

## Notes from the Field

## Two Imported Cases of New Variant COVID-19 First Emerging in Nigeria — Guangdong Province, China, March 12, 2021

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On February 19, 2021, a 48-year-old male (Case A, XG2275) returning from Nigeria and a 38-year-old female (Case B, XG2276) returning from Ukraine via airplane were tested by the laboratory of Guangzhou Customs using nose swabs to test for coronavirus disease 2019 (COVID-19). Both of them tested positive and were transported by ambulance from the isolation point to Guangzhou Eighth People's Hospital. They are still undergoing centralized medical observation in the hospital after recovery.

On March 5, Guangdong CDC received the samples and began virus isolation and genome sequencing analysis. On March 10, the 2 samples were sequenced using Nanopore GridION. On March 12, the sequencing analysis concluded that the 2 virus genomes belonged to lineage B.1.525, a new COVID-19 variant first emerging in Nigeria, which was first detected by genome sequencing in mid-December in Nigeria but was also quickly found in cases in the United Kingdom, France, and elsewhere. As of March 8, 2021, a total of 577 counted sequences in 30 countries were found in the world (1).

Compared with the Wuhan reference sequence (EPI\_ISL\_402119) (2–3), the strain from Case A (XG2275) displayed 24 nucleotide variation sites (C241T, C1498T, A1807G, G2659A, C3037T, C6285T, T8593C, C9565T, C14407T, C14408T, C18171T, A20724G, A21717G, C21762T, G23012A, A23403G, G23593C, T24224C, C24748T, T26767C, C28308G, A28699G, C28887T, and G29543T) including the single nucleotide polymorphisms (SNPs) that defined the L-lineage European branch and belonged to the Pangolin lineage B.1.525 (Figure 1). Furthermore, 10 amino acid mutation sites (E:L21X, M:I82T, N:A12G, N:T205I, S:Q52R, S:A67V, S:E484K, S:D614G, S:Q677H, and S:F888L) and 3 amino acid deletions (H69del, V70del, and Y144del) were detected in the protein that corresponded to the features of the Nigerian variant (B.1.525) (4).

Compared with the Wuhan reference sequence (EPI\_ISL\_402119) (2–3), the Case B (XG2276) strain displayed 22 nucleotide variation sites (C241T, C1498T, A1807G, C3037T, C6285T, T8593C, C9565T, C14407T, C14408T, C18171T, A20724G, C21762T, G23012A, A23403G, G23593C, T24224C, C24748T, T26767C, C28308G, A28699G, C28887T, and G29543T) including the SNPs that defined the L-lineage European branch and belonged to the Pangolin lineage B.1.525 (Figure 1). Furthermore, 9 amino acid mutation sites (E:L21X, M:I82T, N:A12G, N:T205I, S:A67V, S:E484K, S:D614G, S:Q677H, and S:F888L) and 3 amino acid deletions (H69del, V70del, and Y144del) were detected in the protein that corresponded to the features of the Nigerian variant (B.1.525).

The variant first emerging in Nigeria (B.1.525) shares the same 3 amino acid deletions (H69del, V70del, and Y144del) with the 501Y.V1 variant (also known as the B.1.1.7). The mutation E484K is also present in the 501Y.V2 variant first emerging in South Africa (also known as the B.1.351) and Brazilian strains (501Y.V3). The amino acid substitution at position 677 (Q677H) is identical to that found in variants recently described in the United States. The amino acid substitutions Q52R and A67V are unique to the B.1.525 (4). This is the third recent detection of a major international variant following the detection of the United Kingdom 501Y.V1 variant and the South African 501Y.V2 variant. The transmissibility and pathogenicity of these mutant variants urgently needs further study (5–6).

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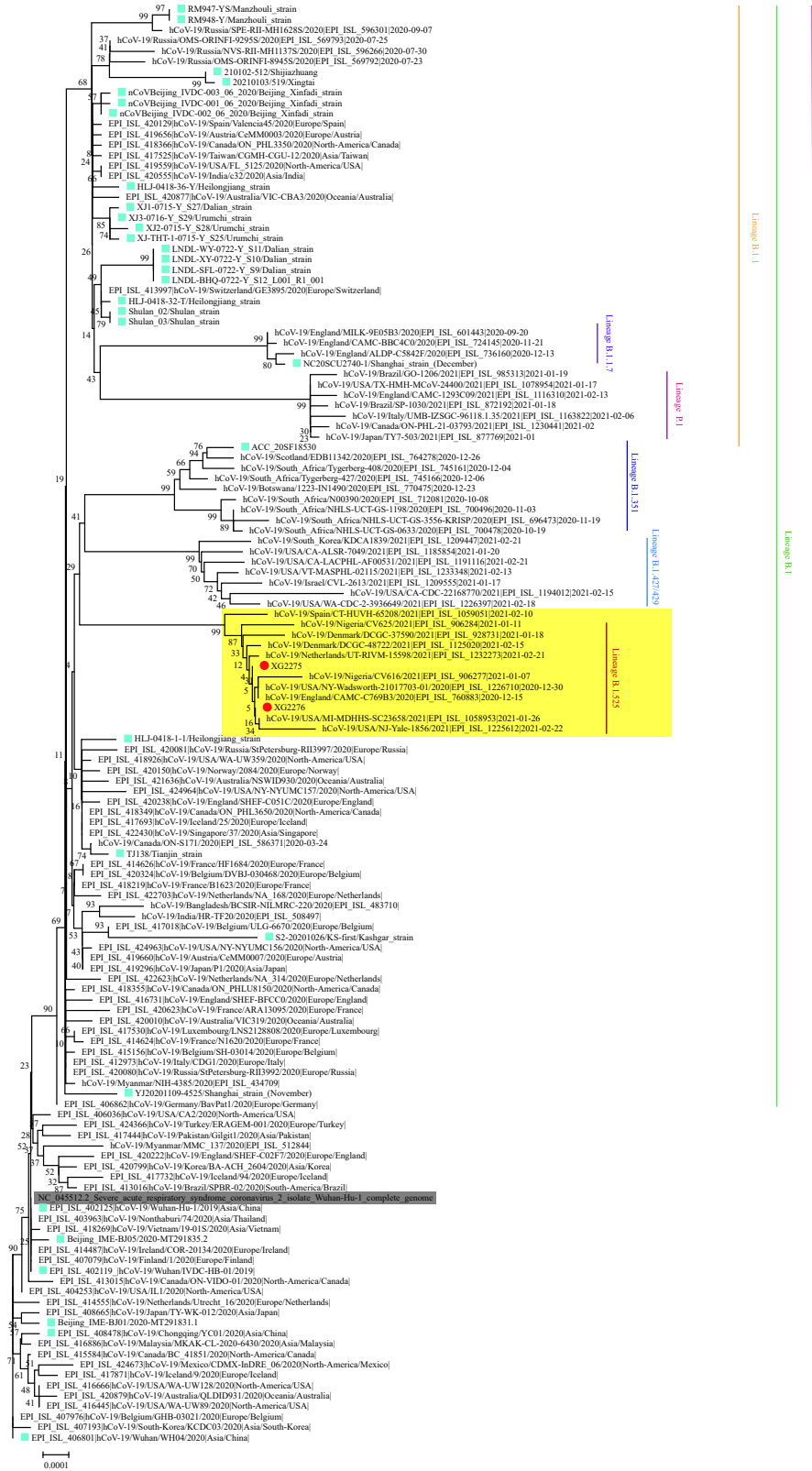


FIGURE 1. Phylogenetic tree based on the full-length genome sequences of the COVID-19 virus. The Nigerian variants (B.1.525) are highlighted in yellow and the Guangdong imported B.1.525 variant cases are marked with red dots. The strains associated with specific outbreaks in China are marked with blue squares. The Wuhan reference strain is shaded in gray. The 5 distinguished COVID-19 mutants are marked and colored on the right. The L(A)- or L(B)-lineage and sublineages of the COVID-19 virus were marked and colored on the right.

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