

Variants of the Novel Coronavirus

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Abstract

The novel coronavirus had emerged in 2019 from the Hubei province in China. Now the world is facing the third and fourth waves of the pandemic caused by this virus. These are due to the new mutants and variants of the virus that have emerged over time due to various reasons. It is important to keep oneself updated about these mutants and variants.

Keywords: variants; mutants; emergence

Introduction

Since March 2020, many new mutants of the novel Coronavirus or SARS CoV2 have emerged. The disease has been recognized as a pandemic in March 2020 by the World Health Organization. The disease is called COVID 19 because it was first recognized in December 2019 in China (1). Right now the third wave is raging across India and the world.

With time, many new mutants and variants of the virus have emerged, which had earlier been given various names and epithets like UK variant, Brazilian Variant and others. They were later replaced by Greek alphabetical letters like Alpha, Beta and Mu. If one or more mutations alters the virus 'behaviour in a significant manner, it is called Variant. If number of cases or deaths due to a variant are not that high or are to be fully investigated, it is simply called VOI or Variant of interest. The properties of a VOI are being investigated. If however the number of cases or deaths due to the variant in question is substantial and is of public health concern, it is called a VOC or Variant of concern(2). VOCs have been observed to be more infectious, and also more prone to cause breakthrough or re-infections in those who have been vaccinated or previously infected. These variants are more likely to cause severe disease, evade diagnostic tests, and resist antiviral treatment. Variants under monitoring or VUM are the SARS-CoV-2 variants with genetic changes which are suspected to affect virus characteristics with some indications that it may pose a future risk, but evidence of phenotypic or epidemiological impact is unclear presently. There is another terminology called Variant of high consequence or VOHC, which is a variant for which current vaccines do not offer protection. As of now, there are no SARS-CoV-2 variants of high consequence. The naming of the variants are done by the Technical Advisory Group on Virus Evolution, also called the Virus Evolution Working Group (3).

Reasons behind emergence of so many SARS CoV2 variants:

Mutations occur normally in RNA viruses. SARS CoV2 has an error prone RNA polymerase which frequently leads to change in its genetic code or mutations. Factors like frequent international travel, man and animal conflict, wet animal markets and non compliance to taking vaccines also help in faster evolution and emergence of mutants and variants. Crowded areas and failure to adhere to COVID protocols like hand washing and social distancing are also important factors behind this. Isolation in geographical areas lead to different mutants and variants being evolved.

Alpha, Beta and other variants

The Alpha VOC of the SARS CoV2 had several mutations in the S or spike protein, due to which existing PCR methods were unable to detect the spike genes. This was called the 'S gene dropout'. The Alpha variant (B.1.1.7) is the first identified COVID-19 variant, detected for the first time in the UK and later emerged as a dominant threat in the US, till March 2021. The Alpha variant is rarely encountered now. The Beta variant was discovered in South Africa. It is actually B.1.351 and also has a high number of mutations. It also has the E484K mutation that may make it escape vaccine induced immunity quite well.

The Gamma variant, first identified in Japan is thought to be the most dominantly spreading variant in Brazil, which became a major COVID hotbed since 2020. With mutations P.1, P.1.1, P.1.2, this variant, has also been found to have difficult mutations in its spike protein, which could help it escape neutralizing antibodies.

Delta and Delta plus VOCs

The Delta VOC and Delta plus are the dominant strains in most countries now. Delta variant emerged and was first detected in India. The Delta VOC caused the second wave of infections in India. It can be neutralized by vaccine induced immunity. The Delta plus VOC emerged later and has led to infections in vaccinated individuals also.

Mu variant

The Mu variant of the novel Coronavirus evolved in 2021 and was first reported from Colombia. It had many mutations and could theoretically evade host immunity, but it did not remain for a long time in circulation as the Delta variant was much more transmissible(4). However it is still abundant in countries like Ecuador and Colombia.

Omicron variant

Since November 2021 a new variant of concern has emerged, called the Omicron variant. It was first identified in Botswana and South Africa in November 2021. The Omicron variant belongs to the pangolin lineage of Coronaviruses. It has possibly emerged via mixing of human and deer coronaviruses. Omicron variant causes clinical features that are different from the parent strain or other strains of the SARS CoV2, like mild fever, bodyache, cough with phlegm, nausea and others. Nausea,found in early part of the illness along with lower back pain which also occurs early, are now pathognomonic features of Omicron variant infection. This variant is about twice more transmissible than the Delta variant but causes milder symptoms and has still not been reported to cause pneumonia. Only few deaths have so far been reported worldwide due to the Omicron variant. It also has the S gene dropout in PCR like the Alpha variant, due to so many mutations in the spike gene. It also has the E484K mutation that may make it prone to escape vaccine induced immunity (5). Now Omicron is spreading very rapidly and fast becoming the dominant strain in all countries due to it's high transmissibility. It is now responsible for the chunk of the third wave of infections in India and other countries.

Subsets of omicron variant:

There is also a subset of the Omicron variant that does not have so many mutations in the spike gene. It is called BA2 subset or subclass. The original Omicron variant is called BA1 subset.

IHU variant

The new IHU variant of the SARS CoV2 has been identified in a university in France (Instituts hospitalo-universitaires) and hence called IHU variant. It may already have spread to many countries. It is also called B.1.640.2 and has been detected in 12 patients near Marseille in France recently (6). The first of these 12 patients had returned from The Cameroons. Till now this variant has been also seen in Germany, UK, Congo and India.

It reportedly has even more mutations in the spike region than the Omicron variant. In fact, it has 46 mutations and 37 deletions in its genetic code. There are many mutations in the spike region of this variant. However as of now it does not seem to be spreading so rapidly. However one case of IHU variant has been detected in India.

New Nigerian variant

A new variant of SARS CoV2 has emerged in Nigeria in December 2021. Although it is said to have emerged from the UK variant, it is different from both the UK and South African lineages of SARS CoV2(7). More information is awaited about this variant.

How to prevent emergence of variants

Simple adherence to COVID appropriate behaviour like proper physical distancing, hand washing and wearing masks properly whenever going out, can go a long way to prevent emergence of new variants. This is also highlighted in Figure 1 below. N95 masks are better than cloth masks in preventing transmission, especially of the highly contagious Omicron variant. People should also be administered available vaccines whenever possible (8). Efforts should also be made to devise newer vaccines targeting the new variants. Also with time, milder but more contagious variants of the virus are set to emerge that may still put the already strained healthcare system into more trouble.



Figure 1: Mass gatherings should be avoided or spacing should be done. (image source: authors)

Discussion

More and more information is now coming up with respect to the mutants and variants of the novel coronavirus. Newly emerging SARS-CoV-2

variants need to be carefully and continuously monitored for their potentially increased transmission rate, altered pathogenicity, and resistance to vaccine induced or disease induced immunity(9).

Epidemiological surveillance is therefore very important. Genomic surveillance is needed to track the paths of the new variants and mutants in the wake of emergence of new variants like IHU(10). Whenever needed, home isolation and home quarantine should be advised for the ill and the exposed, respectively so that the spread of infection is checked. Also important are booster doses of the available vaccines for the frontline warriors and the highly susceptible population in order to mitigate disease severity.

Conclusion

Public health measures should be spruced up to prevent emergence of new variants and mutants of the SARS CoV2. Emergence of the mutants and variants should be monitored and studied well. COVID appropriate behaviour is also very important in this aspect to prevent health emergencies.

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