POLICY BRIEF #24

Genomic surveillance detects local transmission of the global variants of concern in nine counties in Kenya

Background

Continuous genomic surveillance of SARS-CoV-2 in Kenya has detected circulation of three global variants of concern (VOC) in the country i.e. (a) the Alpha variant (i.e., lineage B.1.1.7, first identified in United Kingdom), (b) the Beta variant (i.e., lineage B.1.351, first identified in South Africa), and (c) the Delta variant (i.e., lineage B.1.617.2, first identified in India). The Delta variant has higher transmissibility (around 60%) compared to Alpha and Beta variants[1]. These VOCs are currently the dominant sources of COVID-19 cases in the country.

Although it remains unclear as to whether the WHO designated VOCs (Beta, Gamma and Delta) are associated with severe COVID-19 presentation compared to non-VOC, there is growing evidence for an increased risk of hospitalization and death following infection with the Alpha variant [2,3].

Keypoints

- We sequenced 58 SARS-CoV-2 PCR-positive samples collected between 3rd May and 18th June 2021 from nine counties in Kenya: Homa-bay, Kisii, Kilifi, Laikipia, Migori, Mombasa, Nairobi, Nyamira and Taita Taveta.
- All recovered sequences classified as variants of concern:
  - Alpha (B.1.1.7, first identified in UK) (37.9%, n=22)
  - Beta (B.1.351, first identified in South Africa) (5.1%, n=3)
  - Delta (B.1.617.2, first identified in India) (56.9%, n=33).
- Delta variant was detected in eight out of the nine surveyed counties
- None of the cases reported here had a recent history of international travel suggesting ongoing local transmission of these variants.

Methods

On 25th June 2021, we sequenced 58 SARS-CoV-2 PCR positive samples collected between 3rd May and 18th June 2021. The samples were obtained from nine counties namely Kilifi (n=28), Migori (n=7), Kisii (n=7), Mombasa (n=5), Laikipia (n=4), Homa-Bay (n=3), Nairobi (n=2), Nyamira (n=1) and Taita Taveta (n=1)
We classified the recovered genome sequences using the Pango lineage assignment tool (Pangolin version v3.1.5). Variants of concern (VOC) and variants of interest (VOI) were designated based on the WHO framework as of 31st May 2021 (https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/).

Findings from sequence data obtained on 25th June 2021

The newly sequenced genomes belong to three Pango lineages: B.1.1.7 (i.e., Alpha VOC, n=22), B.1.351(i.e., Beta VOC, n=3) and B.1.617.2 (i.e., Delta VOC, n=33) (Figure 1). None of the sequenced cases had a recent history of international travel (defined as the preceding 14 days). Delta variant was detected in eight out of the nine counties (**Table 1**). Alpha variant was detected in five counties, while Beta variant was detected in Migori and Kisii counties. (**Table1**). Information on clinical status was available for 46 cases: 34 were symptomatic while 12 were asymptomatic (***Table 1***).

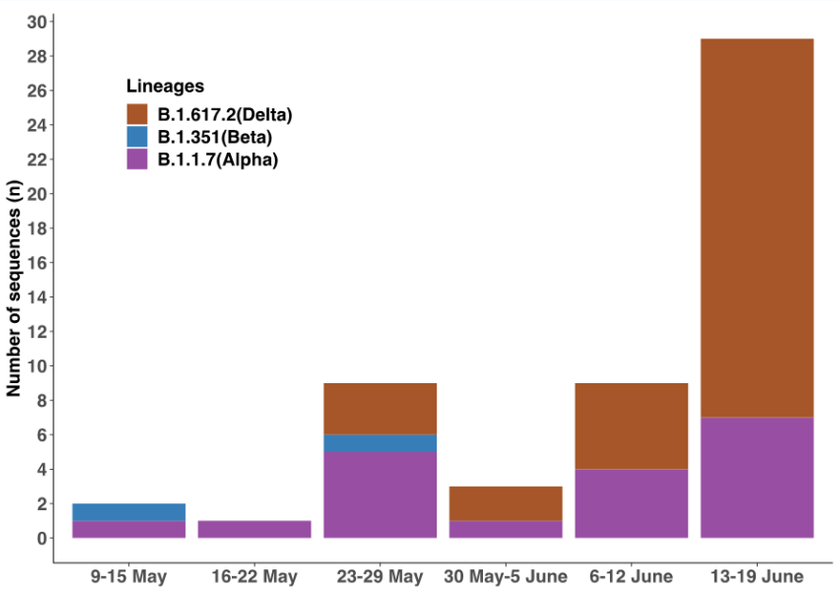

Figure 1. A bar plot showing the weekly number of each of the lineages detected among the 58 sequenced samples collected from 3rd May and 18th June 2021 from nine counties in Kenya.

Temporal lineage dynamics.

We observe replacement of previously circulating lineages by VOCs overtime; Beta variant was first detected in our surveillance in December 2020, Alpha variant was first detected in our surveillance in February 2021, while Delta variant was first detected in April 2021 (**Figure 2**). The VOCs are now the dominant lineages from our genomic surveillance data (**Figure 2**).

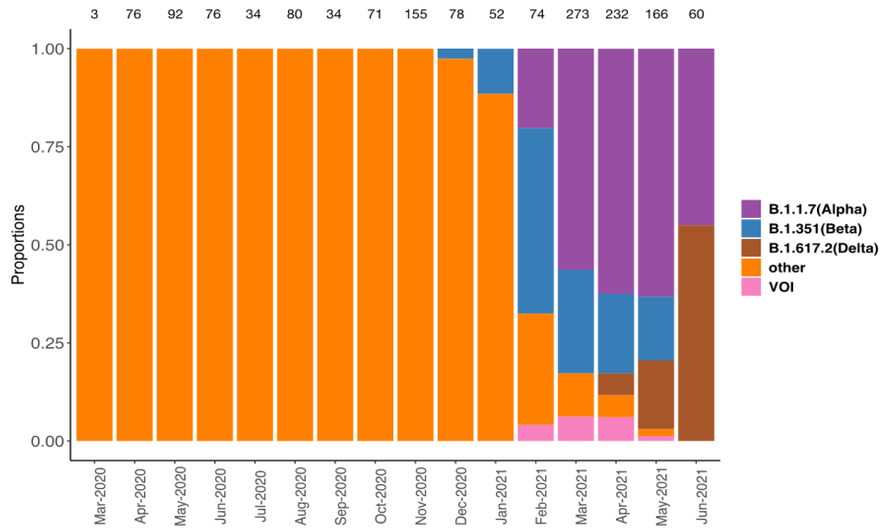

Figure 2. Temporal distribution of the common Pango lineages identified from our geneomic sureveillance from March 2020 to 25 June 2021. The values on top of the bars indicate the total number of sequences per month.

Table 1. A summary of 58 SARS-CoV-2 RT-PCR positive samples collected between 3rd May and 18th June 2021 in 9 counties in Kenya.

	B.1.1.7 (Alpha) (n=22)	B.1.351 (Beta) (n=3)	B.1.617.2 (Delta) (n=33)
Location			
Homabay	1	0	2
Kilifi	10	0	18
Kisii	5	1	1
Laikipia	0	0	4
Migori	5	2	0
Mombasa	0	0	5
Nairobi	1	0	1
Nyamira	0	0	1
Taita Taveta	0	0	1
Clinical Presentation			
Asymptomatic	3	0	9
Symptomatic	13	2	19
Data not Available	6	1	5
Travel History			
Local	22	3	33
Testing Criteria			
Contact with confirmed case	3	0	3
Presented to health facility	3	0	8
Surveillance	8	2	8
Data not Available	8	1	1

Discussion

Our genomic surveillance provides evidence of ongoing local spread of three SARS-CoV-2 VOCs in the nine surveyed counties. All sequences come from individuals none of whom have a recent history of international travel (Table 1).

This report provides evidence of the circulation of the Delta (B.1.617) variant in eight out of the nine surveyed counties; Kilifi, Kisii, Laikipia, Mombasa, Nairobi, Homa-Bay, Nyamira and Taita Taveta.
Temporal prevalence pattern of lineages in Kenya indicate that VOC have become the predominant cause of COVID-19 cases in the country.

Recommendation

Emphasis should be placed on:

a. Enhanced genomic surveillance to monitor local transmission and evolution of these lineages and variants of concern across Kenya as both naturally acquired immunity and vaccine derived immunity increase in the local population.
b. Linking clinical data to the genomic data we generate to establish whether or not the locally circulating VOCs are associated with severe clinical outcomes. This requires access to samples from patients who are showing severe illness symptoms while receiving care in either public or private hospitals.

Data Availability

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

Reference:

1. Campbell F, Archer B, Laurenson-Schafer H, et al. Increased transmissibility and global spread of SARS-CoV-2 variants of concern as at June 2021. Eurosurveillance. 2021;26(24). doi:https://doi.org/10.2807/1560-7917.ES.2021.26.24.2100509
2. Challen R, Brooks-Pollock E, Read JM, Dyson L, Tsaneva-Atanasova K, Danon L. Risk of mortality in patients infected with SARS-CoV-2 variant of concern 202012/1: Matched cohort study. BMJ. 2021;372:1-10. doi:10.1136/bmj.n579
3. Horby AP, Bell I, Breuer J, et al. NERVTAG paper. 2021;63:1-14.

Acknowledgments

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