

Letter to the Editor

Is SARS CoV-2 viral mutation leading us to a virtual world?

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It's nearly a year, when in December 2019 few cases of atypical pneumonia were detected in the Wuhan province of china. During that time, in a very short span, the number of cases was sky rocketing not only in china, but in various countries. Eventually, on 11th March 2020, world health organization (WHO) declared this new infection, Corona virus disease (COVID-19) as pandemic. Since its inception, the world has witnessed devastating effects of COVID-19 on every aspect of human life. According to the recent data available, the pandemic has affected over 200 countries with nearly 7.5 million people affected across the world. Although, it has low mortality in comparison to Middle East respiratory syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS), it has accounted for about 1.6 million deaths across the globe.¹

The journey from its first case to the present day has observed various phases. Regular updates and advisories from the international health agencies

such as WHO and Centers for Disease Control and Prevention (CDC) have been instrumental during this period.²In the beginning; huge surge in the number of infected cases with the established role of human transmission has thrown the world into a complete lockdown. It was suppose to break the chain of human transmission and to bring halt to the fast spreading infection.

Realizing the infective nature and fatality rate, simultaneous efforts were started in the direction of developing effective vaccine. With the forced compliance of infection control measures including social distancing, and disinfection, the disease was brought under partial control. With the decline in cases, relaxation in the daily life was gradually introduced. Fortunately, the development in the vaccine research was also about to see the daylight. Sadly, the information about new mutated strain of corona virus hit the world, with instant reaction of putting yet another halt to international travel and

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lockdown in the countries claiming the point of origin. This viral mutation has made many countries again in a stand still condition forcing the humankind for another episode of lockdown.

By nature, whenever virus replicate, it tends to change its genetic codes. These changes in the genetic base pairs can be non-consequential, as known as synonyms mutations. On the other hand, alterations which tend to change the sequence of amino acids and eventually protein makeup can have grave consequences, known as non-synonyms mutations. Like any other viral infection, COVID-19 has also undergone various mutations in the recent past. In the month of October 2020, Spain reported a mutant of coronavirus, known as 20A.EU1. It is well understood that it was originated during the summers, when the travel restrictions were relaxed leading to transmission in many European countries inclusive of UK. In the recent past, another instance of mutation was seen in the Denmark, where the mutated strain was identified in mink, an animal which is reared for various commercial purposes. Most recently, a new lineage of coronavirus namely VUI-202012/01 has been identified in the UK. Supposedly different lineage of coronavirus known as 501.V2 has also been identified in the South Africa.³ These random mutations in the viral genome is not always adverse to the host, rather can be harmful for the virus itself. The mutations that hamper the basic existence of virus such as attachment to the host and replication are generally lost. The other set of mutations which sustain, are deleterious to the host, as they create new mutagenic determinants. Thus, the virus becomes more virulent and resistant to conventional treatment modalities. In this way, new group of individuals are identified as high-risk with probable alterations in clinical presentation. This holds true for all newly emerged variants of coronavirus in different parts of the world.

Coronavirus being a RNA virus has an exceedingly higher tendency for mutations compared to DNA viruses. The inherent tendency of nucleic acid, frailty of replication enzymes and the absence of inherent proof-reading enzymes are seen as the main reasons for their high rate of mutations.⁴

The emergence of VUI-202012/01 has given rise to various concerns and led to many speculations. The first and foremost concern is regarding the 70% higher rate of transmission of the infection compared to its established variant. Another apprehension is with

the children being identified as high-risk group. Additionally, there is an increasing anxiety about the effectiveness of recently developed vaccine.

Among the mentioned worrisome issues, there is also a reason to simmer down, its relatively low mortality rate. Taking into account of the transmissibility, the decision of complete lockdown of the non-essential activities in the places of origin is praiseworthy. As far as efficacy of vaccine is concerned, the health authorities have shown confidence over its effectiveness. It was 8th December 2020 when the first roll out of BNT162b2 vaccination was administered in the UK. It is an m-RNA based vaccine that is developed against multiple SARS-CoV-2 spike protein as targets. The claim over the effectiveness of vaccine is also based on the multimodal immune response seen during the trials. Dose-dependent titers of IgG antibody which are specifically directed towards the receptor binding domain (RBD) were evident after every dose of vaccine. Also, high levels of SARS-CoV-2 neutralizing antibodies were observed in a dose-dependent manner. In addition to humoral immune response, T-cell mediated response (CD4+ and CD8+) was also observed. However, authenticity about the effectiveness of vaccine still needs to be confirmed, considering the highly mutating nature of coronavirus.⁵

There are even more questions which should draw our attention. Why only in UK and few European countries have been successful in identifying the mutated strain? This situation can be either because of some geographical, regional or environmental factors that had hastened the viral mutations. During the post-lockdown phase, the policies regarding the easing of restrictions also might have contributed towards mutations. Another aspect to this scenario can be the robust and vigorous U.K.'s practice of COVID-19 testing of their population. In that case, it might be possible that other nations might have mutated version, but remain undetected.

In the past, we had seen the fast spreading infection across the geographic boundaries leading to the imposition of worldwide lockdown. While doing so, our lives had changed drastically with an introduction of "New normal" in all aspects of life. SARS-CoV-2 rising to unprecedented levels^{6,7}, at the same time, we cannot ignore the fact that human beings are seen as social creatures and they can't survive in a virtual world for a long time. So, we need to think seriously about our future course of action. Since we cannot

control the viral mutations, the only way to deal with this infection is to prevent its transmission, detailed identification of the viral genome and subsequently developing a potent vaccine. The self-discipline among the community by following the policies and procedures led by the governmental agencies is the need of the hour. At the same time, CDC has already launched a National SARS-CoV-2 Strain Surveillance (NS3) program which will ensure the

identification of any new strains.³ This in turn will aid in characterizing the viral genome in order to develop and improvise an effective vaccine.

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