

**INTERNATIONAL OUTBREAKS OF IMPORTANCE**

## Emergence of a new SARS-CoV-2 lineage in South Africa

The Network for Genomics Surveillance in South Africa (NGS-SA), which includes the NICD, UKZN, UCT, SUN and UFS, has been monitoring changes in SARS-CoV-2, the virus which causes COVID-19, since March 2020. While SARS-CoV-2, like all viruses, mutates with time, between March and September 2020, this virus mutated at a relatively slow rate, as evidenced by over 2 000 sequences from across eight of the nine provinces.

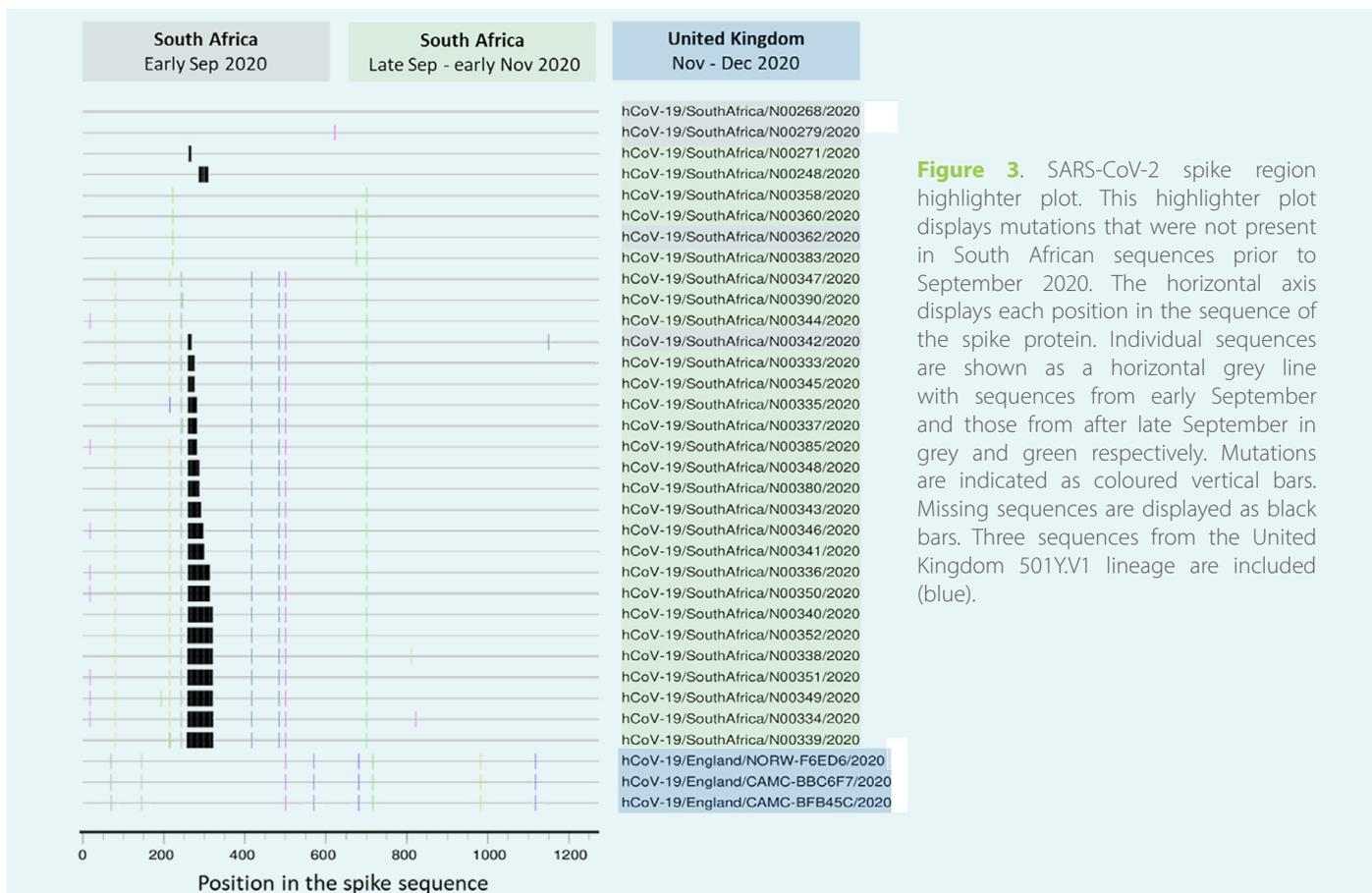
We have recently detected a new lineage, which is a group of mutated viruses of SARS-CoV-2 in the Eastern Cape, Western Cape and KwaZulu-Natal provinces. This lineage, named 501Y.V2, possesses between up to 20 mutations that were not previously seen in viruses from South Africa prior to September 2020. This lineage has been detected in 219 infections thus far from the three provinces mentioned previously. The spike region of this virus is under constant scrutiny, because it is used by the virus to infect human cells and is a target for neutralising antibodies. Figure 3 shows that between September and November 2020, eight lineage-defining mutations accumulated in the spike region of viral sequences in the Eastern Cape Province.

One of these spike mutations has been shown to increase binding to the human cell receptor, which could make it easier for the virus to cause infection. Two of these spike mutations reduce virus sensitivity to some antibodies, meaning that these

antibodies may not be as effective against this new mutated lineage compared to the previous lineage, which caused the initial wave of infections in South Africa. These mutations will not affect PCR testing sensitivity. The mutated lineage from the Eastern Cape Province has already been detected in 219 samples, using South Africa's current repertoire of real-time PCR tests. In addition, our tests typically detect at least two or three different SARS-CoV-2 gene targets, which serves as a backup in the case of a mutation arising in one.

Another lineage with a significant number of mutations across the genome and within the spike region has also been described in the United Kingdom (UK), and accounts for over 1 000 infections (Figure 3). The UK lineage, named 501Y.V1, is different from the South African lineage, with only one mutation, N501Y, common to both lineages.

We remain cautious about the implications of these mutations, until we perform the necessary experiments. However, we advise the public to remain vigilant and continue to follow COVID-19 protocol by wearing masks (which cover your nose, mouth and chin), washing or sanitising your hands and surfaces regularly, and keeping 1.5m distance from others as much as possible. These non-pharmaceutical interventions are still proven to prevent the spread of all SARS-CoV-2 viruses.



**Figure 3.** SARS-CoV-2 spike region highlighter plot. This highlighter plot displays mutations that were not present in South African sequences prior to September 2020. The horizontal axis displays each position in the sequence of the spike protein. Individual sequences are shown as a horizontal grey line with sequences from early September and those from after late September in grey and green respectively. Mutations are indicated as coloured vertical bars. Missing sequences are displayed as black bars. Three sequences from the United Kingdom 501Y.V1 lineage are included (blue).

Source: Centre for Respiratory Diseases and Meningitis, NICD-NHLS; cherylc@nicd.ac.za