SARS-CoV-2 Variant of Concern 202012/01 (B.1.1.7) in a Traveler from the United Kingdom to China

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Highlight

We report the complete genome of SARS-CoV-2 VOC 202012/01 in a traveler from the United Kingdom to China, representing the first such case in North China. This study highlights that intensive genomic sequencing enables early identification and rapid characterization of the SARS-CoV-2 importing to China.

Dear editor - A new SARS-CoV-2 variant, designated Variant of Concern 202012/01 (VOC 202012/01), has caused a surge of COVID-19 in England since December 2020. On January 4, 2021, the UK government imposed a national lockdown on England to contain this variant. Evidence from mathematical modelling suggested that VOC 202012/01 is up to 70% more contagious than previously circulating forms of SARS-CoV-2. VOC 202012/01 has since then quickly spread globally and been reported in multiple countries. The COVID-19 genomic surveillance system in China has since closely monitoring the importing of this variant to China. Here we describe the recovery and characterization of a VOC 202012/01 genome in a traveler returning to China from the United Kingdom.

A 27-year-old male student returning from London, the United Kingdom, arrived in Qingdao, Shandong province, China, on December 19, 2020. Throat swab and blood samples taken upon his arrival were tested negative for SARS-CoV-2 using polymerase chain reaction (PCR) and antibody assay, respectively. He was then escorted to a hotel for 14-day mandatory quarantine. PCR testing result of a second throat swab taken on December 23 was negative. He was asymptomatic until December 26 when he developed symptoms of fever (39.0°C), body aches, and fatigue. PCR testing result of a third throat swab taken on January 1, 2021 was positive for SARS-CoV-2. He was immediately transferred to a local hospital and subsequently diagnosed with COVID-19. No COVID-19 case has been reported from other passengers on the same flight with this traveler.

We conducted RNA extraction, cDNA preparation and amplification, and Illumina sequencing for the SARS-CoV-2 positive throat swab. From over 17 million sequencing reads, we recovered a full-length SARS-CoV-2 genomic sequence of 29,824 bp, referred to as SD01 (deposited in the Global Initiative on Sharing Avian Influenza Data database). To investigate the genetic relationship between SD01 and previously published SARS-CoV-2 genomes, we retrieved >100,000 complete and high coverage UK SARS-CoV-2 genomes (length > 29,000 bp and undefined bases <1%) from the COVID-19 Genomics UK consortium (https://www.cogconsortium.uk). BLAST results showed that SD01 genome is most closely related to a group of UK SARS-CoV-2 genomes recovered in November and December 2020, differing by 2 nucleotides. SD01 genome clustered within genetic lineage B.1.1.7 in the genome phylogenetic tree (Fig. 1). SD01 genome possesses 17 signature mutations of VOC 202012/01, among which 3 mutations (N501Y, P618H, deletion 69_70) are in the spike

glycoprotein that could plausibly influence ACE2 binding and viral replication. In addition, SD01 genome possesses the dominant D614G mutation in the spike protein. Two mutations in the receptor-binding domain of the spike protein, E417N and E484K, that characterizes another emerging SARS-CoV-2 variant from South Africa (B.1.351) are not present in the SD01 genome.

VOC 202012/01 was estimated to be 56% more transmissible than the original virus. In addition, there is possibility that VOC 202012/01 may cause more severe infection, while further studies are needed. In term of vaccination, the Oxford ChadOx1 vaccine shows very similar efficacy against the VOC 202012/01 and the original virus, despite slightly lower effectiveness for VOC 202012/01. The South African variant B.1.351 emerged independently of VOC 202012/01. This variant contains the N501Y mutation to the spike protein but has a number of other mutations, among which E484K is associated with neutralizing antibody escape. Recent research shows that ChadOx1 vaccine provides minimal protection against mild-moderate COVID-19 infection from B.1.351 in young South African adults. Therefore, B.1.351 variant is of great public health concern due to its reduced vaccine effectiveness.

International travel facilitated the rapid spread of COVID-19 around the world [1]. In order to mitigate importing cases via international travel, almost every country in the world has imposed some form of travel restriction, including border closures, flight suspensions, and testing and quarantine for travelers [2,3]. These measures are clearly very beneficial for countries that have no or few COVID-19 domestic cases. All travelers entering China are requested to take molecular test pre-travel, receive test by the customs authorities, and subject

to a 14-day mandatory quarantine in the first entry point city [4,5]. Singapore implemented a Stay-Home-Notice strategy to minimize the risk of importing cases for the community [6,7].

Our study highlights that intensive genomic sequencing enables early identification and rapid characterization of the SARS-CoV-2 VOC 202012/01 importing to China. The emergence and spread of this highly contagious variant raised global concern. However, our understanding is still at an early stage. It's urgent and critical to assess the full implication of this variant, such as transmissibility and spread, disease severity, and potential influence on vaccine effectiveness.

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Potential conflicts of interest

No Conflict of interest.

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Figure legend

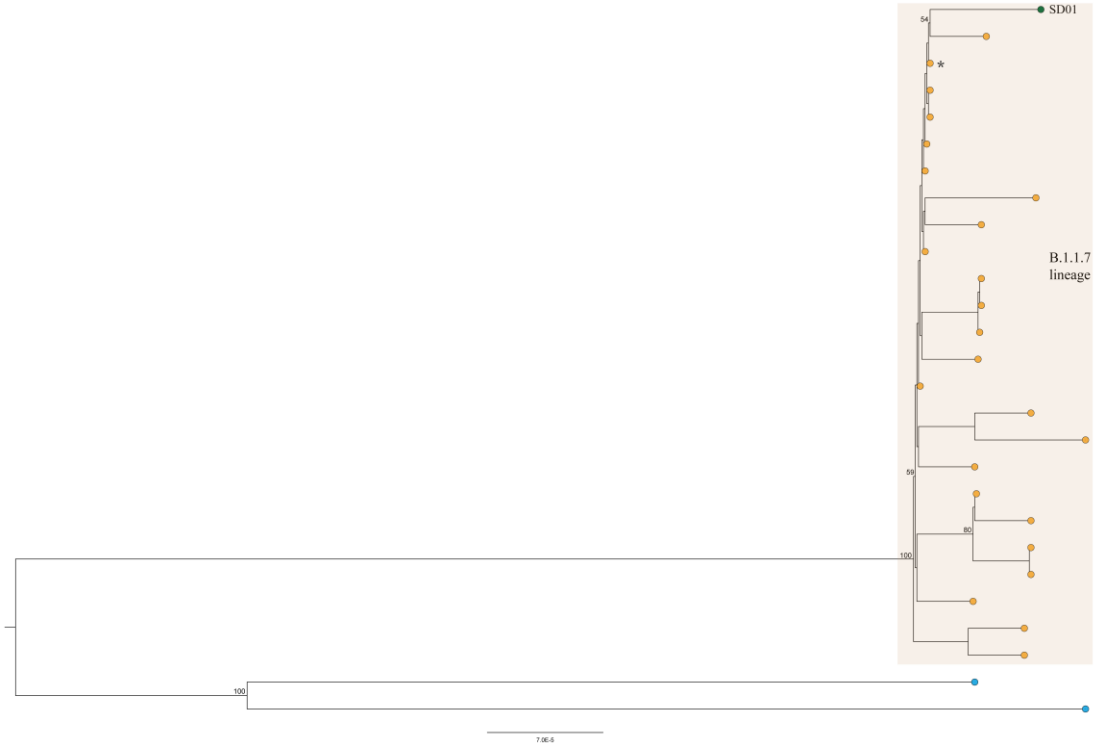

Figure 1. Maximum-likelihood phylogenetic trees of SARS-CoV-2 VOC 202012/01 genome recovered in a traveler returning to China from the United Kingdom. VOC 202012/01 genome recovered from the traveler in this study is marked in green, reference genomes representing B.1.1.7 lineage are marked in yellow, and reference genomes representing B.1 lineage are marked in blue. The earliest publicly available VOC 202012/01 genome (GISAID accession number, EPI_ISL_601443) is denoted by a black asterisk. The tree was generated using IQ-TREE V2.0.3. Numbers at the nodes indicate bootstrap support evaluated by 1000 replicates.