**The new variants of coronavirus**

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The covid-19 infection has been threatening the world for the past year. First the front-line workers, and now the older population of India, are being vaccinated to curb the infection. Alongside, there is a rapid spread of new *variants* of coronavirus, alarming researchers, health organizations and the general public. This is concerning because the new variants spread faster than the previous virus, which means more people would likely get infected and lead to the next pandemic. It also raises the question of whether the vaccines currently being administrated will control the infection.

*What is the coronavirus structure?*

Viruses have very simple geometrical structure. They contain the genetic material (which may be DNA or RNA) surrounded by a protein coat called capsid. Some larger ones have an additional outer coat called an envelope. All viruses have a protein coating or capsid, but some viruses, such as the flu virus, have an additional envelope made of **lipids** (fats). Viruses without this extra membrane are called *naked* *viruses*. The presence or absence of an envelope is an important determining factor in how a virus interacts with the host's membrane, how it enters a host, and how it exits the host after maturation. The novel SARS-Coronavirus-2, for instance, has an envelope. At some point, caused by an unknown trigger, the virus becomes active and causes the disease. More details about the Sars-Cov-2 virus were discussed in last year’s Mar-Apr issue of JM. Other viruses were discussed in last year’s May-June issue.

The key structure of the virus is its spiked appearance (see picture) which helps the virus invade the human host cells and cause the Covid-19 disease. These are made of proteins and give the virus a crown-like appearance so they are called “corona viruses”. These spikes bind to cells in humans and help the virus release its genetic material to infect them.

*What is the coronavirus variant?*

**Genetic mutations** are common in all viruses. In general, RNA viruses mutate faster than DNA viruses and the coronavirus (named SARS-CoV-2) is a positive-sense single-stranded RNA virus. The GISAID, a global science initiative, continually monitors the spread of infectious viruses and genetic mutations acquired in their genomes. This organization's survey reports that several mutations have occurred in the coronavirus since the outbreak of Covid-19. Most of them do not cause any significant effects. However, some mutations can have serious consequences depending on where they occur in the genome.

If the virus acquires several mutations that lead to changes in its immunological response, it becomes a new strain. For example, SARS-CoV-2 and SARS-CoV-1 are different strains of the coronavirus family. On the other hand, a variant of the virus results from a small number of mutations with no significant effect on the immunological response. Notably, in the last mid-year, the D614G mutation has resulted in a new variant.

Many new variants of coronavirus have now emerged from various parts of the world. Such variants evolve through mutations from the previous virus in persons who suffered from long-term infection.

*What is the effect of mutations in the spike protein?*

Spike protein interacts directly with the human *ACE2* protein, thereby allows the virus to enter human cells. ACE2 is a protein that is found on the surface of many cell types such as in the lungs, heart, digestive system, etc. It is an enzyme that generates small proteins that are important to regulate different kind of cell functions and processes such as blood pressure, wound healing and inflammation. Since the spike protein facilitates the primary step for viral infection, this protein has been used to design vaccines.

*How do vaccines work?*

When a virus (called antigen) enters our system, the body produces anti-bodies to fight these viruses. It also creates memory cells that produce anti-bodies the next time the virus invades our body, so that we are protected against it. Vaccines stimulate this process: they contain weakened or inactive parts of an antigen that triggers an immune response within the body.

*Variants and vaccine efficacy*

Variants containing mutations (alterations or changes) in the spike protein have the potential of cheating the human host into not recognising the virus and hence delaying the anti-body response. This thus alters the on-going pandemic and causing reinfection.

A widely spoken coronavirus B.1.1.7 (or alpha variant ) contains eight mutations in the spike protein. This variant, which was first identified in the UK, has now spread to more than eighty countries, including India.

*Reproductive rate*

If an infected person infects four anothers, the reproductive rate is said to be four. Typically, the virus's reproductive rate should be less than one to show a decline in the infection because this will mean that there are fewer people getting newly infected. However, the reproduction rate of the B.1.1.7 variant is 1.2-1.3, which means that the number of infections caused by this virus is likely to increase.

*Variants of concern*

The spike protein contains more than a thousand amino acids (1273 aa). According to preliminary research, amino acid change at 501st position in the spike protein i.e., N501Y mutation, allows the variant to spread 30-50% faster than the previous virus. Besides, seven other mutations (A570D, P681H, T716I, S982A, D1118H and deletion of H69-V70 and Y144) may contribute to the rapid spread of this variant. The graphic shows the important variants that are driving the spread of the disease and the location of the mutations/deletions on the SARS-COV2 genome.

The B.1.351 (or beta) variant, originated in South Africa, contains the same N501Y mutation along with two addition mutations E484K and K417N, in the spike protein. New research shows that this variant binds more tightly to the human ACE2 protein than the original virus. As the B.1.351 variant harbours more mutations than the B.1.1.7 variant, it is predicted to be more vulnerable.

Parallelly, the emergence of other new variants in Nigeria and Brazil has been reported to be predominant. The Brazilian variant (called gamma) has already been observed in the USA and UK and was responsible for a large increase in infection in the city of Manaus in Brazil.

In the case of India, 19 variants of coronaviruses have been identified. Specifically, a new variant with N440K mutation has recently emerged in Amravati, Yavatmal, and Akola in Maharashtra and shows enhanced infectivity. It was listed as the B.1.617, but the variant B.1.617.2 (called delta) is considered to be highly contagious and is majorly responsible for the very severe second wave in India that has cost so many lives. Currently it is the dominant variant spreading in the UK and the rest of the world since it is 40% more transmissible than the alpha variant.

*Variants vs. current vaccines*

Vaccines are biomolecular entities that mimic elements of the infecting virus. They raise antibodies against the virus in humans upon administration. Most vaccines that are currently being used mimic the spike protein of the virus. Antibodies induced by such vaccines specifically bind to the spike protein protruding from the infecting viral surface and induce immune responses to kill the virus.

Since the vaccines were designed based on the spike protein of the original virus, mutations in spike protein, especially at the ACE2 binding region, may affect its interaction with antibodies. Nonetheless, spike protein has a large surface in which mutations have thus far been observed in a small region. Also, antibodies use several regions that have not been affected by mutations. Therefore, vaccine developers and researchers believe that currently available vaccines would potentially work against these new variants. Indeed, new results report the successful actions of existing vaccines.

It should be cautioned, however, that constant evolution of the coronavirus may lead to more mutations in the spike protein. As a consequence, the activity of the antibodies induced by these vaccines may decrease. Moreover, if these vaccines are given to only a small population, there is a risk of variants evolving against them.

*How to deal with the virus mutation?*

Vaccination of larger populations on time can reduce the viral spread and emergence of new variants.

It is important to monitor the nature of the coronaviruses spread across populations and examine whether a new variant has emerged. Such activity can be done by genome sequencing and comparative genomics. Although India is currently practicing these activities, it is of utmost importance to expand them across various parts of the country.

Recent research has shown that saliva can be used for the Covid-19 test. With this effortless method, a person who may be severely affected by the infection can be identified before the disease becomes worse. Given the high number of infections caused by rapidly spreading new variants, this testing method can guide timely medical treatment to the needed people.

Progressive research like this and the constant follow of precautionary measures, i.e., wearing masks, frequent hand sanitization, and social distancing, will help us control and eventually eradicate the Covid-19 catastrophe.