

Indian 'double mutant' strain named B.1.617

April 9, 2021

In News: The 'double mutant' virus that scientists had flagged last month as having a bearing on the spread of the pandemic in India, has a formal scientific classification: B.1.617.

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- The variant is common in India – how much in every state though is unclear – and has a couple of defining mutations, E484Q and L425R, that enable them to become more infectious as well as evade antibodies.
- Though these mutations have individually been found in several other coronavirus variants, the presence of both these mutations together have been first found in some coronavirus genomes from India.
- Certain variants of the coronavirus, for instance, B.1.1.7 and B.1.351 – have been termed the 'United Kingdom' and 'South Africa' variant respectively because they have mutations associated with large spikes in these countries or reduce the efficacy of vaccines and are termed 'Variants of Concern (VOC)'.

Not yet of concern

- Sample of genomes from coronavirus patients in India, B.1.617 was first detected in India on December 7, 2020
- Though now present in at least eight countries, nearly 70% of the genome sequences that have the mutations characterising B.1.617 and submitted to the global database GISAID (Global Initiative on Sharing Avian Influenza Data) are from India. This is followed by the United Kingdom (23%), Singapore (2%) and Australia (1%)
- It is worrying because the mutations E484Q and L452R are linked to increased infectivity.

- It's been linked to 20% of the cases in Maharashtra but we have to also see the role of the variant (from further genome studies) in say West Bengal, Uttar Pradesh where there are massive crowds from elections, the Kumbh Mela

Resistant to T cells

- L452R, some studies show, could even make the coronavirus resistant to T cells, that is the class of cells necessary to target and destroy virus-infected cells.
- They are different from antibodies that are useful in blocking coronavirus particles and preventing it from proliferating.

Global Initiative on Sharing Avian Influenza Data

- It is a public platform started by the WHO in 2008 for countries to share genome sequences.
- Created as an alternative to the public domain sharing model, GISAID's sharing mechanism took into account the concerns of Member States by providing a publicly accessible database designed by scientist for scientist, to improve the sharing of influenza data.
- In 2010 the Federal Republic of Germany became the official host of the GISAID platform.
- In 2013 the European Commission recognized GISAID as a research organization and partner in the PREDEMICS consortium, a project on the Preparedness, Prediction and the Prevention of Emerging Zoonotic Viruses with Pandemic Potential using multidisciplinary approaches.
- GISAID's database access agreement ensures that contributors of genetic sequence data do not forfeit their intellectual property rights to the data.