Notes from the Field

The First Case of COVID-19 by an A.27 Lineage Variant Detected in a Returning Employee — Sichuan Province, China, January 7, 2021

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On January 7, 2021, a 32-year-old returning employee arrived in Chengdu from Algeria via airplane and tested positive for coronavirus disease 2019 (COVID-19) by nucleic acid tests. He was transferred to the designated hospital for further diagnosis and treatment. The patient was diagnosed as a mild COVID-19 case on January 16. After medical treatment, this patient recovered and left the hospital on February 18.

According to the manufacturer's instruction, Viral RNA from the patient's specimen was extracted using the QIAamp® Viral RNA Mini Kit (Qiagen, Valencia, CA, USA). Amplicon-based enrichment and sequencing approach were applied. The viral genome was reverse-transcribed and amplified using ULSEN® 2019-nCoV Whole Genome Kit (Micro Future). The sequencing libraries were prepared using the Illumina Nextera® XT Library Prep Kit. The final viral-enriched libraries were sequenced using the Illumina MiSeq platform. The whole genome sequence of this COVID-19 virus strain, designated SCSR-455, was assembled and obtained using Geneious v11.0.3 (https://www.geneious.com). The published genomes from the Global Initiative on Sharing All Influenza Data (GISAID) and the genome of SCSR-455 were aligned with the reference genome (Wuhan-Hu-1, Genbank: NC_045512, GISAID: EPI_ISL_402125) (*1*) using MAFFT v7.4 (https://mafft.cbrc.jp/alignment/software/) (*2*). The maximum likelihood (ML) phylogeny was estimated with IQ-TREE v1.6.12 (*3*) with 1000 bootstraps and the best-fit model autodetected.

The genomes of SCSR-455 had the single nucleotide polymorphisms (SNPs) 8782T and 28144C, which represent the Pangolin A lineage (*4*). The A lineage was prevalent during the early stage of the COVID-19 epidemic in China (*5*). So far, however, it has been less frequently detected than the B lineage. Phylogenetic analysis revealed that SCSR-455 was located in the Pangolin lineage A.27 which was designated in February 2021. This lineage of COVID-19 viruses was first detected in Denmark on December 14, 2020, and then transmitted to several other countries, including Belgium, France, the Netherlands, Nigeria, Rwanda, Switzerland, the United Kingdom (UK), and Turkey (Figure 1). Apart from 8782T and 28144C, viruses in the A.27 lineage had 21 SNPs (A361G, C1122T, C2509T, A9204G, A11217G, C16466T, A18366G, A20262G, C21614T, G22468T, T22917G, A23063T, C23520T, C23525T, G23948T, G25218T, T25541C, C27247T, A28273T, G28878A, and G29742A) compared with the Wuhan-Hu-1 reference sequence. The genomes of SCSR-455 shared all these lineage-defining SNPs with the A.27 lineage strains and also had another 6 SNPs, including C3096T, C5974T, C12241T, C16293T, C19895T, and C21658T. The genomes of 4 strains of the A.27 lineage, collected in France (EPI_ISL_934974), Rwanda (EPI_ISL_1020288), and the UK (EPI_ISL_769875 and EPI_ISL_769876), respectively, shared 26 SNPs with SCSR-455. These 4 strains were phylogenetically most closely related to SCSR-455 within the A.27 lineage (Figure 1).

A total of 7 amino acid mutation sites (L18F, L452R, N501Y, A653V, H655Y, D796Y, and G1219V) that correspond to the features of the A.27 lineage were detected in the spike protein of SCSR-455. The A.27 is the first sub-lineage of the A lineage that evolved to obtain N501Y mutation in the spike protein, despite the amino acid mutation D614G, which might increase viral transmissibility (*6*) not being identified. Residue 501 is a key contact residue within the receptor-binding domain (RBD), and the N501Y mutation has been shown to enhance binding affinity to human and murine hACE2 (*7*–*8*). N501Y has been associated with some faster-growing COVID-19 virus lineages throughout the world (e.g.,

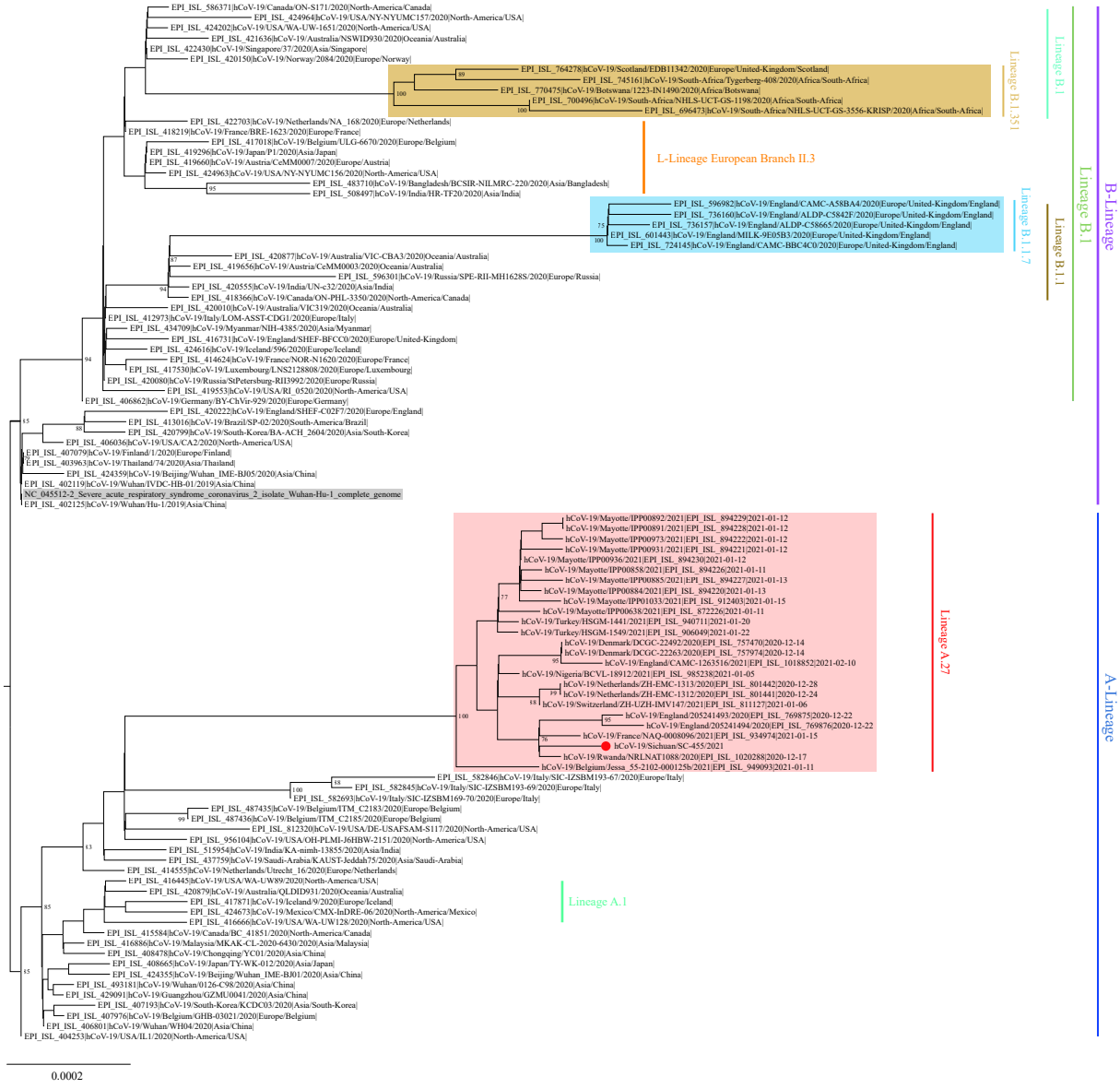

FIGURE 1. The maximum likelihood (ML) phylogenetic tree is based on the genome sequences of the COVID-19 virus.
Note: The A.27 variants are highlighted in red, and the Sichuan imported A.27 variant is marked with a red dot. The Wuhan reference strain is shaded in gray. The A or B-lineage and sub-lineages of the COVID-19 virus were marked and colored on the right. All labeled clades are supported by ML bootstrap values >75%.

the UK lineage B.1.1.7, also known as the 501Y.V1; and the South African lineage B.1.351, also known as the 501Y.V2). The A.27 lineage shared only one amino acid mutation, N501Y, with the B.1.1.7 and the B.1.351 lineage. In Addition, the A.27 lineage obtained the L452R mutation, which might alter the antibody recognition sites, and D796Y, which might be associated with changes in ligand binding surface.

The strain SCSR-455 is the first imported A.27 lineage variant in China. Previous investigations showed that the A lineage was less prevalent than the B lineage. Given the importance of N501Y in the sustained human-to-human transmission of COVID-19, ongoing epidemiological and genomic surveillance are needed to monitor the potential expanded transmission of the A lineage. Further laboratory investigations are required to test the efficiency of the existing vaccines against this newly described A.27 lineage.

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