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GENOME SEQUENCES

New SARS-CoV-2 Variant from Jordan

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ABSTRACT A variant of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) from Jordan was identified during the second wave of infection. The genome of this variant has a unique set of mutations that suggest local evolution. Due to the continuous emergence of new variants worldwide, molecular surveillance is crucial for fighting the pandemic.

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2; the causative agent of COVID-19) belongs to the family *Coronaviridae* and the genus *Betacoronavirus* (1, 2). In viral outbreaks, new variants are expected to emerge as part of the virus's natural evolution (3). The assumption that SARS-CoV-2 was a slowly mutating virus began to change by the end of 2020, with the emergence of novel variants such as those reported in the United Kingdom (20I/501Y.V1/B.1.1.7), South Africa (20H/501Y.V2/B.1.351), Brazil (P.1/20J/501Y.V3/B.1.1.248), and India (B.1.617). These lineages contained mutations in the spike protein that are expected to increase the infectivity and virulence of the virus (4, 5). Since new SARS-CoV-2 variants continue to emerge globally, and Jordan is amid a second wave of COVID-19 infections, we analyzed SARS-CoV-2 variants in Jordan to see if one of these known strains had emerged. Here, we report the complete genome sequence of a SARS-CoV-2 variant isolated in Jordan.

Strain SARS-CoV-2/human/JOR/AM-HU-16/2021 was recovered (nasopharyngeal swabs) from a 57-year-old female inpatient at the Prince Hamza Hospital, Amman, Jordan. The patient was identified as positive for COVID-19 by reverse transcription-PCR (RT-PCR; Zybio, China). A QIAamp viral RNA minikit (Qiagen, Germany) was used to extract viral RNA, which was then converted into cDNA and amplified using the QIAseq SARS-CoV-2 primer panel kit (Qiagen, Germany). The Qubit 4 fluorometer was used to combine, purify, and quantify the generated 400-bp amplicons for library preparation. Nextera DNA Flex libraries were prepared and sequenced on the iSeq 100 system (Illumina) with an output of 2 × 150-bp paired ends.

The raw data were analyzed using the Illumina BaseSpace pipeline. The FASTQ Toolkit v 2.2.5 was used to remove low-quality and short reads. DRAGEN COVID Lineage v 3.5.1 was used for mapping/aligning, variant calling, and consensus sequence generation of the SARS-CoV-2 genome compared to the reference genome (Wuhan-Hu-1, GenBank accession number MN908947.3). Default parameters were used for all software unless otherwise specified.

Analysis allowed us to obtain a SARS-CoV-2 genome of 29,886 bp in length. From 1,157,905 reads, 1,080,169 reads were mapped, covering 99.15% of the total genome with a median coverage of 2,330×. This genome was defined by multiple spike (S) protein mutations based on viral genome sequence data (deletions 69-70, S12F, W152R, L176F, R346S, L452R, T547I, D614G, Q677H, and A899S) and is classified as a subclade of 20D (Fig. 1). The L452R mutation in the S protein is found within a known receptor binding domain that is resistant to monoclonal antibodies to the S protein (6). Clinical

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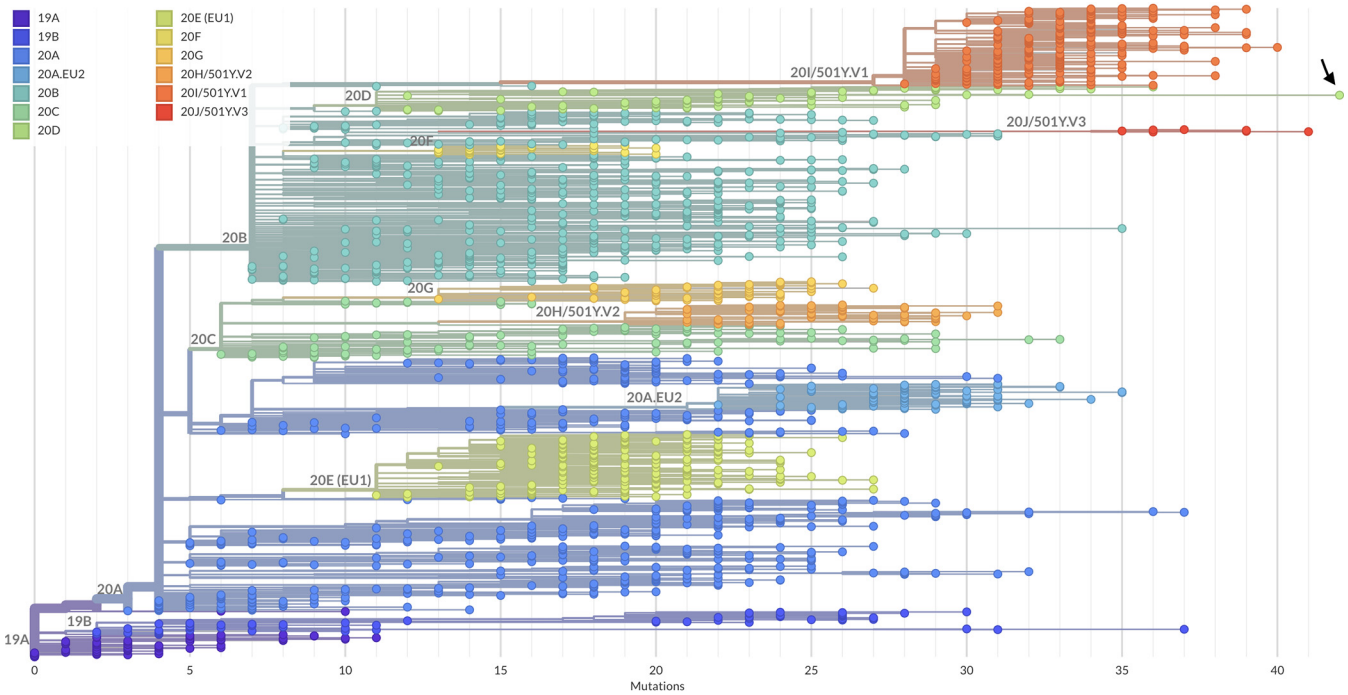

FIG 1 Phylogenetic relationship of SARS-CoV-2/human/JOR/AM-HU-16/2021 (black arrow) to the global SARS-CoV-2 genomes. The phylogenetic tree was constructed using the Nextclade tool v 0.14.3 (https://clades.nextstrain.org/).

outcomes have yet to be determined, and the strain's functional impact on infectivity and disease severity is unknown. Even though there are 618 genome sequences of SARS-CoV-2 from Jordan uploaded to the GISAID database, none of them is close to this variant.

Data availability. The genome sequence of this sample has been uploaded to the GISAID database under the accession number EPI_ISL_1336652 and to GenBank (accession number MZ266636). The raw data are available at the NCBI SRA (BioProject number PRJNA733775).

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