

'DOUBLE MUTANT' STRAIN NAMED B.1.617

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Genome study:The B.1.617 strain of the novel coronavirus was first detected on December 7, 2020.AP

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.

The variant is common in India — how much in every State is unclear though — and has a couple of defining mutations, E484Q and L425R, that enable it to become more infectious and evade antibodies.

Though these mutations have individually been found in several other coronavirus variants, the presence of both mutations together were 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)”.

According to a note from the INSACOG, the consortium of laboratories that is sequencing a sample of genomes from COVID-19 patients in India, B.1.617 was first detected 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%).

“That suggests that this variant is fairly common in India. 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 and Uttar Pradesh where there are massive crowds from elections and the Kumbh Mela [respectively],” said Shahid Jameel, virologist and Director, Trivedi School of Biosciences, Ashoka University.

An explainer note by the INSACOG on the significance of the mutations says that it has as many as 15 “lineage defining mutations”. Other than the two mutations, there is a third significant mutation, P614R. All three concerning mutations are on the spike protein, the operative part of the coronavirus that binds to receptor cells of the body.

Resistant to T cells

L452R, some studies show, could even make the coronavirus resistant to T cells, a class of cells necessary to target and destroy virus-infected cells.

India has not yet conducted studies on how vaccine efficacy is influenced by variants, except for limited laboratory trials, but 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.

So far, only three global VOCs have been identified: the U.K. variant, the South African and the

Brazilian (P.1) lineage. Of the 10,787 samples from international passengers, 771 instances of these VOCs have been identified in 18 States of the country, according to a statement from the Health Ministry in March.

A scientist associated with the INSACOG said vaccine makers should now be accounting for the variations in the spike protein in designing future vaccine.

“That’s the real purpose of genomic analysis. To design appropriate vaccines but so far there are hardly such studies out of India,” the scientist pointed out.

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