

Detection of Additional SARS-CoV-2 B.1.351/501Y.V2 Variants and one B.1.1.7/501Y.V1 variants in Kenya

Key Points

- We sequenced a total of 58 samples collected between 26th October 2020 and 8th February 2021. A total of 14 samples were collected from coastal counties, 14 from Nairobi county and 30 from Western Kenya counties.
- 4 sequences collected from truck drivers of Tanzanian nationality in Kwale and Taita Taveta counties were classified as variants of concern (B.1.351/501Y.V2).
- One sequence, recovered from a sample obtained from a 28-year-old individual in Nairobi county with no travel history, was classified as a variant of concern B.1.1.7/501Y.V1

Background

At KEMRI-Kilifi, we have continued to undertake SARS-CoV-2 genome sequencing of samples identified as SARS-CoV-2 positive during the national testing effort. In our previous policy briefs we reported detection of 6 B.1.352/501Y.V2 variants: two from international visitors, two from truck drivers seeking entry into Kenya and two from Kenyan residents who had no recent history of international travel. We have also previously reported detection of a single B.1.1.7/501Y.V1 case from a sample collected from Mombasa county in an individual who had no history of recent travel.

Findings from sequence data obtained on 22nd February 2021

We sequenced an additional 58 samples collected between 26th October 2020 and 8th February 2021 from 14 counties. A total of 14 samples were collected from Mombasa, Kwale and Taita Taveta, 14 samples from Nairobi county, and 30 samples collected from 9 Western Kenya counties. We classified the recovered genome sequences into 10 lineages (**Figure 1**). Most of the sequenced samples belong to the lineage B.1 (n=37).

The persons infected with the A.23.1 Lineage

One sample from Taita Taveta and three from Nairobi were classified as **A.23.1** lineage, the dominant lineage in Kampala Uganda based on a recent report [1]. The baseline characteristics are summarized in **Table 1**.

The persons infected with the 501Y.V1 and 501Y.V2 variants

The baseline characteristics for the nine individuals, eight from Kwale and Taita Taveta counties and one from Nairobi country, whose sequences were placed in the 501Y.V1 and 501Y.V2 phylogenetic clade are described in **Table 1**. Four samples collected from Kwale and Taita Taveta counties were classified as **B.1.351/501Y.V2** and an additional four lacked the defining mutations at position 501 and 484 on the spike protein and were classified B.1/501Y.V2 and B.1.526/501Y.V2. Seven individuals with the 501Y.V2 variant individuals had recent travel history to Tanzania and one to Zambia. The individual with the 501Y.V1 variant had no travel history and had difficulties in breathing.

Date Collected	County	Lineage	NextStrainClade	Travel Location
2021-01-25	Nairobi	A.23.1	19B	None
2021-01-27	Nairobi	A.23.1	19B	None
2021-01-28	Taita Taveta	B.1.351	501Y.V2	Tanzania Tanga
2021-01-28	Nairobi	A.23.1	19B	None
2021-01-29	Kwale	B.1.351	501Y.V2	Tanzania
2021-02-02	Nairobi	B.1.1.7	501Y.V1	None
2021-02-04	Taita Taveta	B.1	501Y.V2	Tanzania
2021-02-04	Kwale	B.1	501Y.V2	Tanzania Mafinga
2021-02-05	Kwale	B.1	501Y.V2	Zambia Ndola
2021-02-05	Kwale	B.1.526	501Y.V2	Tanzania
2021-02-05	Taita Taveta	B.1.351	501Y.V2	Tanzania
2021-02-05	Taita Taveta	B.1.351	501Y.V2	Tanzania
2021-02-06	Taita Taveta	A.23.1	19B	None

Table 1: Baseline characteristics of individuals who tested positive for the SARS-CoV-2 501Y.V1 and 501Y.V2 variant in Kenya sorted by the sample's date of collection. All the samples belonging to the 501Y.V2 clade were obtained from male truck drivers at points of entry. The variants of concern are highlighted in bold.

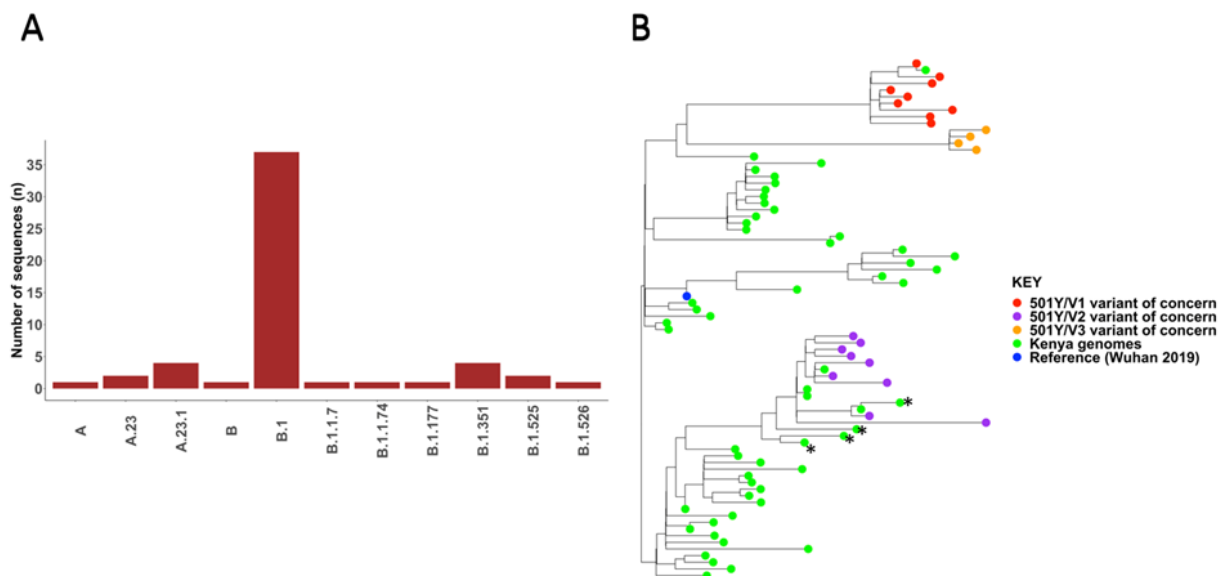


Figure 1. Analysis of 58 SARS-CoV-2 sequences from samples collected between 26th October 2020 and 8th February 2021 (A) A bar plot showing the frequency of lineages (x-axis) circulating in Kenya based on the 58 sequences. **(B)** A phylogenetic tree of the sequenced genomes (light green markers) in relation to the three global variants of concern (501Y.V1 in red, 501Y.V2 in purple, 501Y.V3 in orange). Asterisks show discrepant sequences that were placed in the 20H/501Y.V2 phylogenetic clade although they were not classified as variant B.1.351 because they lack key mutations at position 501 and 484 on the spike protein.

Implications

There is also an increased risk of local transmission of the SARS-CoV-2 variants of concern based on the increase in the number of B.1.351/501Y.V2 and other variants of concern detected at points of entry. Out of 58 samples, 49 were non-variant, and therefore the majority of the transmission for the period covered by the samples described here was not attributable to the variants of concern.

Recommendations

- Enhanced genomic surveillance of SARS-CoV-2 variants in the country.

Data availability

Whole genome sequence data are available from GISAID to allow global scientific community access.

References

1. D. Lule Bugembe, M. VTPhan, I. Ssewanyana, P. Semanda, B. Dhaala, S. Nabadda, Á.O. Niamh, A. Rambaut, P. Kaleebu, M. Cotten, A SARS-CoV-2 lineage A variant (A.23.1) with altered spike has emerged and is 1 dominating the current Uganda epidemic 2, MedRxiv. (2021) 2021.02.08.21251393. <https://doi.org/10.1101/2021.02.08.21251393>.

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