Coronavirus Pandemics Era and Cancer Patients

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A Era do Coronavirus Pandêmico e os Pacientes Oncológicos

Era de Coronavirus Pandémico y Pacientes con Cáncer

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INTRODUCTION

There are more and more studies that establish that viruses similar to the coronavirus (SARS) can be transmitted from animals to people hundreds of thousands of times a year, facilitating new adaptations in humans and therefore the development of pandemics[1]. Recently, a work under review based on samples from the Indochinese peninsula, concludes that these viruses can move rapidly in wide geographic ranges in bat reservoirs, frequently infecting people who work in caves, such as guano collectors, or certain ascetic religious communities who spend time in or very close to caves, as well as tourists who visit caves, at particular risk of exposure[2]. In addition, it must be considered that it will also depend on the evolution of the SARS-CoV-2 (COVID-19) variants associated with global vaccination campaigns in order to maintain the efficacy of current vaccines[3]. It is therefore of vital importance to continue innovating in new vaccination strategies that allow covering the majority of coronaviruses of animal origin, as well as new variants derived from SARS-CoV-2.

DEVELOPMENT

Variants SARS-COV-2

The progress of national and global vaccination programs, the emergence and spread of Variants of Concern (VOC) and Variants of Interest (VOI), as well as public responses to non-pharmaceutical interventions (NPI) will be the key factors in the development of the COVID-19 pandemic. In the short term, in those countries with a low vaccination rate, a reduction of restriction measures will produce the spread of the SARS-CoV-2 virus, which favors the development of variants (VOC and VOI) by increasing mobility and mixing of population[4]. In this article the Variants of Concern (VOC) and Variants of Interest (VOI) which are being tracked by WHO (World Health Organization) and ECDC (European Centre for Disease Prevention and Control) were analyzed, as well as future perspectives in relation to the development of the innovative vaccines against new COVID-19 variants and new species of coronavirus and a brief perspective of cancer patients in this scenario.

Four categories have been defined by WHO[5] as established on May 31st 2021: Variant of concern (VOC), Variant of interest (VOI), Variant Under monitoring and De-escalated variants.

a. Variants of Concern (VOC) are those involving one or more of the following changes at a degree of global public health significance in relation with the increase of: i) transmissibility or virulence; ii) change of clinical presentation; and finally, iii) Decrease in efficacy of public health and social measures or available diagnostics, vaccines, or therapeutics.

The variants were designated by one or more Pango lineages[6] and any additional characteristic spike protein changes due to additional mutations.

Figure 1 shows the VOC variants described so far: Beta, Gamma and Delta (as well as not defined variant from United Kingdom).

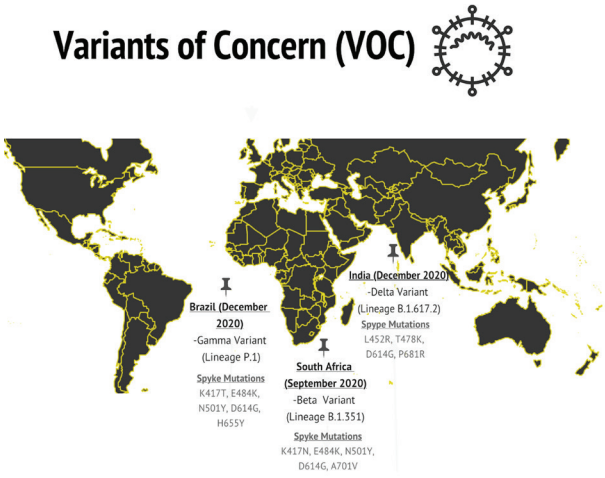

Figure 1. Variants of Concern (VOC) of the SARS-CoV-2 virus[7]

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Among the VOC variants it must be highlighted the Delta variant, which was detected in India on December 2020, belonging to the B.1.617.2 variant and displaying a community transmission that favored its wide spread throughout the world[8].

Multiple studies were carried out about the effectiveness of the COVID vaccines against Delta variant. The analysis of the serum from individuals who had received one dose of the mRNA[9] vaccine revealed that it had barely discernible inhibitory effect on the Delta variant. Administration of two doses of the vaccine generated a neutralizing response in 95% of individuals, with antibodies titers three-to-five-fold lower against the Delta variant than against the Alpha variant.

Thus, the spread of the Delta variant is associated with an escape from antibodies that target non-RBD and RBD epitopes of the spike protein[9]. According to a different study, to guarantee an adequate response to individual and collective protection, it is necessary to use the best weapon against the virus: vaccines. A study published in the New England Journal of Medicine[10], with 14,000 people who had tested positive for the Alpha variant and more than 4,000 with the Delta variant, points to the high protection against infection of full vaccination against the Delta variant (88% with Pfizer and 67% with AstraZeneca), but a low percentage with a single dose (35% with Pfizer and 30% with AstraZeneca)[10]. Finally, Cascella et al.[11] analyzed briefly the different variants of SARS-CoV-2 and the efficacy of different available vaccines for prevention and treatments against COVID-19 and its variants.

b. Variant of interest (VOI). For these variants, evidence is preliminary (or not clear) available on genomic characteristics, epidemiological evidence or in-vitro results that could imply in an important impact on transmissibility, severity and/or immunity, realistically having an impact on the epidemiological situation. This information is available on the website of the European Centre for Disease Prevention and Control[7].

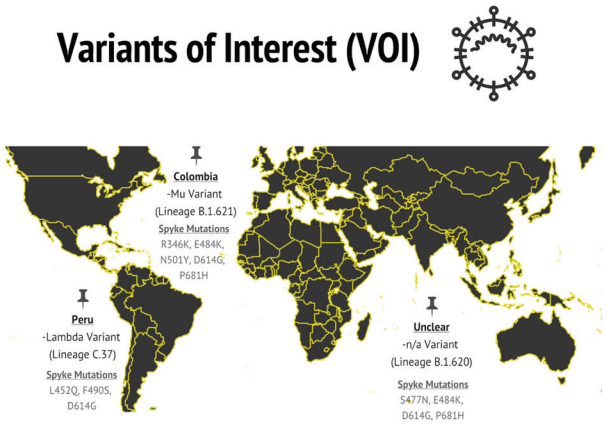

Figure 2. Variants of Interest (VOI) of the SARS-CoV-2 virus[7]

Among the VOI variants it must be highlighted the **Mu variant** detected in Colombia in January 2021 and belonging to the B.1.621 lineage, due to its scientific interest. Since then, sporadic cases and some outbreaks have been reported in South American countries. Cases have also been reported in the United Kingdom, Europe, United States, and Hong Kong. Currently, this variant is located mainly in Colombia and Ecuador, where it represents 39% and 13% of COVID-19 cases, but worldwide it only represents 0.1% of infections. Although more scientific studies are required in relation to immune escape, a mutation of interest E484K associated with immunological resistance has been described[12].

c. Variant under monitoring have been detected in countries as Egypt (COVID variant lineage C.36 more mutation L452R), Russia (COVID variant lineage AT.1), Italy (COVID variant lineage P.1 more mutation P681H), United Kingdom (COVID variant lineage B.1.617.2 more mutation K417N), South Africa (COVID variant lineage C.1.2) and India (two COVID variants, the first belonging to B.1.617.2 with mutation E484Q and the second, COVID variant lineage B.a.617.2 associated to the mutation Q613H).

Among them, the main COVID variant with mutations of the spike protein associated to higher transmission and putative decrease of the immune response are from Egypt[13], Italy[14] and finally, Russia and South Africa where the E484K mutation from spike protein has been described[7,12].

d. De-escalated variants, additional SARS-CoV-2 variants whose detection has been reduced due to at least one of the following points: (1) the variant has been circulating for a long time without any impact on the health public epidemiological situation, (2) the variant is no longer circulating, (3) scientific evidence shows that the variant is not associated with any public health problem. The monitoring of these variants can be carried out through the ECDC website)[7].

SARS-COV-2 VARIANTS AND CANCER PATIENTS

More and more studies appear where the ability to mutate the SARS-CoV-2 virus is analyzed in immunocompromised patients such as lymphomas[15,16]. Moreover, in this study carried out by Siqueira et al.[17], the authors concluded that cancer patients had a greater capacity to develop SARS-CoV-2 variants, with four globally dominant SARS-CoV-2 haplotypes (C241T, C3037T, C14408T and A23403G) as the majority of consensus sequences analyzed.

Therefore, it is essential to carry out vaccination in immunocompromised patients such as cancer patients to prevent the development of new variants of SARS-CoV-2.

Future perspectives

Scientists must continue to work in search of a new universal vaccine that covers the majority of variants SARS-CoV-2 and coronaviruses (pan-coronavirus). With this objective, there are several studies that have shown important results. First, scientists from the Gillings School of Global Public Health at the University of North Carolina (United States) developed a vaccine targeting sarbecoviruses. Sarbecoviruses, which are part of the great family of coronaviruses, have been responsible for the most devastating diseases of the last 20 years, SARS, and COVID-19. The orientation of the study is based on the use of mRNA, like the Pfizer and Moderna vaccines, but instead of using the mRNA code of a single virus, they mixed multiple viruses showing efficacy in animal models[18]. Along the same lines, researchers from the United States, France, Italy, Belgium, and Switzerland have used a cocktail of nanoparticles of binding domain to the spike protein receptor, giving rise to an important immunogenic response against sarbecoviruses[19]. In a third work published in the journal Science, the authors analyzed the structure and activity of antibodies with a broad neutralization capacity of beta-coronaviruses, a genus to which the coronaviruses responsible for SARS, MERS and COVID-19 also belong. Knowledge of these antibodies allows the guided design of a new generation of vaccines against these viruses[20].

Finally, Schmidt and collaborators studied the presence of neutralized pseudotypes bearing highly resistant SARS-CoV-2 polymutant spike (PMS proteins), or diverse sarbecovirus spike proteins in the plasma from individuals who had been infected and subsequently received mRNA vaccination. The authors concluded that PMS proteins encoding numerous neutralization escape mutations may represent useful immunogens to broaden the polyclonal antibody response elicited by first generation SARS-CoV-2 vaccines[21].

CONCLUSION

After the lesson learned in this SARS-CoV-2 (COVID-19) pandemic, it should be anticipated the possible success of variants of SARS-CoV-2 and/or new coronaviruses, using science as the basis for monitoring possible animal reservoirs together with the development of prevention measures such as universal vaccines applied to populations at higher risk of infection, including cancer patients.

DECLARATION OF CONFLICT OF INTEREST

There is no conflict of interest to declare.

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