**Importance of SARS CoV-2 variants**

[**Dr Zareen Fatima and Dr Muhammad Munir Akram**](https://nation.com.pk/Columnist/dr-zareen-fatima-and-dr-muhammad-munir-akram)

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The advent of COVID-19 is remarkable and it has divided time into the pre-COVID-19and COVID-19 eras. This infection is not just significant in terms of health and disease, but was able to uncover the disproportional distribution of wealth and resources in communities. Many studies from western countries such as Canada and the US have reported discrimination in healthcare among races and ethnicities where the Latino and Black populations had to face a lack of healthcare facilities.

One thing which COVID-19 made possible was the realisation of the importance of science and researchers. Now we all know about the existence of words like R2, exponential growth, spike protein, mRNA, and so on. A new word added to the dictionary of the average human is “variant”. But what these variants are, how we know these are variants, and what their effects are, is still vague and unclear. To help the general public, these concepts are described in easy words for better understanding.

[IHC extends Zardari's interim bail till Jan 28](https://nation.com.pk/12-Jan-2021/ihc-extends-zardari-s-interim-bail-till-jan-28)

Mutations are sudden changes in genetic code of cells and viruses. Evolutionary scientists study selective pressures which shape the evolution of organisms. Selective pressure, also known as selection pressure or evolutionary pressures are living (biotic) or non-living (abiotic) factors that affect the growth of a population at a place. Biotic factors can be disease, predation, or parasitism and abiotic factors can be sunlight, temperature, or pressure etc.

Viruses are non-living i.e., they do not need food nor they reproduce like other living organisms do. Viruses are either enveloped or not. They are entities that contain genetic material as DNA or RNA. The mutations in viruses occur because they have to maintain their population in circulation. Selective pressures lead to natural selection. This phenomenon was extensively developed by naturalist Charles Darwin. Positive (Darwinian) selection promotes the spread of beneficial mutations in viruses, and negative (or purifying) selection hinders the spread of harmful mutations. Those RNA viruses which do not have a correcting protein (polymerase enzyme) to correct mutations while the genetic code is replicating are mostly under negative selection. The lack of the proof-reading ability of the polymerase enzyme is balanced by negative selection. Also, RNA viruses tend to be under more negative selection than DNA viruses.

[MPAs to elect PTI senate candidates from Sindh](https://nation.com.pk/12-Jan-2021/mpas-to-elect-pti-senate-candidates-from-sindh)

We might think that all the mutations that occur in genetic material of viruses provide an advantage (are advantageous) to the virus. However, such mutations are low in number and there are more harmful mutations (deleterious) for the virus. The ones which make a virus strong and let itself copy more are advantageous while the ones which make a virus prone to destruction are deleterious. One may think; why does a virus not mutate to a point where it is impossible to finish it? In nature, this does not happen because viruses replicate in bodies of living organisms and these organisms have developed immunological processes that keep trying to kill the virus from the body. Hence, the fight between the body’s immune system and the virus keeps going on until one of them loses.

Some viral mutations become deadly to the host and kill it before the host could infect and spread the virus to another host. This way, the mutation will disappear from the population. Some mutations occur which make viruses lose their ability to infect, attach, and enter the host cell completely. This also removes the mutation from the population. Helpful mutations keep the virus from infecting new hosts and cells. Scientists yet do not know where a mutation will occur. Coevolution algorithms are used to extract any pattern of grouped mutations in viruses and science is still trying to define which parts of the virus mutate together. But we do know certainly that if a mutation arises on the part of the virus which attaches to the cell, it has considerable effect on the overall infectivity of the virus.

[Almost 13,000 healthcare workers infected with COVID-19: NCOC](https://nation.com.pk/12-Jan-2021/almost-13-000-healthcare-workers-infected-with-covid-19-ncoc)

‘Isolate’ is the term given to the virus taken from a patient. Strains can be defined as types of a virus which have certain properties and immunological response. When a strain has a number of mutations those are termed as variants. If mutations lead to changed properties and immune response then such a variant becomes a different strain of that virus.

We study evolution by plotting the genetic code of viruses on a ‘phylogeny’. It is a treelike structure in which we get to know which viruses are distant or together, based on their appearance on the tree. The International Committee on Taxonomy of Viruses classifies viruses till species level. Below it, there are no formal guidelines to characterise virus species in clades or lineages. Each of these is defined by set rules of a particular virus. On a tree, lineages are portions containing clades. Clades are the last part of a tree with descendants of the same ancestor.

[Pak Navy launches Missiles, torpedoes to safeguard submarines](https://nation.com.pk/12-Jan-2021/pak-navy-launches-missiles-torpedoes)

Up till now, scientists are working to define how many strains SARS CoV-2 has and how many variants of these strains are circulating. A Chinese study at the beginning of the COVID-19 pandemic defines two strains, L and S based on the mutation differences they had. However, they may have grown into six—the original L strain, its first mutation S, strains V and G. To date, strain G is the most widespread: it mutated into strains GR and GH at the end of February 2020.

Although the word “strain” has clear meanings, many times even scientists use them wrongly. A new strain will appear if the biological properties of that strain differ from others. However, all the SARS CoV-2 attach to the same human receptor (hACE2) and they do not have any different infectivity or severity of disease. These nomenclatures are yet to be defined. Rambaut and colleagues have defined 81 lineages of SARS CoV-2. In terms of variants, there are 3667 UK variants as mentioned by Dr Derek Fairley of Belfast Health and Social Care Trust.

[WhatsApp breaks silence over policy update controversy](https://nation.com.pk/12-Jan-2021/we-want-to-address-some-rumours-whatsapp-breaks-silence-over-policy-update-controversy)

According to Professor Matt Holden of the University of St Andrews and Public Health Scotland, more than 40 UK lineages circulated in Scotland, many were introduced by other countries through travel from Spain, Greece, Turkey, and Croatia, while two lineages in Scotland emerged from within the UK (England). Three main lineages were seen in Scotland, two in the first wave and the third emerged and spread in the second phase. One of the first phase lineages emerged and disappeared in the first wave because of lockdowns and SOPs followed strictly. Re-importation of cases and international travel caused the spread of lineages and their re-introductions and cross border outbreaks.

Professor David Robertson of the University of Glasgow noted that 2 amino acid mutations per month in global lineage can be misleading if we see the phylogeny without time. As SARS CoV-2 is a slow-evolving virus, there was not enough positive selection in the beginning of the pandemic because it had no pressure in the form of immunity against it. The newly highlighted variant which originated from the UK in lineage B.1.1.7 has no evidence of the mutation effect so far. The spread of this variant may be due to increased sampling, travelling and movement in population.

[IHC disapproves NAB appeal against Nandipur case](https://nation.com.pk/12-Jan-2021/ihc-rejects-nab-appeal-against-babar-awan-s-acquittal-in-nandipur-case)

An extremely important point to note is computational modelling (by taking log-odds), which tells us that the growth of the new variant is by chance; another concept in the evolution of viruses in a population, Dr Erik Volz from Imperial College, London explains. It means due to less immunity, there is not any selection pressure of antibodies on the new variant, hence it spread because of travel and movement across the UK. The high point of this variant’s spread coincides with the travel of October.

Although there are certain laboratory and epidemiological studies which show that the new circulating variants may have high transmissibility, these variants are not causing severe infections. Scientists around the globe are worried that the virus can accommodate changes. Antibodies target the accessible region on a spike protein of the virus and there are not many mutations in that region. This is a worrying situation which requires extra surveillance but it does not by any means prove that the new variants are more deadly or super contagious as they are being termed. Professor David Robertson, University of Glasgow cited Harvey and colleagues (2020), this can be due to less selection pressure on the virus right now as most of the population is susceptible. There is no scientific evidence so far that vaccines will not work. However, the current lineage has 17 changes as compared to the Wuhan strain upon which vaccines are constructed, which is a worrying situation.

[Children to play responsible citizens' role: Firdous Ashiq](https://nation.com.pk/12-Jan-2021/children-to-play-responsible-role)

The new variants of the UK and South Africa have been identified in over 40 countries including Pakistan, US, Canada, Europe, and Asia. What remains important is the surveillance of cases and genetic changes so that scientists can prophesise any major issue in the future.

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