

## RISK ASSESSMENT VARIANT B.1.1.529

RAG 26/11/2021

### Risk assessment

- The genomic profile of the B.1.1.529 is worrisome and is compatible with higher transmissibility and possibly immune evasion. For this reason, the variant was classified as a VOC by ECDC on 26/11/2021.
- The epidemiological trend in South Africa and the very rapid increase of the share of infections caused by the new variant appear to confirm a substantial higher transmissibility than the Delta variant. Of note is that the sequencing results in South Africa might be biased, because of possible preferential tracing & sequencing contacts of cases infected with the variant.
- The variant is likely to be associated with significant immune escape because of the many mutations and their nature.
- There are still no data available to assess a possible impact on severity of disease.
- There is no reason to expect that the classic preventive measures as they currently apply (social distance, limited contacts, mouth masks, ventilation, etc.) would not be effective to this variant.
- Previous experience with Alpha and Delta have shown that it is not possible to stop the introduction of a new variant into the country, even with travel ban. However, the purpose of travel restrictions is to delay the introduction and widespread circulation. For that purpose, these measures should be taken as fast as possible.
- The variant has been reported in other countries than South Africa, including in 6 cases in Botswana, 2 cases in Hong Kong (of which one traveler from South Africa) and at least one case in Malawi (imported in Israel). Genomic surveillance in African countries is generally limited and under detection/reporting is expected. Undetected circulation in neighboring countries is likely (Eswatini, Zimbabwe, Malawi, Lesotho, Mozambique, Botswana, Namibia and Zambia), however difficult to assess to what extent.
- In South Africa, the variant represents 59% of the sequences during the last 30 days. Although the incidence or PR [criteria](#) are not fulfilled (yet), the country is classified as a VOC-country based on the worrisome evolution.

### Recommendations

- While waiting for more scientific data on the possible impact of the new variant (transmissibility, severity, immune escape), the principle of precaution should be applied. Therefore, in addition to the measures that apply for VOC-countries, the RAG advises a travel ban (activation of the emergency brake) for the following countries: South Africa, Eswatini, Zimbabwe, Malawi, Lesotho, Mozambique, Botswana, Namibia and Zambia. This implies that travelers exempted from the ban (such as returning residents) follow the same procedures with regards to quarantine and testing as travelers arriving from a VOC country. The duration of this measure is at least until more scientific evidence is available on the severity and cross-protection of the vaccines.

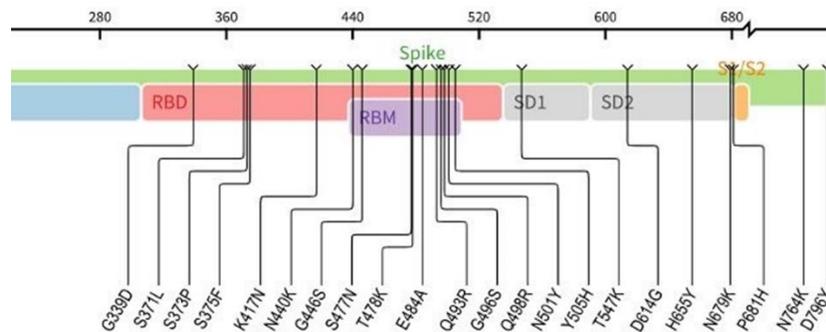
- To avoid indirect incoming travelers through other airports in the EU, there is a need to have coherent European measures. Discussions are ongoing.
- In addition, more strict measures are recommended for all travelers returning from countries from Africa and the Middle East, that are not on the white list:
  - Request of a negative test pre-travel.
  - Tests performed after arrival should be PCR tests (no RAT), ideally using a VOC PCR that detects S-gene dropout. These tests can be performed by the federal platform and some main clinical laboratories. Especially tests performed in Zaventem should use this PCR. Positive samples from these travellers should be systematically sequenced.
  - Two tests should be done after arrival: one immediately after arrival and a second test on day 7. The traveller has to remain in quarantine until a negative second test.
  - Testing is recommended for children from the age of 6, instead of 12, since children also play a role in transmission.
  - No distinction should be made for vaccinated and unvaccinated travellers, as long as there is no data on possible immune escape of the variant. The current procedure in which fully vaccinated travellers from non EU/Schengen countries or countries on the white list only have to be tested once does therefore temporarily not apply to travellers from countries from Africa and the Middle East.
- Priority should be given for contact tracing to confirmed infections with the variant strain and infected returning travelers, especially if there is a link to South-Africa and neighboring countries.

## Background

### *Virological characteristics*

The variant raises concerns because of the large number and unusual constellation of mutations, with multiple mutations across the genome of which 32 in the spike protein (Figure 1). Some mutations are known to affect transmissibility and immune evasion, but many others have been rarely observed until now.

Figure 1: Mutations in the spike protein of B.1.1.529



The variant can be identified with a particular PCR assay that detects S-gene dropout (similar to the Alpha variant).

### *Epidemiological evolution*

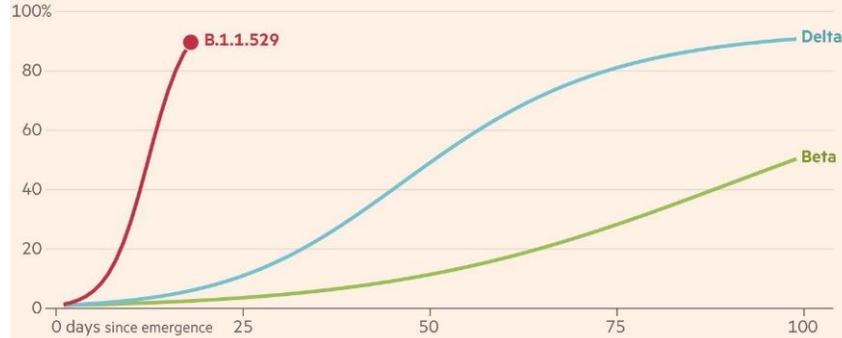
#### *1) International context*

B.1.1.529 was first detected in South Africa. The African CDC reports that by November 25, 77 cases have been detected in the country. ECDC data on 26/11/2021 report 100 cases. According an analysis of data from Gisaïd and the South African National Health Laboratory Service, published in the Financial Times, the share of B.1.1.529 among sequenced samples is more rapidly increasing than it was for previous VOCs (Figure 2). By November 25, it already represented more than three quarters of the sequenced samples and it is expected to soon reach 100% (Figure 3).

Figure 2

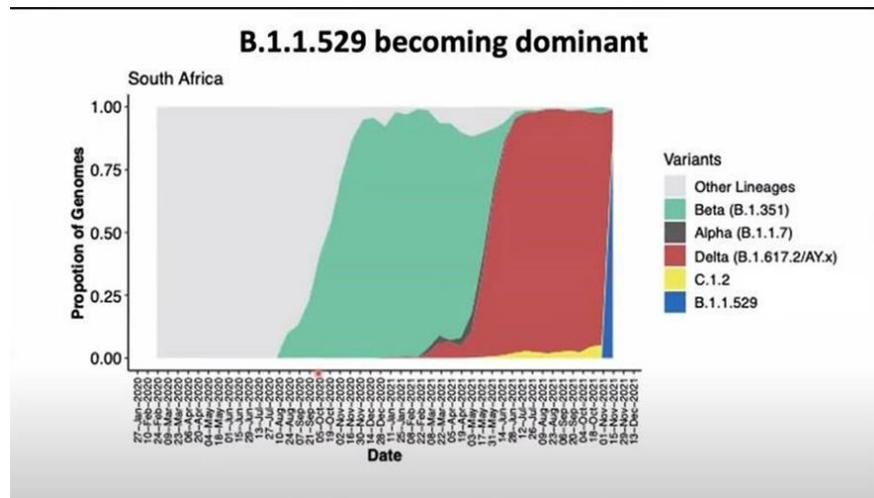
A new variant is spreading rapidly in South Africa, and appears to be out-competing other variants much faster than previous variants of concern did

Share of all sequenced cases\* in South Africa accounted for by each variant, by number of days since it passed 1%



\*Growth of B.1.1.529 is modelled from SGTF data rather than full genomic sequences  
Source: FT analysis of data from Gisaidd and the South African National Health Laboratory Service  
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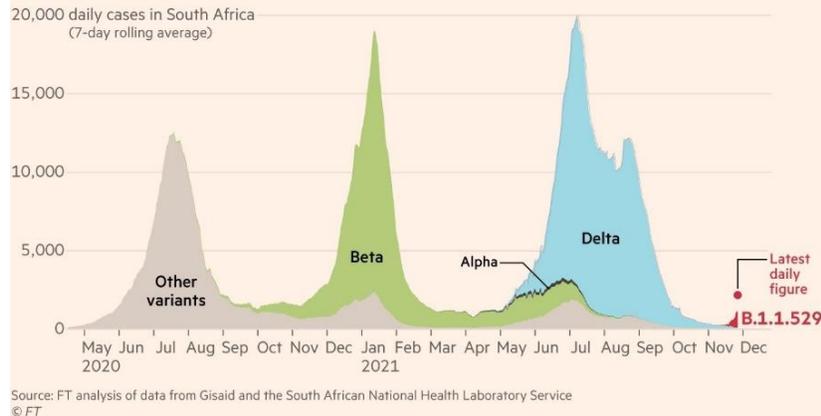
Figure 3



According a rapid calculation, using the GISAID data and press conference data, by Prof. Tom Wenseleers, the variant could have a growth rate advantage over Delta of as high as 38% (Twitter communication). The same analysis of data from Gisaidd and the South African National Health Laboratory Service also showed a recent increase in the number of daily cases in South Africa, possibly as a result of the new variant (Figure 4). The increase is mostly observed in the same provinces where the new variant was detected (Gauteng, North West and Limpopo).

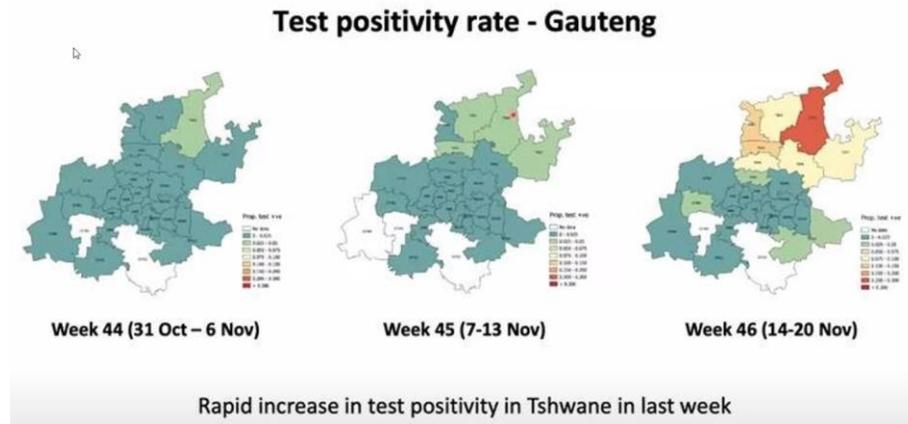
Figure 4

There are signs that B.1.1.529 may be triggering a new wave in South Africa



Also the positivity ratio is increasing in those provinces. In Gauteng province the PR increased from 0.7% in the week of 31 October-6 November to 4.3% in the week of 14-20 November (Figure 5).

Figure 5



A rapid and sharp increase is recently also observed in S-gene dropout, in all provinces (Figure 6 and 7). Being a good marker of B.1.1.529 (77/77 of SGTF sequences from Gauteng were confirmed as B.1.1.529), it is likely that almost all SGTF samples in South Africa are this variant.

Figure 6

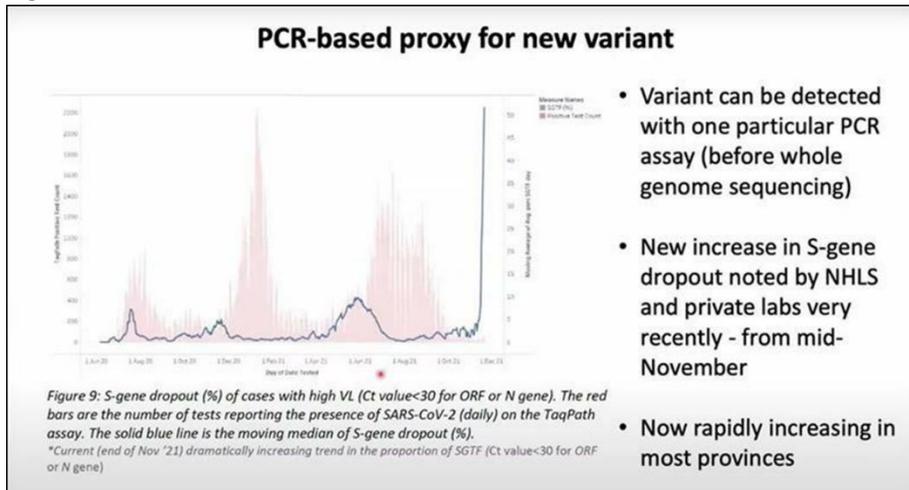
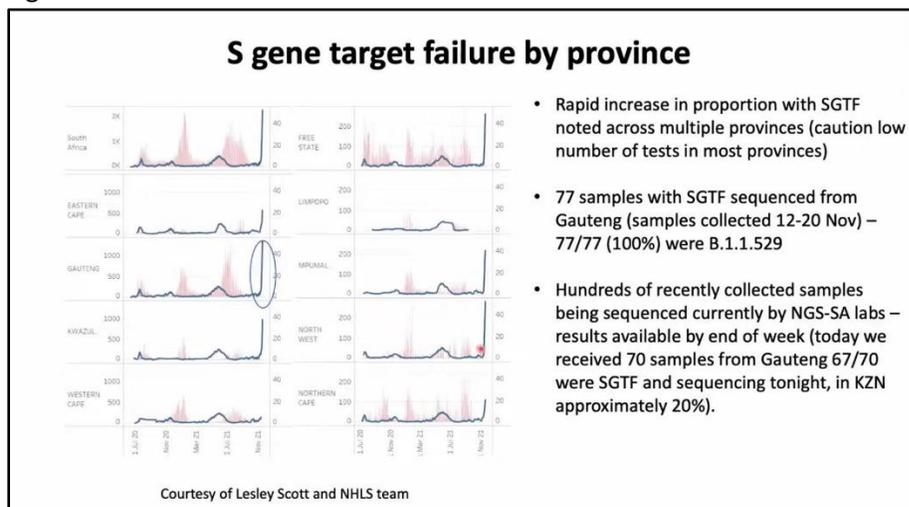


Figure 7



The variant has meanwhile also been detected in Botswana, Hong-Kong and Israel. According to data from GISAID, By 25th November 2021, the B.1.1.529 variant had been detected in 6 samples from Botswana (out of 98 sequences reported in the last 30 days). The variant was not detected in other countries neighboring South Africa, but these countries reported less than 10 sequences in the last 30 days. The variant was also detected in 2 samples in Hong Kong, of which one was a traveler coming from South Africa. The Israeli Ministry of Health communicated that the variant was detected in a vaccinated traveler returning from Malawi.

## 2) Belgian data (source NRC)

Over the last month, 47 positive test results were identified associated with both a Cq < 26 and a SGTF (S-gene dropout), with a higher frequency during the last week. SGTF is typically caused by a 69-70 deletion in the Spike gene, which is systematically present in the Alpha and B.1.1.529 variants, but also occasionally among other variants of concern. The numbers above can therefore not be considered as B.1.1.529 alone. The samples will be systematically investigated in the coming days.

Two samples were already sequenced and one of those tested positive for B.1.1.529. It concerns a young adult woman who developed symptoms 11 days after travelling to Egypt via Turkey. The patient did not report any link with South Africa or other Southern African countries, had not previously been vaccinated and had not yet been infected. She developed flu-like symptoms, but does not present at this stage signs of severe disease. The source of infections remains unclear, and further investigation is ongoing.

The patient did not report high risk contacts outside her household. None of her household members have developed symptoms, but have nevertheless been referred for testing.

The table below gives an overview of the number of travelers currently arriving from South Africa and neighboring countries.

Number of average daily arrivals from selected countries in the period 1-25 November 2021

South Africa	66
South Africa, Namibia, Zimbabwe, Eswatini, Lesotho	74
All Southern African countries*	82

\*Includes also Botswana, Mozambique, Malawi and Zambia

#### Sources:

[New COVID-19 variant detected in South Africa - NICD](#); [‘The virus is always searching for its next move’: why science is alert to new variants | Financial Times \(ft.com\)](#); [WEEKLY EPIDEMIOLOGICAL BRIEF - NICD](#); [WEEKLY TESTING SUMMARY - NICD](#); @TWenseleers; presentation shared by Patrick Smits; ECDC presentation; [Africa Centres for Disease Control and Prevention’s Statement regarding the new SARS-COV-2 virus variant B.1.1.529 – Africa CDC](#); [Israel detects its first case of new, highly mutated COVID-19 strain | The Times of Israel](#); <https://www.gisaid.org/>

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