

# Genomic surveillance indicates dominance of local transmission of the global variants of concern in Kilifi, Taita Taveta and Mandera 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; (a) the Alpha variant i.e., lineage B.1.1.7 that was first identified in United Kingdom, (b) the Beta variant i.e., lineage B.1.351 that was first identified in South Africa, and (c) the Delta variant i.e., lineage B.1.617.2, that was first identified in India. There is some evidence for an increased risk of hospitalisation and death following infection with the Alpha variant 1,2, but the evidence is unclear for other variants.

## Methods

On 11<sup>th</sup> June 2021, we sequenced 22 additional SARS-CoV-2 PCR positive samples collected between 7<sup>th</sup> May and 3<sup>rd</sup> June 2021. These samples were collected from three counties: Kilifi (n=16), Taita Taveta (n=3) and Mandera (n=3). None of the cases had a recent history of international travel (defined as the preceding 14 days). Information on clinical status was available for 17 cases, 10 were symptomatic while 7 were asymptomatic. (Table 1). Amongst the symptomatic, 2 out of 10 individuals were recorded as deceased and both were from Mandera county. The deceased cases were between 40 and 70 years of age.

We classified the recovered genome sequences using the PANGO lineage assignment (PANGO version v3.1. Variants of concern (VOC) and variants of interest (VOI) were designated based on the WHO framework as of 31<sup>st</sup> May 2021 (<https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/>).

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## Findings from sequence data obtained on 11<sup>th</sup> June 2021

The newly sequenced genomes belong to three Pango lineages: B.1.1.7 (i.e., Alpha VOC, n=16), B.1.351 (i.e., Beta VOC, n=3) and B.1.617.2 (i.e., Delta VOC, n=5, Figure 1). The Alpha VOC was the predominant strain among the sequenced samples and was reported in all the 3 counties we included in our analysis. Delta variant was only detected in Kilifi county. All cases detected as VOCs had no history of travel. Three and one of the individuals infected with Alpha and Delta variants were contact of confirmed cases, respectively.

**Table 1** provides epidemiological details associated with the cases.

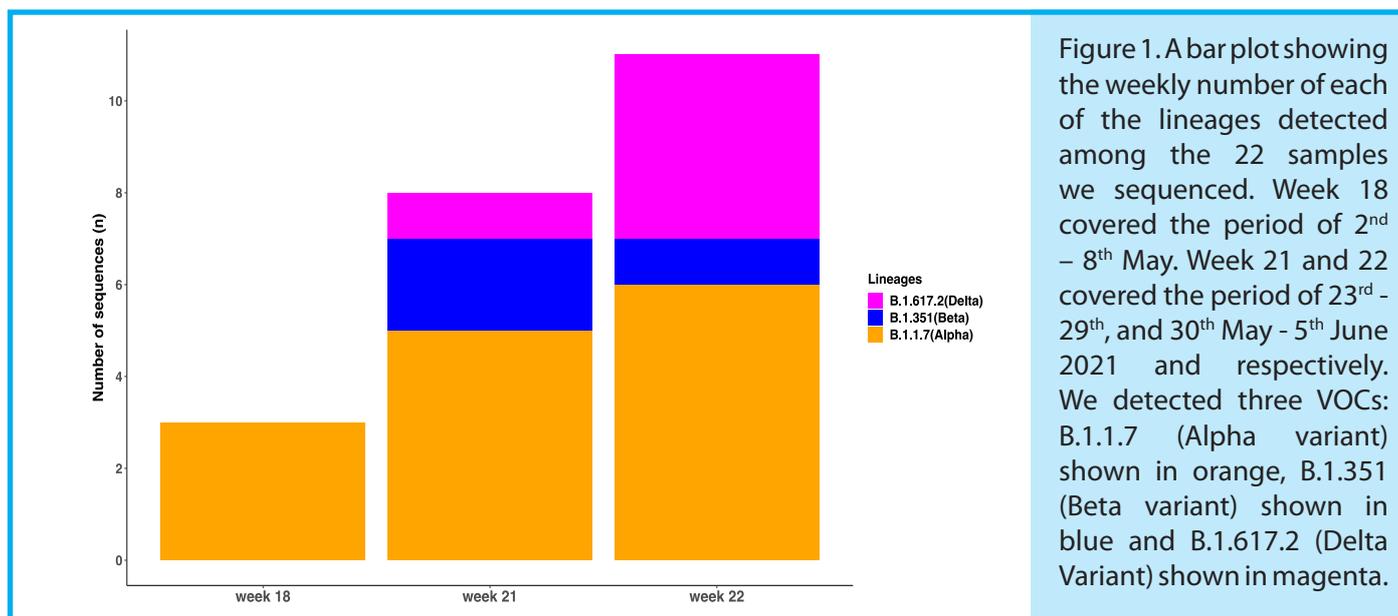


Figure 1. A bar plot showing the weekly number of each of the lineages detected among the 22 samples we sequenced. Week 18 covered the period of 2<sup>nd</sup> – 8<sup>th</sup> May. Week 21 and 22 covered the period of 23<sup>rd</sup> – 29<sup>th</sup>, and 30<sup>th</sup> May – 5<sup>th</sup> June 2021 and respectively. 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.

## Key points

- We sequenced 22 SARS-CoV-2 PCR-positive samples collected between 7<sup>th</sup> May and 3<sup>rd</sup> June 2021 from Kilifi, Taita Taveta and Mandera counties.
- Recovered whole genome sequences were classified as variants of concern:
  - Alpha (B.1.1.7, first identified in UK) (64%, n=14)
  - Beta (B.1.351, first identified in South Africa) (14%, n=3)
  - Delta (B.1.617.2, first identified in India) (23%, n=5).
- None of the cases reported here had a recent history of international travel which suggests local transmission.
- The data suggest a trend for an increasing proportion of cases with the Delta variant

**Table 1.** A summary of 22 SARS-CoV-2 RT-PCR positive samples collected between 7th May 2021 and 3rd June 2021 in Kilifi, Taita Taveta and Mandera county

	<b>Alpha (B.1.1.7) (N=14)</b>	<b>Beta (B.1.351) (N=3)</b>	<b>Delta (B.1.617.2) (N=5)</b>
<b>Location</b>			
Kilifi	8	3	5
Mandera	3	0	0
Taita Taveta	3	0	0
<b>Clinical Presentation</b>			
Asymptomatic	5	0	2
Symptomatic	6	1	3
Deceased	2	0	0
Data not Available	1	2	0
<b>Travel History</b>			
Local	14	3	5
<b>Testing Criteria</b>			
Contact with confirmed cases	3	0	1
Presented to health facility	6	1	2
Data not Available	5	2	2
Variants of Concern: B.1.1.7, B.1.351 and B.1.617.2			

## Discussion

Our genomic surveillance provides evidence of ongoing local spread of three SARS-CoV-2 VOCs in the three surveyed counties. The individuals providing samples had no recent history of international travel (Table 1).

This report provides evidence of the circulation of the Alpha (B.1.1.7) variant in Mandera county which is being included in our genomic surveillance for the first time.

The results provide early evidence of an increasing proportion of cases with the Delta variant.

## Recommendation

Emphasis should be placed on:

- Enhanced genomic surveillance to detect importation of global VOC into Kenya and understand the extent of local transmission, including the newly introduced Delta VOC.
- Linking clinical data to 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 will be made available on GISAID database to allow access to the global scientific community.

## Reference

- Challen, R. et al. Risk of mortality in patients infected with SARS-CoV-2 variant of concern 202012/1: Matched cohort study. *BMJ* 372, 1–10 (2021).
- Horby, A. P. et al. NERVTAG paper. 63, 1–14 (2021).
- Bager, P. et al. Increased Risk of Hospitalisation Associated with Infection with SARS-CoV-2 Lineage B.1.1.7 in Denmark. (2021) doi:10.2139/ssrn.3792894.

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