Research Article

NEW SARS-COV-2 VARIANTS ON THE CURRENT PANDEMIC SITUATION IN INDIA.

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Abstract

Coronavirus 'SARS-CoV-2' infection is the primary cause of the global pandemic of novel coronavirus disease. It affects people of all ethnicities, races, and communities. Corona viruses are enveloped RNA viruses with spike-like projections on their tops and a diameter of 60 to 140 nm. With 3,52,991 people testing positive for coronavirus infection in a day, the highest so far, India's total tally of COVID-19 cases has climbed to 1,73,13,163 while active cases have crossed the 28-lakh mark, according to the Union Health Ministry data updated on Monday. The death toll increased to 1,95,123 with a record 2,812 new fatalities. Registering a steady increase, the active cases have increased to 28,13,658 comprising 16.25 per cent of the total infections, while the national COVID-19 recovery rate has further dropped to 82.62 percent. To conclude, governments should enact or strengthen sick leave entitlements to prevent unnecessary pressure to work while sick, incentivize industries to provide better working conditions, financially support temporary business closures when appropriate, and provide housing for those living in cramped or shared housing. Such interventions may help to reduce group transmission significantly. The local COVID-19 rates and risk factors will determine which of these steps should be implemented.

Keywords: Coronavirus, Immunization, Variants, Vaccines

I. Introduction

The pandemic of the 21st century in the entire world is infection with the coronavirus.[1] Coronaviruses are pathogenic agents that cause serious diseases in a variety of animal species including infections in humans. Coronavirus is a large, approximately spherical particle with bulbous surface projection. The viral envelope is mainly

consisted of lipid bilayer in which the structural proteins Membrane (M), Envelope (E) and Spike (S) are intercalate and the ratio of E:S:M in lipid bilayer is approximately 1:20:300 coronavirus has approximately 74 surface spikes. The surface spikes of coronavirus are homotrimeric to S protein and consist of S1 and S2 subunits. S1 protein is indeed a class I fusion protein that helps in receptor binding and membrane fusion between the host cell and the virus and the S1 subunit forms the spike 's head and has a receptor-binding domain, while the S2 subunit forms the spike's stem and allows protease activation to be fused and the E and M proteins are critical in viral envelope formation and help to maintain shape and structure.[2] The world health organization, urges people to follow a healthier lifestyle, saying it will increase their chances of a quick recovery.[3,4] On 23 March 2020 India's government took all necessary measures to avoid COVID-19 pandemic.[5] The dissemination of COVID-19 has contributed to the closing of educational institutions around the world.[6] Pandemic of Novel Corona Virus disease is rampant and self-isolation or quarantine is one of the core strategies in flattening the curve of infection rates. [7,8] The COVID-19 pandemic has devastated healthcare systems, shut down schools and communities, and plunged the world into an economic recession. While 2020 was a challenging year, 2021 looks to be difficult with the emergence of multiple variants of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The race to vaccinate the world will need to respond to the pathogen's constant evolution to evade immunity.[9]

New SARS-COV-2 Variants

Immune-escape variants have raised concerns about the effectiveness of vaccines as the world scales up SARS-CoV-2 immunisation. COVID-19 vaccines have shown up to 95% efficacy in preventing clinical cases and up to 100% efficacy in preventing severe disease or admission to hospital in settings with pre-existing variants. New variants, especially 501Y.V2 (B.1.351), which escape natural-induced and vaccine-induced immunity, have created uncertainty on whether the vaccines are effective in preventing both mild and severe COVID-19.[10,11] Three new variants that have rapidly become dominant within their countries have aroused concerns: B.1.1.7 (also known as VOC-202012/01), 501Y.V2 (B.1.351), and P.1 (B.1.1.28.1). These lineages are each characterized by numerous mutations in the spike protein, raising concerns that they may escape from therapeutic monoclonal and vaccine-induced antibodies. The B.1.1.7 variant (23 mutations with 17 amino acid changes) was first described in the United Kingdom on December 14, 2020, is N501Y located in the receptor-binding domain (RBD) of spike. This variant is seemingly more transmissible and possibly more virulent.[12] The 501Y.V2 variant (23 mutations with 17 amino acid changes) was initially reported in South Africa on December 18, 2020; and the P.1 variant (approximately 35 mutations with 17 amino acid changes) was reported in Brazil on January 12, 2021. By February 22, 2021, the B.1.1.7 variant had been reported in 93 countries, the 501Y.V2 variant in 45, and the P.1 variant in 21. All three variants have the N501Y mutation, which changes the amino acid asparagine (N) to tyrosine (Y) at position 501 in the receptor-binding domain of the spike protein. The 501Y.V2 and P.1 variants

both have two additional receptor-binding–domain mutations, K417N/T and E484K. These mutations increase the binding affinity of the receptor-binding domain to the angiotensin-converting enzyme 2 (ACE2) receptor. Four key concerns stemming from the emergence of the new variants are their effects on viral transmissibility, disease severity, reinfection rates (i.e., escape from natural immunity), and vaccine effectiveness (i.e., escape from vaccine-induced immunity[13] The 501Y.V2 variant spread rapidly in South Africa, accounting for 11% of the viruses sequenced (44 of 392) in the first week of October 2020, for 60% of those sequenced (302 of 505) in the first week of November 2020, and for 87% of those sequenced (363 of 415) in the first week of December 2020. In Western Cape, a South African province where the 501Y.V2 variant is predominant, a threshold of 100,000 cases of Covid-19 was reached approximately 50% more quickly in the second wave of infection than in the first wave (54 vs. 107 days). The 501Y.V2 variant has been estimated to be 50% more transmissible than pre-existing variants in South Africa, and B.1.1.7 to be between 43% and 82% more transmissible than pre-existing variants in the United Kingdom.

Earlier study on B.1.351 demonstrated that this variant is refractory to neutralization by a number of monoclonal antibodies directed to the top of RBD, including several that have received emergency use authorization. Moreover, this variant was markedly more resistant to neutralization by convalescent plasma and vaccine sera. Importantly, these effects were largely mediated by the E484K mutation. These finding are worrisome in light of recent reports that two vaccine trials showed a substantial drop in efficacy in South Africa. Nearly all of the newly identified B.1.526 variants have a set of common mutations in the spike protein: L5F, T95I, D253G, E484K, D614G, and A701V.[12,14,15]

Discussion

As the world ramps up SARS-CoV-2 immunization, immune-escape variants have sparked questions about vaccine efficacy. In settings with pre-existing versions, COVID-19 vaccines have demonstrated up to 95% efficacy in preventing clinical cases and up to 100% efficacy in preventing serious disease or hospitalization. New variants, especially 501Y.V2 (B.1.351), which evade both natural and vaccine-induced immunity, have cast doubt on whether vaccines are successful in preventing both mild and serious diseases. COVID-19.[10,11] D614G was one of the first variants to appear and quickly become globally dominant. Although some studies have shown that this strain is more contagious, we and others discovered that sera from convalescent people effectively neutralized both wild type and D614G forms. Recent genomic surveillance in the United Kingdom, however, has revealed the rapid spread of a novel lineage known as B.1.1.7 (also known as VOC-202012/01 or 501Y.V1). B.1.1.7 has three amino acid deletions and seven missense mutations in spike, including D614G and N501Y in the ACE2 receptor-binding domain (RBD), and is more contagious than D614G. Several studies have shown that convalescent and vaccine sera cross-neutralize B.1.1.7 variants with only slightly reduced potency, implying that previous infection or vaccination with wild-type SARS-CoV-2 can still protect against B.1.1.7 variants.[16,17]

Conclusion

As the number of COVID-19 cases linked to variants rises in the nation, the degree of urgency and volume of messaging, as well as local control programs should grow. Furthermore, depending on the level of local community transmission, enhanced mitigation measures may be needed. The following are some of them:

1) Emphasizing the importance of wearing face coverings in all indoor public spaces, classrooms, offices, and congested outdoor spaces.
2) Considering the temporary closure of non-essential indoor spaces where face coverings are not permitted.
3) Considering extending the 2 m (6 ft) rule.
4) Enhancing indoor ventilation.
5) Resolving social disparities, which in many countries are the primary drivers of context group transmission.

To conclude, governments should enact or strengthen sick leave entitlements to prevent unnecessary pressure to work while sick, incentivize industries to provide better working conditions, financially support temporary business closures when appropriate, and provide housing for those living in cramped or shared housing. Such interventions may help to reduce group transmission significantly. The local COVID-19 rates and risk factors will determine which of these steps should be implemented.

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