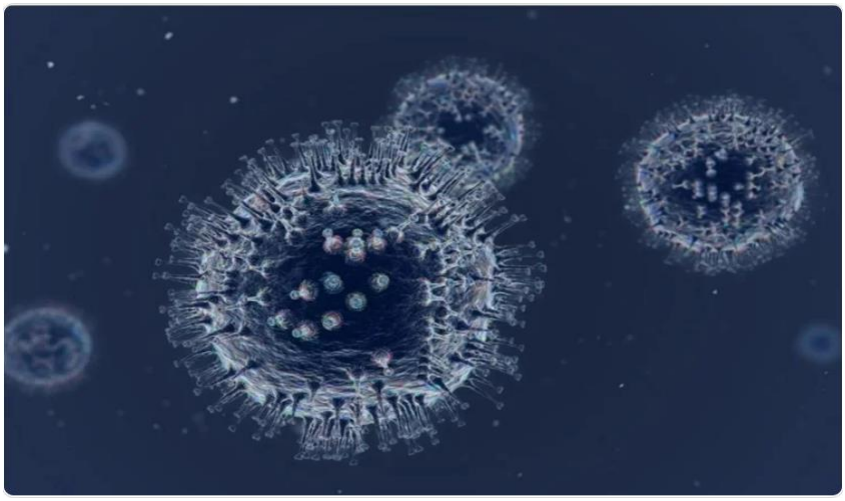
Immune Response of T-cell in Previously Infected and Vaccinated Individuals Effective Against SARS-CoV-2 Omicron Variant

As the ongoing coronavirus disease 2019 (COVID-19) pandemic approaches its third year, the focus has shifted towards the emergence and spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants of concern (VOCs) capable of escaping the complex immune response generated by prior infections or vaccinations. Throughout the pandemic, each of these variations of concern (VOCs) has been linked to widespread infection.



Introduction

While most of these VOCs exhibit varying degrees of antibody resistance in vitro, vaccination and prior infection with SARS-CoV-2 provide significant protection against breakthrough or re-infections – particularly in terms of mitigating serious disease and mortality. The new B.1.1.529 or Omicron variant harbors a greater number of mutations than the previous VOCs.

If the Omicron VOC mutations evade anti-SARS-CoV-2 immune response—whether triggered by vaccination or infection—it would have serious implications on the efforts to curb this pandemic. Additionally, the variant has been reported from every continent except Antarctica, indicating that, like other VOCs, it has a high potential for dissemination.

A significant proportion of the mutations linked to the Omicron VOC are present in the virus's Spike protein, probably due to selection for evasion of antibody responses. Moreover, this might impact the ability of pre-existing antibodies to neutralize the virus; however, to what extent, remains uncertain. It's also unclear how these mutations alter non-neutralizing binding antibody responses.

While it is important to identify whether or not Omicron is susceptible to existing humoral responses, T-cell-associated immunity is complicated for viruses to overcome, considering the wide and adaptable response generated in a given individual, as well as the variety of human leukocyte antigens (HLA) haplotypes between individuals.

A prior study of CD8+ T cell responses to the original SARS-CoV-2 variant in convalescent individuals revealed a broad and variable immune response in nearly all patients studied, even those with relatively low anti-SARS-CoV-2 antibody responses. A succeeding analysis found that mutations associated with the Alpha, Beta and Gamma VOCs had minimal cross-over with the epitopes identified

in this earlier study (1/52 epitopes affected), implying that the CD8+ T cell response from a previous infection would almost definitely still be efficient against the new variant.

The mutations related to Omicron VOC are studied in the same way in the present investigation published.

Findings

The detailed procedures of the prior two pieces of research were already published. This study selected peripheral blood mononuclear cell (PBMC) samples from polymerase chain reaction (PCR)-confirmed, recovered COVID-19 convalescent plasma donors for examination of their anti-SARS-CoV-2 CD8+ T cell responses. All samples were acquired in April and May 2020 in the Baltimore, MD and Washington, DC region from patients who possessed at least one of six different HLA haplotypes (HLA-A*01:01, HLA-A*02:01, HLA-A*03:01, HLA-A*11:01, HLA-A*24:02, and HLA-B*07:02).

Among the samples, only one mutation associated with the Omicron variant, in the Spike protein (T95I), out of 50, overlapped with a CD8+ T-cell epitope (GVYFASTEK) and was identified in this population. This epitope was restricted to HLA*A03:01 and HLA*A11:01. Meanwhile, two individuals elicited a T-cell reactivity – typed as HLA: A03:01 and HLA: A03:01/ HLA: A11:01, respectively.

Considering the ability to induce T-cell responses against GVYFASTEK on both alleles in one individual, this epitope was a low-prevalence target in both of these individuals. This accounted for 0.1% and 0.4% of all CD8+ T-cell responses in each individual, respectively. Furthermore, this epitope was one of five and one of thirteen of the anti-SARS-CoV-2 epitopes targeted by the two individuals, respectively.

The previously unknown Omicron variant of concern has more mutations than any other variant uncovered until now. Further, several of the mutations linked to the Omicron variant are located in areas likely to be bound by neutralizing antibodies – signifying that the first line of immune defense against COVID-19 may be weakened.

T-cell-based responses, in addition to antibodies, are produced by both natural infection and vaccination. Here, the researchers wanted to assess if sections of the virus or epitopes, that were targeted by the CD8+ T-cell response—in 30 people who recovered from COVID-19 in 2020—were mutated in the Omicron variety.

The results revealed that one of the 52 epitopes identified in this cohort included an Omicron-mutated amino acid. These findings imply that the T-cell immune response in previously infected, and most likely vaccinated, individuals should still be effective against Omicron.

Conclusion

These findings illustrate that despite the continuous pattern of the ongoing evolution of SARS-CoV-2, it has not resulted in any significant accumulation of CD8+ T-cell escape mutations. The results also reveal that existing CD8+ T-cell responses from a previous SARS-CoV-2 infection, and most likely vaccination, will recognize the Omicron VOC and should provide significant protection against COVID-19.

Source:

https://www.news-medical.net/news/20211215/T-cell-immune-response-in-previously-infected-and-vaccinated-individuals-effective-against-SARS-CoV-2-Omicron-variant.aspx