

# The Delta VOC is the dominant SARS-CoV-2 variant in Kenya

## Background

Continuous genomic surveillance of SARS-CoV-2 has detected circulation of three global variants of concern (VOC) in Kenya. The Delta variant has higher transmissibility compared to Alpha and Beta variants<sup>1</sup>. These VOCs are the dominant sources of COVID-19 cases in the country based on sequenced samples collected in recent months.

## Methods

On 2<sup>nd</sup> July 2021, we sequenced 212 SARS-CoV-2 PCR positive samples collected between 13<sup>th</sup> May and 24<sup>th</sup> June 2021. The samples were obtained from 12 counties namely, Coast (Kilifi (n=36), Kwale (n=1), Lamu (n=1), Mombasa (n=32) and Taita Taveta (n=12)), Nyanza (Kisumu (n=73), Migori (n=14) and Siaya (n=27)), Rift Valley (Laikipia (n=3), Nakuru (n=1) and Nandi (n=1)) and Western (Vihiga (n=11)).

## Key points

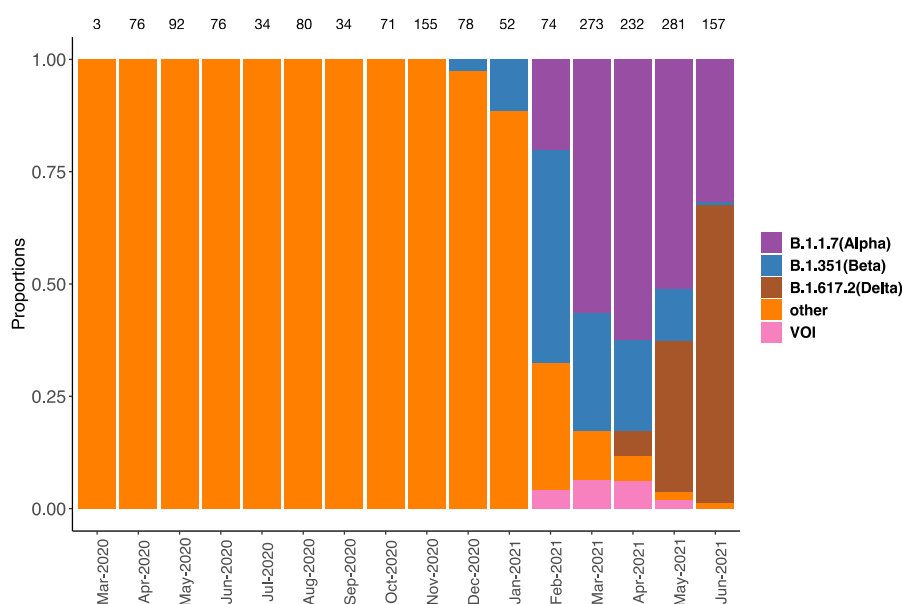
- We sequenced 212 SARS-CoV-2 PCR-positive samples collected between 13<sup>th</sup> May and 24<sup>th</sup> June 2021 from twelve counties in Kenya: Coast (Kilifi, Kwale, Lamu, Mombasa and Taita Taveta), Nyanza (Kisumu, Migori, Siaya), Rift Valley (Laikipia, Nakuru and Nandi) and Western (Vihiga).
- The recovered sequences included three variants of concern; Delta (B.1.617.2, first identified in India) (65%, n=137), Alpha (B.1.1.7, first identified in UK) (29%, n=62) and Beta (B.1.351, first identified in South Africa) (3%, n=6), and included one variant of interest; (A23.1, first identified in Uganda (1.4%, n=3).

## Findings

The newly sequenced genomes belonged to seven Pango lineages: B.1.617.2 (n=137, Delta VOC), B.1.1.7 (n=62, alpha VOC), B.1.351 (n=6, Beta VOC), A.23.1 (n=3, VOI) B.1.1 (n=3), B.1 (n=2) and B.1.596.1 (n=1). Delta variant is the predominant VOC in the new sequences (**Table 1**). Demographic characteristics of patients providing samples are shown in **Table 1**. The total number of sequenced SARS-CoV-2 genomes from the KEMRI-Kilifi laboratory is now 1768, and the temporal lineage patterns since March 2020 to date is shown in Figure 1.

## Conclusion

The VOCs are now the dominant lineages from our genomic surveillance data with a predominance of the Delta Variant of concern in the most recent weeks.



**Figure 1.** Temporal distribution of the common Pango lineages<sup>1</sup> identified from our genomic surveillance from March 2020 to 2 July 2021. The values on top of the bars indicate the total number of sequences per month.

### <sup>1</sup>Variant of concern (VOC):

A variant for which there is clear evidence of a significant increase in transmissibility, more severe disease, significant reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures. For example, B.1.351, B.1.1.7, B.1.617.2.

The WHO has recommended renaming of the variant of concern as follows:

1. Alpha: B.1.1.7, first identified in the United Kingdom
2. Beta: B.1.351, first identified in South Africa
3. Gamma: P.1, first identified in Brazil
4. Delta: B.1.617.2, First identified in India.

### Variant of Interest

A variant with specific genetic markers that have been associated with changes to receptor binding, reduced neutralization by antibodies generated against previous infection or vaccination, reduced efficacy of treatments, potential diagnostic impact, or predicted increase in transmissibility or disease severity.

**Table 1.** A summary of 212 SARS-CoV-2 RT-PCR positive samples collected between 13th May and 24 June 2021 in eleven counties in Kenya.

	<b>B.1.1.7 (Alpha) (n=62)</b>	<b>B.1.351 (Beta) (n=6)</b>	<b>B.1.617.2 (Delta) (n=137)</b>	<b>A.23.1 VOI (n=3)</b>	<b>Others<sup>1</sup> (n=4)</b>
<b>Location</b>					
Kilifi	5	0	31	0	0
Kisumu	22	0	49	1	1
Kwale	0	0	1	0	0
Laikipia	1	0	2	0	0
Lamu	0	0	1	0	0
Migori	7	4	0	2	1
Mombasa	0	1	29	0	2
Nakuru	0	0	1	0	0
Nandi	1	0	0	0	0
Siaya	9	1	17	0	0
Taita Taveta	11	0	1	0	0
Vihiga	6	0	5	0	0
<b>Clinical Presentation</b>					
Asymptomatic	40	4	57	3	2
Symptomatic	21	1	48	0	0
Data not available	1	1	32	0	2
<b>Travel History</b>					
Local	62	6	137	3	4
<b>Testing Criteria</b>					
Contact with confirmed case	1	0	6	0	0
Presented to health facility	3	0	16	0	0
Surveillance	46	6	105	3	4
Data not available	12	0	10	0	0

<sup>1</sup>Lineages B.1.1, B.1 and B.1.596.1

## 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.

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