ABSTRACT

The COVID-19 pandemic is a worldwide threat caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). This highly contagious virus has dramatically impacted the world's demographics, including Indonesia. Some method to reduce the number of COVID-19 is by developing and implementing vaccination programs. Peptide-based vaccines, especially those developed based on the T-cell epitopes, could be the solution for the emergence of SARS-CoV-2 variants. Here, the development of T-cell epitope-based vaccines will use immunoinformatic tools. It starts with obtaining the Indonesian SARS-CoV-2 sequences and the Indonesian HLA allele. Using IEDB tools, epitopes for MHC class I, class II, and B cells were acquired. The epitopes were evaluated based on several criteria: immunogenicity, IFNγ inducing ability for MHC class II, promiscuity in HLA alleles, conservancy analysis, and homology analysis to the human proteome. Several epitopes were chosen as VC which are six of MHC class I, four of MHC II, and three of B cells epitopes which were linked using linkers. Once again, it was evaluated based on having antigenicity, allergenicity, toxicity, and having a good physicochemical characteristic like pI, half-life, good stability, good GRAVY score, high population coverage, and non-homologous to human microbiome. The final vaccine construct consisted of 249 AA sequences with coverage of 99% in Indonesia. Lastly, the interaction between TLR4 was evaluated and visualized. With this, specialized vaccines -that are highly specific, eliciting long-lasting adaptive immunity, and did not have unwanted immune responses- for the Indonesian population could be developed.