# Review Form 1.7

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| Journal Name: | **Asian Journal of Research in Infectious Diseases** |
| Manuscript Number: | **Ms_AJRID_101833** |
| Title of the Manuscript: | **Balance and genetic mechanisms in the covid-19 process of mutation.** |
| Type of the Article | **Review Article** |

**General guideline for Peer Review process:**

This journal's peer review policy states that **NO** manuscript should be rejected only on the basis of '**lack of Novelty'**, provided the manuscript is scientifically robust and technically sound.
To know the complete guideline for Peer Review process, reviewers are requested to visit this link:

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## Review Form 1.7

**PART 1:** **Review Comments**

| | **Reviewer's comment** | **Author's comment** *(if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)* |
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| **Compulsory** REVISION comments<br>1. **Is the manuscript important for scientific community?** yes (Please write few sentences on this manuscript)<br>2. **Is the title of the article suitable?** Yes (If not please suggest an alternative title)<br>3. **Is the abstract of the article comprehensive?** Yes<br>4. **Are subsections and structure of the manuscript appropriate?** yes<br>5. **Do you think the manuscript is scientifically correct?** Yes<br>6. **Are the references sufficient and recent? If you have suggestion of additional references, please mention in the review form.** Please add 5 modern references at last 5 years<br>**(Apart from above mentioned 6 points, reviewers are free to provide additional suggestions/comments)** | **1-Discuss the following statement: "All viruses mutate over time to adapt to changes in the host or environment and COVID-19 is no exception. Most of these mutations have little or no effect on the characteristics of the virus."**<br>**2- There are two classifications of SARS-CoV-2 variants according to the World Health Organization (WHO): surveillance (alpha, beta, gamma, epsilon, eta, iota, kappa, mu, zeta) and alert variants (delta and omicron) on what did these two depend The two ratings?**<br>**3- Increasing the genetic mutations of the virus gives it a greater ability to infect cells and insert its genetic material into it, as it allows it to evade better from the immune system. Is there a vaccine that is compatible with all mutations?**<br>**4- That the Ómicron arose from the first sequences of SARS-CoV-2 and not from the closest previous variant, which is delta, why?**<br>**5- Why the mutation rate of this virus is not as high as expected, but it should be noted that it is very well balanced, and the mutations that occur are selected precisely through these regulatory mechanisms, only those that improve transmissibility or increase the ability to evade the immune system able to continue explain it?**<br>**6- The omicron variant has some common variants with other VOCs, but 45 of its mutations are unique to it. Do you think that this property made it less or more effective and why?**<br>**7- Mutation of the S protein, mainly in the receptor-binding domain (RBD), the most prominent of which is N501Y, which exchanges bases generating a change in 1 amino acid. Another related mutation in this protein is D614G, which is present in almost all variants. What is its significance for viral infection?**<br>**8- Despite the fact that most of the population complied with the safety measures, the** | |

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| | alternative spread with an ease it had never seen before. Fortunately, the virus genome favored transmissibility rather than pathogenicity, but what if that was not the case, is the world ready to face new mutations and variants? Explain this?<br>9- It has been proven that SARS-CoV-2 enters epithelial cells through the interaction of surface glycoprotein with the human angiotensin-converting enzyme 2 (ACE2) located on the surface of the epithelium. Explain how this was done? | |
| **Minor** REVISION comments<br>1. **Is language/English quality of the article suitable for scholarly communications?** | Yes | |
| **Optional/General** comments | 10- It is known that within the COVID-19 mutation line, some mutations were relatively unrelated. There are 15 distinct mutations represented in the protein S domains out of the 15 mentioned, 8 of which were detected in the S1 domain, the other 6 in the S2 domain, and 1 of them Belongs to peptide signals. Can you classify the severity of these mutations compared to mutations of other types?<br>11- These mutations will continue to appear as long as there is a lack of adherence to public health methods. What are the measures that can reduce or eliminate virus transmissions? | |

**PART 2:**

| | **Reviewer's comment** | **Author's comment** *(if agreed with reviewer, correct the manuscript and highlight that part in the manuscript. It is mandatory that authors should write his/her feedback here)* |
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| **Are there ethical issues in this manuscript?** | *(If yes, Kindly please write down the ethical issues here in details)* | |

**Reviewer Details:**

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