## EXPLAINED

Relevant for: Developmental Issues | Topic: Health & Sanitation and related issues

In remembrance: A person walks past the National Covid Memorial Wall, after new measures were announced yesterday due to the Omicron coronavirus variant, in London on November 28, 2021. | Photo Credit: <u>Reuters</u>

**The story so far:** A new lineage of SARS-CoV-2 has been identified in samples sequenced and deposited in public domain from Botswana, South Africa and Hong Kong and was assigned as B.1.1.529. The variant has been designated as a Variant of Concern (VoC) by the World Health Organisation (WHO) and has been named Omicron.

## Explained | What is the new coronavirus variant in South Africa?

The Omicron variant is interesting due to the fact that it has a large number of mutations compared to other prevalent variants circulating across the world. This includes 32 mutations in the spike protein. Many of these mutations lie in the receptor-binding domain of the spike protein, a key part of the protein required for binding to the human receptor proteins for entry into the cell, and thus may play an important role in recognition by antibodies generated due to a previous infection or by vaccines.

The variant was reported in South Africa and epidemiologically linked to a recent rise in cases in the Gauteng province of South Africa and has been identified among travellers from South Africa apart from other countries in the region.

Many of the mutations in the spike protein have been previously suggested to cause resistance to antibodies as well as increased transmission. Thus, there is a possibility that this variant could be more likely to reinfect people who have developed immunity against previous variants of the virus. While the behaviour of the virus is not accurately predictable based on the evidence on individual mutations, as the effect of the combination of mutations is not the sum total of individual mutations, such analysis can provide useful insights and directions to explore even further. Further in-depth analysis on the effect of these mutations on transmissibility and vaccine escape is underway.

From a diagnostic point of view, some of the mutations in the spike protein cause primers used in some of the RT-PCR kits to not function as expected. This is otherwise known as a spike gene dropout or spike gene target failure (SGTF). While most kits use multiple primer sets targeting different genes in SARS-CoV-2 RNA for diagnosis, this should not adversely affect the diagnosis, but can be used as a surrogate for quick identification of the variant. Nevertheless this approach is not specific to Omicron, as other variants could also have similar mutations which can cause a spike in gene dropout.

Some of the initial individuals identified to be infected with the variant have been vaccinated for COVID-19 and therefore the variant can indeed cause vaccine breakthrough infections. This should not be of concern, since the prevalent variants of concern including Delta have been shown to cause breakthrough infections. Whether the variant causes more breakthrough infections than Delta is not currently known.

As of date, nine countries have confirmed the presence of Omicron. This includes South Africa, Botswana, England, Hong Kong, Australia, Italy, Israel, Czech Republic, and Belgium.

Suspected cases are being followed up in a number of other countries. Countries have identified the variant through genomic surveillance programmes. The initial reports of the variant has been made possible through the tireless efforts of researchers in Botswana and South Africa as well as countries which reported infections in incoming travellers.

India has a national programme on genomic surveillance (INSACOG) as well as focussed surveillance programmes in Kerala, Maharashtra, Delhi and Karnataka, apart from independent research programmes. In INSACOG's latest Bulletin, none of the sequenced samples in India have the Omicron variant until date. Heightened surveillance of the variant is ongoing.

Enhanced surveillance and genome sequencing efforts are essential to detect and track the prevalence of the Omicron variant. Rapid sharing of genome sequences of the virus and the epidemiological data linked with it to publicly available databases will help in developing a better understanding of the variant. Existing public health and social measures need to be strengthened to control and prevent transmission.

Enhancing vaccination coverage across different regions along with access to testing, therapeutics and support will be essential for combating the new variant. Equitable access to vaccines would be key to controlling the Omicron variant, and slowing down the emergence of any future variants.

## Our code of editorial values

The extension was approved by the Central Drugs Standard Control Organisation

## END

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