POLICY BRIEF #10

Further detection of SARS-CoV-2 501Y.V1 and 501Y.V2 variants from samples collected in Nairobi and Coastal Kenya

Key Points

- We sequenced a total of 33 samples collected between 28th January and 5th March 2021 from Nairobi (n=7), Kilifi (n=8), Mombasa (n=7), Kwale (n=7), and Taita Taveta (n=4) counties.
- A total of 19 sequences (i.e., 3 from Nairobi and 16 from coastal counties) were classified as variants of concern; 501Y.V1 (n=6) and 501Y.V2 (n=13).

Background

At KEMRI-Kilifi, we have continued to undertake whole genome sequencing of SARS-CoV-2 RT-PCR positive samples to support genomic surveillance and the national testing effort. Our whole genome sequencing work is geared towards monitoring circulating SARS-CoV-2 variants, identifying new variant introductions and monitoring the spread of known variants of concern in the population. We have sequenced 559 samples collected between 10th November 2020 and 5th March 2021 and identified 15 SARS-CoV-2 variants of concern, (501Y.V1 (n=1) and 501Y.V2 (n=14), among travellers and in individuals without a history of travel. Here we report additional detection of 501Y.V1 and 501Y.V2 from samples collected in Nairobi and at the Kenyan coast.

Findings from sequence data obtained on 12th March 2021

Between 28th January 2021 and 05th March 2021, we sequenced 33 samples from Kilifi (n=8), Kwale (n=7), Mombasa (n=7) and Taita Taveta (n=4) and Nairobi county (n=7). We classified the recovered genome sequences into 5 Pango lineages; A.23.1 (n=4), B.1 (n=8), B.1.1.7 (a.k.a501Y.V1, n=6), B.1.351 (a.k.a 501Y.V2, n =13) and B.1.525 (n=2), (Figure 1). B.1.351 (i.e. 501Y.V2) was the dominant lineage from the sequenced samples, comprising 39.4% of all sequences. Table 1 provides a descriptive summary of the recovered genomes with basic demographic characteristics.

Four of the eight viruses that classified as lineage B.1 had 2-3 of the amino acid changes in the spike protein that define 501V.V2 variant of concern, and this observation was supported by their classification under the Nextstrain clade assignment system, **Table 1**. Clearly, the more recent sequencing runs have detected an increasing proportion of variants of concern, variants of interest or samples with mutations of concern but without the full set of changes to assign them as VOC. However, for the majority of these cases, they were either Tanzania nationals or information on travel history was not available, making it difficult to conclude if these variants are now causing widespread outbreaks locally.

Table 1: *A summary table of SARS-CoV-2 Rt-PCR positive samples collected from Nairobi and Coastal Kenya counties sorted by the date of sample collection*

Collection Date	Pango Lineage	NextStrain clade	County	Gender	Nationality	Travel history	Mutations of Concern (MoC) in the Spike Protein
28-01-2021	B.1.351	20H/501Y.V2	Taita Taveta	Male	Tanzanian	Tanzania	D80A, K417N, E484K, N501Y
29-01-2021	B.1.351	20H/501Y.V2	Kwale	Male	Tanzanian	Tanzania	D80A, K417N, E484K, N501Y
02-02-2021	B.1.1.7	20I/501Y.V1	Nairobi	-	-	Missing	N501Y, A570D
05-02-2021	B.1.1.7	20I/501Y.V1	Mombasa	Female	Kenyan	Missing	N501Y, A570D
05-02-2021	B.1.351	20H/501Y.V2	Kwale	Male	Zambian	Zambia	D80A, K417N
05-02-2021	B.1.351	20H/501Y.V2	Taita Taveta	Male	Tanzanian	Missing	D80A, K417N, E484K, N501Y
12-02-2021	B.1.1.7	20I/501Y.V1	Nairobi	-	-	Missing	A570D
13-02-2021	B.1.351	20H/501Y.V2	Mombasa	Male	Kenyan	Missing	D80A, K417N, E484K, N501Y
13-02-2021	B.1.351	20H/501Y.V2	Nairobi	Male	-	Missing	D80A, K417N, N501Y
18-02-2021	B.1	20H/501Y.V2	Kwale	Male	Tanzanian	Tanzania	D80A, E484K, N501Y
18-02-2021	B.1	20H/501Y.V2	Mombasa	Male	Tanzanian	Tanzania	D80A, E484K, N501Y
18-02-2021	B.1	20H/501Y.V2	Taita Taveta	Male	Kenyan	Missing	D80A, K417N
19-02-2021	B.1.351	20H/501Y.V2	Taita Taveta	Male	Kenyan	Missing	D80A, K417N
24-02-2021	B.1.351	20H/501Y.V2	Mombasa	Male	Kenyan	Missing	D80A, K417N, E484K, N501Y
25-02-2021	B.1.351	20H/501Y.V2	Mombasa	Male	Kenyan	Missing	D80A, K417N, E484K, N501Y
25-02-2021	B.1.351	20H/501Y.V2	Mombasa	Male	Kenyan	Missing	D80A, K417N, E484K, N501Y
25-02-2021	B.1.351	20H/501Y.V2	Kwale	Male	Tanzanian	Tanzania	D80A, K417N, E484K, N501Y
26-02-2021	B.1.351	20H/501Y.V2	Mombasa	Male	Kenyan	Missing	D80A, K417N, E484K, N501Y
26-02-2021	B.1.351	20H/501Y.V2	Kwale	Male	Tanzanian	Tanzania	D80A, K417N
03-03-2021	B.1.1.7	20I/501Y.V1	Kilifi	Male	-	Missing	N501Y, A570D
03-03-2021	B.1	20H/501Y.V2	Kilifi	Female	-	Missing	D80A, K417N
04-03-2021	B.1.1.7	20I/501Y.V1	Kwale	Female	-	Missing	N501Y, A570D
05-03-2021	B.1.1.7	20I/501Y.V1	Kilifi	Female	Kenyan	Missing	N501Y, A570D

Highlighted cells in yellow represent sequences with low coverage at positions N501Y and E484K, and we could not ascertain the presence of these mutations. "Missing" in travel history means that the information wasn't provided during sample collection

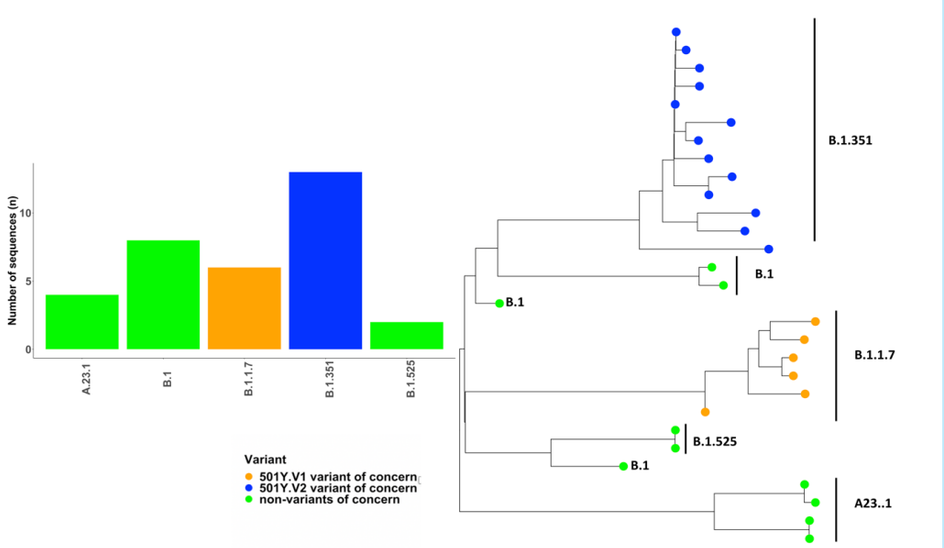

Figure 1: Analysis of 33 SARS-CoV-2 sequences from samples collected between 28th January 2021 and 5th March 2021 (A) A bar plot showing the frequency of lineages (x-axis) circulating in Kenya based on the 33 sequences. (B) A phylogenetic analysis of 33 SARS-CoV-2 sequences from samples collected between 19th January and 5th March 2021 from Nairobi in addition to four coastal counties.

Implications

The detection of the SARS-CoV-2 variants 501Y.V1 and 501Y.V2 among samples collected from Nairobi and coastal counties samples provides evidence for potential local transmission of these two SARS-CoV-2 variants of concern in Kenya. A considerable fraction of individuals found to be infected with these variants were screened at points of entry and were non-Kenyan nationals emphasizing the importance of Border Point screening for SARS-CoV-2 to stop importation of variants of concern.

Recommendations

Enhanced local genomic SARS-CoV-2 surveillance and submission of samples from local surveillance with complete metadata information, including recent travel histories of the sampled persons.

Data availability

Whole-genome sequence data will be available from the GISAID database to allow access to the global scientific community.

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