

# SARS-CoV-2 genomic diversity in Kenya, June – October 2020

## Key Points

- We previously sequenced 294 genomes sampled from the coastal region and Nairobi and identified 10 circulating SARS-CoV-2 lineages in Kenya between March and June 2020
- Additional sequencing of 205 genomes sampled from the coastal region between June and October 2020 identified 16 circulating lineages
- None of the variants of concern identified in the United Kingdom (named B.1.1.7/501Y.V1) or South Africa (named B.1.351/501Y.V2) were found in the sequence data we have produced so far
- However, some of the Kenyan SARS-CoV-2 genomes have mutations whose significance is yet to be fully understood
- We plan to sequence approximately 400 samples between January and the end of February 2021 across multiple sites in Kenya and provide a monthly report

## Background

Genomic surveillance of local SARS-CoV-2 genetic sequences will contribute to the COVID-19 outbreak response through spatial and temporal tracking of novel variants of public health importance in a timely manner. Furthermore, monitoring of evolutionary changes within the SARS-CoV-2 genome enables (i) identification of new virus strains or variants that could lead to additional outbreaks, (ii) spotting failure of diagnostic tests and (iii) assessment of vaccine effectiveness.

## Variants of Concern

Currently there are two SARS-CoV-2 genetic variants that are of global concern. One was first identified in the United Kingdom (named B.1.1.7/501Y.V1) and the other identified in South Africa (named B.1.351/501Y.V2). A virus variant is detected by changes in the RNA sequence (virus' genetic material). RNA sequence changes may result in a change of the protein structure of the virus if they change the amino acid sequence. The RNA sequence changes in the two variants of concern

share in common a change at amino acid position 501 on the immunogenic spike protein, which is abbreviated N501Y. Most RNA sequence changes do not lead to amino acid changes that significantly modify the virus properties (e.g. transmissibility, virulence) and such changes are not regarded as "variants of concern". There are several previous RNA sequence changes that have led to amino acid changes, but these have not been regarded as "variants of concern" because of limited spread compared with the UK or South African "variants of concern".

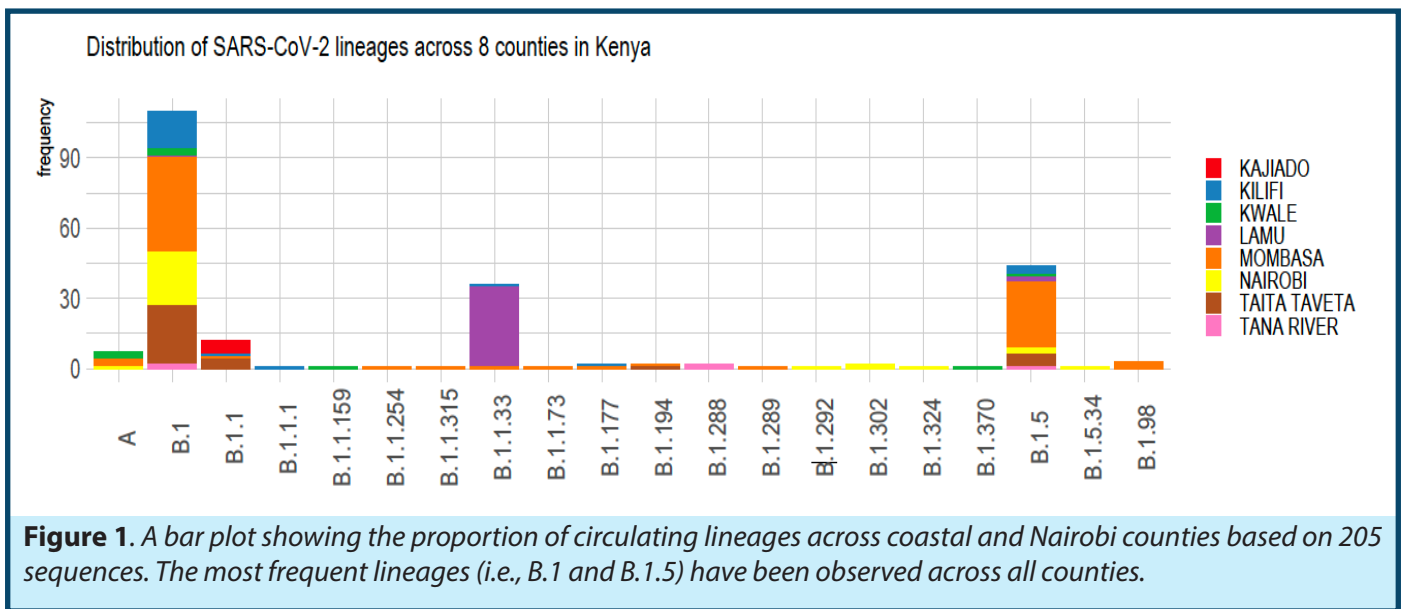
To date, 11<sup>th</sup> January 2021, the two "variants of concern" Lineage B.1.1.7/501Y.V1 (first reported in the UK) and Lineage B.1.351/501Y.V2 (first reported from South Africa) have been reported in 47 and 11 countries respectively. The UK variant B.1.1.7/501Y.V1 has not been reported in any African country yet, and the South African variant B.1.351/501Y.V2 has now been reported in Botswana. However, genomic surveillance across Africa is very limited and therefore introduction and spread in Africa cannot be ruled out.

## 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 our further sequencing effort (June – October 2020)

From a collection of 205 genome sequences, sampled between June and October, we observed that the local lineage composition of the epidemic expanded to 16 lineages. The lineages B.1, B.1.5 and B.1.1.33 and B.1.1, which were observed in the initial phase (March-June 2020), have continued to predominate. We observed 12 new lineages at low frequency but have not expanded locally to give rise to many cases.



### Has Kenya seen the new SARS-CoV-2 variants of concern (VOC) yet?

Has Kenya seen the new SARS-CoV-2 variants of concern (VOC) yet? None of the lineages that are described as “variants of concern” (B.1.1.7/501Y.V1 and B.1.351/501Y.V2) were detected in this new Kenyan dataset. This includes 20 samples collected from October which coincide with the start of the 2nd wave.

The UK variant of concern (lineage B.1.1.7/501Y.V1) was first observed in the UK on 20-Sept-2020. This variant has a unique set of 14 amino acid changes across the genome. From the data we have so far, we do not find evidence of this variant in Kenya before October 2020. We will need more sequencing covering the period October 2020 to January 2021 to conclude on the local status of these variants. Given the widespread global transmission of this lineage, there is a significant risk of its eventual introduction to Kenya.

### Amino acid changes

We scanned the spike protein of the local SARS-CoV-2 genomes for amino acid changes including the N501Y mutation that is shared by both variants of concern. We identified a single sequence containing a N501Y mutation from a 43-year-old asymptomatic individual from Lamu in August. The significance of this is uncertain, since subsequent sampling does not suggest that viruses with this mutation have expanded. Several other amino acid changes are noted (Table 1), the significance of which is also uncertain.

**Table 1.** Summary of some of the known important amino acid changes observed in the Kenya genomes data (June-October).

Amino acid change	Type	No. of observations	Sample	Comment
<b>Del 69-70</b>	Two amino acids deleted	2	P46146/Mombasa/18-Aug-2021 P46914/Kilifi/21-Aug-2020	<ul style="list-style-type: none"> <li>May facilitates immune escape.</li> <li>Potentially influences ACE2 binding and viral replication</li> </ul>
<b>D80Y</b>	Aspartic acid -> Tyrosine change	16	14 samples from TAITA TAVETA, 1 from Lamu, 1 from Nairobi	<ul style="list-style-type: none"> <li>This same position as seen in B.1.351 (SA variant) but different amino acid change – i.e., D80A</li> </ul>
<b>D614G</b>	Aspartic acid -> glycine change	>97% of our data		<ul style="list-style-type: none"> <li>Possible increased transmissibility, but present since March 2020</li> </ul>
<b>N501Y</b>	Asparagine -> Tyrosine change	1	P43612/Lamu/15-Aug-2020	<ul style="list-style-type: none"> <li>Seen in both B.1.1.7 (UK variant) and B.1.351 (SA variant).</li> <li>Possibly better binding to ACE-2 receptor and may enhance replication.</li> </ul>
<b>P681H</b>	Proline -> Histidine change	1	KLS2/Nairobi	<ul style="list-style-type: none"> <li>One of the mutations in the B.1.1.7 lineage (i.e., UK variant)</li> <li>Potentially influence ACE2 binding and viral replication.</li> <li>Has been observed in several other lineages across the globe</li> </ul>

## **Next steps**

We are sequencing samples from October to present and going forward we propose surveillance of 50 samples each week from across the various testing laboratories and ports of entry to monitor for new variants and will report our findings on a monthly basis.

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