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Maharashtra says no worrying mutations but geneticists question sampling method

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MUMBAI: State health officials on Saturday said genome sequencing conducted on 52 Covid-19 samples had not shown any particular mutation that could have led to the sudden surge in Covid-19 cases in Maharashtra.

Experts, though, fear the state's method of drawing samples randomly is a problem and that it isn't scientific enough to draw the right conclusions.

On Saturday, state health services director Dr Archana Patil told TOI that 52 samples tested by the National Institute of Virology in Pune had not found any predominant mutation in the SARS-CoV-2 virus that was triggering the present surge in cases in the state.
Dr Nerges Mistry of the Foundation for Medical Research (FMR), though, questioned the state's decision to randomly select Covid-19-positive samples for genome sequencing.

Earlier in February, as cases rose in Amravati and Yavatmal, samples were randomly selected for whole genome sequencing; the results showed mutations that had been in circulation in India for a few months.

"Cluster-based sampling will provide a more robust picture," said Dr Mistry, who was the first to discover totally drug-resistant TB strains in circulation in Mumbai more than a decade ago.

For example, 229 students and teachers from a school in Washim district should be looked at as a super-spreader event that led to a cluster. “We need to pick up 80% of these samples for genome sequencing and then relate the findings with epidemiological tracking of affecting persons,” she said.

Genome sequencing hasn’t been widely used in India, with around 6,000 out of the 1.1 crore Covid-19 cases sequenced so far. “That is only 0.054%,” said Dr Kayzad Nilgiriwala who specializes in whole genome sequencing.

He said while all viruses mutate, the Covid-19 situation in the state pointed to two possibilities vis-a-vis the theory that variants are the cause for the surge. “The surge could have been caused by an influx of external (from foreign countries) variants or it could be the occurrence of new mutations within Indian viral strains,” he said.

To be able to analyse to such an extent, India should have conducted studies to identify a standard Indian viral strain. “One of the main problems in India is most samples are still tested against the Wuhan strain that caused the pandemic in 2019,” said Dr Nilgiriwala. Dr Mistry concurred it is time to identify a standard Indian viral strain to understand the evolution of Indian variants.

In districts such as Amravati, where the surge was first noticed, the state should have picked up between 1,000 and 1,500 samples for whole genome sequencing to get the right answer.