

Notes from the Field

A Case of New Variant COVID-19 First Emerging in South Africa Detected in a Security Guard at the Isolation Point — Shenzhen, China, January 23, 2021

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On January 22, 2021, a 34-year-old male, who served as a security guard at the isolation point in Shenzhen, tested positive for coronavirus disease 2019 (COVID-19) during the every-three-day routine test. After the nasopharyngeal swab was further confirmed as positive for COVID-19 by Shenzhen CDC, the patient was transferred to the Third People's Hospital of Shenzhen and was diagnosed as a COVID-19 asymptomatic infection. On January 25, 2021, Shenzhen CDC identified the 20H/501.Y.V2 (B.1.351) variant, which was a variant of COVID-19 virus first emerging in the South Africa.

The epidemiological investigation indicated that the patient (ACC-XG00731) began working as a security guard at the isolation point on July 25, 2020 in Shenzhen. On January 19, his test result was negative. According to his statement, in the last 14 days, he had worked on the isolation floor occasionally but had not been exposed to the individuals who were in quarantine, had no exposure to the household or medical waste generated from the isolation personnel, and did not participate in the sewage treatment of the isolation point. On January 22, 2021, 1 case (ACC-XG00741) of COVID-19 infection in this isolation point was detected in entry isolation personnel from South Africa and was diagnosed on January 22. It was considered possible that case ACC-XG00731 is a descendant of the case ACC-XG00741.

On January 25, 2021, the sample of the 2 cases were sequenced by Shenzhen CDC using the second-generation (MiSeq) and third-generation sequencing technology (Nanopore). Compared with the Wuhan reference (EPI_ISL_402125) (1), these 2 strains exhibited 23 to 24 nucleotide variation sites, belonging to the Pangolin lineage B.1.351 (2), which were all classified as the 20H/501.Y.V2 variant (Figure 1). The genomic sequence of ACC-XG00731 and ACC-XG00741 strains were highly homologous (99.997%), sharing 23 variation sites (G174T, C241T, C1059T, A2692T, C3037T, G5230T, C9808T, A10323G,

C14408T, C21614T, A21801C, A22206G, G22813T, A23403G, C23664T, G25477T, G25563T, C25904T, C26456T, C26645T, C28253T, C28887T, and G29737T). The 2021A-XG00731 strain only had one specific variation site (C16428T). As is characteristic of 501.Y.V2 variant, the ACC-XG00731 strains carried several amino acid mutation sites, including K417N, E484K, and N501Y.

The 501Y.V2 lineage, which was connected to a fast-growing epidemic, emerged in early August in South Africa (3). The 501Y.V2 lineage includes several specific mutations (D80A, LAL242-244del, R246I, K417N, E484K, N501Y, D614G, and A701V) in the spike protein of the COVID-19 virus, also known as severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2). The N501Y mutation had also been identified in the B.1.1.7 variant (also known as 501Y.V1) first emerging in the United Kingdom (4); recently, the B.1.1.7 variant was estimated to be approximately 56% more transmissible than existing viruses in circulation (5). The N501Y mutation may influence the function of spike receptor binding domain that promotes the interaction to ACE2 on the host cells, making infection easier (6).

In the case that the 501Y.V2 variant first emerging from South Africa was detected in returnees and further spread to the security guard at the isolation point in Shenzhen, the management measures of the isolation points should be heightened. The 501Y.V2 and 501Y.V1 variant had been detected in Guangdong (7) and Shanghai in China, respectively (8), and had been identified in tens of countries worldwide, posing a more serious challenge to the global epidemic. Understanding the faster-spreading variants of COVID-19 virus may be beneficial for the policy decisions to contain their spread.

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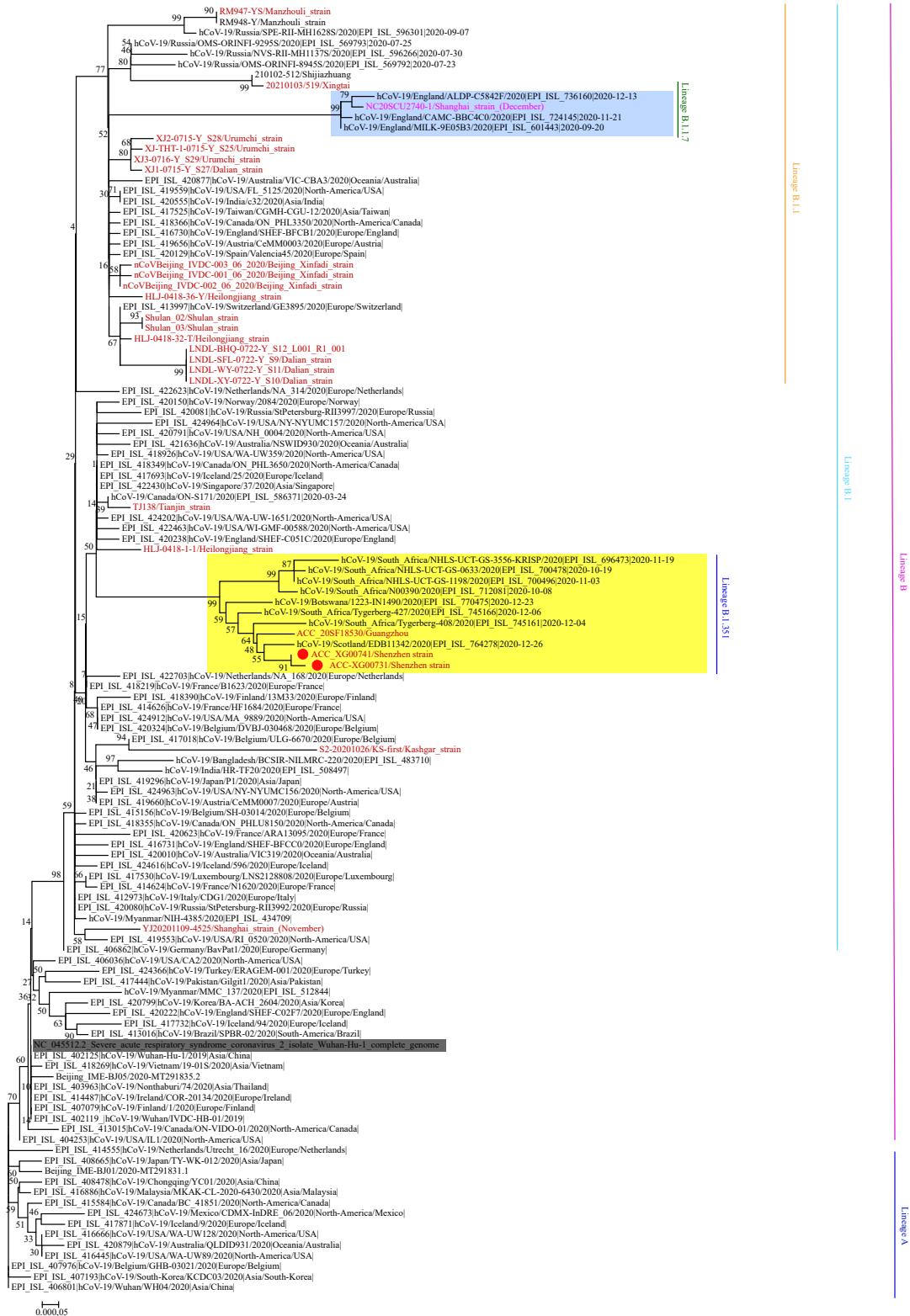


FIGURE 1. Phylogenetic tree based on the full-length genome sequences of the COVID-19 virus. The strains associated with specific outbreaks in China are marked in red. The South African 501Y.V2 variants are highlighted with yellow color and the Guangdong imported 501Y.V2 variant are marked in red, and the Shenzhen 20H/501.Y.V2 variant are exhibited with the red dots. The UK VUI-202012/01 variants are highlighted in blue. The Wuhan reference strain is marked in gray. The S(A)- or L(B)-lineage and sublineages of the COVID-19 virus were marked and colored on the right.

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