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SCIENTISTS FIND SECOND MOST COMMON CORONAVIRUS TYPE IN INDIA

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The A2a type has emerged dominant the world over. | Photo Credit: Getty Images

Scientists at multiple CSIR laboratories have identified a coronavirus type that maybe the second most prevalent in India and may comprise 3.5% of the genomes globally.

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The most dominant coronavirus clade in India is the A2a and of 213 genomes analysed by the group, 62% of them were A2a. The newly identified, that the scientists have christened A3i, comprised 41% of those analysed. With the new clade, there are 11 SARS-CoV-2 types identified globally with at least six of them identified in India.

The coronavirus type, or clade, is a cluster of SARS-CoV-2 viruses that share evolutionary similarities and are grouped together based on characteristic mutations or similarities in parts of their genomes.

Such classifications are useful in establishing whether certain strains are particularly virulent, spread more easily, how they are likely to evolve over time and whether some could be less vulnerable to certain kinds of vaccines.

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Previous studies have shown that while type O was the first ancestral family of the virus identified from China, it’s the A2a type — that has emerged dominant the world over because of a mutation in its genes that allow that coronavirus’ spike to more efficiently infiltrate the lungs.

“Epidemiological assessments suggest that the common ancestor [of this subtype of viruses] emerged in the month of February 2020 and possibly resulted in an outbreak followed by countrywide spread,” say the scientists from the CSIR-Centre for Cellular and Molecular Biology and the CSIR-Institute of Genomics and Integrative Biology in their paper that’s not yet peer-reviewed but available on the bioRxiv pre-print server for scientific criticism.

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“While we rely on samples from the State authorities, it appears that this originated from a person in Telangana who had travelled from Indonesia, Singapore or some place in South-East Asia,” Rakesh Mishra, Director, CSIR-CCMB, and one of the authors of the study, told *The Hindu*.

The A2i type, once it took root, became the dominant clade in Telangana and also Tamil Nadu, Maharashtra, and Delhi, three States that are among those that, as of Tuesday, collectively account for a little over 1,00,000 cases. India now has close to 1,90,000 confirmed infections.

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So far, there is no evidence of whether A3i is more virulent — that is, it’s linked to more deaths.

“It is too early to comment about the virulence right now. We are in the process of acquiring more data, and we’ll have more clarity on this when that data get analysed. This should be in a couple of weeks,” Divya Tej Sowpati, a co-author and a scientist at the CCMB, told *The Hindu* in an email.

“The A3i clade stood out from other clades due to differences at four different places in its sequence. Also, our analyses suggest that the A3i clade mutates slowly compared to the A2a clade [the other prevalent clade in Inda]. This is often disadvantageous for the virus, but more data [and time] is needed to see if this is actually the case,” he added.

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