

Detection of SARS-CoV-2 Variant of Concern (B.1.617) that is common in India among returning travellers at Jomo Kenyatta International Airport (JKIA)

Background

Global genomic surveillance of SARS-CoV-2 has identified at least four variants of concern (VOC). B.1.617 is a recently declared variant of concern with high prevalence in India [1]. This variant has now spread to other global geographic regions and countries. The B.1.617 has characteristics that might make antibodies to older variants or existing vaccines less effective, but this has yet to be confirmed. There is no strong evidence to suggest that B.1.617 is associated with severe disease. Here we report SARS-CoV-2 whole genome sequences obtained from 17 samples collected from

individuals with a history of very recent travel to India (either returning into the country or transiting) who tested positive at the Jomo Kenyatta International Airport (JKIA) in Nairobi.

Key Points

- We sequenced 17 SARS-CoV-2 PCR positive samples collected from travelers that arrived from India and who tested positive on 29th April 2021 at the Jomo Kenyatta International Airport (JKIA) in Nairobi Kenya.
- A total of 15 sequences were classified as the new SARS-CoV-2 variant of concern (B.1.617) that is common in India.
- One sample was classified as B.1.1.7, a variant of concern first identified in the United Kingdom and spread across the globe.

Findings from sequence data obtained on 7th May 2021

We received 18 samples collected on 29th April 2021 from individuals who arrived from India at Jomo Kenyatta International Airport (JKIA) in Nairobi Kenya. We obtained partial genomes from 17 of the 18 samples. One sample failed processing quality control steps and was not taken forward for sequencing.

We classified the recovered genome sequences using the two main SARS-CoV-2 genomic classifications systems (i.e., the Pango lineage and the NextStrain clade classification). The newly sequenced genomes fell into 4 Pango lineages; B.1.617.2 (n=12), B.1.617.1 (n=3), B.1.1.7 (also known as clade 501Y.V1) (n=1) and B.1 (n=1), **Figure**.

Discussion

The sequenced samples were dominated by the recently declared VOCs of Indian origin (88% (15/17)). The sub-lineage B.1.617.1 occurred in 18% (n=3) samples and the sub-lineage B.617.2 (n=12) occurred in 76% (n=12) samples. Notably, these samples were collected from individuals who had travelled from India to Kenya suggesting importations rather than local transmission.

(See **Table** below)

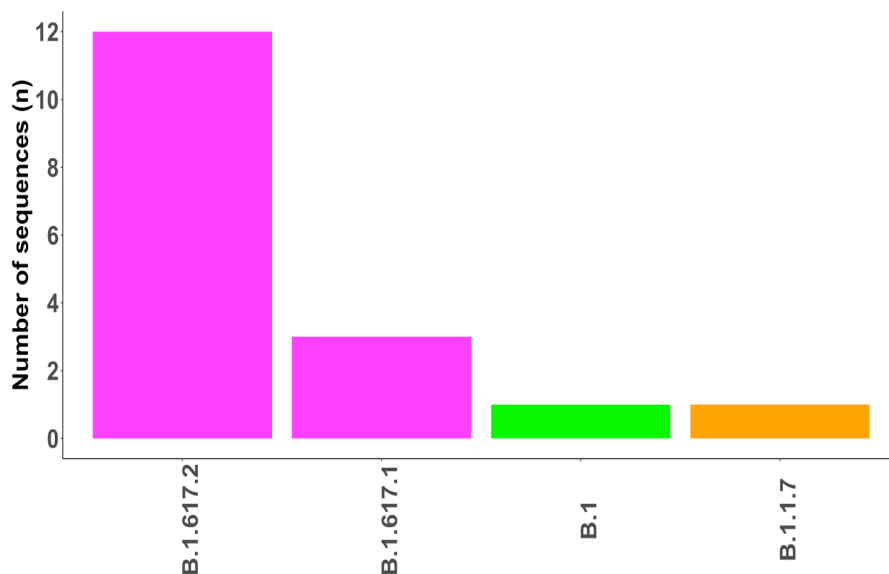


Figure: A bar plot showing the frequency (y-axis) of lineages (x-axis) detected among 17 samples collected from returning travellers at JKIA on 29th April 2021.

Table: A summary of 17 SARS-CoV-2 Rt-PCR positive samples collected on 29th April 2021 at JKIA in Nairobi, Kenya from individuals arriving from India.

	501Y.V1 (UK origin) (n=1)	B.1.617 (Indian origin) (n=15)	Other Variants (n=1)
Location			
JKIA	1	15	1
Clinical Presentation			
Asymptomatic	0	2	0
Symptomatic	0	0	0
Deceased	0	0	0
Data not Available	1	13	1
Travel history			
Travelled	1	15	1
Local	0	0	0
Testing criteria			
Point of Entry	1	12	0
Routine Surveillance	0	0	0
Presented at health facility	0	0	0
Travelling/In-transit	0	3	1
Contact with confirmed case	0	0	0
Data not Available	0	0	0
Other Variants: B.1			
JKIA: Jomo Kenyatta International Airport			

Implications

The sequencing results provide evidence of travellers importing to Kenya variants of concern from India detected through surveillance at the international airport. Given that such surveillance is unlikely to detect all cases and that the VOCs were spread widely in India prior to the recent travel restrictions, it is possible that these VOCs are already introduced to Kenya.

Recommendation

Emphasis should be placed on surveillance to identify local transmission of the B.1.617 VOC in Kenya.

Data availability

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

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. 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

Reference:

1. S. Cherian, V. Potdar, S. Jadhav, P. Yadav, N. Gupta, Convergent evolution of SARS-CoV-2 spike mutations , L452R , E484Q and P681R , in the second wave of COVID-19 in Maharashtra , India, (2021).