

COVID-19 VS COVID-20: IS IT A SINGLE OR MULTIPLE MUTATION?**Manal A. Hamed***

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ABSTRACT

The objective of this study is to explore a new insight in the transformation of COVID-19 to COVID-20. This report believes that COVID-19 undergo either one or multiple mutations that can change it to a new virus. COVID-20 is going to be more potent and complex than COVID-19. The change of the spike protein represents one of the first coronavirus mutations that have made it more infectious. These mutations may allow the variant to replicate and transmit more efficiently. The implications of the changes in these mutations are not yet well understood to get steps towards controls, treatments, and virus eradication or prevention.

KEYWORDS: COVID-19; COVID-20, Mutation, Spike protein, Control; Treatment; Prevention.**INTRODUCTION**

In December 2019, Wuhan, China, became the center of an outbreak of pneumonia of unknown etiology with severe acute respiratory syndrome belongs to coronavirus (SARS-COV-2 or COVID-19).^[1] In December 2020, the confirmed cases of COVID-19 was 76,858,506, including 1,711,498 deaths.^[2] Although the virus is linked to bats, but the virus origin and its intermediate host (s) have not yet been identified. The virus is predominantly transmitted between people through respiratory droplets and close contact, while there are also many examples of transmission between humans and animals. Several animals that have been in contact with infected humans, such as dogs, domestic cats, lions and tigers, have tested positive for SARS-COV-2.^[3] The rapid spread of this virus through many countries and its efficient killing have been labeled it as an international emergency.

Virus Control

SARS-COV-2 can target different tissues other than lung including gastrointestinal tract, liver, kidney and nervous system where it can cause severe illness and death.^[4] Many attempts were done to overcome disease progression. Certain drugs that are clinically approved for other diseases were tested against SARS-COV-2 as Chloroquine, Hydroxychloroquine, Ivermectin, Favipiravir, Ribavirin and Remdesivir. Traditional herbal medicine was also considered. Due to the absence of effective treatment against SARS-COV-2 so far, the only way to confront this crisis is to develop an effective vaccine.^[3]

Virus Mutations

While scientists are working to find an appropriate vaccine against SARS-COV-2, the world was surprised by the emergence of another strain of the virus namely "VUI-202012/01". The virus variation was found in United Kingdom in mid-September 2020 and its mutations have occurred on the genetic material that controls the spike protein, which allows SARS-COV-2 and other similar viruses to penetrate host cells, causing infection.^[5] According to the U.K.'s chief scientific adviser, Patrick Vallance, there are 23 changes in the virus's genetic material. These large number of variations helps the virus to spread more quickly with 70% more transmission rate. However, there is no evidence that the strain causes a more intense illness or leads to a higher fatality rate.^[6] Higher transmission rate means more cases and a higher hospitalization rate.

In general, viruses that encode their genome in RNA like SARS-COV-2 tends to pick up mutations quickly when they are copied inside their hosts because enzymes that copy RNA are prone to making errors. Since the beginning of the pandemic, at least 1,000 minor variants have been detected in SARS-COV-2 genetic code. These variations appeared to be susceptible to antibodies that target the earlier strain and did not associated with more severe illness.^[7]

COVID-20 Prevalence

However, the change to the spike protein found in southeast England represents one of the first coronavirus mutations that have made it more infectious. These mutations may allow the variant to replicate and transmit more efficiently. Therefore, COVID-20 is a highly

contagious new variant of coronavirus, circulating in England and consider as a large-scale crisis that is deeply enmeshed in social and environmental factors.^[8]

In South Africa, a similar version of the virus has emerged, sharing one of the mutations seen in the British variant. That virus has been found in up to 90 percent of the samples whose genetic sequences have been analyzed.^[6]

In June 2020, Denmark confirmed 214 cases of COVID-19 that had been identified as SARS-COV-2 variants associated with farmed minks, including 12 cases with a unique variant. The cases ranged in age from 7 to 79 years, and eight had a link to the mink farming industry and four cases were from the local community.^[9] To date, six countries, namely Denmark, the Netherlands, Spain, Sweden, Italy and the United States of America have reported SARS-CoV-2 in farmed minks.^[9]

Mutations and Vaccine Response

Now, the question being raised is whether the mutation could affect people's response to vaccines and scientists say this is unlikely. Several coronavirus vaccines are designed to create antibodies targeting the spike protein. The vaccines target multiple regions on the spike, while a mutation refers to a change in a single point. So, if there is one mutation, it does not mean vaccines would not work. One reason to be concerned is that eight mutations appear in the gene that encodes the spike protein on the viral surface, two of which are particularly worrisome. One, called N501Y, has previously been shown to increase how tightly the protein binds to the angiotensin-converting enzyme 2 receptor, its entry point into human cells. The other, named 69-70del, leads to the loss of two amino acids in the spike protein and has been found in viruses that eluded the immune response in some immunocompromised patients.^[10]

Ravi^[11] said that it is likely to be a mutation in the spike protein. From his point of view that there has been a single nucleotide change in one portion of the spike protein, so there would be no bearing on the disease biology or even diagnostics. Contradictory, Kang,^[12] said that there would be more concern about a mutation in the spike region than other regions of the coronavirus genome. It is the coronavirus spike protein that binds to a human protein to initiate the process of infection. So, changes here could possibly affect how the virus behaves in terms of its ability to infect, or cause severe disease, or escape the immune response made by vaccines.

The original form of amino acid in spike protein is *D614*, while the mutant form is referred to as *D614G*, or just *G614*. The spike protein is a string of 1,273 amino-acids. The 614th of these amino acids has the chemical symbol "D" (aspartic acid), while in the mutated form, the 614th amino acid is abbreviated "G" (glycine). So *D614G* is short for having a spike protein with aspartic acid at position 614 mutated to glycine.^[13] The *D614G* mutation

is being carried along as a part of a clade called the "G clade". A "clade" is a lineage in a phylogenetic tree with a shared ancestral state. A phylogenetic tree can be thought of like a family tree, and a shared ancestor like a grandmother who is a shared ancestor of all of her grandchildren.^[13] The G clade differed from the original Wuhan form by 4 mutations. *G614* is almost always found linked to the other 3 mutations.^[13] Fortunately, the clinical data showed that even though patients with the new G virus carried more copies of the virus than patients infected with D, there wasn't a corresponding increase in the severity of illness.

Mutations will keep happening and the new virus variants will survive or disappear depending upon our immune response and their ability to multiply and transmit.^[14] But all SARS-COV-2 strains are genetically similar to one another, and scientists do not expect these mutations to have a significant impact on their ability to cause more severe disease than what has been observed so far.

CONCLUSION

Finally, the rapid development of this virus and the specific mutations it causes have made it more epidemic, so all scientists have to recognize the importance of sharing the epidemiological, virological and full genome sequence information with their research teams for specific treatment or vaccine development shortly.

CONFLICT OF INTEREST

The author declared no conflict of interest.

Ethical statements

This is an observational study and no ethical approval is required.

This work has not been published before and not under consideration for publication anywhere.

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