

## Notes from the Field

## Detection of Variants of B.1.617 Lineage from Five Returning Chinese Nationals at a Guangxi-Vietnam Border Port — Guangxi Zhuang Autonomous Region, China, April 2021

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A 47-year-old male (Patient A) passenger from Vietnam whose nucleic acid results for coronavirus disease 2019 (COVID-19), also known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), were positive at Pingxiang Customs on April 29, 2021, and subsequently confirmed by Guangxi CDC laboratories on April 30.

On April 30, four accompanying persons (Patient B–E) of Patient A returned from Vietnam. After being tested by the laboratory of Pingxiang Customs using nasopharyngeal swab tests for COVID-19, the results for patients showed COVID-19 positive. All five patients were transported to the Pingxiang Emergency Medical Center for isolated treatment by ambulance. Clinical conditions of the five patients included normal body temperature, blood tests, and liver-kidney functions. Abnormalities in chest computed tomography (CT) suggested infectious lesions, four patients (A/B/D/E) classified as mild type of COVID-19, and one (patient C) was classified as severe type.

Preliminary epidemiological investigation revealed those patients were on a business trip from April 9, when they came to Yen Bai Province, Vietnam, and were isolated in a designated isolation hotel until April 22. From April 23 to 28, all five patients performed their business and travel in Vietnam. The latest negative results for Patients A, B, and C were on April 22 and were on April 27 for Patients D and E, respectively.

Further investigations demonstrated a group of Indian nationals who were isolated in the hotel on April 18, and four of these individuals eventually tested positive for COVID-19 on April 19. In addition, guests of the hotel had activity unrestricted in the hotel during the quarantine, and there was only one attendant who took no relevant precautionary measures against COVID-19 when on duty. The attendant was later confirmed positive for COVID-19

on April 26.

The specimens of the confirmed patients were sent to Guangxi CDC and sequenced by Illumina MiSeq Sequencing platform using a 500-cycles MiSeq v2 Reagent Kit between April 30 to May 4. On May 3, one patient's whole genome sequence was obtained, and on May 7, the other four patients' sequences were obtained. In comparison with the COVID-19 reference strain (Gene Bank Accession: NC\_045512), these isolates possessed 28–34 variation sites in nucleic acids, including 11 variations in the spike protein (T19R, G142D, A222V, L452R, T478K, D614G, P681R, D950N, E156del, F157del, and R158del). Notably, eight variation sites of amino acid residues (T19R, L452R, T478K, D614G, P681R, D950N, F157del, and R158del), which were identical to those in Indian B.1.617.2 variants, were observed in all five isolates. Phylogenetic analysis of genome sequence indicated these isolates belonged to the PANGO lineage (1) B.1.617.2 (Figure 1), an emerging variant first identified in India in October 2020 and has recently been designated as a variant of concern (VOC) which labeled as Delta by the World Health Organization (WHO) (2–3). The COVID-19 infection in these five patients probably occurred when they were staying in the designated isolation hotel in Vietnam and sharing space with the Indian nationals that were confirmed positive for COVID-19. Furthermore, the hotel attendant was confirmed as COVID-19 positive on April 26. The B.1.617 variant had been detected in Chongqing (4) and had been identified in dozens of countries worldwide, posing a serious challenge to the global pandemic. Among the sub-variants of B.1.617, the B.1.617.3 shares the L452R and E484Q mutations found in B.1.617.1 (VOI, Kappa), whereas B.1.617.2 does not have the mutation E484Q but has the T478K mutation not found in B.1.617.1 and B.1.617.3. Since most of B.1.617 variants reported in 17 countries contained 2 key mutations, L452R and E484Q, these imported

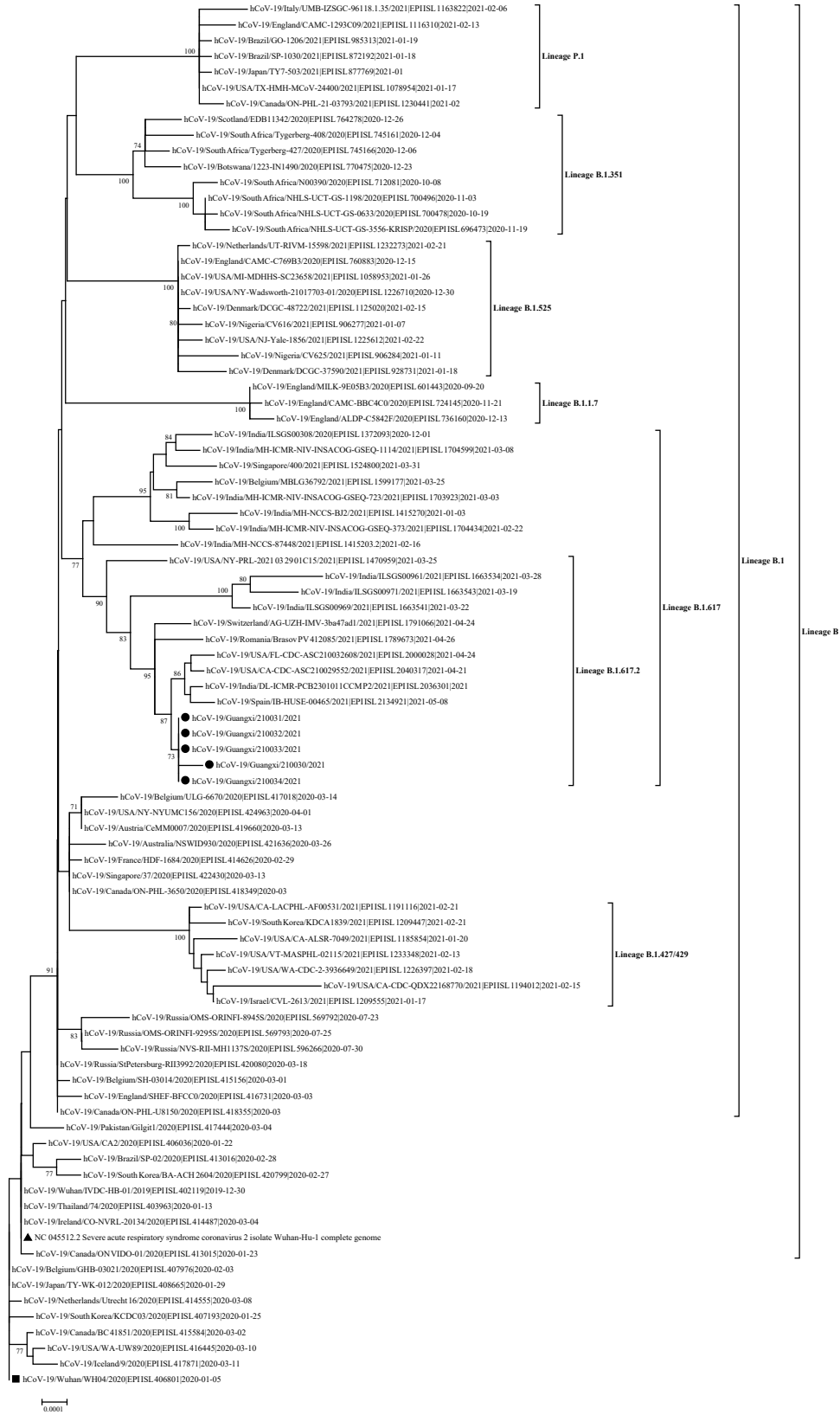


FIGURE 1. Neighbor-joining phylogenetic tree based on the whole genome sequences of COVID-19 representative strains. Note: The five Guangxi strains are indicated by dots; the Wuhan reference strain is indicated by triangle. The PANGOLIN lineages were marked on the right. The tree was rooted using strain WH04 (EPI\_ISL\_406801) in accord with the root of PANGOLIN tree.

cases in Guangxi were excluded from such double-mutant variants.

Guangxi Zhuang Autonomous Region is adjacent to Association of Southeast Asian Nation (ASEAN) countries by land and sea and is an important provincial-level administrative division for China open to ASEAN. During the 13th Five-Year Plan period, the import and export trade of Guangxi to ASEAN accounted for 48.9% of the total foreign trade value. However, over the past year, cases of COVID-19 rose 40-fold to 162 million globally, while the number of deaths has increased 11-fold to more than 3.3 million. To prevent COVID-19 cases from entering, Guangxi has taken strict restrictions on all entry-exit personnel. The five patients were found among returning Chinese nationals from Vietnam at a border port for the first time, suggesting that the COVID-19 (B.1.617.2 variants) still poses a risk of transmission in some ASEAN countries. Therefore, constant surveillance of genome sequences in imported cases is required to track the transmission and evolution of the COVID-19 virus during the ongoing COVID-19 pandemic. The pathogenicity and transmissibility of these mutant variants urgently need further study (5–6).

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