

The Alpha (B.1.1.7) variant of concern continues to predominate SARS-CoV-2 infections in Kenya

Background

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 variant recently named “Alpha” by WHO, lineage B.1.1.7, that was first identified in United Kingdom, (b) the variant recently named “Beta” by WHO, lineage B.1.351, that was first identified in South Africa, and (c) the variant recently named “Delta” by WHO, lineage B.1.617.2, that was first identified in India. While it remains unclear as to whether the WHO designated variants of concern Beta, Gamma and Delta are associated with more severe COVID-19 presentation compared to non-variants of concern, there is some evidence for an increased risk of hospitalisation and death following infection with the Alpha variant [1,2].

Key Points

- We sequenced 41 SARS-CoV-2 PCR-positive samples collected between 17th and 28th May 2021 from 6 counties across Kenya.
- A total of 40 out of 41 (98%) samples were classified as variants of concern as follows;
 - Alpha (B.1.1.7, first identified in UK) (76%, n=31)
 - Beta (B.1.351, first identified in South Africa) (7%, n=3)
 - Delta (B.1.617.2, first identified in India) (15%, n=6).
- All the 6 cases infected with Delta variant of concern were from Kilifi county. Five did not have a history of international travel, but 1 was a truck driver who had recently travelled to Uganda.

Methods

On 4th June 2021, we sequenced 41 additional SARS-CoV-2 PCR positive samples collected between 17th and 28th May 2021. These samples were collected from Kilifi (n=26), Taita Taveta (n=8), Laikipia (n=6), and Mombasa (n=1) counties. Two of the sequenced cases had a recent history of international travel to Uganda (defined as the preceding 14 days). Information on symptom status was available for 38 cases, and 25 were asymptomatic while 13 had symptoms (Table 1).

We classified the genome sequences using the new WHO classification and the PANGO lineage designation (PANGO version v1.2.6).

Findings from sequence data obtained on 4th June 2021

The newly sequenced genomes fell into 4 Pango lineages: B.1.1.7 (i.e., Alpha VOC, n=31), B.1.351 (i.e., Beta VOC, n=3), B.1.617.2 (i.e., Delta VOC, n=6) and B.1.525 (n=1), **Figure 1**. The Alpha VOC was the predominant strain among the sequenced samples. The 6 samples infected with the Delta VOC were collected from individuals from Kilifi county of whom 5 had no history of international travel and 1 was a truck driver who had recently travelled from Uganda. Three of the six individuals infected with the Delta VOC were contacts of confirmed cases. Table 1 provides epidemiological details associated with the cases.

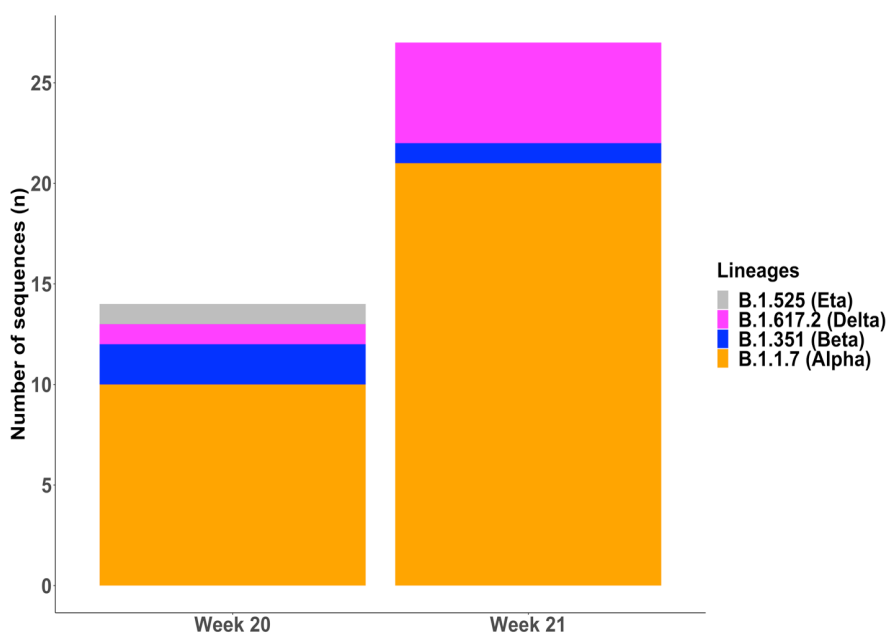


Figure 1. A bar plot showing the weekly number of each of the lineages detected among the 41 samples we sequenced. We detected three VOCs: B.1.1.7 (Alpha variant) shown in orange, B.1.351 (Beta variant) shown in blue and B.1.617.2 (Delta Variant) shown in magenta. We also detected a VOI B.1.525 (Eta variant; International lineage with E484K, del69-70 among other defining mutations) shown in grey. Week 20 and 21 covered the period of 16th-22nd and 23rd-29th May 2021 respectively.

Table 1. A summary of 41 SARS-CoV-2 RT-PCR positive samples collected between 17th and 28th May 2021 in 3 counties at the Coast, 2 counties in the Rift Valley and 1 county in Central Kenya.

	Alpha (B.1.1.7) (n=31)	Beta (B.1.351) (n=3)	Delta (B.1.617.2) (n=6)	Eta (B.1.525) (n=1)
Location				
Kilifi	19	1	6	0
Mombasa	0	1	0	0
Taita Taveta	6	1	0	1
Laikipia	6	0	0	0
Clinical Presentation				
Asymptomatic	19	2	4	0
Symptomatic	10	1	1	1
Deceased	0	0	0	0
Data not Available	2	0	1	0
Travel history				
Travelled	1	0	1	0
Local	30	3	5	1
Testing criteria				
Point of Entry	0	0	0	0
Routine Surveillance	8	2	1	1
Presented at health facility	8	1	0	0
Travelling/In-transit	0	0	0	0
Contact with confirmed case	12	0	3	0
Data not Available	3	0	2	0
Variants of interest: B.1.525 Variants of concern ¹ : B.1.1.7, B.1.351 and B.617.2				

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.

Recommendation

Emphasis should be placed on enhanced genomic surveillance to understand the extent of local transmission and importation of global variants of concern in Kenya, especially the newly introduced Delta variant of concern.

Data availability

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

References

1. R. Challen, E. Brooks-Pollock, J.M. Read, L. Dyson, K. Tsaneva-Atanasova, L. Danon, Risk of mortality in patients infected with SARS-CoV-2 variant of concern 202012/1: Matched cohort study, *BMJ*. 372 (2021) 1–10. <https://doi.org/10.1136/bmj.n579>.
2. A.P. Horby, I. Bell, J. Breuer, M. Cevik, R. Challen, N. Davies, G. Dabrera, J. Edmunds, N. Ferguson, S. Funk, A. Hayward, B. Humberstone, C. Huntley, J. Mcmenamin, P. Mckeigue, G. Medley, C. Semple, NERVTAG paper, 63 (2021) 1–14.

Acknowledgements

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. The samples from Laikipia were provided by KEMRI-CBRD.