

# **Vaccine-induced mutation in SARS-CoV-2, a matter of concern?**

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# Vaccine-induced mutation in SARS-CoV-2, a matter of concern?

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## Abstract

The emergence of new lineages of corona virus over the different continents has illustrated a significant public health concern. These new strains have a higher rate of transmissibility and have become dominant within a short period of time. The virus strains were also witnessed with an extensive range of mutations in the spike (S) protein, particularly in the receptor-binding domain (RBD) and amino-terminal domain (NTD). The studies concerning the genomic epidemiology of the COVID-19 virus have assisted the scientific community to unveil the evolutionary aspect of viruses and track the transmission dynamics over the world. At present all the mutations are vaccine sensitive, but vaccine-resistant variety may emerge at any time. It is very important that we should close the door quickly, although, strategic problems are there. Mutations are more possible in partially vaccinated areas rather than fully vaccinated areas. The present policy of vaccinating on an age structure leaves many non-vaccinated in the same home. In a population with very few vaccinated people there are viruses in many hosts and the chances of mutation is high. If the population is fully vaccinated, the virus is eradicated from that community and hence mutation chances are less. This locality specific fast and total vaccination will curtail the mutagenesis of the virus, lead to its eradication and to be preferred rather than vaccinating based on age structure.

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## Original Manuscript

## Title Page

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## Vaccine-induced mutation in SARS-CoV-2, a matter of concern?

### Abstract

The emergence of new lineages of corona virus over the different continents has illustrated a significant public health concern. These new strains have a higher rate of transmissibility and have become dominant within a short period of time. The virus strains were also witnessed with an extensive range of mutations in the spike (S) protein, particularly in the receptor-binding domain (RBD) and amino-terminal domain (NTD). The studies concerning the genomic epidemiology of the COVID-19 virus have assisted the scientific community to unveil the evolutionary aspect of viruses and track the transmission dynamics over the world. At present all the mutations are vaccine sensitive, but vaccine-resistant variety may emerge at any time. It is very important that we should close the door quickly, although, strategic problems are there. Mutations are more possible in partially vaccinated areas rather than fully vaccinated areas. The present policy of vaccinating on an age structure leaves many non-vaccinated in the same home. In a population with very few vaccinated people there are viruses in many hosts and the chances of mutation is high. If the population is fully vaccinated, the virus is eradicated from that community and hence mutation chances are less. This locality specific fast and total vaccination will curtail the mutagenicity of the virus, lead to its eradication and to be preferred rather than vaccinating based on age structure.

**Keywords:** Vaccination policy; mutation; COVID-19; Corona virus

## Introduction

Within a short period of time, the COVID-19 pandemic has touched every continent, resulting in 158 million confirmed cases and 3.29 million deaths (as of May 12, 2021). Equally fast has been the progress in the development of an effective vaccine with clinical trials.<sup>1</sup> The year 2021 has witnessed the launch of a plethora of COVID-19 vaccines around the globe.<sup>2,3</sup> Advanced molecular strategies like Whole-Genome Sequencing (WGS) have allowed the scientific community to track the spread of corona viruses with special inference on the recent problem, the development of different lineages through mutation. In addition to the aforementioned concepts, the urgency of vaccination in a different stratification rather than age wise as practiced now has been put forward as the principal core of this article.

## The scenario

The Corona viruses are known for their ability to illustrate the clinical spectrum that may range from the common cold to severe respiratory disease problems.<sup>4</sup> That means, here, we can find a close link between the human host and the virus, like a constant relationship. In order to maintain their close relationship, all viruses have inserted their genetic materials into the infected cells. The corona virus has also made prominent alterations in the apoptosis pathways of the host cells, transcriptional and translational patterns, cytoskeleton and cell cycle.<sup>5</sup> During this time, the corona virus has maintained its genetic makeup to continue its relationship with the human host. It is evident that the genetic and phenotypic structure of the virus has a prominent role in pathogenesis. Probably due to this, after the vaccination, the virus has been forced to break the usual relationship with the human host by altering its genetic makeup through mutation. As a result of mutation, which was probably instigated by the vaccination, different virus strains have been developed within a short period of time.

In order to combat the mutating strains of the virus, it is crucial to block enough time, which is essential to develop the mutation that happens in the spike regions of the virus. That means delays in taking vaccination will provide enough time for the virus to develop a mutation in the spike region. The significant thing is that we must not put off getting vaccinated since there is a chance for the development of new strains of the virus. At present all the mutations are vaccine sensitive, but vaccine-resistant variety may emerge at any time. It is very important that we should close the door quickly, although, strategic problems are there. Mutations are more possible in partially vaccinated areas rather than fully vaccinated areas. The present policy of vaccinating on an age structure leaves many non-vaccinated at the same home and niche. In a population with very few vaccinated people

there are viruses in many hosts and the chances of mutation is high. If the population is fully vaccinated, the virus is eradicated from that community and hence mutation chances are less. This locality specific fast and total vaccination will curtail the mutagenicity of the virus, lead to its eradication and to be preferred rather than targeting entire nation and vaccinating on age structure.

### **Public Health Implications**

In order to diminish the opportunities for the coronavirus to instigate mutation, the amount of transmission rate needs to be reduced. From the author's view, it was clearly witnessed that the availability and rolling out vaccines as hurriedly and extensively as possible will definitely be illustrated as one of the major and critical ways of protecting humans over the world before they are infected by the new strains of corona viruses. As more people will be exposed to effective vaccination, the circulation of the virus will be started to decrease, thereby leads to the diminishing level of mutated strains. The authors suggest that vaccination based on age structure will give more chances to the virus to remain in the same niche with diverse mutations. On an evolutionary point of view this vaccination programme acts as a selective force against the virus and it adapts to the new environment by way of varied mutations. Of this several mutations, a few of them, form the founder principle and get established. Hence the authors propose the concept of vaccination start from a locality, vaccinating everyone and spread in a radiating style including everyone rather than age stratification. Certainly virus will be pushed back and leads to its diminishing presence and finally to eradication. It is reported that all the known new mutations are vaccine sensitive, but vaccine-resistant variety may emerge at any time before which we have to act.

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