

# Detection of SARS-CoV-2 variant 501Y.V2 at Lunga Lunga Border Point, Kwale County

## Key Points

- We recently presented results from sequencing 69 SARS-CoV-2 PCR positive samples collected between October 2020 and December 2020 (Policy Brief #3), and from sequencing 499 SARS-CoV-2 PCR positive samples collected between March 2020 and October 2020 (Policy briefs #1 and #2).
- We have now performed whole genome sequencing for an additional 66 SARS-CoV-2 PCR positive samples collected between 7<sup>th</sup> October 2020 and 15<sup>th</sup> January 2021 from across coastal Kenya.
- Analysis of the genetic sequence data identified a 501Y.V2 variant from SARS-CoV-2 PCR-positive sample collected at Lunga Lunga Border Point, Kwale county, obtained from a truck driver of Tanzanian nationality. The traveller did not cross the border.
- From the obtained genome dataset (n=66) we conclude that SARS-CoV-2 variant 501Y.V2 is not the dominant variant circulating at the Kenyan coast, but there is a high probability of introductions of the variant, three of which we have detected to date.

## Background

Three SARS-CoV-2 genetic variants have been described as variants of concern given their potential impact on control efforts of COVID-19 pandemic. These variants have been designated as: 501Y.V1/B.1.1.7), 502Y.V2 /B.1.351, and 501Y.V3/P.1. These variants were first reported in the UK, South Africa and Brazil, respectively. In Policy Brief #3 dated 16<sup>th</sup> January 2021, we reported the detection of SARS-CoV-2 variant 501Y.V2 in two asymptomatic South African Nationals who visited the Kenyan coast in mid-December. Based on our recent genomic surveillance, we report the detection of an additional variant 501Y.V2 from a Tanzanian national who sought to enter the country from the Lunga Lunga border point.

## Genomic surveillance work at KEMRI-Kilifi

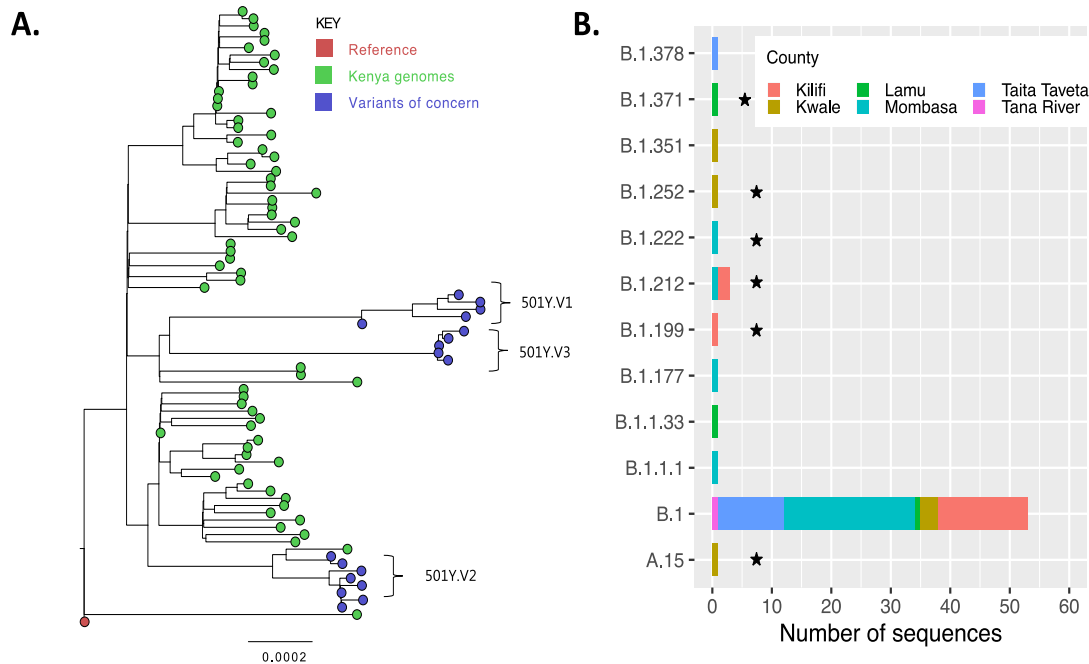
At KEMRI-Kilifi, we have continued to undertake SARS-CoV-2 genome sequencing mostly from samples diagnosed in our laboratory as part of the national testing effort. These samples are received from all six coastal Kenya counties namely, Kilifi, Taita Taveta, Tana River, Mombasa, Kwale and Lamu.

## Findings from sequence data obtained on 28<sup>th</sup> January 2021

We performed whole genome sequencing for 66 SARS-CoV-2 PCR positive samples collected between 7<sup>th</sup> October 2020 and 15<sup>th</sup> January 2021 from across coastal Kenya. We classified the obtained whole genome sequences into 12 lineages (**Figure 1**), 6 of which we have described in previous reports including the 501Y.V2 variant and 6 which we report for the first time. Most of the sequenced samples belong to the lineage B.1 (n=53), the predominant lineage in Coastal Kenya. The additional lineages we detected are, B.1.212 (n=3), B.1.199 (n=1), B.1.222 (n=1), B.1.252 (n=1), B.1.371 (n=1), and A.15 (n=1). These lineages are not associated with variants of concern.

## The person infected with the 501Y.V2 variant

The sequence identified as 501Y.V2 was obtained from a sample that was collected on 15<sup>th</sup> January 2021 from an individual of Tanzanian nationality sampled at Lunga Lunga border point in Kwale County as part of the routine surveillance of SARS-CoV-2 for persons entering the country. The individual did not cross the border into Kenya.



**Figure 1. (A)** A phylogenetic tree showing the placement of the samples classified as 501Y.V2 relative to other SARS-CoV-2 sequences from the coastal region (coloured green) and in relation to global subset of B.1.1.7/501Y.V1 (UK origin), B.1.351/501Y.V2 (SA origin) and P.1/501Y.V3 (Brazil origin), coloured blue. **(B)** A bar plot showing the frequency of lineages (x-axis) circulating in the coastal counties based on 66 genetic sequences collected between 7th October 2020 and 19th January 2021. New lineages identified for the first time from our recent sequencing work are marked in black Asterix.

## Implications

The identification of variant 501Y.V2 in an asymptomatic truck driver at a port of entry highlights the importance of surveillance at international ports of entry and the potential for new introductions through the ports of entry. There is no evidence that variant 501Y.V2 has spread widely in Kenya since the other 65 samples were not 501Y.V2. However, there is potential and high risk for more introductions of new SARS-CoV-2 variants, and the small sample size means we cannot reliably identify virus types that circulate at low levels.

## Recommendations

- Continue and extend genomic surveillance of circulating SARS-CoV-2 across Kenya.
- 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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