POLICY BRIEF #23

Genomic surveillance of SARS-CoV-2 Variants of Concern 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; (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. Emerging data indicate that most recently detected Delta variant is around 60% more transmissible compared to the Alpha variant[1]. It is unclear if this variant is associated with an increased risk of hospitalisation and death following infection. In our KEMRI-Kilifi Kenya genomic surveillance work, we have detected 51 Delta variant infected cases as of 23rd June 2021, but the full extent of spread of this variant in the country is unclear. Here we report on the most recent data from coastal Kenya.

Key points

- We sequenced 22 SARS-CoV-2 PCR positive samples collected between 2nd and 10th June 2021 from Kilifi (n=15), Lamu (n=1), Mombasa (n=3), and Taita Taveta counties (n=3).
- All the recovered sequences were classified as variants of concern:
  - Alpha variant (n=16, 72.7%)
  - Delta variant (n=6, 27.3%).
- None of the sequenced cases had a recent history of international travel thus all these infections were a result of local transmission.

Methods

On 18th June 2021, we sequenced 22 SARS-CoV-2 PCR positive samples collected between 2nd and 10th June 2021. These samples were collected from four counties: Kilifi (n=15), Taita Taveta (n=3), Mombasa (n=3) and Lamu (n=1).

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

Findings from sequence data obtained on 18th June 2021

The newly sequenced genomes belong to two Pango lineages: B.1.1.7 (i.e., Alpha VOC, n=16) and B.1.617.2 (i.e., Delta VOC, n=6) **(Figure 1)**. None of the sequenced cases had a recent history of international travel (defined as the preceding 14 days). Information on clinical status was available for 15 cases, 10 were asymptomatic while 5 were symptomatic **(Table 1)**. Three and one of the individuals infected with Alpha and Delta variants were contacts of confirmed cases, respectively. Table 1 provides epidemiological details associated with the sequenced cases.

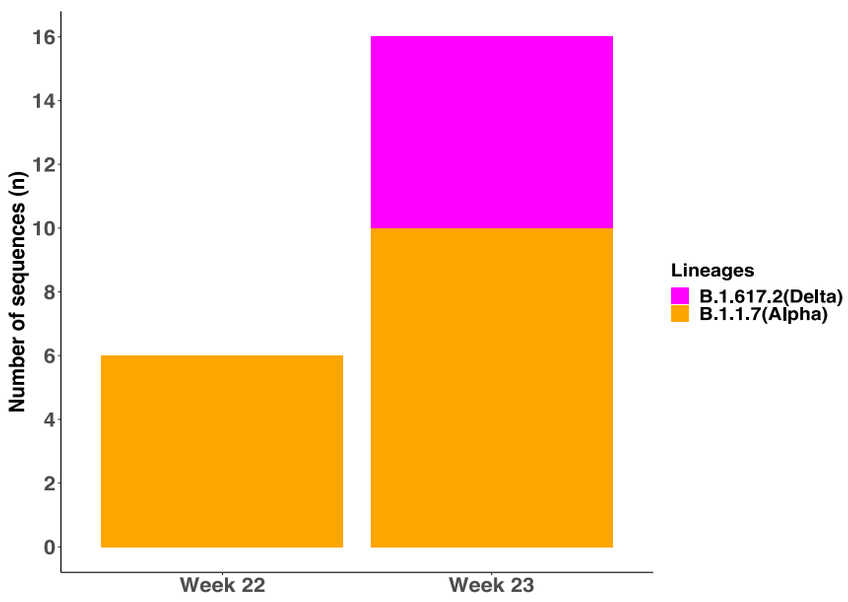

Figure 1. A bar plot showing the weekly number of each of the lineages detected among the 22 sequenced samples collected from four coastal counties. Week 22 and 23 covered the period of 30th May - 5th June 2021 and 6th – 12th June, respectively. We detected two VOCs: B.1.1.7 (Alpha variant) shown in orange and B.1.617.2 (Delta Variant) shown in magenta.

Table 1. A summary of 24 SARS-CoV-2 RT-PCR positive samples collected between 2nd and 10th June 2021 in Killfi, Taita Taveta, Mombasa and Lamu county.

	B.1.1.7 (Alpha) (n=16)	B.1.617.2 (Delta) (n=6)
Location		
Kilifi	9	6
Lamu	1	0
Mombasa	3	0
Taita Taveta	3	0
Clinical Presentation		
Asymptomatic	7	3
Symptomatic	2	3
Data not Available	7	0
Travel History		
Local	**16**	**6**
Testing Criteria		
Contact with confirmed case	3	1
Presented to health facility	4	2
Surveillance	1	1
Data not Available	8	2

Discussion

The Alpha variant was the predominant strain among the sequenced samples and was reported in all the 4 counties included in our analysis. Like our most recent shared report, the Delta variant was detected in Kilifi county in individuals without history of recent travel, suggesting ongoing local transmission of this variant in the county. The sample sizes for counties other than Kilifi were very small and hence solid conclusions on the presence or absence of the Delta variant elsewhere on the Coast cannot be drawn.

Recommendation

Emphasis should be placed on:

a. Enhanced genomic surveillance across the Coastal counties to identify the extent of the spread of VOCs and, in particular, the Delta variant.
b. Linking clinical data to genomic data we generate to establish whether the locally circulating VOCs are associated with severe clinical outcomes. This requires access to samples from patients with severe illness symptoms turning up in either public or private hospitals

References

1. Campbell, F. et al. Increased transmissibility and global spread of SARS-CoV-2 variants of concern as at June 2021. Eurosurveillance 26, (2021).

Data Availability

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

Acknowledgments

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