POLICY BRIEF #5

Detection of SARS-CoV-2 Variant 501Y.V1 in Coastal Kenya

Background

As of 22nd January 2021, three SARS-CoV-2 genetic variants have been described as variants of concern (VOC) given their potential impact on control efforts of COVID-19 pandemic. These variants have been designated as: 1) lineage B.1.1.7/501Y.V1 (first detect in the UK in September 2020); 2) B.1.351/502Y.V2 (first detected in South Africa in October 2020); and 3) B.1.1.28/501Y.V3 (first detected in Brazil in January 2021). The 501Y.V1 variant has been reported extensively in UK and has been reported in 59 other countries across the globe.

Key Points

- We sequenced an additional 18 SARS-CoV-2 PCR positive samples collected between 29th December 2020 and 14th January 2021 from across coastal Kenya.
- Our finding confirms the presence of SARS-CoV-2 variant 501Y.V1 (UK origin) in a sample collected from a male symptomatic case in Mombasa.
- Based on the limited data that is restricted to sampling from the Coast, it is not possible to describe the extent of spread of the new variant in Kenya.

Findings from sequence data obtained on 20th January 2021

Our report dated 16th January 2020 provided a snapshot of genetic diversity of circulating SARS-CoV-2 in Kenya based on whole genome sequences of 57 samples collected between October and December 2020 from 6 coastal counties. Here, we update our findings based on whole genome sequencing of an additional 18 samples which yielded genomes that were more that 80% complete (i.e., they passed quality control checks). The samples were collected between 29th December 2020 and 14th January 2021.

The newly sequenced samples were classified into a total of 6 lineages (**Figure 1**) including the novel B.1.1.7/501Y.V2 lineage. Most SARS-CoV-2 sequences from coastal Kenya belong to the lineages B.1 lineage (n=12).

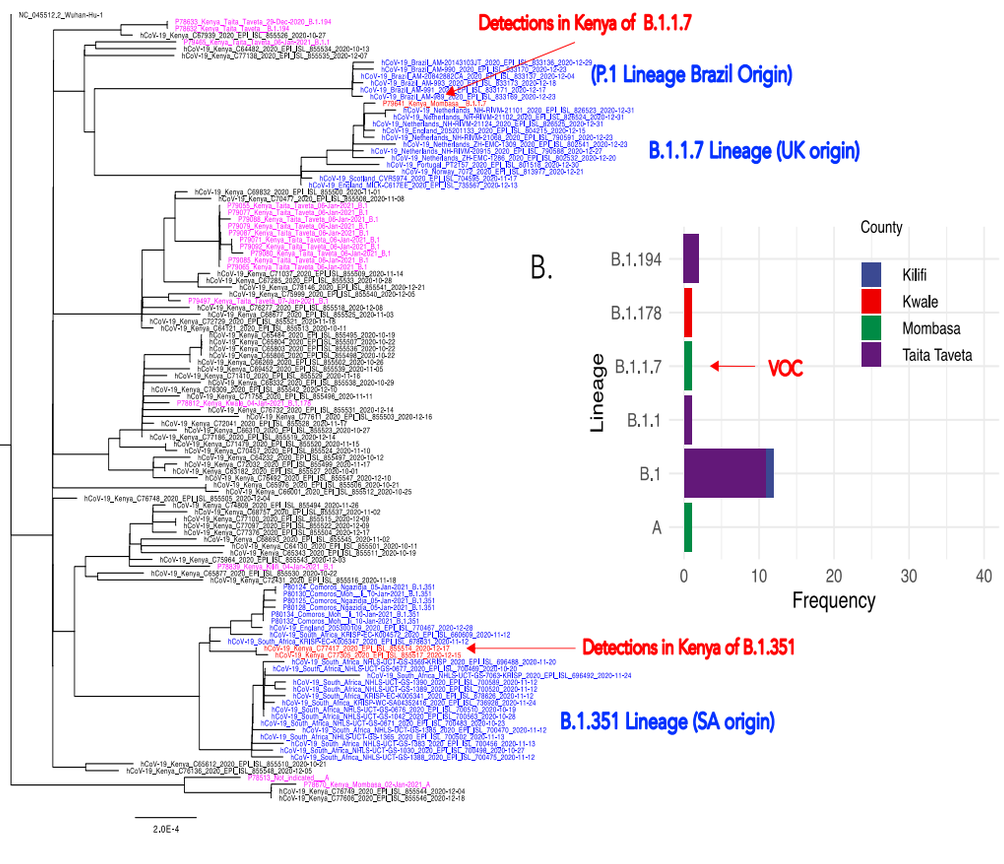

Figure 1. (A) A phylogenetic tree showing the placement of a single sequence belonging to the B.1.1.7/501Y.V1 (UK origin) and two samples belonging to B.1.351/501Y.V2 (SA origin) relative to other SARS-CoV-2 sequences from the coastal region (coloured black) and in relation to global subset of B.1.1.7/501Y.V1 (UK origin) and B.1.351/501Y.V2 (SA origin), coloured blue. The samples sequenced at Kilifi in this latest round are coloured pink. Three sequences representing the variants of concern are coloured in red. **(B)** A bar plot showing the lineage frequency (x-axis) of a subset of circulating SARS-CoV-2 sequences from coastal counties based on 18 newly sequenced cases sampled between 29th December 2020 and 14th January 2021. Red arrow points to the detected lineage/variant of concern.

The persons infected with the 501Y.V1 variant

The positive sample was obtained from a 32-year-old male who presented a Mombasa-based clinic with fever and headache. They were handled as COVID-19 suspected case and put in an isolation centre. They were subsequently moved to treatment centre following PCR positive confirmatory COVID -19 test result. The individual is currently undergoing treatment. The patient does not have a history of travel and has no known contact with a person with a history of travel.

Implications

Detection of an additional variant of concern B.1.1.7/501Y.V1 sequence confirms the entry of new variants to Kenya. We cannot infer how much transmission has arose from the new variant given the limited sample size. The variant may not have spread sufficiently to dominate the Kenyan epidemic. However, given the extent of transmission in other countries there is a clear risk of spread of new variants in Kenya.

Recommendations

a. Continue and extend genomic surveillance of circulating SARS-CoV-2 across Kenya.
b. Genomic surveillance should include Nairobi and Kisumu SARS-CoV-2 samples from November to date.

Data availability

The whole genome sequence data will be available from GISAID.

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