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New unknown Sars-Cov-2 virus variants and hidden pandemics within them in developing countries

Shohreh Ghasemi [1], Zohreh Mortezania [2], Sanaz Gholami Toghchi [3] and Mahmood Dashti [4,*]

[1] *OMFS Department of Augusta University, GA, USA.*
[2] *Faculty of Medicine, Shahid Beheshti University of Medical Sciences, Tehran, Iran.*
[3] *Department of Oral and maxillofacial pathology, Dental school, Shahid Beheshti University of Medical Sciences, Tehran, Iran.*
[4] *School of Dentistry, Faculty of Dentistry, Shahid Beheshti University of Medical Sciences, Tehran, Iran.*

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Abstract

It is unclear whether the combination of one or several mutations alters the clinical and epidemiological symptoms, infectivity, pathogenicity, or vaccine efficacy of the virus. The transmission of new mutants by asymptomatic carriers is also unidentified. Antiviral drugs or vaccines have not yet been induced. Mutation pressure; however, other mutations are expected after global vaccination and after introducing verified treatments. Therefore, it is wise to be willing to bring new options to life quickly. Low-toxicity but highly genetic mutants can also be expected, which might be part of herd immunity. Clinical and rapid laboratory tests need to be developed to monitor vaccinated individuals for secondary infections caused by new variants. Significantly, personal hygiene, spatial distancing, restrictive countermeasures, facial disguises, and travel bans remain applicable fighting against the virus.

Keywords: Sequencing; Pandemic; Sars-COV2; Contamination; Developing countries

1. Introduction

Covid-19 paralyzed humanity with isolation, death, and quarantine last year, but the fear is expected to end with the advent of new vaccines such as Pfizer, Oxford AstraZeneca, and Modana. The virus develops over time as the virus copies or replicates. Sometimes it changes slightly, which is a characteristic of viruses. These changes are called "mutations." A virus having one or more than one new mutation is known as a "variation" of the previous virus. As the virus spreads commonly in the population and sources more infections, the virus is more likely to be transformed. The more chances the virus spreads, the more opportunities and their replicas have for change [1]. Numerous variants of SARS-CoV-2 are distributed worldwide. During 2020, several new variants were there, mainly [2].

In the United Kingdom, a new variant of SARS-CoV-2 (known as B.1.1.7or 20I / 501Y.V1, VOC 202012/01) has emerged with numerous mutations. It is found in many countries around the world, including the United States (USA). On January 28, 2021, British scientists presented proof [3], revealing that option B.1.1.7 might have been associated with an augmented risk of death compared to other possibilities. This new variant was informed in the USA at the end of December 2020. We need to confirm this conclusion.

* Corresponding author: Mahmood Dashti
DDS, School of Dentistry, Faculty of Dentistry, Shahid Beheshti University of Medical Sciences, Tehran, Iran.

While in South Africa, one more variant of SARS-CoV-2 (B.1.351 or 20H / 501Y.V2) occurred self-reliantly of B.1.1.7. This mutant has few transformations with B.1.1.7. Cases Related to this Option were reported in and outside of South Africa and around the world. It was reported in the USA at the end of the first month of 2021.

The SARS-CoV-2 variant (known as P.1) in Brazil was first identified among four Brazilian travelers tested in a routine survey at Haneda Airport, Tokyo, Japan. Rice field. This variant has 17 specific mutations and three other mutations inside the spike protein of the receptor-binding domain of the virus. This variant was discovered in the United States in late January 2021 [2-4].

COVID-19 has impacted oral and maxillofacial region, for example there has been reports of dermal fillers interaction with COVID-19 vaccination [5], dental practitioner can use various oral manifestation to diagnose COVID-19 even before any test or sign [6]. Due to the high load of COVID-19 particles in aerosol that is produced during dental treatments, dental practitioner has been advised to use mouthwashes for their patients before doing any treatments [7].

2. Discussion

2.1. More Variant details

2.1.1. Alpha: B.1.1.7 Linage (also known as 20I / 501Y.V1 Variant of Concern (VOC) 202012/01)

In this variation, the RBD (receptor binding domain) of the pedplomer at position 501 is altered, replacing the corrosive aminoasparagine (N) with tyrosine (Y). The abbreviation for this change is N501Y. This variation also has some different changes, including:

- This variant is supposed to have first appeared in the United Kingdom in September 2020.
- Several countries since December 20, 2020, including the United States, have reported strain B.1.1.7.
    - This option is related to increased transparency (that is, more efficient and faster transmission).
    - British scientists presented evidence in January 2021 [3], revealing that option B.1.1.7 might be associated with an enhanced risk of death compared to other variants.
    - Initial reports found no proof that this option affected disease severity or vaccine efficacy [4,8,9].

2.1.2. Beta: strain B.1.351 (also known as 20H / 501Y.V2)

- This variation has numerous alterations in spike protein, such as N501Y, E484K, and K417N. Unlike the B.1.1.7 strain found in the United Kingdom, this variation does not comprise the 69/70 deletion.
- This change was first recognized in Nelson Mandela Bay, South Africa, in a preliminary study dating back to early October 2020. Various cases have since been reported around South Africa, containing the USA.
- Options were also identified in Zambia at the end of December 2020 and proved to be the primary option in Zambia.
- Currently, there is no evidence that this option affects the harshness of the disease.
- There is evidence that one of the peplomer mutations, E484K, might affect with neutralization by few polyclonal and monoclonal antibodies [9,10].

2.1.3. Gamma: P.1 lineage (a.k.a. 20J/501Y.V3)

- Option P.1 was first reported by the National Institute of Infectious Diseases (NIID) in Japan by four Brazilian travelers sampled during a routine inspection at Haneda Airport on the outskirts of Tokyo Line B.1.1. 28.
- Line P.1 comprises three spike protein receptor-binding domain mutations, E484K, N501Y, and K417T.
- There is proof to advise that specific mutations in the P.1 mutant might affect its antigen profile and infectivity. This can affect the ability of antibodies from previous natural infections or vaccinations to recognize and neutralize the virus.
- The new report discloses numerous cases in Manaus, the largest city in the Amazon region, with variation P.1 recognized in 42% of tests sequenced since late December 2020 [10]. Approximately 75% as of October Development of this variation raises concerns about the potential for increased infectivity or people's approach to recontamination with SARS-CoV-2.
- This new variant was recognized in the United States in late January 2021.

2.1.4. Delta: B.1.617.2 Linage

- First of all, this variant peaked in India [11] in December 2020 and then in the United Kingdom [12].
- Delta variations are categorized by mutations in proteins T D614G, D950N, Δ157-15, 19R, T478K, P681R, and L452R [13]. These alterations can affect the direct immune response to deleting the critical antigen region (452 and 478) P681R. This is located at the S1-S2 cleavage site, and strains with mutations appear to have more replication, more viral load and more infection rate [14,15].
- Bernal et al. showed that vaccine efficacy after a single dose (BNT162b2 or ChAdOx1 of-19) was found to be significantly lower among people with the delta mutant (30.7%) compared to the alpha mutant (48.7%). With the ChAdOx1 nCoV-19 vaccine, the efficacy of two doses was 74.5% for the alpha mutant and 67.0% for the delta mutant [12].

2.1.5. Lambda: C.37 lineage

- The C.37 or the lambda variant was first informed in December 2020 in Peru. The genome pattern of the mutant exposed a deletion 1a (ORF1a), an open reading frame (Δ3675-3677) of the wild-type. C.37 mutants also have new deletions F490S, and L452Q mutations are present in RBD spikes F490S mutations are linked with decreased susceptibility to antibody neutralization. Nineteen mutations have been identified in this variant; therefore it is more resistant or contagious to antibodies made by previous exposure to the virus or vaccination [16_18].
- Acevedo et al. revealed that greater infectivity facilitated by Lambda pepromeras was detected compared to alpha and gamma mutants or D614G (line B). In addition, neutralization was 3.05 times for the lambda mutant, 2.33 times for the gamma mutant, and 2.03 times for the alpha mutant [18]. Tada et al. revealed an average 2.3-3.3-fold decrease in antibody titers beside lambda mutants [17].

2.1.6. Mu: B.1.621 lineage

- It was classified on August 30, 2021, as a Variation of Interest (VOI) and received the WHO name "Mu."
- The overall prevalence of Mu variability between sequenced cases dropped to less than 0.1%, but the occurrence in Colombia (39%) and Ecuador (40%) remains high (13%).
- Despite some peak changes, SARS-COV-2B.1.621 is counteracted by Pfizer vaccine-induced antibodies, but despite the success, the balance is better than other coronavirus variations. They also said it was low [19,20]. Snell et al. suggest that there are two potential vaccine cases for MU variations: escape. They characterized that some of the spike variations inside Mu 'have been detailed to show decreased balance by antibodies.
- The Mu variant was also found to have the same spike variations that have been debilitated immunization response and the Beta Variations. The presence of transformation associated with immunization escape may warrant retitling of this variant to a variant of concern [21].
- We also found that the Mu mutation shows the same differentiation as the peak, which is the intentional immune response of the beta mutant.

2.1.7. Delta Plus: AY.1 and B.1.617.2.1 Linage

- Since the emergence in India, the Delta Plus variant has spread to several countries, including the United States. The first state to report Delta Plus was Washington (May 3, 2021), followed by New York (May 6, 2021) [22].
- Delta plus is anticipated to have even more antibody-eluding properties due to the K417N mutation seen previously in the Beta variant [23].
- In India, the Delta Plus variant was found to have lower neutralization in COVID-19 naive or recovered patients vaccinated with the BBV152 (Covaxin) vaccine [24].
- It has been reported to be resistant to monoclonal antibodies such as casiribimab and imdevimab used for COVID-19, and it is argued that the affinity and infectiousness of the lung mucosa is higher than that of other alternatives [25].

2.2. Other variations

- The B.1.525 (Eta variation) was first recognized in December 2020 in Nigeria. Its spike alterations contain Q677H, D614G, and E484K, which affect antibody transmission and neutralization [26].
- The epsilon mutant (B.1.427 / B.1.429) was first identified in the USA in September 2020 and revealed D614G, L452R as spike alterations but showed effects on antibody transmission and neutralization [26].

- P.3 (Theta mutant) was first recognized in January 2021 in the Philippines, and P681H, N501Y, E484K, and D614G were detected as peak mutations affecting antibody transmission and neutralization [26].
- B.1.617.1 (Kappa mutant) was first recognized in December 2020 in India, with P681R, L452R, D614G, and E484Q identified as peak mutations that also affect antibody transmission and neutralization [26].
- B.1.526 (The Iota variant) was first recognized in December 2020 in the USA using A701V, D614G, and E484K as peak changes affecting antibody neutralization [26].
- In Brazil, P.2 (The Zeta mutant) was first recognized in January 2021, and D614G and E484K were perceived as spike alterations affecting antibody neutralization [26].
- It has been shown that not all of the variants as mentioned earlier have been revealed to cause serious illness [26].

2.3. Booster dose

There are numerous reasons why a booster dose of the COVID vaccine might be needed.

- With the passage of time, your defenses against infectious illnesses and diseases, severe illnesses, decline (i.e., your immunity response declines).
- (ii) Decreased protection against concerns (VOCs)
- (iii) Insufficient protection from the currently suggested primary series for few risk groups that might not have proof from Phase 3 clinical trials.

The basis for booster doses might vary by vaccine type, vaccination rate, risk group, and epidemiological situation. However, in situations where restrictions on the global supply of vaccines continue, booster doses will increase demand and become deficient. In national or local situations, you have not yet received a series of primary vaccinations. For now, the focus is on increasing the overall vaccination rate of the primary series (one or two vaccinations of the recent EUL vaccine) [27].

2.4. Fungal pandemic

- The current increase in coronavirus disease (COVID-19) is linked with reports of fungal infections such as mucor disease and aspergillosis, especially among critically ill patients treated with steroids. Recent cases of COVID-19 in India during the second wave of the pandemic have been associated with increased reports of invasive zygomycosis after COVID-19 [28].
- Various factors might be involved in the development of zygomycosis in COVID-19 patients, including diabetes mellitus, obesity, the progression of cytokine storms, and corticosteroid use. However, the presence of spores and other factors can also play a role [29].
- An increasing number of critically ill patients infected with ongoing COVID-19 and SARS-CoV-2 pandemics, mucormycosis, prevalence risk of patients at risk of mucormycosis due to the epidemiological burden of diabetes is essential for developing basics, COVID-19 disease severity, and use of immunomodulators, including combinations of corticosteroids and immunosuppressants in transplant and cancer patients [28].

The COVID-19 immunizations, as of now being affirmed or developed, are required to give probably some protection against new variations of the virus, as these antibodies get an expansive invulnerable reaction, including the scope of antibodies and cells. Consequently, changes or transformations in the infection ought not to deliver antibodies incapable. If any of these immunizations end up being less potent against at least one variation, the creation of the antibodies can be changed to secure against these variations [1,30,31].

Increasing vaccine production and introducing the vaccine as quickly and widely as possible are also necessary to defend people before they are directly exposed to the virus and prevent the risk of new emerging variations. Maximize global protection against new variants and minimize the risk of infection. In addition, ensuring equal access to the COVID-19 vaccine is more important than ever to address the development of the pandemic. As more people are vaccinated, it is expected that the circulation of the virus will decrease, and mutations will decrease.

Developing countries, even if that happens, do not have the equipment to identify new options. Given the strange outbreaks of death and viral infections, it is very likely that new and old methods of safe storage, treatment and infection have already emerged. These new variants can threaten not only these developing and developing countries but also other countries. The new virus can move without worrying about borders, infect the entire world again, and cause new pandemics that can easily endanger human survival [31,32].

3. Conclusion

Good public health policies must take into account the appearance of new viral variations. In addition, more study and extensive research are needed to address new variants of the virus. Never give up current regulations such as national quarantine, travel bans, especially strict social distances during vacations, respiratory hygiene and frequent hand washing. Characterization of the new viral variation needs molecular biology experimentation, contact tracing, and COVID-19 testing. Organizations such as CDC and WHO need to monitor the Covid-19 mutation and the USA and other European and developing countries to prepare for the mutation and stay one step ahead of the virus. Vaccines need to be prepared for new mutants to achieve the desired results.

Compliance with ethical standards

Disclosure of conflict of interest

all authors have consent for publication in the journal.

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