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B.1.617 mutation found in 1/3rd samples from Mumbai

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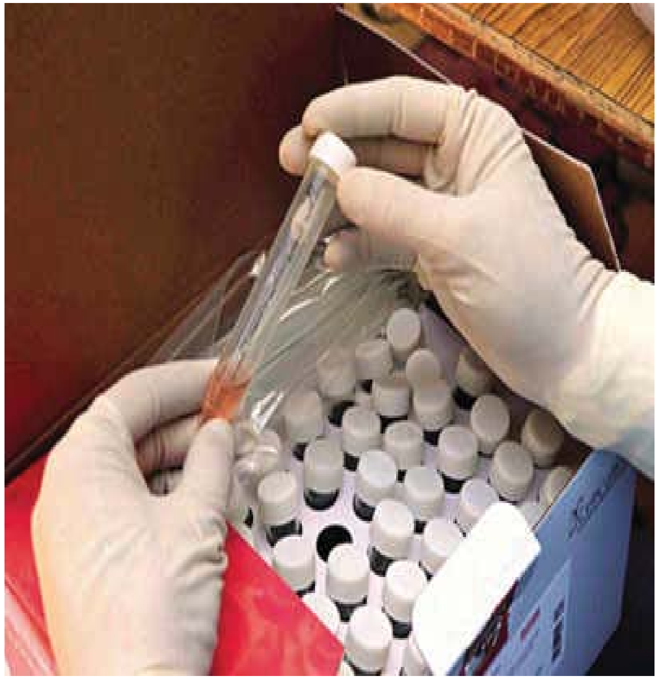

MUMBAI: The B.1.617 variant of the Covid-causing SARS-CoV-2 virus is in circulation in Mumbai and was found in at least a third of the samples from the city reported online recently. While the Union government hasn't yet given city-specific data on B.1.617 and its sub-lineages—which were labelled as variants of concern (VoC) by World Health Organisation—data from global initiatives such as GISAID confirm the presence of B.1.617's three sub-lineages 1, 2 and 3 in Mumbai and surrounding cities. (The B.1.617 was first detected in Covid-positive samples collected for genome sequencing from Maharashtra's Vidarbha region and has since been found in 44 other countries.)

GISAID is a collaboration among scientists and enables them to share genetic sequencing data related to Covid-19 in a freely accessible database. While not all scientists may upload data on GISAID, it gives a fair idea of variants in circulation in various parts of the world.The GISAID data, shared by Foundation for Medical Research director Dr Nerges Mistry, showed that of the 165 samples sequenced from Mumbai, B.1.617.1 was found in 51 samples (31%) and the other two sub-lineages were found in 2 and 1 samples respectively. Officially, however, there is no word on the variant’s presence in Mumbai; foreign scientists have, meanwhile, linked the emergence of the B.1.617 variants with the second wave.

When contacted, BMC additional municipal commissioner Suresh Kakani said the central government had not shared information about the detection of B.1.617 in Mumbai (every week, samples are sent from Mumbai to National Institute of Virology for genetic sequencing). The state task force on Covid-19 held a briefing on genomic sequencing for its members on Monday.

GISAID data for Maharashtra showed that of 3,882 samples sequenced, the B.1.617.1 variant was found in 24% samples. Across the country, 10% of the 15,282 samples had B.1.617.1 while the other sub-lineages accounted for 1,255 (8%) and 77 (1%).

The breakup is of significance because the Centre—despite having set up a consortium of 10 laboratories called INSACOG for gene sequencing—has so far given out only broad figures. On Monday, Union health minister Harsh Vardhan said B.1.617 has become the dominating Covid-19 variant in India, accounting for 55% of all variants of concern detected in India through genome sequencing so far.

He said 25,739 Covid-positive samples were sequenced by INSACOG till Monday morning. Of these, 9,508 had VoC and the B.1.617 variant was found in 5,261 samples, making it the most common mutation till now.

Dr Mistry, who found the B.1.617 sub-lineage 3 in a couple of samples sequenced in her Worli lab, said sequencing is important for public health measures. “We can find out which cluster has variants and plan accordingly,” she said.

She said Mumbai/India could start sequencing from waste water samples. ``We cannot always take samples from individuals, but we could take samples from toilets in hospitals, homes, water treatment plant to find the variants in circulation,’’ said Dr Mistry. One of the most important uses of surveillance is to get information for vaccines. ``We have to start getting information for preparation of second generation Covid vaccine,'' she added.