

Notes from the Field

A Nosocomial COVID-19 Outbreak Initiated by an Infected Dockworker at Qingdao City Port — Shandong Province, China, October, 2020

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On October 10, 2020, 3 cases of coronavirus disease 2019 (COVID-19) were detected via routine pre-admission nucleic acid screening of inpatients and their visitors at Qingdao Central Hospital. The 3 cases were all related to the Qingdao Chest Hospital. An additional 9 cases were discovered and confirmed through tracing and testing contacts of the 3 initial cases. Viral isolates from all 12 cases were found to have high degrees of genetic homology with the viral isolate from a dockworker at Qingdao Port, referred to as Patient A in this report. A joint investigation team was formed to determine the source of infection and the scale of the outbreak, and to prevent further spread of the virus.

On October 11, all inpatients, visitors, and hospital staff who had been at Qingdao Chest Hospital after September 1 underwent COVID-19 virus nucleic acid screening; close contacts of the cases were traced and provided medical care in isolation. An additional 9 new confirmed cases of COVID-19 were found, for a total of 12 cases. Among these, 7 were tuberculosis (TB) patients in Qingdao Chest Hospital, 3 were visitors of the tuberculosis patients, and 2 were family members of the tuberculosis patients or visitors. From October 11 to 17, more than 200,000 people from the community where the initial patients resided and residents of the surrounding areas were screened with PCR testing. Subsequently, all Qingdao City residents were tested. In total, 10.92 million people were tested, and no additional cases were found. Among the 12 outbreak cases, 2 infections were mild, 7 were moderate, 2 were severe, and 1 was critical. Their average age was 49 years, ranging from 23–83 years old; 6 were men and 6 were women.

Virus isolates from the 12 cases underwent whole genome sequencing. Sequences were compared and analyzed by Shandong Provincial CDC and were sent to China CDC for comparison with genetic sequences of recent COVID-19 cases. The sequences of the 12 cases' virus isolates were found to be 99.9%

homologous with a virus sequenced from Patient A, a COVID-19 case diagnosed in Qingdao on September 24. Patient A is a dockworker who was infected after loading and unloading imported frozen seafood at Qingdao Port on September 19. The phylogenetic diagram of Patient A's virus isolate is shown in [Figure 1](#), demonstrating that he was the source of infection of this outbreak. After being diagnosed on September 24, he had been transferred to Qingdao Chest Hospital, which is a designated hospital for COVID-19 care and treatment ([1](#)).

Big data screening and tracking showed that there was no temporal or spatial correlation between the patients and the close contacts in this outbreak and Patient A or his contacts before he was transferred to Qingdao Chest Hospital. A surveillance video confirmed that Patient A had been escorted from the isolation ward on the afternoon of September 24 to undergo a computerized tomography (CT) examination, possibly contaminating the CT examination room with virus due to lack of standardized disinfection. Contamination of the CT room most likely led to infections of Patients B and C, who had CT exams the following morning. They, in turn, likely brought the virus into the area for TB patients, and thus continued the spread of COVID-19.

From October 11 to 15, Qingdao City CDC collected 129 environmental samples at Qingdao Chest Hospital, including from the CT room, tuberculosis patient wards, and sewage pipes. All samples had negative nucleic acid test results. Close contacts of all cases, close contacts of the close contacts, and all staff of Qingdao Chest Hospital and their visitors underwent a total of 5 nucleic acid tests each; all tests were negative. As of October 20, no new cases have been detected in Qingdao.

This outbreak was likely an in-hospital infection caused by a lack of standardized disinfection of the hospital's CT room. Recommendations have been

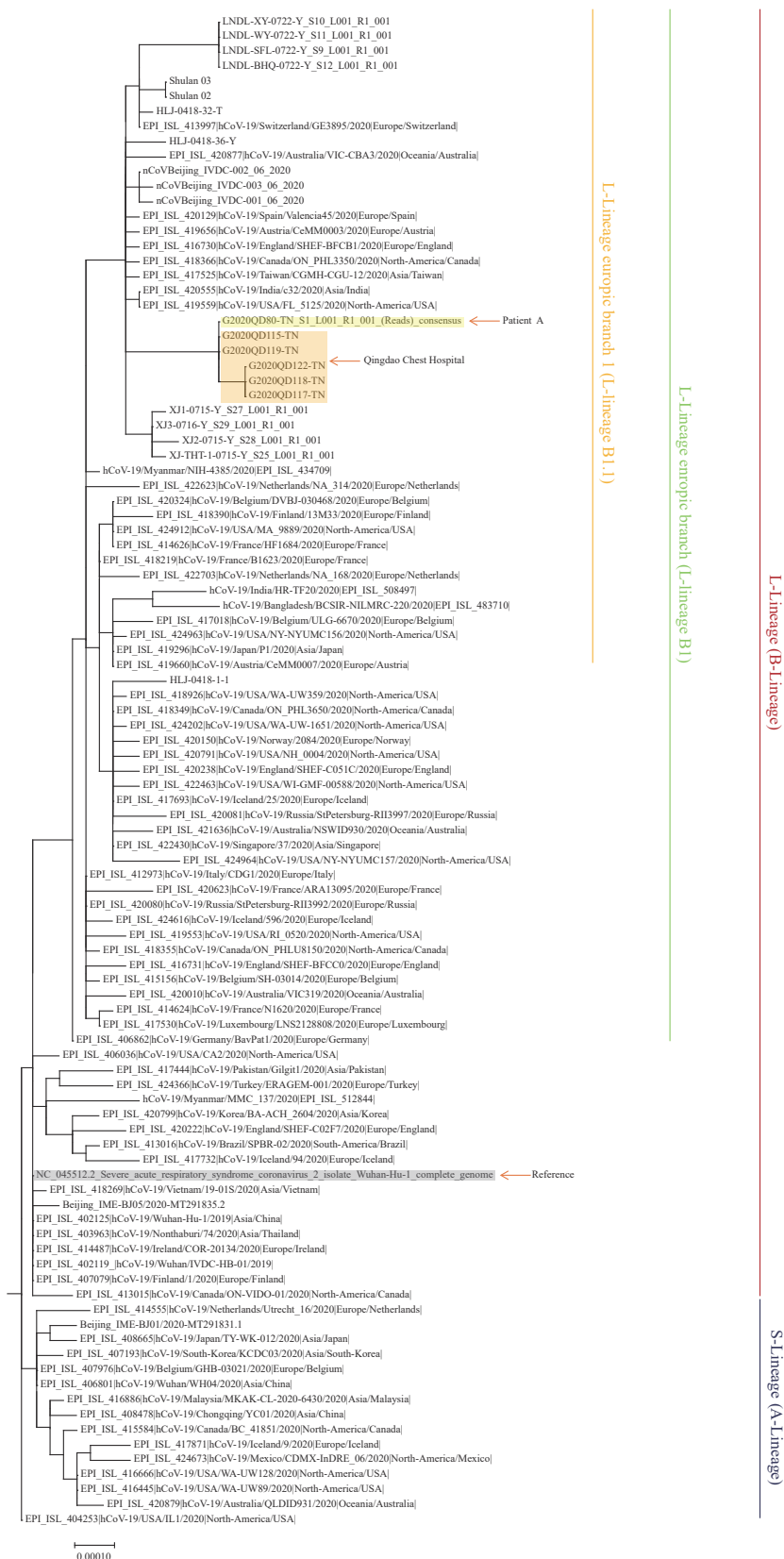


FIGURE 1. Phylogenetic tree based on the genome sequences of the COVID-19 virus. The genome of the COVID-19 virus from 5 patients infected at Qingdao Chest Hospital and Patient A were highlighted in shades of orange and yellow, respectively.

made to strengthen the prevention and control of nosocomial COVID-19 infections to prevent transmission at these COVID-19-designated medical institutions.

Acknowledgements: The authors would like to thank all the team members in the nation-province-prefecture joint investigation team for their contribution to this article.

doi: [10.46234/ccdcw2020.224](https://doi.org/10.46234/ccdcw2020.224)

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Submitted: October 20, 2020; Accepted: October 22, 2020

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