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Review Article

A review of the SARS-CoV-2 viral genome mutation and its effects

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ABSTRACT

The pandemic-starting SARS-CoV-2 novel coronavirus was found in Wuhan, China. WHO declared this pandemic, which began in late 2019, in March 2020. Experts say this was the first SARS-CoV-2 outbreak. It was the first of many. This virus constantly mutates in response to its replication environment, causing waves, the deadliest of which was the delta variant-caused second wave, which killed millions worldwide. This review examines viral genome alterations and their global effects. We used references from previous research articles on this or similar issues to make our review more data-driven. We found that the virus' mutation has caused major health problems in humans, including deaths. The viruses changed genome, proteins, local food, sanitation, immunity, and milieu may be involved. We also found that while some of the impacted variations are milder and less contagious, some have had record-breaking peaks and significant death rates in a short time. This analysis examines COVID-19's impact on diabetes, cardiovascular disease, asthma, aging, and community hygiene. SARS-CoV-2 increases stress and blood glucose in diabetics. Clinical investigations have linked COVID-19 to cardiovascular disease, although the mechanism is uncertain. Asthmatics are more vulnerable to respiratory infections. Its effects change as one age. Cleanliness campaigns are needed to put an end to the epidemic.

1. Introduction

The outbreak of coronavirus disease 2019 (COVID-19), which began in the city of Wuhan in China, has been traced back to a virus that has been designated as SARS-CoV-2/novel coronavirus. This virus is principally responsible for the pandemic. Even though it started to spread in the last months of 2019, the World Health Organization (WHO) did not wait too long before recognizing this virus as a pandemic. This recognition came in March 2020. This highly contagious virus has an estimated case fatality rate (CFR) of between 2 and 3 percent, but it has the potential to produce a severe acute respiratory syndrome with symptoms similar to those of the flu and even death (Singhal et al., 2022). In addition to persons of all ages, the elderly are disproportionately impacted. This virus has a positive-sense, single-stranded RNA genome that is between 26 and 32 kilobases in size (Kumar et al., 2020). Membrane protein M, structural protein P, and spike proteins are all components of the lipid bilayer that forms the viral envelope. Due to changes in its structural parts, especially its envelope protein, this virus has made a lot of different types that are now found in every part of the world (Schoeman et al., 2019). During the course of this pandemic, several variants of this virus have been discovered; however, only a few of these numbers have been accepted by various agencies as being of concern. This virus had never been seen in humans before; it was initially zoonotic (like bats), but it

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somehow changed and spread to humans. Within a few months of its first break, it took the form of a pandemic, which was unheard-of at the time. Even though a large number of preventative measures were put into places, such as quarantines and complete lock downs of cities and nations, none of them were successful. This was because the disease not only spread rapidly but also continuously mutated. COVID-19 causes hypoxia in its severe sufferers, which can lead to cardiac arrest and lung collapse if the patient is not closely monitored and treated immediately. Vaccination efforts on a global scale have helped us emerge from the worst of this pandemic, but the virus might still mutate and spread. In this study, we will take a look at the various global patterns of mutation. The study highlights the some of the essential mutations that turned the lifestyle of the humans under this huge and violent pandemic.

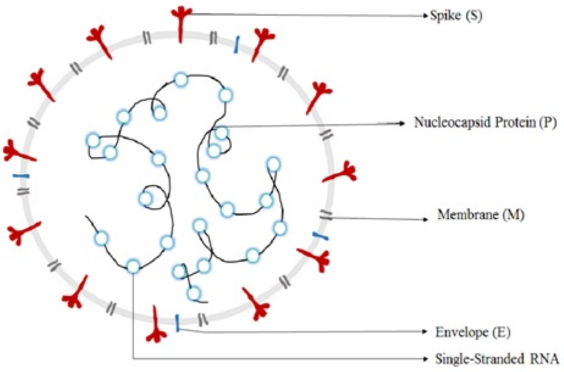

Fig. 1: Human SARS-CoV-2

2. Crucial Mutations in SARS-CoV-2

SARS-CoV-2 is a member of the coronavirus family, which is a large family of viruses that includes a number of other viruses. There are three different virus families that belong to the order Nidovirales. These families are the Coronaviridae, Roniviridae, and Arteriviridae. The coronaviruses are the most numerous and widespread of this group of viruses. RNA viruses with a positive sense that are single-stranded, encapsulated, and members of the family Coronaviridae make up this family. The genomes of these organisms can be anything between 26 and 32 kilobases in length. This viral group consists of four unique genera, which are known as Alpha, Beta, Gamma, and Delta, and it covers a vast variety of coronaviruses that can harm both people and animals.[1] Each of the four genera is named after a letter of the Greek alphabet: Alpha, Beta, Gamma, and Delta. Scientists didn't find out about the human coronavirus for the first time until the middle of the 1960s. Seven human coronaviruses belonging to the Alpha and Beta genera have been discovered presently, genus Alpha, including human coronavirus NL63 (HCoV-NL63) and human coronavirus 229E (HCoV-229E), and genus Beta, including human coronavirus OC43 (HCoV-OC43), human coronavirus HKU1 (HCoV-HKU1), and severe acute respiratory syndrome. They are the root cause of a wide variety of diseases, the most common of which is the common cold. They also cause other respiratory problems with mild to severe symptoms.[2]

There is evidence to imply that bats serve as an essential host for specific coronaviruses.[3] For instance, the severe acute respiratory syndrome coronavirus (SARS-CoV), which was responsible for the deaths of hundreds of people in China in the years 2003 and 2004, expanded throughout the country and caused the deaths of hundreds more. Following that, in 2012, MERS-CoV was discovered in the Middle East; both viruses were transmitted by bats and were responsible for the infection and deaths of a significant number of people.[4,5] The World Health Organization assigned the name COVID-19 to a new disease in the year 2020 that was showing signs of becoming more widespread in every region of the world. Not so long ago, the COVID-19 epidemic made its first appearance, and since then, it has rapidly spread over more than 200 countries all over the world. The World Health Organization announced on the 16th of October that COVID-19 has been confirmed in 39.8 million people all across the world, with a mortality rate of 3.4%. It has been observed that new genetic lineages of SARS-CoV-2 have been developing and spreading all over the world ever since the pandemic of COVID-19 began. This has been the case ever since the beginning of the pandemic.

3. Mutation Due to Multiple Outbreaks During Pandemic

Viruses like SARS-CoV-2 continue to evolve as a result of modifications to their genetic code that take place throughout the process of genome replication. This was found in the research done by V'kovski and colleagues in the year 2021. A SARS-CoV-2 variant can have one or more mutations that separate it from other SARS-CoV-2 variants. This is how the variant is distinguished from other SARS-CoV-2 variants.[6] Scientists examine the genetic differences between viruses to identify virus variants and determine how these variants are related to one another to aid in the investigation of local outbreaks. This allows the scientists to gain a better understanding of national patterns and to assist in the investigation of local outbreaks. Even though the evolution of viruses is likely to result in the production of new viral variants, we must monitor every new virus variant that emerges so that we may ensure that we are ready for anything that may come. This is especially important to keep in mind if a new strain of the virus emerges that is more dangerous, extremely contagious, resistant to immunization, able to cause sickness of a more severe nature, or possesses any combination of the traits listed above. The World

Health Organization (WHO) uses the Greek alphabet as a mechanism for recognizing novel coronavirus variants, starting with the Alpha variety, which was found for the very first time in the year 2020. This practice began in 2020. In this analysis, we looked at the country of origin, the mutational protein, how contagious it is, how many people die from it, and when it first appeared. All of these factors are important in different parts of the world.

This shows that the virus has mutated all across the world, and with each new mutation, it creates a new risk for the population as a whole, increasing the likelihood that it will kill people. While not all of the variants in question are equally infectious, some have showed unprecedented spikes in a short amount of time, while others have travelled to other regions of the world via people, eventually giving rise to yet another variant as a result of environmental and host-immunity alterations. There are several varieties, some of which have a high mortality rate while others have symptoms that are not as severe. If we pay particular attention to the timing of the introduction of any new kinds, we will see that, with a few notable exceptions, the vast majority of new variations arise between the months of September and January. On the other hand, we do not have sufficient data to draw any conclusive judgements regarding this. The delta form was the most notorious of all the other types of the disease since it was responsible for millions of fatalities in India and other countries where it had spread. Because of their varied beginnings and histories, diverse variants display mutations in a variety of structural proteins. These mutations are dependent on the environment in which the variants are found as well as the immune response of the host.[7] In the past one to two years, only a select few nations and private companies have invested significant time and resources into the research and development of a number of vaccinations that are nearly effective against all strains of the disease. However, at this time, we are unable to guarantee that these vaccinations will be as effective against future versions. Further investigation is necessary for the creation of enhanced vaccinations and the identification of any new strains of concern. This can be accomplished with the assistance of next-generation sequencing (NGS) of viral genomes and a variety of tests that look for a rise in positive cases. As we can see, the absence of a specific treatment for this virus has posed a significant problem for everyone, whether in developed nations like the United States and the United Kingdom or in developing nations like India and Brazil. This virus has been a severe problem because there is no known cure for it. As a result, a comprehensive immunisation programme targeting a large population should be given top priority.

4. Dilemma in Covid Infection Positivity

When fighting the ongoing coronavirus disease 2019 (COVID-19) pandemic, having efficient, sensitive, and reliable diagnostic reagents is of the utmost importance because there is neither a prophylactic vaccine nor a particular medicine available for severe acute respiratory syndrome caused by coronavirus 2. This is due to the fact that the condition is currently incurable (SARS-CoV-2). Inaccurate positive and negative test findings will grow dramatically if the diagnostic reagents now in use are compromised. The genotyping of 31,421 SARS-CoV-2 genome samples collected up to July 23, 2020, revealed that nearly all of the current COVID-19 diagnostic targets have undergone mutations. We were able to determine this based on our research. We further show that numerous primers and probes used to analyse the nucleocapsid (N) gene of SARS-CoV-2 have the highest mutation rates. The diagnosis of COVID-19 has greatly benefited from the widespread use of these primers and probes. We used their mutation rates and mutation h-indices to figure out if the SARS-CoV-2 genes have changed in the same way or in different ways.[8] According to our findings; the N gene is highly variable within the SARS-CoV-2 genome. We show that diagnostic targets should also be selected to avoid cytidines in order to account for the editing of APOBEC mRNA that is caused by the human immune response (C > T). By letting the most effective SARS-CoV-2 genes and proteins be chosen, our results may pave the way for the design and development of COVID-19 diagnostic reagents, preventative vaccines, and therapeutic drugs.[9]

5. Effects of Non-communicable Diseases During SARS-CoV-2 Infection

People who have a history of certain health conditions, such as asthma, diabetes, or cardiovascular disease, are at a greater risk of developing problems and passing away as a result of COVID-19. Different age groups have their own perspectives on what the implications will be. Similarly, unhygienic communities have their drawbacks. Diabetes and the SARS-CoV-2 infection can make things more difficult by:

1. Raising blood glucose levels, which cause inflammation and oxidative damage
2. Acinar cells' binding to ACE2 results in tissue injury.
3. Limiting lymphocyte proliferation as a result of high blood sugar.

In diabetic patients, infection with SARS-CoV-2 causes the release of glucocorticoids and catecholamines, which leads to an increase in both stress and glucose levels. Increased levels of glucocorticoids and catecholamines both lead to a lowered immune response and may also increase the likelihood of infection.[10] In addition, research conducted in laboratories has demonstrated a connection between COVID-19 and cardiovascular disease. The pre-existing cardiovascular disease appears to be linked to poorer outcomes and an increased risk of death in people with the condition. This is even though COVID-19 can cause myocardial injury, arrhythmia, and acute coronary syndrome on its own.

It is not quite known how these relationships function at this time. People who suffer from asthma are generally thought to be at a significantly increased risk of developing respiratory illnesses such as the flu.[11] When the COVID-19 pandemic first started, there was a widespread misconception that those who suffered from asthma were more likely to contract the virus. However, when more information became available, the connection between asthma and COVID-19 became less evident. Nevertheless, we still can't rule out the risk in situations like these.[12] Clinical symptoms appear in 21% (95% credible interval: 12-31%) of infections in adults aged 10 to 19, rising to 69% (57-82%) of infections in people over the age of 70, according to a study that was conducted by Davies et al. In addition to this, they projected that the risk of contracting an illness among people under the age of 20 is around one-half that of adults over the age of 20.[13,14]

In places like slums and colonies with a lot of people, where this disease can spread quickly if proper hygiene isn't taken care of, it's important to keep the whole community clean to stop the disease from spreading.

6. Conclusion

In addition to several other known and unknown factors, as well as the genetic susceptibility of the host, mutations and genetic variabilities of the virus itself has a significant impact on the varying clinical symptoms associated with COVID-19 infection. In general, at this point, it is practically impossible to detect all of the mutations that have emerged in SARS-CoV-2 and their link with clinical changes. This is mostly due to the presence of asymptomatic people. It is important to note that the absence of symptoms in certain individuals who have been diagnosed with the disease in question may be the result of attenuated mutations in SARS-CoV-2. This hypothesis has to be investigated further so that it can be verified. In addition, to substantiate the findings of the research that was conducted, it will be necessary to repeat those investigations in a variety of settings and on a wide range of individuals. By finding out how SARS-CoV-2 is spread genetically, this kind of research could help make patient-specific treatments. In addition to this, the glycosylation sites were removed, which resulted in a decrease in the infectious potential of the virus as well as a change in its reactivity to antibodies that neutralize it. This finding adds credibility to the concept that glycan may have a major impact on both the reproduction of the SARS-CoV-2 virus and the immune responses that are generated by vaccination. When looked at as a whole, our results show what happens when certain strains of circulating viruses change, especially in terms of how easy they are to spread and how they affect the immune system.

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None.

8. Conflict of Interest

None.

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