NATIONAL INSTITUTE FOR COMMUNICABLE DISEASES
Division of the National Health Laboratory Service

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Frequently asked questions about the B.1.1.529 mutated SARS-CoV-2 lineage in South Africa

The Network for Genomics Surveillance in South Africa (NGS-SA, www.ngs-sa.org), which includes the National Institute for Communicable Diseases (NICD), KRISP at the University of KwaZulu-Natal (UKZN), University of Cape Town (UCT), Stellenbosch University (SUN), the University of the Free State (UFS), the University of Pretoria, the University of the Witwatersrand (WITS) and the National Health Laboratory Service (NHLS), has been monitoring changes in SARS-CoV-2, the virus which causes COVID-19, since March 2020.

What is the B.1.1.529 lineage?
On 22 November 2021, we detected a group of related SARS-CoV-2 viruses in South Africa named the B.1.1.529 lineage. B.1.1.529 has been detected in Gauteng at relatively high frequency, with >70% of genomes sequenced (n =71) from specimens collected between 14-23 November 2021 belonging to this lineage. This lineage possesses a high number of mutations previously seen in other SARS-CoV-2 variants of interest (VOI) or variants of concern (VOC) but also other mutations which are novel. One of these changes can be detected through standard diagnostic tests that target the S gene, which allows detection of this lineage in South Africa without sequencing data.

The World Health Organization and the South African National Department of Health were alerted to this lineage earlier this week. The NGS-SA is continuing to monitor the frequency of this lineage, and laboratory tests to assess the functional impacts of these mutations are underway. Thus far the virus has not fulfilled the WHO criteria for VOC or VOI. This will be revisited, especially as the virus spreads and data is accumulated.

How do the C.1.2, Beta or Delta variants differ from the B.1.1.529 lineage?
While the B.1.1.529 lineage shares a few common mutations with the C.1.2, Beta and Delta variants, it also has a number of additional mutations. At the present, the B.1.1.529 lineage is relatively distinct from the C.1.2, Beta and Delta variants and has a different evolutionary pathway.

Does infection with B.1.1.529 result in similar symptoms as with other variants?
Currently no unusual symptoms have been reported following infection with the B.1.1.529 variant and as with other variants some individuals are asymptomatic.

What are the implications? Will these mutations affect vaccine effectiveness, disease severity, and transmissibility?
SARS-CoV-2, like all viruses, changes with time, with mutations that afford the virus some kind of advantage being selected for in recent infections. While some of the mutations in the B.1.1.529 lineage have arisen in other SARS-CoV-2 variants of concern or variants of interest, we are being cautious about the implications, while we gather more data to understand this lineage.

Work is already under way to look at the immune escape potential of B.1.1.529 in the laboratory setting. We are also establishing a real time system to monitor hospitalisation and outcome associated with B.1.1.529. Based on our understanding of the mutations in this lineage, partial

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immune escape is likely, but it is likely that vaccines will still offer high levels of protection against hospitalisation and death.

We expect new variants to continue to emerge wherever the virus is spreading. Vaccination remains critical to protect those in our communities at high risk of hospitalisation and death, to reduce strain on the health system, and to help slow transmission. This must be in conjunction with all the other public health and social measures, so we advise the public to remain vigilant and continue to follow COVID-19 protocols by: ensuring good ventilation in all shared spaces, wearing masks (which cover your nose, mouth and chin), keeping 1.5m distance from others as much as possible and washing or sanitising your hands and surfaces regularly and keeping 1.5m distance from others as much as possible. These non-pharmaceutical interventions (NPIs) are still proven to prevent the spread of all SARS-CoV-2 viruses.

Will these mutations affect test sensitivity?
The B.1.1.529 lineage has a deletion (Δ69-70) within the S gene that allowed for rapid identification of this variant in South Africa and will enable continued monitoring of this lineage irrespective of available sequence data. However, most other targets (including the N and RdRp genes) remain unaffected from specimens tested in over 100 specimens from testing laboratories in Gauteng so it is unlikely that overall PCR test sensitivity is affected. These PCR tests typically detect at least two different SARS-CoV-2 targets, which serves as a backup in the case of a mutation arising in one.

Analysis of the mutations in the nucleocapsid (N gene) of B.1.1.529 viruses suggests that rapid antigen tests should be unaffected, however verification of this is underway.

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