POLICY BRIEF #26

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[1]. These VOCs are the dominant sources of COVID-19 cases in the country based on sequenced samples collected in recent months.

Methods

On 9th July 2021, we sequenced 76 SARS-CoV-2 PCR positive samples collected between 12th April and 6th July 2021. The samples were obtained from four counties namely, Kilifi (n=57), Siaya (n=13), Laikipia (n=5), and Busia (n=1).

Key points

- We sequenced 76 SARS-CoV-2 PCR-positive samples collected between 12th April and 6th July 2021 from four counties in Kenya: Kilifi, Siaya, Laikipia and Busia county.
- The recovered sequences included three variants of concern; Delta (B.1.617.2, first identified in India) (82.9%, n=63), Alpha (B.1.1.7, first identified in UK) (13.1%, n=10) and Beta (B.1.351, first identified in South Africa) (2.6%, n=2), and included one variant of interest; (A23.1, first identified in Uganda (1.3%, n=1).

Findings

The newly sequenced genomes belonged to four Pango lineages: B.1.617.2 (n=63, Delta VOC), B.1.1.7 (n=10, alpha VOC), B.1.351 (n=2, Beta VOC) and A.23.1 (n=1, VOI).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 1864, 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.

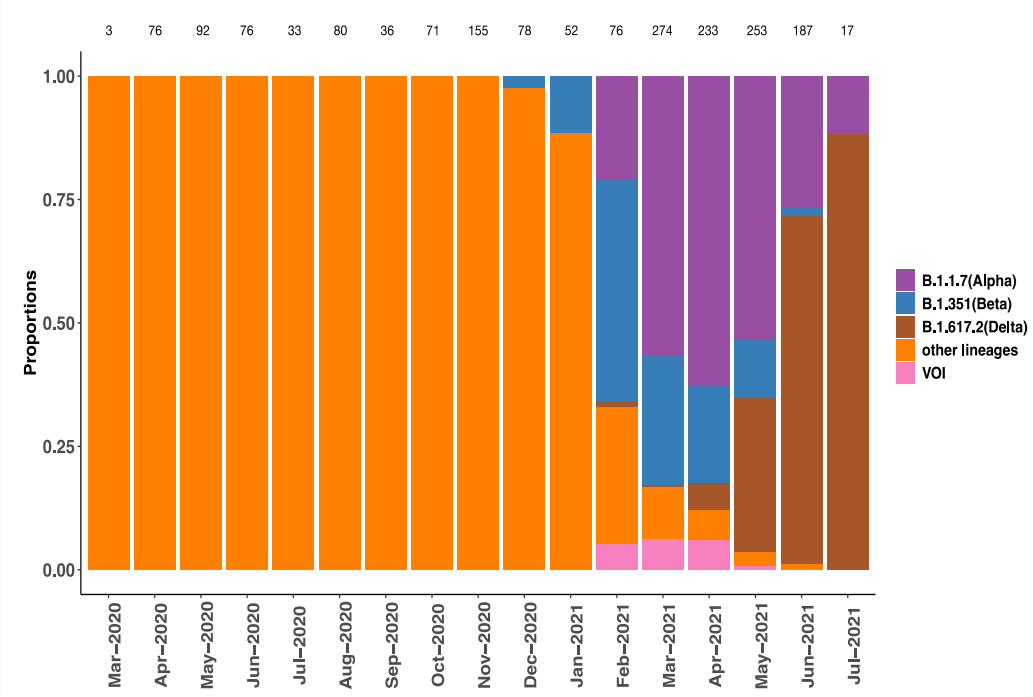

Figure 1. Temporal distribution of the common Pango lineages[1] identified from our genomic surveillance from March 2020 to 12th July 2021. The values on top of the bars indicate the total number of sequences per month.

[1]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 76 SARS-CoV-2 RT-PCR positive samples collected between 12th April and 6th July 2021 in four counties in Kenya.

	A.23.1 (n=1)	**B.1.1.7 (Alpha) (n=10)**	**B.1.351 (Beta) (n=2)**	**B.1.617.2 (Delta) n=63)**
Location				
Busia	0	1	0	0
Kilifi	0	1	2	54
Laikipia	0	1	0	4
Siaya	1	7	0	5
Clinical Presentation				
Asymptomatic	0	0	2	19
Symptomatic	1	10	0	39
Data not available	0	0	0	5
Travel History				
Local	1	10	2	63
Testing Criteria				
Contact with a confirmed case	0	0	0	6
Presented to health facility	1	10	0	31
Surveillance	0	0	2	10
Data not available	0	0	0	16

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

Acknowledgments

This work was supported by the National Institute for Health Research (NIHR) (project references 17/63/82 and 16/136/33) using UK aid from the UK Government to support global health research, The UK Foreign, Commonwealth and Development Office and Wellcome Trust (grant# 220985/Z/20/Z). The views expressed in this publication are those of the author (s) and not necessarily those of NIHR or the Department of Health and Social Care, Foreign Commonwealth and Development Office. In addition, this work was supported by the KEMRI Internal Research Grant (Grant # KEMRI/COV/SPE/012). This work is supported by the Rapid Response Teams (RRTs) from Kwale, Tana River, Lamu, Taita-Taveta, Mombasa and Kilifi and the dedicated effort from the various health care and testing facilities across the coast region and the country at large