



## The persons infected with the 501Y.V2 variant

The two genome sequences that were identified as 501Y.V2 were obtained from samples that were collected on the 15<sup>th</sup> and 17<sup>th</sup> December 2020, from two South Africa nationals who visited the country. Their samples were taken as part of the routine surveillance of visitors arriving in coastal Kenya during the month of December. None of the travellers had symptoms at the time of sample collection and they have since left the country.

## Implications

The identification of variant 501Y.V2 among 2 asymptomatic travellers of different age categories confirms the entry of new variants to Kenya. We cannot infer how much transmission has arisen from new variants because of the small sample size. With a small sample size, we are limited to concluding that the South African variant has not spread sufficiently to dominate the Kenyan epidemic, as it has done in South Africa. However, given the extent of transmission in other countries there is a clear ongoing risk of spread of new variants.

## Recommendations

- a. Continue and extend genomic surveillance of circulating SARS-CoV-2 across Kenya.
- b. Genomic surveillance should include Nairobi SARS-CoV-2 samples from November to date.

## Data availability

The whole genome sequence data will be available from GISAID.

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