

The Alpha (B.1.1.7) variant of concern continues predominating SARS-CoV-2 infections on the Kenyan Coast

Background

Genomic surveillance of SARS-CoV-2 in Kenya has detected circulation of three global variants of concern (VOC) in the country including the variant recently named “Delta” by WHO, B.1.617.2 by Pango lineage, that was first identified in India, among 27 samples collected between 29th April and 13th May 2021. The Delta variant was identified in: (a) 14 recent travellers (from India); and (b) 13 long term residents of Kenya with no history of international travel (6 from Kisumu, 3 from Mombasa and 4 from Kilifi). It remains unclear as to whether any of the four WHO designated variants of concern (Alpha, Beta, Gamma and Delta) are associated with more severe COVID-19 presentation.

Methods

We sequenced 35 further SARS-CoV-2 PCR positive samples collected between 9th and 20th May 2021.

These samples were collected from Kilifi (n=26), Mombasa (n=8) and Taita Taveta (n=1) counties. None of the cases had a recent history of international travel (defined as the preceding 14 days). Information on symptom status was available for 21 cases, and 13 were asymptomatic while 8 had symptoms (Table 1).

We classified the genome sequences using the new WHO classification and the PANGO lineage designation.

Findings from sequence data obtained on 28th May 2021

The newly sequenced genomes fell into 5 Pango lineages; B.1.1.7 (i.e. Alpha VOC, n=19), B.1.351 (i.e. Beta VOC, n=9), B.1.617.2 (i.e. Delta VOC, n=5), B.1 (n=1) and B.1.1 (n=1), **Figure 1**. The Alpha VOC was the predominant strain. The 5 samples infected with the Delta VOC were collected from Kilifi among individuals who had no history of international travel. One of the five individuals infected with the Delta VOC was a contact of a confirmed case. Table 1 provides a epidemiological details associated with the cases.

Key Points

- We sequenced 35 SARS-CoV-2 PCR-positive samples collected between 9th and 20th May 2021 from Kilifi (n=26), Mombasa (n=8) and Taita Taveta (n=1) counties.
- A total of 33 out of 35 (94%) samples were classified as variants of concern as follows (described by WHO classification, Pango lineage classification and Country of first identification, respectively);
 - Alpha (B.1.1.7, first identified in UK) (54%, n=19)
 - Beta (B.1.351, first identified in South Africa) (26%, n=9)
 - Delta (B.1.617.2, first identified in India) (14%, n=5).
- All the 5 cases infected with Delta variant of concern were from Kilifi and did not have a history of international travel.

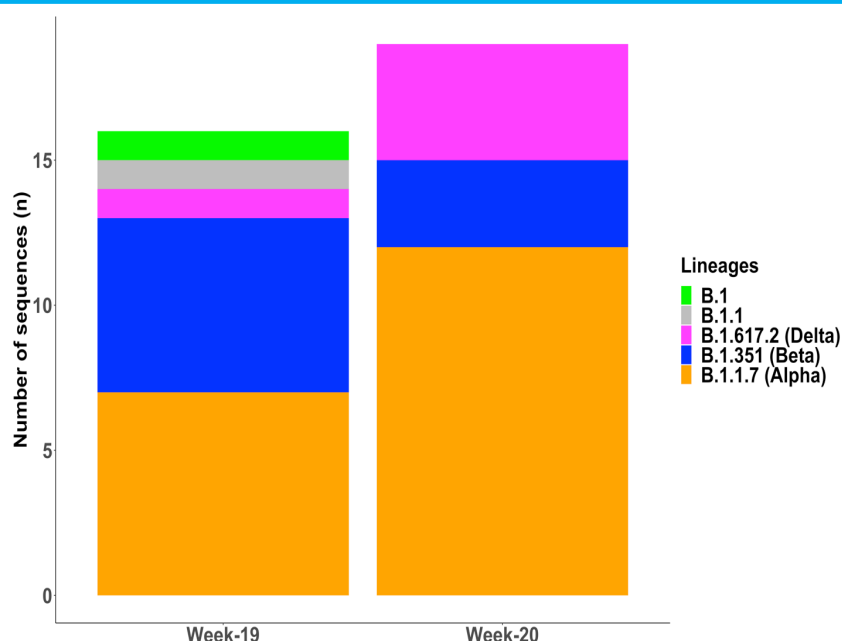


Figure 1. A bar plot showing the weekly number of each of the lineages detected among the 35 samples we sequenced. We detected three VOCs: B.1.1.7 (Alpha variant) shown in orange, B.1.351 (Beta variant) shown in blue and B.1.617.2 (Delta Variant) shown in magenta. We also detected other variants B.1.1 (European lineage) and B.1 (Large European lineage the origin of which roughly corresponds to the Northern Italian outbreak early in 2020) shown in grey and green respectively.

Table 1. A summary of 35 SARS-CoV-2 RT-PCR positive samples collected between 9th and 20th May 2021 in 3 counties at the coastal region.

	Alpha (B.1.1.7) (n=19)	Beta (B.1.351) (n=9)	Delta (B.1.617.2) (n=5)	Other Variants (n=2)
Location				
Kilifi	17	3	5	1
Mombasa	1	6	0	1
Taita Taveta	1	0	0	0
Clinical Presentation				
Asymptomatic	7	3	2	1
Symptomatic	5	1	2	0
Deceased	0	0	0	0
Data not Available	7	5	1	1
Travel history				
Travelled	0	0	0	0
Local	19	9	5	2
Testing criteria				
Point of Entry	0	0	0	0
Routine Surveillance	5	1	2	1
Presented at health facility	11	8	2	1
Travelling/In-transit	0	0	0	0
Contact with confirmed case	2	0	1	1
Data not Available	1	0	0	0
Other Variants: B.1.1, B.1 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.

Discussion

The SARS-CoV-2 infections in coastal Kenya are predominantly arising from three global variants of concern: (a) Alpha, (b) Beta, and (c) Delta which have established local transmission. The Alpha VOC has continued to predominate in the region, but the newly introduced Delta VOC is also gaining foothold in the region especially Kilifi County. The distribution of the cases among the asymptomatic and symptomatic was roughly similar across the lineages.

Recommendation

Emphasis should be placed on enhanced genomic surveillance to understand the extent of local transmission of global variants of concern in Kenya, especially the newly introduced Delta variant of concern. There is need to collect a purposeful set genomic and epidemiological data of infections across the disease spectrum to understand if any of the variants circulating locally has higher propensity to cause severe infection.

Data availability

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

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