especially trains, are the most important means of transportation for people in China; they have enclosed spaces, which greatly facilitates virus transmission. Therefore, further attention is warranted on measures that can reduce the likelihood of transmission on trains.

Author contributions: S.F.Q. and H.B.S. designed the project. H.J.J., X.Y.D., H.b.L., H.W., L.G.W. and M.J.Y. carried out the data collection. S.F.Q., P.L. and H.B.L. analyzed the data and prepared the figure. S.F.Q., H.B.L. and H.B.S. drafted the manuscript. All the author have revised the manuscript, approved the version submitted for publication and have agreed to be accountable for all aspects of the work.

Conflict of Interest: The authors have declared no conflicts of interest.

Funding: This work was supported by grants from the National Science and Technology Major Project of China (nos. 2018ZX10101003 and 2018ZX10714002).

References

1. Zhu N, Zhang D, Wang W, et al. A Novel Coronavirus from Patients with Pneumonia in China, 2019. N Engl J Med 2020;382(8):727-733.
2. Chan JF, Yuan S, Kok KH, et al. A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. Lancet 2020;395(10223):514-523.
3. Huang C, Wang Y, Li X, et al. Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. Lancet 2020;395(10223):497-506.
4. Olsen SJ, Chang HL, Cheung TY, et al. Transmission of the severe acute respiratory syndrome on aircraft. N Engl J Med 2003;349(25):2416-22.
5. Pongpirul WA, Pongpirul K, Ratnarathon AC, et al. Journey of a Thai Taxi Driver and Novel Coronavirus. N Engl J Med 2020;382(11):1067-1068.

Figure legend

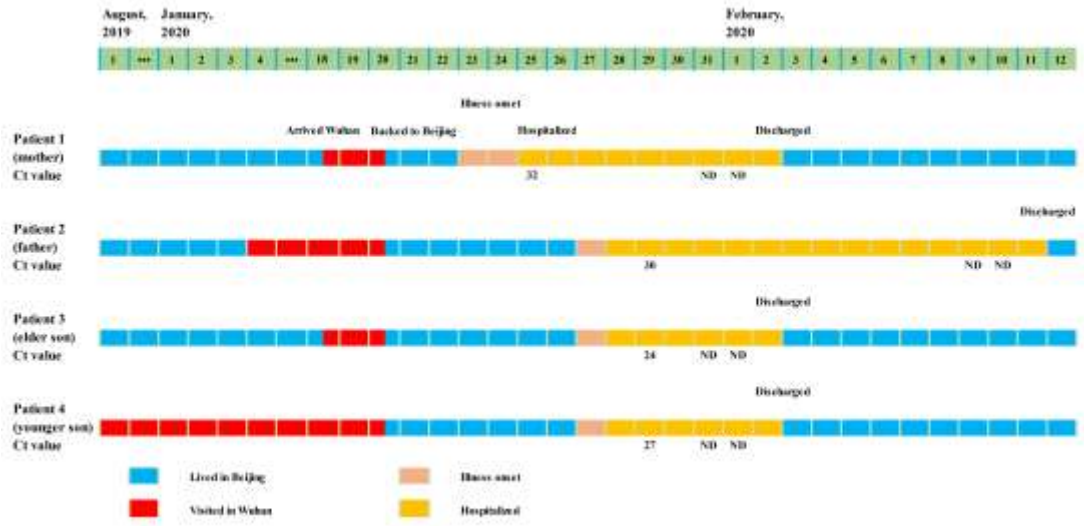

Figure 1. Timeline of SARS-CoV-2 infection within a family cluster

Cycle threshold (Ct) values of RT-PCR are shown, and ND indicates negative results for SARS-CoV-2.