

The Corona virus and its variants

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In news : COVID-19 was in the news for its mutations and variants

What is coronavirus?

Coronaviruses are a large family of viruses that cause illness ranging from the common cold to more severe diseases. A novel coronavirus (nCoV) is a new strain that has not been previously identified in humans.

COVID-19 is caused by infection with the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) virus strain

Coronavirus variants

The cases of infection with new variants of the coronavirus SARS-CoV-2 have been rising. Three of them are of particular concern, and were first detected respectively in the UK, South Africa and Brazil. **They are defined as variants of interest (VOIs).**

What is SARS-CoV-2 SARS-CoV-2 VOI?

According to WHO, A SARS-CoV-2 isolate is a VOI if:

- it is phenotypically changed (it has a different structure and properties) compared to a reference isolate, or has a genome with mutations that lead to amino acid changes associated with phenotypic implications; and
- it has been known to cause community transmission/multiple Covid-19 cases or has been detected in multiple countries.

Three types of phenotypic changes

WHO has specified three types of phenotypic changes associated with a VOI, they are:

1. Increase in transmissibility or detrimental change in Covid-19 epidemiology⁴
2. Increase in virulence or change in clinical disease presentation
3. Decrease in the effectiveness of available vaccines and treatment.

UK variant of Coronavirus:

Known as B.1.1.7 or VOC 202012/01, it first emerged in the UK last December. Compared to the reference, all three variants have shown changes in the spike protein, the part of the coronavirus that attaches to the human cell.

Multiple mutation of B.1.1.7

In this variant are multiple mutations in the spike protein:

- One mutation, called N501Y, makes the variant more effective at binding to the ACE2 receptor (the human protein that serves as the entry point for the coronavirus).
- Other significant spike protein mutations are D614G, A570D, P681H, H69/V70 deletion, and Y144 deletion.
- Public Health England has said these mutations have led to the virus becoming about 50% more infectious and spreading more easily.

Countries with UK variant

- According to the WHO, as of March 2, 106 countries across all six WHO regions have reported cases of this variant.
- Community transmission has been reported in at least 42 countries across four regions; transmission

classification is currently incomplete for 35 countries reporting this variant.

- India has 280 case of this variant

South African Variant:

- It was first detected in South Africa in October 2020.
- It is called 501Y.V2 or B.1.351 (and VOC 202012/02 in the UK)
- It is defined by nine changes in the spike protein in comparison to the reference the “Wuhan-1 D614G spike mutant” that previously dominated in South Africa.
- It is also considered highly transmissible.
- Concerns: The spike mutations could lead to antigenic changes that are detrimental to monoclonal antibody therapies and vaccine protection.
- A paper by Columbia University researchers, accepted for publication in Nature, has examined the loss of plasma’s neutralising activity against this variant
- It found the major contributor to the neutralisation resistance appears to be E484K (one of the mutations).
- Efficacy of vaccines: Both Novavax and Johnson & Johnson vaccines showed a substantial drop in efficacy in South Africa and efficacy of the Oxford-AstraZeneca vaccine against mild and moderate Covid-19 disease was 21.9% in participants in South Africa.

Countries with South African Variant

- According to WHO. as in February, 2021, this variant has now been reported from 56 countries across all six WHO regions.
- Community transmission has been reported in eight countries across three regions, and transmission classification is currently incomplete for 42 countries reporting this variant.
- In India: Only 11 cases of this variant have been detected during surveillance.

Variant from Brazil:

- It is called P.1, a branch of the B.1.1.28 lineage.
- It was first reported by the National Institute of Infectious Diseases in Japan in four travellers from Brazil, during routine screening at Tokyo airport.
- This variant is of concern as it shares some mutations with the South Africa variant, such as E484K and N501Y.
- As per USA's CDC, here is evidence to suggest that some of the mutations in this variant may affect its transmissibility or the ability of antibodies generated through previous infection or through vaccination to neutralise the virus.

Countries with this variant

- According to the WHO, this variant is reported in 29 countries across all six regions.
- Community transmission has been reported in at least three countries in one WHO region; transmission classification is currently incomplete for nine countries reporting this variant.
- In India: only one case of this variant has been detected.

What are the major concerns for India?

According to the Ministry of Health & Family Welfare, there is no scientific evidence to suggest that the recent surge in numbers is linked to these three variants.