CORONAVIRUS: WHAT ARE VARIANTS OF CONCERN?

Relevant for: Developmental Issues | Topic: Health & Sanitation and related issues

Keeping track: Detecting variants relies on whole genome sequencing. Globally, over 1 million SARS CoV-2 genomes have been sequenced to date. | Photo Credit: <u>matejmo</u>

If manuscripts are copied by hand repeatedly, spelling errors are common. Similarly, when 'genetic scripts' encoded in DNA or RNA are copied repeatedly for virus replication, errors do occur. RNA viruses are more error-prone than DNA viruses. SARS-CoV-2 genome is single-stranded RNA, and errors — in biology, mutations — occur frequently.

SARS-CoV-2 is new in humans and as it spreads, mutations are very frequent. Emerging variants with higher transmission efficiency become dominant, tending to replace others. Such frontrunners emerge in different geographic communities where the virus is epidemic, spreading widely. Variants were detected in the U.K. and South Africa because genetic studies were systematically done. Brazil variant was discovered in Japan, in travellers from Brazil, and its origin traced back.

The ability to detect and track variants hinges on laboratory capacity for whole genome sequencing of viruses. Globally, over 1 million SARS CoV-2 genomes have been sequenced todate, providing a high resolution, spatio-temporally granular readout of virus evolution. More importantly, this has allowed the identification and documentation of variant viruses with altered properties compared to the virus that started the pandemic. As the importance of 'variants of concern' (VOC) was appreciated, the Indian SARS CoV-2 Genomic Consortium (INSACOG), a network of ten competent public-sector laboratories for genomic surveillance, was established, and the genetic variant landscape is being surveyed in India.

There are three different schemes of nomenclature of SARS-CoV-2 variants. The widely used one is the 'Phylogenetic Assignment of Global Outbreak Lineages' (PANGOLIN) that uses a hierarchical system based on genetic relatedness – an invaluable tool for genomic surveillance. It uses alphabets (A, B, C, P) and numerals starting with 1. Variant lineages are at the emerging edge of the pandemic in different geographies. Lineage B is the most prolific. The variants in circulation are B.1; B.1.1; B.1.1.7; B.1.167; B.1.17; B.1.351, B.1.427 and B.1.429. Lineage P.1 has deviated from the original B.

For convenience, the three most frequent ones are named by their geography of origin — 'U.K. variant' for B.1.1.7; 'South Africa variant' for B.1.351; and 'Brazil variant' for P.1. They had been detected in 2020 — September (U.K.), October (South Africa) and December (Brazil). Variants in India include the so-called double mutant B.1.617 spreading in Maharashtra and B.1.618 spreading in West Bengal.

Mutations can be pinpointed using the nucleotide position on the genome and the switched amino acids consequent to mutation. The original pandemic virus (founder variant) was Wu.Hu.1 (Wuhan virus). In a few months, variant D614G emerged and became globally dominant.

The 'concern' in VOC comprises three sinister properties – transmission efficiency, disease severity and escape from immunity cover of vaccination.

In many countries, including India, the VOC, by virtue of increased transmissibility, have kicked off new wave(s) of epidemic transmission. Unfortunately, at that precise time, as case counts were low, there was widespread relaxation of COVID-appropriate behaviour. Together, this has

contributed to a rapidly ascending second wave — daily numbers far exceeding those during the earlier wave.

Regarding virulence (propensity to cause severe/life-threatening disease), the U.K. variant is worse. The South Africa and Brazil variants do not seem to have higher virulence.

The third concern is regarding the immunity cover offered by vaccination using antigens made from D614G variant — which applies to most vaccines in current use. Lowered efficacy of vaccines was found more with the South African and less with the Brazil variant. Hence, reinfection can occur in spite of immunity by earlier D614G infection or vaccination. Vaccine efficacy may be lower now than what was determined in phase-3 trials as VOC were not then widely prevalent. Fortunately, mRNA (Pfizer and Moderna) vaccines have broader immunity for different reasons, and they protect better against these two variants.

Karolinska Institute in Sweden created an antigen using new variant RBD peptide with adjuvant, and inoculated monkeys already primed with an older vaccine. The resultant booster response was not only high but also broad, covering new variants. This approach, called 'hetero boosting' by a different vaccine, offers a way to manage the 'vaccine-escape' variants until newer vaccines become available.

An important lesson the pandemic has taught us in India is the critical importance of biomedical research and capacity building – for saving lives and economic growth. We need a foundation of broad-based research, in universities, medical colleges and biotechnology companies, all of which must be funded, encouraged, appreciated, and talent rewarded. While some endeavours have been initiated, they must take off in a big way, and India must invest heavily in biosciences. After a decade, its products and profit will make us healthier and wealthier.

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The Hindu's Political Editor Nistula Hebbar speaks about the recent announcements by vaccine manufacturers about the differential pricing of the COVID-19 vaccines

Systemic effects included headache, fatigue, chills and shiver, diarrhoea, fever, arthralgia, myalgia, and nausea.

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