

Detection of SARS-CoV-2 variants B.1.1.7, B.1.351 and B.1.617.2 in samples collected from Nairobi and Coastal Kenya

Background

Global genomic surveillance has identified four SARS-CoV-2 genetic variants of concern (VOC): B.1.1.7 (first identified in the UK and also known as clade 501Y.V1), B.1.351 (first identified in South Africa (SA) and also known as clade 501Y.V2), P.1 (first identified in Brazil and also known as clade 501Y.V3) and B.1.617.2 (first identified in India, and recently assigned as clade 21A). The latest, B.1.617.2, is a recently declared variant of concern with a high prevalence during India's second wave [1]. The viruses belonging to the B.1.617.2 variant have now been detected in more than 45 countries across the globe.

Findings from sequence data obtained on 14th May 2021

In our latest run, we sequenced 103 SARS-CoV-2 PCR positive samples collected between 1st April and 7th May 2021. These samples were collected from Nairobi County (n=8) between 1st – 28th April 2021 and 3 counties across the coastal region Kilifi (n=56), Taita Taveta (n=31) and Mombasa (n=8) between 17th April and 7th May 2021.

We classified the recovered genome sequences using the two main SARS-CoV-2 genomic classifications systems (i.e., the Pango lineage and the NextStrain clade classification). The newly sequenced genomes fell into 7 Pango lineages; B.1.1.7 (n=56), B.1.351 (n=27), B.1 (n=6), B.1.1 (n=5), B.1.525 (n=2) B.1.617.2 (n=6) and B.1.617.1 (n=1), **Figure 1**.

Key Points

- We sequenced 103 SARS-CoV-2 PCR positive samples collected between 1st April and 7th May 2021 from Nairobi and 3 counties across coastal region.
- A total of 90 (87.4%) out of the 103 samples were classified as variants of concern (VOC):
 - B.1.1.7 (first identified in the UK), (52.3%, n=56);
 - B.1.351 (first identified in SA), (25.2%, n=27) and
 - B.1.617.2 (first identified in India) (5.8%, n=6).
- Four of the six cases infected with B.1.617.2 VOC had no recent history of international travel (3 from Mombasa, and 1 from Kilifi) suggesting ongoing local transmission of this variant.

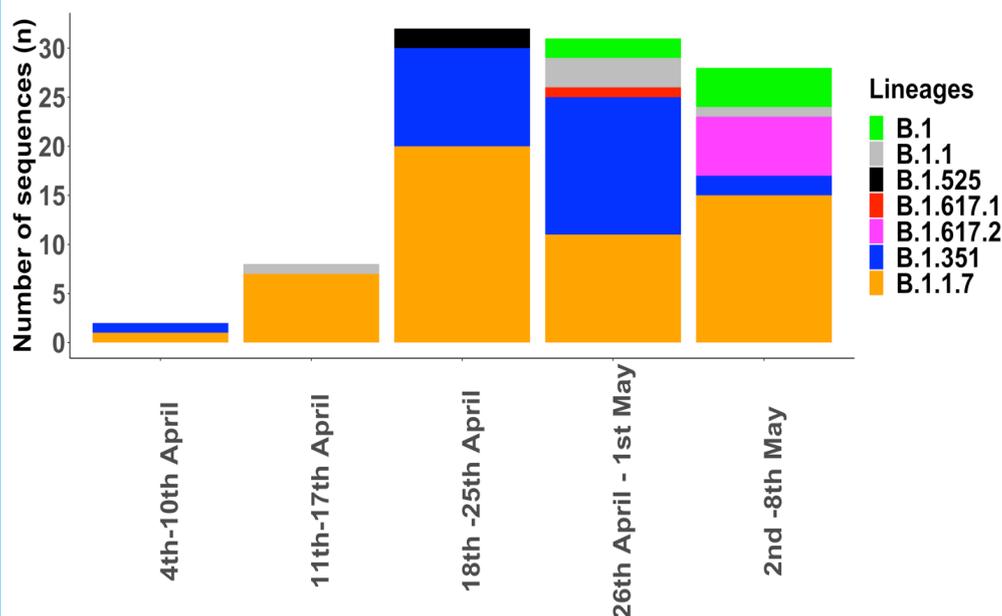


Figure 1 A bar plot showing the weekly number of each of the lineages detected among the 103 samples we sequenced. We detected three VOC: B.1.1.7 (first identified in the UK) shown in orange, B.1.351 (first identified in SA) shown in blue and B.1.617.2 (first identified in India) shown in magenta. We also detected the variants of interest B.1.525 and B.1.617.1 (first identified in India) shown in black and red respectively, and other variants B.1 and B.1.1 shown in green and grey respectively.

Discussion

The sequenced samples for the reported period were dominated by the VOC B.1.1.7 among individuals without a recent history of international travel suggesting ongoing local transmission of this variant in Kenya, Table 1. The B.1.351 VOC showed lower prevalence across the investigated period. Additionally, we report recently declared variant of concern (B.1.617.2) and variant of interest (B.1.617.1) both first identified in India at 6.8% prevalence (7/103). The samples with the VOC B.1.617.2 were collected from: (a) two individuals who had travelled from India to Kenya and (b) four individuals without a history of international travel (3 from Mombasa and 1 from Kilifi) suggesting importations and potential local transmission of this VOC in the country (See Table 1 below).

Table 1. A summary of 103 SARS-CoV-2 RT-PCR positive samples collected between 1st April and 7th May 2021 in Nairobi and 3 counties at the coastal region.

	B.1.1.7 (first identified in the UK) (n=56)	B.1.351 (first identified in SA) (n=27)	B.1.617.2 (first identified in India) (n=6)	Other Variants (n=11)	Variants of Interest (n=3)
Location					
Kilifi	32	18	1	4	1
Nairobi	6	1	0	1	0
Taita Taveta	17	7	0	6	1
Mombasa	1	1	5	0	1
Clinical Presentation					
Asymptomatic	43	26	1	10	2
Symptomatic	13	0	4	1	1
Deceased	0	0	0	0	0
Data not Available	0	1	1	0	0
Travel history					
Travelled	0	1	2	0	0
Local	56	26	4	11	3
Testing criteria					
Point of Entry	0	0	0	0	0
Routine Surveillance	25	16	0	3	1
Presented at health facility	22	10	6	6	1
Travelling/In-transit	0	0	0	1	0
Contact with confirmed case	4	0	0	1	0
Data not Available	5	1	0	1	0

Other Variants: B.1, B.1.1

Variants of interest: B.1.525, B.1.617.1

NOTE: 2 individuals with the B.1.617.2 VOC had previously travelled to India and the other 4 had no history of recent international travel (3 from Mombasa and 1 from Kilifi)

Implications

The sequencing results provide evidence of continuing local transmission of the VOC B.1.1.7 and B.1.351 and also the introduction and local transmission of B.1.617.2 variants into Kenya. There is speculation that SARS-CoV-2 variant B.1.617.2 has enhanced transmissibility as high as that of the B.1.1.7 and some limited laboratory evidence suggesting the potential to evade pre-existing human immunity generated by vaccines [2]. However, there is as yet no conclusive evidence.

Recommendation

Emphasis should be placed on surveillance to understand the extent of local transmission of the variant of concern B.1.617.2 and variant of interest B.1.617.1 in Kenya.

Data availability

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

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Reference:

1. S. Cherian, V. Potdar, S. Jadhav, P. Yadav, N. Gupta, Convergent evolution of SARS-CoV-2 spike mutations , L452R , E484Q and P681R , in the second wave of COVID-19 in Maharashtra , India, (2021).
2. P. I. Ferreira, R. Datir, G Papa, et al., SARS-CoV-2 B.1.617 emergence and sensitivity to vaccine-elicited antibodies, (2021). <https://www.biorxiv.org/content/10.1101/2021.05.08.443253v1.full.pdf>.