

ABSTRACT

The SARS-CoV-2 has been subjected to mutation resulting in the appearance of VOC which are Alpha, Beta, Gamma, Delta and Omicron variants. T-cell is involved in viral infection control and providing immunological memory that is important for long-term protection against the infection. Analyses of conserved epitope, nonconserved epitopes, and phylogenetic trees of T-cells epitope are conducted to shed a bit of light on the evolutionary relationship between the original Wuhan-Hu-1 and the VOCs. The conserved epitopes with good immunogenicity and promiscuity may serve as candidates for vaccine. Many regions were conserved among the variants, indicating those regions may be crucial for the virus development because the regions survived multiple mutations that occurred. The nonconserved epitopes among variants of concern vary with each other, almost all the mutations differ in sequences of amino acids resulting in a completely different epitope peptide. A large portion of mutated epitopes underwent characteristic changes, including changes of immunogenicity value and amount of HLA binder. Phylogenetic trees for MHC Class I and MHC Class II epitopes were also constructed. However, the evolutionary relationship between the epitopes of Wuhan-Hu-1 with other VOCs is still vague despite the fact that all variants originated from Wuhan-Hu-1. One thing that can be seen from the phylogenetic analysis is that sequences with differences but belonging to the same variant category will still be closely related. Additionally, by observing all the mutated epitopes and phylogenetic analyses, it was found that the variants possibly evolved simultaneously from Wuhan-Hu-1 instead of consecutively.

Keyword: SARS-CoV-2; Wuhan-Hu-1; Variants of Concern (VOC); T-cell epitopes; Phylogenetic tree