29th APRIL 2021

POLICY BRIEF #17

Genomic surveillance findings in Kenya: 17th March 2020 to 15th April 2021

Background

Genomic surveillance of SARS-CoV-2 contributes to guiding the COVID-19 pandemic response. Of particular importance is detecting the emergence and spatial and temporal tracking of new variants. Some variants are termed "variants of concern" by the WHO due to their potential for causing outbreaks.

Methods

At KEMRI, we have continued to undertake SARS-CoV-2 genome sequencing mostly from samples collected by KEMRI-CBRD, KEMRI-CGHR and KEMRI-CGMR-C in Nairobi, Western and Coastal Kenya as part of the national genomic surveillance effort.

Results

To date we have sequenced 1,277 SARS-CoV-2 positive samples from 26 counties across Kenya collected between 17th March 2020 and 15th April 2021.

The genomes were classified into 47 distinct lineages including two variants of concern (501Y.V1 in 271 samples, first identified in UK, and 501Y.V2 in 114 samples, first identified in South Africa).

A summary of the temporal detection patterns of the variants of concern in our sequenced samples alongside number of confirmed cases over time is shown in Figure 1.

Since February, most of the cases we sequence are classifying as variants of concern (n=395) with the variant of concern first detected in the UK (501Y.V1) most common (n=271, 69%). The variant of concern first detected in South Africa (501Y.V2) was at 40% in early February but has fallen to 11% in April.

The variants of concern have been detected in 14 of the 26 counties in Kenya with sequence data. We have detected one or both variants of concern from across all locations of Kenya (Table). However, we do not have sequence data from 21 of Kenya's 47 counties.

The detections of variants of concern are seen in many individuals without a history of recent international travel (n=364), implying that these variants have established local transmission, (see Table).

Many of the genomes we have obtained in 2021 are from Coastal Counties (67.6%) and Nairobi County (24.4%). Sampling from the other regions is limited. During February and March different variants were circulating in Nairobi vs Coastal Counties, emphasizing the importance of sampling other counties.

Key Points

- We have sequenced 1,277 SARS-CoV-2 positive samples from 26 Counties across Kenya from samples collected between 17th March 2020 and 15th April 2021.
- Kenya has seen at least 47 distinct SARS-CoV-2 lineages.
- The 47 lineages include two variants of concern 501Y.V1 (UK origin) in 271 samples and 501Y.V2 (South-African origin) in 114 samples.
- The variants of concern have been detected on or after January 2021 and have been seen in 14 of the 26 sampled Counties, including Central and Coastal Counties.
- Variants of concern have been identified from individuals without a history of recent international travel (n=364), suggesting local transmission.
- The variant of concern first detected in South Africa (501Y.V2) was at 40% in early February but has fallen to 11% in April.
- The 501Y.V1 variant of concern, first identified in UK, has become the most common variant in Kenya in April (75% of 103 samples collected in April alone).

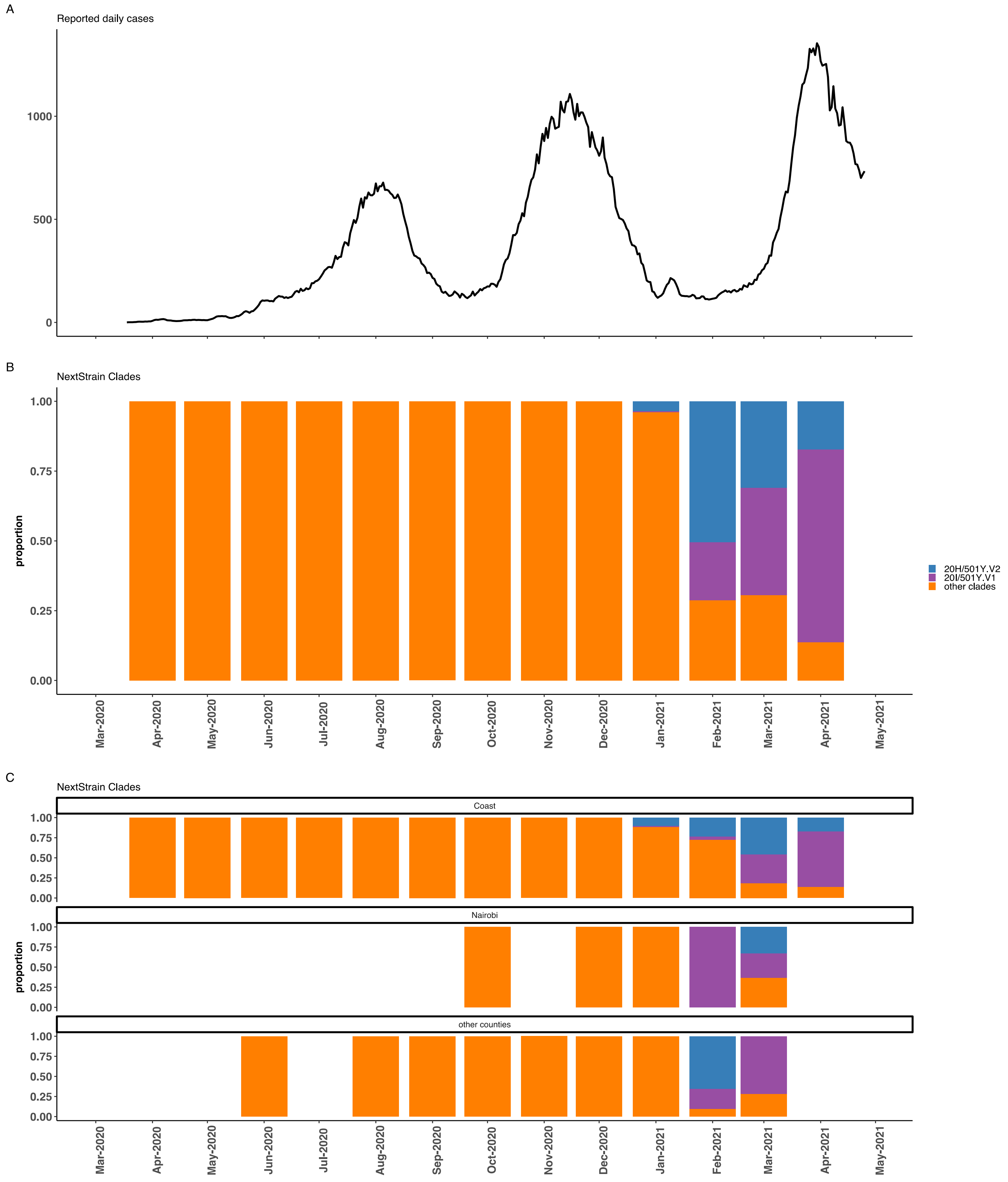

Figure 1: SARS-CoV-2 sequences from Kenya (17th March 2020 – 26th April 2021): A. A summary of the cumulative daily reported COVID-19 confirmed case between March 2020 to 26th April 2021). **B.** A bar plot summary of the proportion of the major phylogenetic clades detected from sequenced samples over the surveillance period. The variants of concern (VOC) are indicated by purple and blue colours denoting 501Y.V1 and 501Y.V2 respectively. **C**. A bar plot showing the major clades stratified by region i.e., the Coast, Nairobi, and other counties across the country (colour code as for B).

Table: Basic epidemiological characteristics: A summary of SARS-CoV-2 Rt-PCR positive samples collected over time between January to April 2021

	501Y.V1 (UK origin) (n=271)	501Y.V2 (South-African origin) (n=114)	Variants of interest * (uncertain significance) (n=41)	Other Variants
Location				
Nairobi	89	5	10	21
Coast	173	95	20	653
Western	1	0	0	11
Central	1	0	1	9
North Eastern	1	0	8	0
Nyanza	3	12	0	26
Rift Valley	2	0	0	19
Eastern	0	0	0	13
Missing	1	2	2	49
Clinical Presentation				
Asymptomatic	177	91	32	591
Symptomatic	74	8	2	105
Deceased	1	0	0	0
Data not Available	19	15	7	105
Travel history				
Travelled	6	15	1	84
Local	265	99	40	717
Testing criteria				
Point of Entry	3	13	3	4
Routine Surveillance	41	24	5	143
Presented at health facility	171	68	17	379
Travelling	2	0	1	0
Contact with confirmed case	47	1	10	4
Data not Available	7	8	5	271
Variants of Interest: A.23.1, B.1.525				

Discussion

These data suggest continuous introduction of SARS-CoV-2 lineages into Kenya from the global pool of SARS-CoV-2 diversity, with at least 47 lineages observed. Most recently, SARS-CoV-2 variants of concern (501Y.V1 and 501Y.V2) have been introduced and are now the dominant circulating SARS-CoV-2 variants.

The findings are not surprising given the known higher transmissibility of the variants of concerns observed in several other countries that have experienced their introduction.

We did not find evidence of circulation of variants of concern during Kenya's first and second SARS-CoV-2 waves of infections, so these might have been driven by other factors for example different social or demographic groups.

Our findings of the dominance of variants of concern in sequenced samples from the last three months suggest that the third wave of infections is, at least in part, driven by local transmission and circulation of variants of concern.

Recommendations

- Enhanced genomic surveillance of SARS-CoV-2 surveillance across the country, especially rural Counties.
- Emphasize to RRT to collect complete the case investigation forms, for example recent travel history is important for genomic surveillance.
- Revise the case investigation forms to capture details such as previous testing history and vaccination history.

Data availability

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

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