

Notes from the Field

Two Reemergent Cases of COVID-19 — Hebei Province, China, January 2, 2021

Shunxiang Qi^{1,✉}; Xiang Zhao^{2,✉}; Peter Hao³; Nankun Liu³; George F. Gao³; Yang Song²; Wenbo Xu^{2,†}; Qi Li^{1,†}

On January 2, 2021, 2 cases of coronavirus disease 2019 (COVID-19) were identified in 2 cities of Hebei Province, and genomic sequencing suggested that the cases likely resulted from the same origin. The first case (Patient A) was identified as positive at 12:18 in Shijiazhuang City, the capital of Hebei Province, and the second case (Patient B) was identified as positive at 21:00 in Xingtai City.

Patient A is a 61-year-old female residing in a rural village in Gaocheng District of Shijiazhuang City and had a history of hypertension and multiple mild cerebral infarctions. Patient A experienced discomfort in her pharynx starting around 21:30 on January 1, 2021 and general malaise and fever around 04:00 on January 2. At 05:00, she took a taxi accompanied by her husband and eldest son (all wearing masks) to a hospital for treatment and was sent to the fever clinic for testing. Her temperature measured 38.6 °C and she tested positive at 12:18. At 17:50, she was transferred by a negative pressure ambulance to a designated hospital in Shijiazhuang for isolation and treatment.

In the two weeks prior to her diagnosis, Patient A had a history of staying at home, visiting family, and attending religious gatherings in the village with sporadic mask wearing. However, on December 28, she attended a wedding in the village at a restaurant with roughly 250 people in attendance. Of these 250 people, several were known to be traveling from Xi'an City of Shaanxi Province and Beijing Municipality.

Patient B is a 34-year-old male residing in Nangong City, a county-level city of Xingtai City. At 14:00 on January 1, he recorded a self-tested temperature of 38.1 °C and drove to the fever clinic of Nangong City for a COVID-19 test at his own expense. His results were found to be positive at 21:00 on January 2, and he was immediately isolated via ambulance and placed under medical observation. He was retested by Xingtai CDC and confirmed to be COVID-19 positive.

In the two weeks prior to his diagnosis, Patient B had a history of performing work-related tasks, staying at home, and meeting guests without going to high-risk areas. He was possibly exposed on December 25

when traveling to Shijiazhuang City to see his daughter at a children's hospital or on December 28 when attending an agricultural conference without wearing a mask. Based on the full investigation of Patient B's epidemiological history, 137 close contacts have been preliminarily identified.

On January 4, the sequences of the COVID-19 samples from Patients A (Shijiazhuang) and B (Xingtai) were obtained using Illumina Miseq and Illumina Nextseq550 platform, respectively (Sequence ID: 512 and 519). Compared with the Wuhan reference sequence (EPI_ISL_402119) (1–2), the Shijiazhuang strain had 21 nucleotide variation sites and the Xingtai strain had 22 nucleotide variation sites. The Xingtai strain shared the 21 nucleotide variation sites presented by the Shijiazhuang strain and also presented an additional unique variation. The 2 strains both contained the 7 single nucleotide polymorphisms (SNPs) that defined L-lineage European branch I (C241T, C3037T, C14408T, A23403G, G28881A, G28882A, and G28883C) (Figure 1). Furthermore, the 2 sequences shared an additional 14 unique nucleotide variation sites (T2392C, C6354T, T7075C, C10747T, A11794G, C15342T, C15360T, G15666A, C16733T, C21727T, T22020C, C25416T, C27213T, and C29835T) and were both identified as belonging to B.1.1.123 Pangolin lineage (3), which suggested that the Shijiazhuang and Xingtai strains had the same transmission route. However, the Xingtai strain had an additional variation site T23227C. The sequencing results indicated that the genomic characteristics of the Hebei strains differed from recent strains detected in several COVID-19 epidemics in China (4–6) and were unrelated to recent variants discovered in the United Kingdom.

After accessing the public database GISAID and GenBank, 3 Russian strains detected in July were found to share the 10 variation sites with the 2 Hebei strains (GISAID IDs: EPI_ISL_596266, EPI_ISL_569792, and EPI_ISL_569793). Despite relatively few shared variation sites, the 3 unique sites detected from the Russian strains were only seen in the Hebei strains

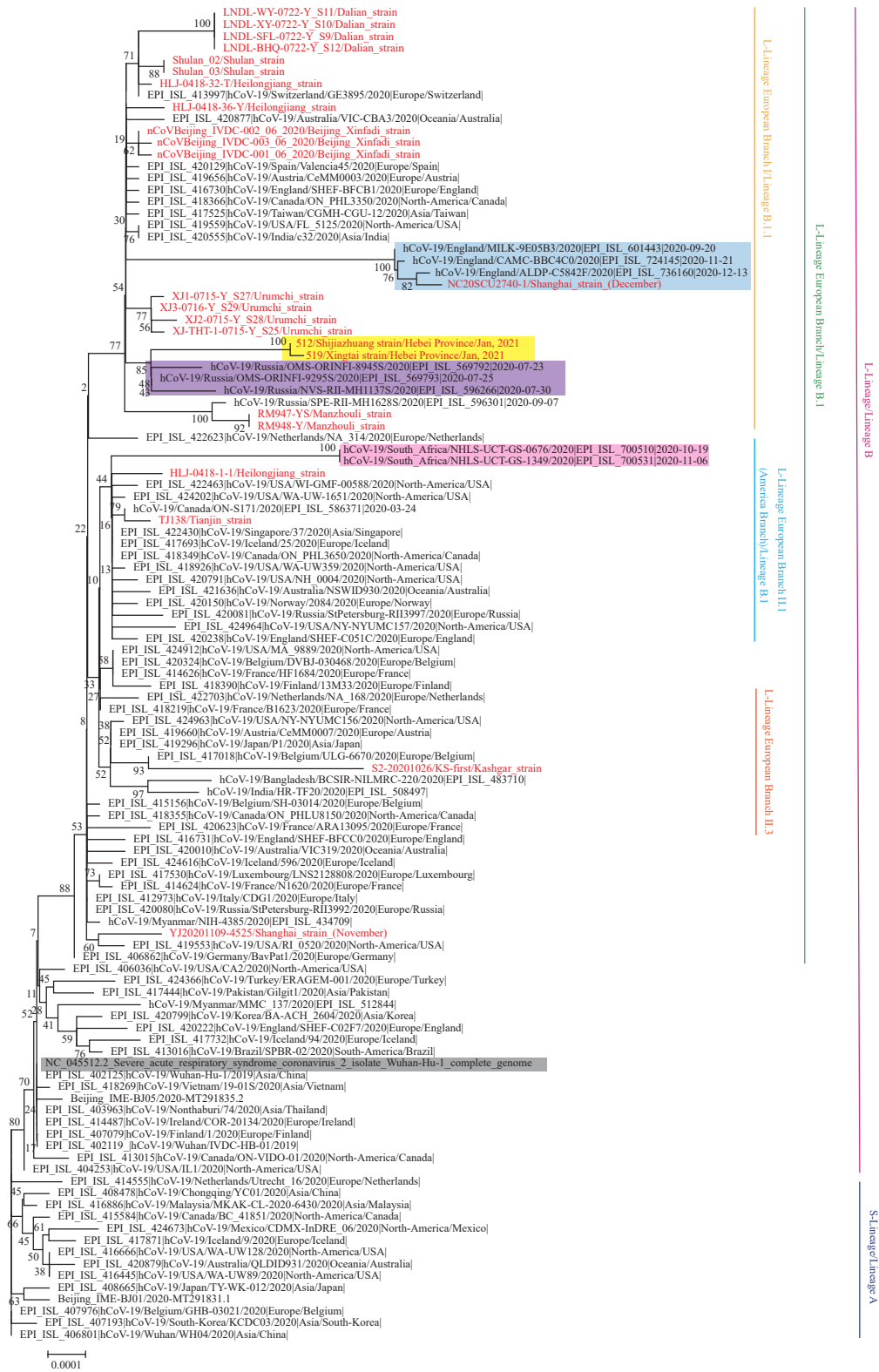


FIGURE 1. Phylogenetic tree based on the full-length genome sequences of the COVID-19 virus. Strains associated with specific outbreaks in China were marked and colored in red letters. The Shijiazhuang and Xingtai strains from Hebei Province are highlighted in yellow, and the Russian strains that shared 10 nucleotide variation sites with the Hebei strains are highlighted in purple. The UK VUI-202012/01 variants and South African 501.V2 variants are highlighted in blue and pink, respectively. The Wuhan reference strain is shaded in gray. The S(A)- or L(B)-lineage and sublineages of the COVID-19 virus were marked and colored on the right.

(Figure 1). The databases have not recorded many recently uploaded strains from Russia, but evidence indicates that these the Shijiazhuang and Xingtai strains may have originated from these Russian strains. Continued monitoring of COVID-19 in Hebei Province is vital to prevent further transmission.

Since the initial identification of the cases on January 2, 2021, 39 confirmed cases and 83 asymptomatic infections in Hebei Province have been identified as of January 5, 2021. Before this outbreak was identified, Hebei Province had no COVID-19 cases for approximately 160 days with the last cases being found on June 25, 2020.

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Corresponding authors: Wenbo Xu, xuwb@ivdc.chinacdc.cn; Qi Li, liqinew@aliyun.com.

¹ Hebei Provincial Center for Disease Control and Prevention, Shijiazhuang, Hebei Province, China; ² National Institute for Viral Disease Control and Prevention, China CDC, Beijing, China; ³ Chinese Center for Disease Control and Prevention, Beijing, China. [†] Joint first authors.

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