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Editorial

SARS-CoV-2 vaccines: evolution and escape

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SARS-CoV-2 was declared a pandemic virus a year ago and has caused more than 140 million confirmed cases and 3 million deaths worldwide (1). In late 2020, vaccines based on the SARS-CoV-2 *spike* protein were the first to be approved in the health emergency. The *spike* protein interacts with the human ACE2 receptor at the beginning of the infection process, this basic knowledge gave rise to a vaccine whose target of action was the *spike* to trigger the action of neutralizing antibodies (2). Vaccines applied in the Western Hemisphere do not follow the traditional route of attenuated or inactive viruses; the new trend is messenger RNA methodologies, some are inserted into viral vectors that present the antigen to the cells of the immune system cells and induce humoral memory. However, vaccines based on recombinant peptides, attenuated and inactive viruses, have been successfully applied in Latin America and Asia, which overcome storage temperature and geopolitical aspects limitations.

Among the vaccines that use the mRNA, Pfizer and Moderna's methodology obtained promising results in phase III clinical trials, showing efficacy> 94% (3,4). Among the vaccines that use the viral vector methodology are AstraZeneca (AZD1222), Johnson & Johnson (JNJ- 78436735), and the Russian Gam-COVID-Vac (Sputnik V), they have shown the efficacy of 63, 66, and 91.6%, respectively. All of them reduce the risk of severe disease by 100% (5,6,7). On the other hand, the Chinese pharmaceutical company Sinovac successfully developed the Coronavac vaccine that uses complete virus inactivated with β-Propiolactone, its protection efficiency against the disease is 50.65% 100% for severe and fatal cases (8).

Despite the rapid design and success of vaccines, in recent months through genomic surveillance viral strains presenting mutations in the *Spike* protein's immunodominant sites have been discovered. Among them are the Receptor Binding Domain (RBD) and the N-terminal Domain (NTD) giving it the ability to escape neutralization by antibodies. One of the most important variants worldwide is the South African, known as B.1.351 or 501Y.V2, which has 3 RBD mutations (K417N, E484K, and N501Y) and has been shown to have the ability to escape neutralization by sera from convalescent patients (9). Besides, cases of reinfection have been observed in patients infected with the UK (B.1.1.7) and Brazil (P.1) variants. These mutations that have happened so quickly should not surprise us, since RNA viruses such as SARS-CoV-2 naturally present a high mutation rate (10).

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Bearing in mind the immunological evasion that the virus shows: how long will the vaccines currently being applied to be able to maintain their efficacy? Some studies suggest that the presence of RBD mutations reduces the efficacy of neutralizing antibodies from individuals immunized with one or two doses of mRNA-1273 (Moderna) between 2.4 and 6.4-fold (11) and approximately 10-fold for BNT162b2 (Pfizer) (12) and could lead patients who have been vaccinated to become infected with variants such as B.1.351 or P.1 (13). In Colombia, the circulation of the P.1 (Brazil), B.1.17 (UK) and B.1.351 (South Africa) haves already been reported and autochthonous variants may be circulating with mutations in RBD and NTD such as B.1+E484K and B.1.160+E484K. One of the impacts that the immune escape of viruses has had on the immune response is reflected in the administration of plasma from convalescent patients. The use of plasma from a patient who has overcome symptomatic infection does not guarantee therapeutic success in recipient patients. The quantification of neutralizing antibodies is essential for its administration since it could not contain a significant amount of antibodies, confronting the virus at suboptimal concentrations of nABs, exert selective pressure for the emergence of new variants resistant to patient's antibodies (14).

Due to the natural evolution of viruses and the selective pressure of the vaccines themselves, it is essential to establish exhaustive genomic surveillance to identify possible mutations that confer viruses the evasion of neutralizing antibodies. For now, mutations that have an impact on the reduction of neutralizing antibodies, which weakens the action of the vaccines have been identified in the main variants such as those in Brazil, the United Kingdom, and South Africa (K417N, E484K, and N501Y). Genomic surveillance of autochthonous variants is important to detect possible mutations. In this way, appropriate decisions could be made regarding the possible modification of the molecular structure of vaccines. The formulation of a new vaccine that contains the mutations of the *spike* protein (K417N, E484K, and N501Y), added to of biosafety, measures, are the prevailing options for the containment of this pandemic virus (10,15).

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