



## B.1.617: Indian Double Mutant Strain

### Why in News

The [‘double mutant’](#) virus that is having a bearing on the spread of the pandemic in India, has been formally classified as **B.1.617**.

- **Mutation** is an alteration in the genetic material (the genome) of a cell of a living organism or of a virus that is more or less permanent and that can be transmitted to the cell’s or the virus’s descendants.

### Key Points

- **Double Mutant (B.1.617):**
  - Earlier Genome sequencing of a section of virus samples by the **Indian SARS-CoV-2 Consortium on Genomics (INSACOG)**, revealed the presence of two mutations, **E484Q and L452R**.
    - Though these mutations have individually been found in several countries, the **presence of both these mutations together** have been first found in coronavirus genomes from India.
  - This double mutant from India has been scientifically named as **B.1.167**. However, it is yet to be classified as **‘Variant of Concern’**.
  - Till now only three global ‘Variants of Concern’ have been identified: the [U.K. variant \(B.1.1.7\)](#), [the South African \(B.1.351\)](#) and the [Brazilian \(P.1\) lineage](#).
- **Spread of B.1.617:** According to the INSACOG, sequencing a sample of genomes from coronavirus patients in India, **B.1.617 was first detected in India** in December, 2020.
  - Today, nearly **70% of the genome sequences** with the mutations **characterising B.1.617 are from India**.
  - This is followed by the **United Kingdom (23%), Singapore (2%) and Australia (1%)**.

### Variant of Concern

- These are variants for which there is evidence of an increase in transmissibility, more severe disease (increased hospitalizations or deaths), significant reduction in neutralization by antibodies generated during previous infection or vaccination, reduced effectiveness of treatments or vaccines, or diagnostic detection failures.
- **Issues Associated with Mutants:**
  - Mutant virus is **associated with large spikes** of Covid-19 cases in some countries.
  - It enables **viruses to become more infectious** as well as **evade antibodies**.
  - It has also been associated with a **reduction in vaccine efficacy**. International studies have shown reduced efficacy of vaccines particularly those by Pfizer, Moderna and Novavax to certain variants.
    - However, the vaccines continue to be significantly protective in spite of this.
- **Another Mutation:**
  - According to INSACOG, there is also a **third significant mutation, P614R** other than the two mutations (E484Q and L452R).

- All three concerning **mutations are on the spike protein**. The spike protein is the part of the virus that it uses to penetrate human cells.
  - Virus' spike protein may increase the risks and allow the virus to escape the immune system.
- **Resistant to T cells:**
  - **L452R** could even make the coronavirus resistant to T cells, that is the class of cells necessary to target and destroy virus-infected cells.
    - T cells are different from antibodies that are useful in blocking coronavirus particles and preventing it from proliferating.

## T Cells

- A type of white blood cell that is of **key importance to the immune system** and is at **the core of adaptive immunity**.
- It creates the body's immune response to specific pathogens.
- The T cells are like soldiers who search out and destroy the targeted invader.

## Indian SARS-CoV-2 Consortium on Genomics

- Indian SARS-CoV-2 Consortium on Genomics (INSACOG) is a **multi-laboratory, multi-agency, pan-India network to monitor genomic variations in the SARS-CoV-2**.
- It helps in the understanding of how the virus spreads and evolves.
- Genomic surveillance can generate a rich source of information for tracking pathogen transmission and evolution on both national and international levels.

[Source: TH](#)

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