

Study: SA variant could have emerged in E Cape after first wave

The Covid-19 strain, known as the South African variant, that became dominant in the country towards the end of 2020 may have emerged from the coast of the Eastern Cape after the first wave of pandemic.



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The rapid displacement of other SARS-CoV-2 lineages in multiple regions indicates that this variant has an advantage over these other strains, possibly owing to increased transmissibility and/or its ability to avoid the immune system a study published in [<https://www.nature.com/articles/s41586-021-03402-9> *Nature*.

Professor Carolyn Williamson from the University of Cape Town's (UCT) Division of Virology, National Health Laboratory Services (NHLS), and a lead member of Network for Genomic Surveillance in South Africa (NGS-SA), said the study was preceded by a call she received from Professor Tulio de Oliveira, head of NGS-SA. "He was worried as he had found a new variant with an unexpected number of mutations in the spike protein – a region included in most vaccines.

"At UCT, we rapidly sequenced viruses and found more than half the viruses transmitted in the Western Cape contained these mutations, and by December, this virus had essentially replaced the previously circulating variants. This rapid emergence suggested this variant was better at spreading, and subsequent data showed that it could also impact on vaccine efficacy," said Williamson.

The second wave of the SARS-CoV-2 epidemic in South Africa began around October 2020 and was notably rapid in parts of the Eastern Cape, Western Cape and KwaZulu-Natal, prompting an intensification of genomic surveillance.

Mutations

"A new SARS-CoV-2 variant (501Y.V2 / B.1.351) was identified by the NGS-SA through the analysis of 2 882 SARS-CoV-2 whole genomes from South Africa, collected between 5 March and 10 December 2020. The data suggested that the new variant emerged around August 2020 in Nelson Mandela Bay, becoming the dominant lineage in the Eastern Cape, Western Cape and KwaZulu-Natal by the end of 2020," she said.

Williamson noted that the 501Y.V2 variant is defined by eight mutations in its spike protein, which mediates cell entry. “One of these mutations, N501Y, is also present in a variant identified in the UK (B.1.1.7) and is associated with enhanced binding to the human ACE2 receptor. Another mutation, E484K, has been associated with resistance to neutralising antibodies. The distribution and spread of 501Y.V2, along with insights from genomic analysis, suggest that the variant may be more transmissible than other SARS-CoV-2 lineages. However, the full import of the mutations is not yet clear and requires further study,” she said.

Professor Koleka Mlisana, executive manager for academic affairs, research & quality assurance at the National Health Laboratory Service (NHLS) commented: “The NHLS laboratories played an important role in acting quickly in the discovery of the new variant as we could quickly sample 100s of health care facilities. We found that the NGS-SA allowed South Africa to quickly and accurately identify the 501Y.V2 variant. We now want to continue working together to expand this technology to other important pathogens in the country, such as HIV, TB, and Hepatitis virus.”

“This was the first paper that described the 501Y.V2 variant. Since the discovery of the variant, scientists in South Africa have worked relentlessly to advance the science,” said Professor de Oliveira, director of the Kwazulu-Natal Research Innovation and Sequencing Platform and lead of NGS-SA. “Novel results show that people recently infected with 501Y.V2 produce broad neutralising antibodies that neutralise 501Y.V2 and other variants. The focused and collaborative way that South African scientists worked so to understand this variant has been inspiring and exciting.”

Source: University of Cape Town

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