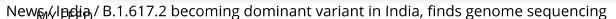


HOME

SCIENCE







B.1.617.2 becoming dominant variant in India, finds genome sequencing

Expants in genomic sequencing of Covid-19 variants in India have revealed cases showing B.1.617.2 are slowly eclipsing most variants including the Kent variant TECH that originated in UK (known as B.1.1.7).













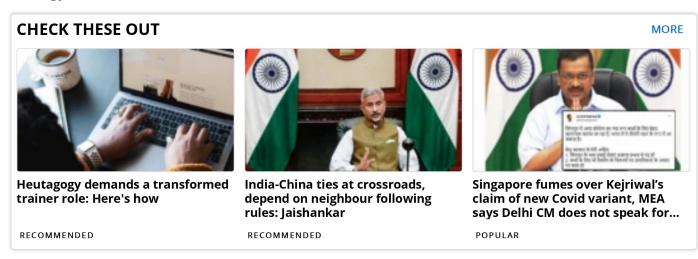
[REPRESENTATIVE IMAGE] File photo of a genome sequencing laboratory in New Delhi. (Photo: PTI)

he United Kingdom has been closely watching the movement of the sub-lineages

In Kerala, Andhra Pradesh, Telangana and Karnataka, the B1.617.2 sub-lineage has almost taken over many cases that are being reported. Uttar Pradesh, Delhi, Gujarat, Maharashtra, Puducherry, Bihar are also showing more cases from this new sub-lineage.

"If 100 samples are being genome sequenced, at least 25-30 samples have the B.1617.2 variant," said a genome sequencing expert in Hyderabad. There is at least a 25-30 per cent chance of having this variant in cases in India.

"B.1.617.2 is the predominant lineage in the recent months. At least in Kerala from the recent analysis done, B.1.617.2 is the predominant sub-lineage in many districts in Kerala. In fact, the present wave during April and May months seems to be because of this variant," said Dr Vinod Scaria, Scientist at CSIR-Institute of Genomics & Integrative Biology (IGIB) in India.



B.1.617.2: A CONCERN FOR THE UK?

As of May, the strain has already reached 48 countries. The British media reported that UK's Prime Minister Boris Johnson was "anxious" about the variant. Some experts also recommended a pause in the planned lifting of restrictions in Britain.

Experts said the variant is 40-50% more transmissible as much as the original parent

OF UTB VARIABLE WITH A CUITIVIATIVE PLEVAIENCE OF 1970 UII MAY 7, 2021.

In the UK, this variant has spread rapidly, showing the highest -- 4,314 total sequences detected, but the cumulative prevalence rate is less than in India, at 6% as of 16 May 2021. (Apparent cumulative prevalence is the ratio of the sequences containing B.1.617.2 to all sequences collected since the identification of B.1.617.2 in that location,) states outbreak.info.

In the United States, 821 sequences show this variant with a small cumulative prevalence of 0.5% till May 17, 2021.

B.1.617.2 EVADING VACCINES?

Experts suggest that it is not complete evasion but lower protection if large populations have only received the first dose of a corona virus vaccine. "With two doses of Covishield, there is about 7% reduction against B1.617.2 as compared to B.1.1.7 in early reports. With one dose there is a more substantial reduction in protection, but it would be important to look at the data in detail to understand what needs to be considered for dosing schedules," said Dr Gagandeep Kang, one of India's leading virologists.

On May 22, the UK government announced, "Vaccine effectiveness against symptomatic disease from the B.1.617.2 variant is similar after two doses compared to the B.1.1.7 (Kent) variant dominant in the UK, and we expect to see even higher levels of effectiveness against hospitalisation and death."

The study found that, for the period from 5 April to 16 May, the Pfizer-BioNTech vaccine was 88% effective against symptomatic disease from the B.1.617.2 variant two

"The UK government feels that the population should also receive the second dose more protection is only possible from taking two doses," said Dr Raman Gangakhedkar, the country's leading expert in epidemiology and former head of epidemiology at the ICMR.

Dr Mary Ramsay, Head of Immunisation at PHE, said: "This study provides reassurance that two doses of either vaccine offer high levels of protection against symptomatic disease from the B.1.617.2 variant."

The analysis included data for all age groups from April 5 to cover the period since the B.1.617.2 variant emerged. It included 1,054 people confirmed as having the B.1.617.2 variant through genomic sequencing, including participants of several ethnicities. Data published on May 20 for vaccine effectiveness covered the period since December for those aged over 65.

HOW SEVERE COULD B.1.617.2 BE?

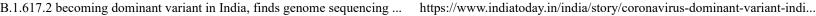
"As with other variants, even higher levels of effectiveness are expected against hospitalisation and death. There are currently insufficient cases and follow-up periods to estimate vaccine effectiveness against severe outcomes from the B.1.617.2 variant. PHE will continue to evaluate this over the coming weeks," the UK government said.

India did 2,902 total sequences for B.1617.2 lineages and of these, India did just 118 samples in the last four weeks. The growth rate is projected at 67%. "118 is too small a number in a country of over a billion people to check for the prevalence rate of the variant. When we see more than 3,000 sequenced data done by the UK, that is a large number. We need more data to see the real picture," said Dr Rajeev Jayadevan, India's top scientific advisor and past president IMA, Kochi, Kerala.

According to GISAID, India has shared 14,063 sequences when the total number of reported cases is 26,289,290, which is only 0.0535% of the Covid-19 cases genome sequenced since January 10, 2020. In the last month, India has shared 264 genome sequences of 10,358,325 cases reported, which comes up to 0.003% of the cases genome sequenced.

The government's Indian SARS-CoV-2 Genome Sequencing Consortia (INSACOG) states that only about 50% of the data has been uploaded to GISAID, as if the data doesn't meet the minimal quality standards, then it cannot be deposited.



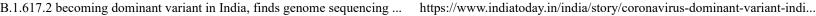


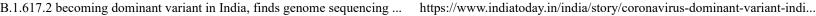
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