

Detection of SARS-CoV-2 501Y.V1 and 501Y.V2 variants of concern in samples collected in Nairobi

Key Points

- We sequenced and obtained partial genomes from 4 out of 9 SARS-CoV-2 positive samples collected between 4th and 15th February 2021 and provided by the UN staff clinic in Nairobi, Kenya.
- A total of 3 of the sequenced samples were identified as variants of concern, two were classified as B.1.1.7/501Y.V1 and one was classified as B.1.351/501Y.V2 based on phylogenetic clade assignment and mutation profiling.

Background

To date, three major variants of concern have been described, B.1.1.7/501Y.V1, B.1.351/501Y.V2 and P.1/501Y.V3. Each variant has been detected in more than 23 countries across the globe including several countries in Africa. In Kenya, we have reported detection of B.1.1.7/501Y.V1 and B.1.351/501Y.V2 during local and border point screening.

Findings from sequence data obtained on 5th March 2021

We received 9 samples collected between 4th and 15th February 2021 from the UN Staff clinic in Nairobi Kenya for the purposed of whole genome sequencing. We obtained partial genomes from 4 of the 9 samples. Five of the nine samples failed quality control steps and were not sequenced.

We classified the recovered genome sequences into 3 lineages; B.1.1.7/501Y.V1 (n=1), B.1.351/501Y.V2 (n=2) and B.1.95 (n=1) (**Figure 1**). **Table 1** provides a detailed summary for each sample.

Date of Collection	County	Nextstrain Clade	Pango lineage	Cycle threshold (Ct) score	Genome recovered (%)	Gender	Age
04-02-2021	Nairobi	20H/501Y.V2	B.1.351	26.31	96.4	Male	
12-02-2021	Nairobi	20I/501Y.V1	B.1.1.7	36.2	55.4		42
13-02-2021	Nairobi	20H/501Y.V2	B.1.351	28.0	81.7	Male	
15-02-2021	Nairobi	20A	B.1.95	22.29	95.8		64

Table 1: A basic summary of sequencing results of the 4 samples collected from the UN staff Clinic in Nairobi, Kenya. The samples are sorted by the date of samples collection from top to bottom.

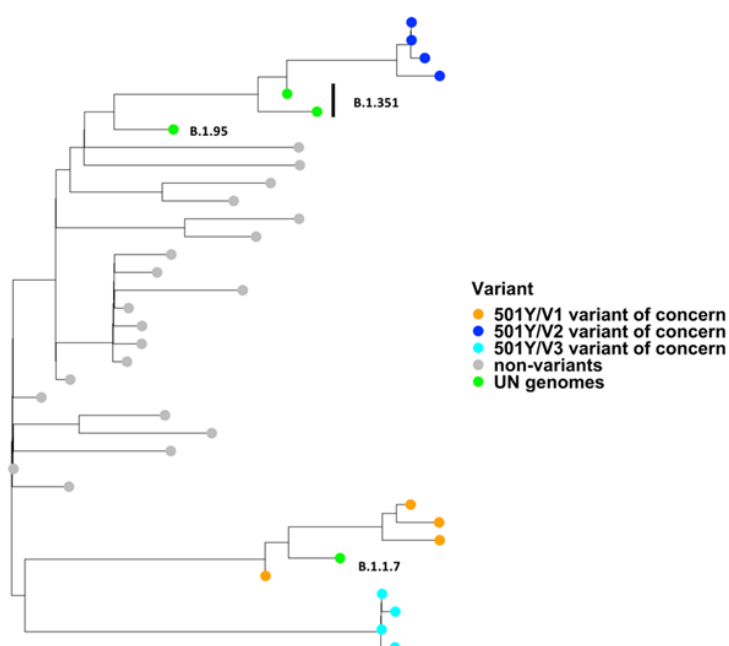


Figure 1. A phylogenetic analysis of four SARS-CoV-2 sequences from samples collected between 4th February 2021 and 15th February 2021 from the UN Staff Clinic in Nairobi, Kenya. The figure shows the relationship between the sequenced genomes (light green markers) and the global variants of concern (501Y.V1 in orange, 501Y.V2 in blue, 501Y.V3 in cyan), non-variants (grey) and previous sequences from western Kenya (grey).

Implications

The detection of the SARS-CoV-2 variants of concern among these samples emphasize the need for enhanced control of SARS-CoV-2 across the region.

Data availability

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

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