ABSTRACT

The COVID-19 global pandemic caused by SARS-CoV-2 has been going on for almost two years and has negatively impacted the global population. The same as other viruses, SARS-CoV-2 is continuously mutating to adapt to the environment, and this may result in negative impacts, such as an increase in virus transmission, virulence, and even resistance to vaccines. Hence, questions regarding whether the currently available vaccines are still effective against the currently circulating SARS-CoV-2 variants have risen and are widely discussed. In this study, next-generation sequencing was done to do genomic surveillance, and a complementary immunoinformatics study was done to predict T-cell epitopes from structural proteins of circulating SARS-CoV-2 variants in Indonesia. Consecutively, conservancy analysis was performed to further study the consequences of mutations in the epitopes of the circulating variants. This study found that the predicted epitopes from the envelope were relatively conserved, while nucleocapsid and spike proteins have a higher percentage of non-conserved epitopes. On the other hand, the predicted membrane epitopes were conserved in VOC Delta, but there were heterogeneous epitopes found in the VOC Omicron in January 2022. It was predicted that mutation in the peptide residue could increase the possibility of T-cell receptor escape and lower the binding affinity of peptides to HLA molecules. However, the consequences and effects of mutation in the SARS-CoV-2 epitopes still need to be further investigated.

Keywords : Next-generation Sequencing; T-cell Epitopes; SARS-CoV-2; Structural Proteins; Vaccine; Indonesia.