Virus Variant - VUI 202012/01 - Transmissibility

Why in news?

- India suspended all flights from and to the UK until December 31, from 21 December 2020, amid concerns about a new variant of SARS-CoV-2 that is spreading and growing rapidly there.
- Several other countries, too, have suspended UK flights and imposed travel restrictions.

What is the new variant?

- The new SARS-CoV-2 variant was revealed to be the reason behind the rapid surge in Covid-19 cases in South and East England.
- It is being referred to as VUI-202012/01 (the first ‘variant under investigation’ in December 2020), or the B.1.1.7 lineage.
- The variant is the result of multiple mutations in the spike protein of the novel coronavirus SARS-CoV-2 as well as mutations in other genomic regions of the RNA virus.
- The variant was identified in genomic surveillance by COVID-19 Genomics UK (COG-UK).
    - It is a consortium that analyses genome sequencing data from the UK.
    - COG-UK is the largest contributor to the global Covid-19 database GISAID (Global Initiative on Sharing All Influenza Data).
- UK authorities have already notified the World Health Organization about the variant.

How significant are mutations?

- Whenever a virus replicates and circulates in a human population, mutations occur naturally.
- This occurs at a rate of around one to two mutations per month in the global phylogeny.
- In fact, for SARS-CoV-2, there are currently around 4,000 mutations in the spike protein.
- It is difficult to predict whether any given mutation is important when it first emerges, given the continuous emergence of new mutations.
- Understanding their significance may be possible based on experimental work that shows a link between the mutation and a subtle change in virus

biology.
- However, it would take considerable time and effort to test the effect of many thousands of combinations of mutations.

What is the case with VUI 202012/01?

- The VUI-202012/01 has 23 mutations in all.
- A few of these are seen in the region of the virus that binds to the human receptor.
- However, a single mutation has been found to increase the binding affinity, making the variant more transmissible.
- COG-UK identified this mutation as “N501Y”, in an area of the spike protein that binds to a key protein in the human cell, the ACE2 receptor.
- The location of the mutations in the receptor-binding domain of the spike glycoprotein raises the possibility that this variant is antigenically distinct from prior variants.
- This was an indication that the alterations may, theoretically, result in the virus becoming more infectious.
- Mutations in the spike protein, the part of the virus that makes it infectious, can change how the virus interacts with human cells.

Why is this notable?

- SARS-CoV-2 being an RNA virus tends to have a higher mutation rate.
- But the presence of 23 mutations strongly suggests that the variant has not emerged through gradual accumulation of mutations.
- According to COG-UK, it is probably due to prolonged infection in a single patient, potentially with reduced immunocompetence.

What is the imminent threat with transmissibility?

- Public Health England (PHE) said data from whole-genome sequencing, epidemiology and modelling suggests that the new variant “transmits more easily than other strains”.
- However, it also emphasised that there is “no evidence” that the variant is more likely to cause severe disease or mortality.
- The variant has the potential to increase by over 0.4 the number of people a person can infect.
- There is “currently insufficient data to draw any conclusion” on the underlying mechanism of increased transmissibility, the age distribution of cases and disease severity.
- Continuing investigations are thus on to understand things better.
- PHE said that mortality was a “lagging indicator” and it would continually

monitor this in the following weeks.
- The cluster differs by 29 nucleotide substitutions from the original Wuhan strain.
- Three sequences from Denmark and one from Australia, from samples collected in November 2020, cluster with the UK variant.
- This most likely indicates that international spread has occurred, although the extent remains unknown.
- Since far fewer SARS-CoV-2 genomes are sequenced at regular intervals in India, it is unclear if the variant is already present here.

Will this affect vaccination processes?

- It is unlikely that the mutations would make the COVID vaccines that have secured emergency use approval and the ones in final stages of testing less effective.
- This is because vaccines produce antibodies against many regions of the spike protein.
- Also, there is the T-cell immunity that would come into play to clear the virus.
- However, as the virus accumulates more mutations, there is a possibility that vaccines might require minor tweaking.
- The emergence of the new variant underlines the compulsion to undertake surveillance following vaccination to track vaccine effectiveness.
- Appearance of vaccine-escape mutants has to be looked for.
- The emergence of the new variant with increased transmissibility is one more reason for strict adherence to non-pharmaceutical interventions.

Source: The Indian Express, The Hindu