

Detection of three additional SARS-CoV-2 501Y.V2 variants at the Kenyan Coast

Key Points

- We sequenced 60 SARS-CoV-2 genomes from PCR positive samples collected between 15th January 2021 and 30th January 2021 from across coastal Kenya.
- We identify three sequences consistent with a 501Y.V2 variant classification, one from each of Kwale, Taita Taveta and Kilifi counties.
- The cases detected from Kilifi and Taita Taveta were not associated with a recent history of travel and raises concern for potential ongoing local transmission.

Background

We have continued to undertake SARS-CoV-2 genome sequencing from samples diagnosed in our laboratory as part of the national testing effort. These samples are received from all six coastal Kenya counties.

In Policy Brief #3 dated 16th January 2021, we reported the detection of SARS-CoV-2 variant of concern 501Y.V2 (the variant first identified in South Africa) in two asymptomatic South African Nationals who visited the Kenyan coast in mid-December and in Policy Brief #6 dated 4th February 2021, we reported a further isolate of the 501Y.V2 variant of concern at the Lunga Lunga border point from an individual with history of travel to Dar-es-salaam, Tanzania.

Findings from sequence data obtained on 5th February 2021

We performed whole genome sequencing for 60 SARS-CoV-2 PCR positive samples collected between 15th January 2020 and 30th January 2021 from across coastal Kenya. We classified the recovered genome sequences into 6 lineages (**Figure 1**), as described in previous reports. Most of the sequenced samples belong to the lineage B.1 (n=26) and the lineage B.1.222 (n=27). In addition, we identified three samples that were positive for the 501Y.V2 variant.

The persons infected with the 501Y.V2 variant

Virus sequences classified as 501Y.V2 lineage were obtained from samples collected from 3 different individuals. The first sample was collected on 20th January 2021 from a 44-year-old individual in Taita Taveta with no history of travel, the second sample was collected on 22nd January from a 32-year-old truck driver of Tanzanian nationality with a recent travel to Njombe, Tanzania and the third sample was on the 28th January from a 44-year-old environmental consultant of British nationality from Malindi, Kilifi County, but without a recent history of travel.

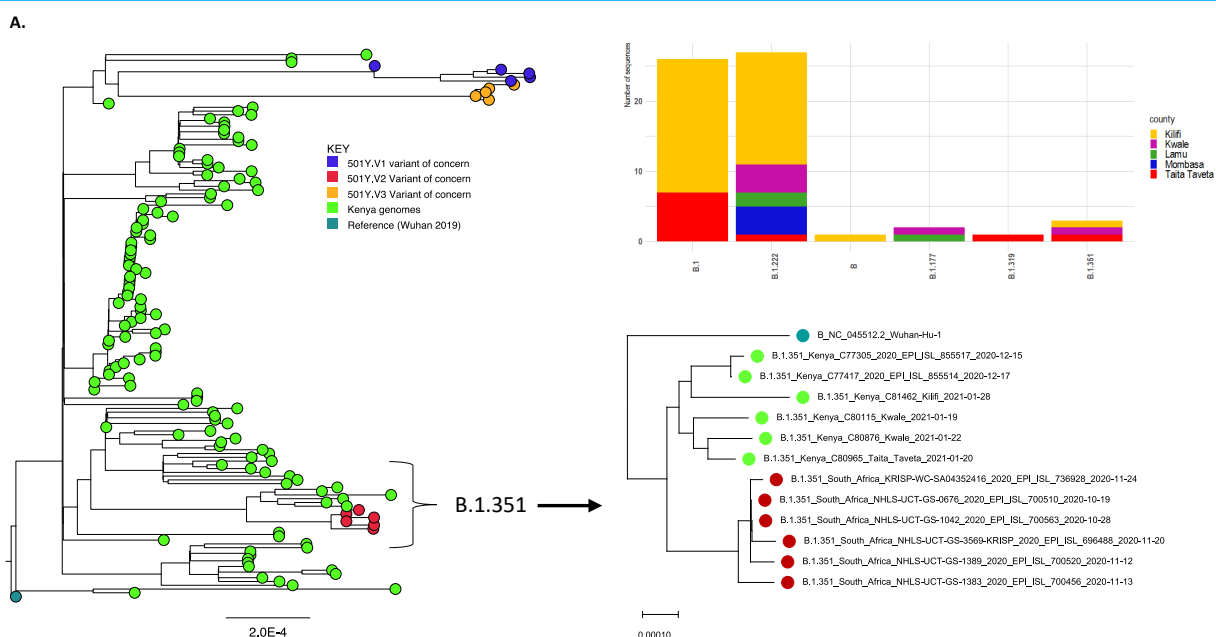


Figure 1. Analysis of 60 SARS-CoV-2 sequences from samples collected between 15th January and 30th January 2021 (A) A phylogenetic tree of the sequenced Kenya Genomes (light green markers) in relation to the three global variants of concern (501Y.V1 blue, 501Y.V2 red, 501Y.V3 orange). (B) A bar plot showing the frequency of lineages (x-axis) circulating in the coastal counties based on the 60 sequences. (C) A phylogenetic tree showing the placement of all the samples classified as 501Y.V2 from coastal Kenya to date relative to other SARS-CoV-2 sequences from South Africa (red).

Implications

The identification of three 501Y.V2 variants from two individuals with no history of travel indicates local transmission of this variant of concern. There is also a continued risk of introductions of new SARS-CoV-2 variants. 57 of the 60 samples were non-variant, and therefore the majority of current transmission is not attributable to the variants of concern.

Recommendations

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

Data availability

We will deposit the whole genome sequence data in GISAID to allow public access.

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