

Detection of SARS-CoV-2 Variant 501Y.V2 (South African origin) in Coastal Kenya

Background

As of 16th January 2021, 3 SARS-CoV-2 genetic variants have been described as variants of concern (VOC) given their potential impact on control efforts of COVID-19 pandemic. These variants have been designated as: 1) lineage B.1.1.7/501Y.V1 (first detected in the UK in September 2020); 2) B.1.351/502Y.V2 (first detected in South Africa in October 2020); and 3) B.1.1.28/501Y.V3 (first detected in Brazil in January 2021). The South African variant has been reported extensively in South Africa (447 genomes publicly available), Botswana (6 genomes publicly available) and 11 other countries across the globe.

Findings from sequence data obtained on 14th January 2021

Our report dated 11th January 2020 provided a snapshot of genetic diversity of circulating SARS-CoV-2 in Kenya based on whole genome sequences of 205 samples collected between June and October 2020 from 8 counties. Here, we update our findings based on whole genome sequencing of an additional 69 samples, 57 of which yielded genomes that were more than 80% complete (i.e., they passed quality control checks). The samples were collected between 01-Oct-2020 and 21-Dec-2020.

The newly sequenced samples were classified into a total of 11 lineages (**Figure 1**), six of the lineages have been described from our previous sequence data while five were novel. Two of the sequenced samples were classified as 501Y.V2, a known variant of concern that was first reported in South Africa. Most viruses belong to the lineages B.1 (n=29) and B.1.5 (n=13), which were the predominant lineages among Coastal Kenya samples based on our previous report. The other additional lineages include (B.1.179 (n=2), B.1.178 (n=1), B.1.113 (n=3) and B.1.102 (n=1).

Key Points

- We sequenced an additional 69 SARS-CoV-2 viruses from PCR positive samples collected between 01-Oct-2020 and 21-Dec-2020 across coastal Kenya. 57 sequences passed quality control checks.
- Our finding confirms the presence of the South African variant of concern (501Y.V2) in two travellers in Kenya.
- Based on the other 55 sequences, we can conclude that the South African variant has not spread sufficiently to dominate the Kenyan epidemic, but with only 55 sequences limited to the Coast, we would not be able to detect more limited spread of the new variant in Kenya.

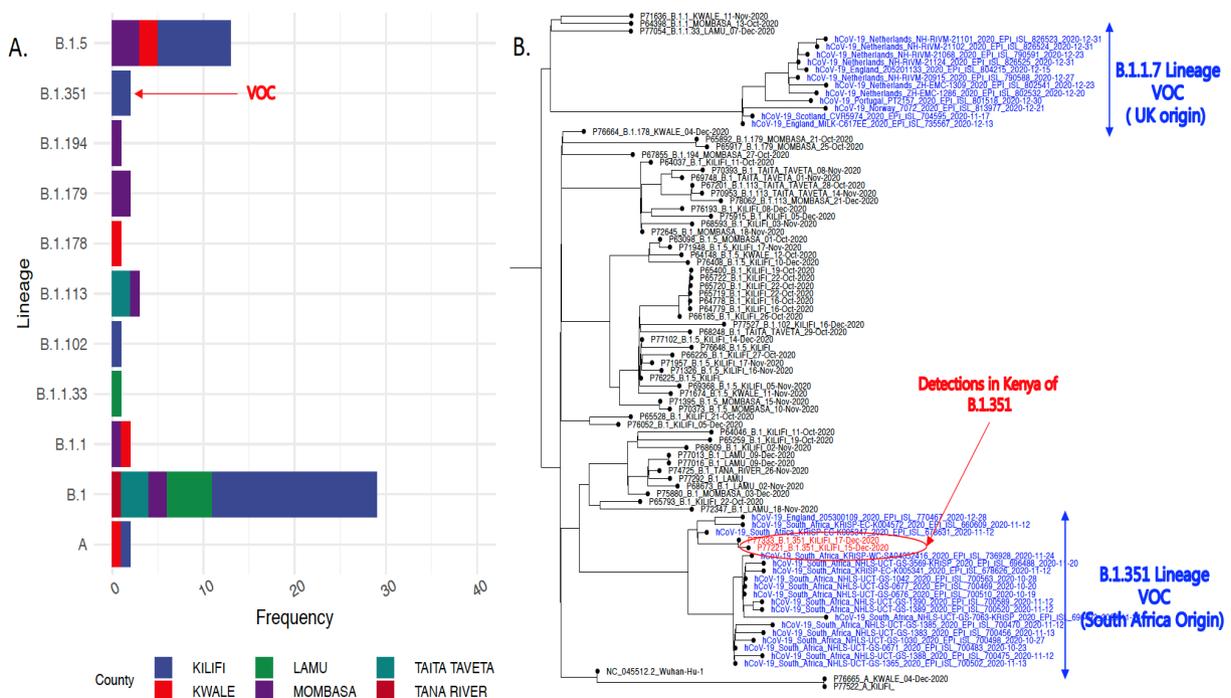


Figure 1. (A) A bar plot showing the lineage frequency (x-axis) of the circulating SARS-CoV-2 cases from coastal counties based on 57 newly sequenced cases sampled between October-December 2020.

(B) A phylogenetic tree showing the placement of the two samples classified as 501Y.V2 relative to other SARS-CoV-2 sequences from the coastal region (coloured black) and in relation to global subset of B.1.1.7/501Y.V1 (UK origin) and B.1.351/501Y.V2 (SA origin), coloured blue. The two sequences from identified in Kenya from two travellers from South Africa are coloured red.

The persons infected with the 501Y.V2 variant

The two genome sequences that were identified as 501Y.V2 were obtained from samples that were collected on the 15th and 17th December 2020, from two South Africa nationals who visited the country. Their samples were taken as part of the routine surveillance of visitors arriving in coastal Kenya during the month of December. None of the travellers had symptoms at the time of sample collection and they have since left the country.

Implications

The identification of variant 501Y.V2 among 2 asymptomatic travellers of different age categories confirms the entry of new variants to Kenya. We cannot infer how much transmission has arisen from new variants because of the small sample size. With a small sample size, we are limited to concluding that the South African variant has not spread sufficiently to dominate the Kenyan epidemic, as it has done in South Africa. However, given the extent of transmission in other countries there is a clear ongoing risk of spread of new variants.

Recommendations

- a. Continue and extend genomic surveillance of circulating SARS-CoV-2 across Kenya.
- b. Genomic surveillance should include Nairobi SARS-CoV-2 samples from November to date.

Data availability

The whole genome sequence data will be available from GISAID.

Funding Disclaimer:

This work was supported by the National Institute for Health Research (NIHR) (project references 17/63/82 and 16/136/33) using UK aid from the UK Government to support global health research, The UK Foreign, Commonwealth and Development Office and Wellcome Trust (grant# 102975; 220985). The views expressed in this publication are those of the author (s) and not necessarily those of NIHR, the Department of Health and Social Care, Foreign Commonwealth and Development Office, Wellcome Trust or the UK government.