



COMMENTARY

High Mutation Rate in SARS-CoV-2: Will It Hit Us the Same Way Forever?

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The COVID-19 pandemic that currently plagues the world has infected over 37,601,848 people, killed 1,077,799 over people, and daily infects around 300,000 people [1]. Different genomic studies indicate that SARS-CoV-2 originated from the bat or the pangolin [2], however, these conclusions are not substantial and it remains a global priority to detail all the characteristics of this agent, looking to discover therapeutic targets, explain the pathophysiological process it produces in humans, and describe its dynamics among populations [3]. As a result of these investigations, a large number of viral subtypes have been identified arising from the constant mutations of SARS-CoV-2 [4], which would explain the different pathological phenotypes found in the reported case series, and allows us to understand heterogeneous lethality rates. This high mutation rate is a serious problem since it causes the virus to adapt to conditions that may be unfavorable to it and may perpetuate its stay among humans [5].

Yang, et al. [5] conducted a study, the mutation rate of SARS-CoV-2 was evaluated in more than 3,100 genomic sequences [5]. These authors detected 2,096 simple nucleic variants and seven short deletions, with 58.4% missense mutations (1,224). Also, they found that there is very frequent substitution at locus 23.403, causing a change in the 614 amino acid, of the spike glycoprotein, which potentially affects the function of this protein [5]. Similar results were exhibited by van

Dorp, et al. [6], where they found that about 80% of SARS-CoV-2 genome mutations occur in the spike protein. The Orf1ab gene is one of which expresses a large number of mutations in its regions, generating changes in the protein described above, and in the structural and nonstructural proteins Nsp6, Nsp11, and Nsp13, which confirms that this is a heavy evolutionary agent, due to its adaptive ease [6].

Tillet, et al. [7] recently published a case study, in which a 25-year-old boy living in the United States consulted twice for viral respiratory symptoms, with two tests being performed, the first in April and the second in June, both of which were positive, while during the follow-up in May, the test came back negative. The genomic analysis of SARS-CoV-2 on both occasions presented significant differences in each variant, being the second more severe than the first. This suggests that due to the high mutation rate of the virus, there is no guarantee to develop total immunity, therefore, biosecurity measures remain as the best tool to decrease the probability of contagion and death by this agent [7]. It is important to consider this data during the process of creating a vaccine, to ensure its effectiveness and safety.

On the other hand, Wang, et al. [8] argued that the homology between all the found strains of SARS-CoV-2 was very high, both at the nucleotide level (99.91%-100%) and at the amino acid level (99.79%-100%) [8].

They also support that the rate of mutation in the reading frame is low, (around 30%) where the most frequent variant was ORF 1a, found in 13 sites [8]. It should be noted that unlike the first findings, the latter was published at the beginning of 2020, and a clear manifestation of the level of the mutability of SARS-CoV-2 can be observed.

It is very important to take into account the genetic aspects of the viral agent since it allows stipulating the prognosis of the pandemic by COVID-19 in the short, medium, and long term. Likewise, other regions can be expected to begin to mutate, and the virulence of this microorganism may increase due to an increase in affinity towards other receptors [9]. The dynamic research process is the only instrument that currently exists, which allows characterizing this virus in a real and constant way. For this reason, the human talent and the equipment of both public and private laboratories must be strengthened, to typify the genome of SARS-CoV-2 in a singular way depending on the region where it is located. This to establish public policies that adhere to the particular needs of each nation, and to determine the magnitude of the pandemic in a particular way, as currently contemplated, where there is a significant difference between the distribution of incidence and mortality at the global level.

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None.

Authors Contribution

All authors have contributed for this manuscript.

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