Brief #13

Ongoing genomic surveillance of SARS-CoV-2 in Nairobi and Coastal Kenya

Background

In our previous policy briefs (#3, #9 and #10), we have reported a total of 34 variants of concern (VOC) from two major clades; 501Y.V1 (n=7) and 501Y.V2 (n=27) from travellers at Points of Entry and in individuals without history of travel. Here we report additional detection of 501Y.V1 ("UK variant") and 501Y.V2 ("South Africa variant") VOC in samples collected in Nairobi county and across four counties at the Kenyan coast.

Key Points

- We sequenced 23 samples collected between 4th February and 12th March 2021 from Nairobi (n=2), Kilifi (n=12), Mombasa (n=4), Kwale (n=1), and Taita Taveta (n=4) counties.
- Fifteen sequences (1 from Nairobi and 14 from coastal counties) were classified as variants of concern; 501Y.V1 (n=4) and 501Y.V2 (n=11).
- We identified 4 samples that typed as variants of concern without any travel history, indicating likely local transmission of these variants

Findings from sequence data obtained on 19th March 2021

We sequenced 23 samples collected between 4th February 2021 and 12th March 2021, from Nairobi (n=2), Kilifi (n=12), Mombasa (n=4), Kwale (n=1), and Taita Taveta (n=4) counties **(Figure 1)**. We classified the recovered genome sequences into 7 lineages using the Pangolin classification; A.23.1 (n=4), B (n=1), B.1 (n=2), B.1.241 (n=1), B.1.1.7 (also referred to as 501Y.V1) n=4), B.1.351 (also referred to as 501Y.V2) n=10) and B.1.525 (n=1) **(Figure 2)**. The lineage B.1.351 was the dominant lineage from the sequenced samples, comprising 43% of the 23 sequences. A summary of the genetic classification/changes for each sample we sequenced is provided in **Table 1**.

Travel information was missing or not captured for several of the sequenced samples. SARS-CoV-2 variants 501Y.V1 (B.1.1.7, n=1) and 501Y.V2 (B.1.351, n=3)), were observed in individuals from Kilifi and Mombasa who did not have a history of travel, implying potential local transmission. We also observed a variant of interest, B.1.525 with a E484K mutation of concern (first observed in the USA) but without the full set of amino acid changes necessary to assign it as VOC. Four samples from Kilifi (n=2), Mombasa (n=1) and Taita Taveta (n=1) were classified as A.23.1 lineage, the dominant lineage in Kampala Uganda based on a recent report [1].

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

#	Collection date	Next strain clade	Pango lineage	County	Gender	Nationality	Travel history	Mutations of concern in the spike Protein
1	2021-02-04	20H/501Y.V2	B.1.351	Nairobi	Male	Missing	Missing	D80A, K417N, N501Y, D614G, A701V
2	2021-02-12	19B	A.23.1	Taita Taveta	Male	Kenya	Missing	None
3	2021-02-15	19B	A.23.1	Kilifi		Kenya	Missing	None
4	2021-02-15	20H/501Y.V2	B.1	Nairobi		Missing	Missing	D80A, K417N, D614G
5	2021-02-16	20A	B	Taita Taveta	Male	Kenya	Missing	D614G, P681H
6	2021-02-19	20A	B.1.241	Taita Taveta	Male	Kenya	Missing	D614G
7	2021-02-22	19B	A.23.1	Mombasa	Female	Kenya	Missing	None
8	2021-02-23	20H/501Y.V2	B.1.351	Mombasa	Male	Kenya	Missing	D80A, K417N, E484K, N501Y, D614G, A701V
9	2021-02-26	20H/501Y.V2	B.1.351	Kilifi	Male	Kenya	Missing	D80A, K417N, E484K, N501Y, D614G, A701V
10	2021-02-27	20I/501Y.V1	B.1.1.7	Mombasa	Male	Kenya	Missing	N501Y, A570D, D614G, P681H
11	2021-03-04	20H/501Y.V2	B.1.351	Mombasa	Male	Kenya	No	D80A, K417N, N501Y, D614G, A701V
12	2021-03-06	20I/501Y.V1	B.1.1.7	Kwale	Male	Tanzania	Kenya, Kwale	N501Y, A570D, D614G, P681H
13	2021-03-08	19B	A.23.1	Kilifi	Male	Kenya	Missing	None
14	2021-03-08	20A	B.1.525	Kilifi	Male	Kenya	Missing	E484K, D614G
15	2021-03-09	20H/501Y.V2	B.1.351	Kilifi	Male	Kenya	No	D80A, K417N, E484K, N501Y, D614G, A701V
16	2021-03-09	20A	B.1	Taita Taveta	Male	Kenya	Missing	D614G, P681H
17	2021-03-10	20H/501Y.V2	B.1.351	Kilifi	Female	Kenya	Missing	D80A, K417N, E484K, N501Y, D614G, A701V
18	2021-03-11	20I/501Y.V1	B.1.1.7	Kilifi	Female	Kenya	Missing	N501Y, A570D, D614G, P681H
19	2021-03-11	20H/501Y.V2	B.1.351	Kilifi	Male	Kenya	Missing	D80A, K417N, E484K, N501Y, D614G, A701V
20	2021-03-11	20I/501Y.V1	B.1.1.7	Kilifi	Male	Kenya	No	N501Y, A570D, D614G, P681H
21	2021-03-11	20H/501Y.V2	B.1.351	Kilifi	Male	Kenya	Missing	D80A, K417N, E484K, N501Y, D614G, A701V
22	2021-03-12	20H/501Y.V2	B.1.351	Kilifi	Female	Kenya	No	D80A, K417N, E484K, N501Y, D614G, A701V
23	2021-03-12	20H/501Y.V2	B.1.351	Kilifi	Male	Kenya	Missing	D80A, K417N, E484K, N501Y, D614G, A701V

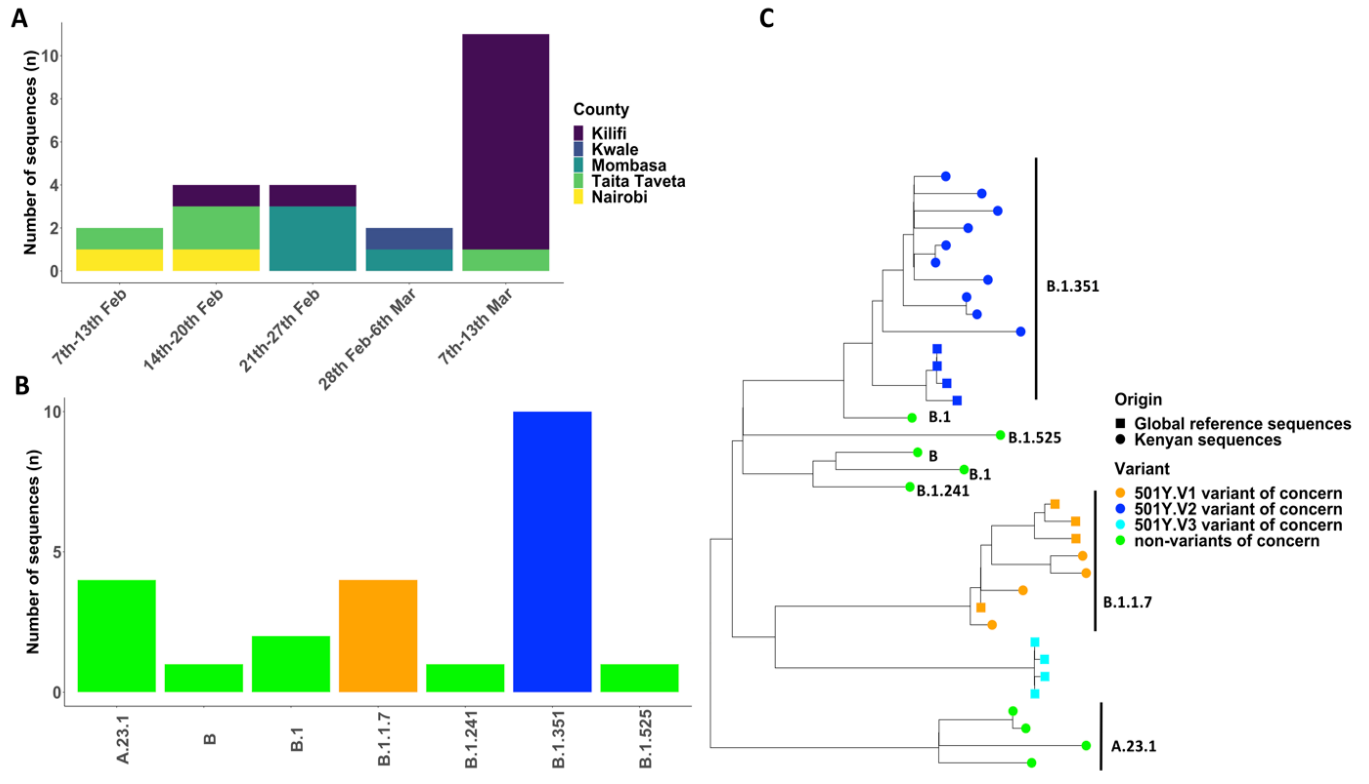

Figure 2: Analysis of 23 SARS-CoV-2 sequences from samples collected between 04th February 2021 and 12th March 2021 A bar plot showing the distribution of the 23 sequenced samples over time in weeks per county (x-axis). (B) A bar plot showing the frequency of lineages (x-axis) circulating in Kenya based on the 23 sequences. (C) A phylogenetic analysis of 23 SARS-CoV-2 sequences from samples collected between 04th January and 12th March 2021 from Nairobi in addition to four coastal counties. The figure shows the relationship between the sequenced genomes (circular tip-points) and the global variants of concern (square tip-points).

Implications

The detection of the SARS-CoV-2 variants 501Y.V1 and 501Y.V2 among samples collected from Nairobi and coastal counties among individuals who had no recent history of travel, is suggestive of local transmission of SARS-CoV-2 variants 501Y.V1 and 501Y.V2 in the population.

Recommendations

1. 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 and patient status.
2. Sequencing of additional samples from Nairobi will provide a clearer picture of circulating diversity associated with recent cases.
3. Editing the case investigation form to capture details on re-infection, vaccination status and travel history at the county/subcounty level.

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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