Abstract

SARS-CoV-2 pandemic is still ongoing in Indonesia, and multiple variants are identified to emerge along the progress. Study of vaccines found out that the newer variants had mutations within the target sites of currently available vaccines, especially on the spike region of the genome, thus reducing most vaccines effectiveness. Thus as precaution for possible future mutation, a multi-epitope vaccine was designed using consensus sequences within Indonesian population. The sequences of Indonesian SARS-CoV-2 samples were taken from GISAID database which undergoes multiple sequence allignment for identification of consensus sequences which were used for epitope prediction. The epitopes were selected as vaccine candidate considering their immunogenicity, toxin characteristic, antigenicity, allergenicity, and Interferon inducing capability. The vaccine construct was further validated through docking prediction and immune simmulation. The resulting design is a 881 amino acids long vaccine that contains CTL, HTL ,and B cell epitopes. Each of the vaccine component was validated to be non-toxin, non-allergen, and antigenic. Trial of docking the vaccine and TLR4 showed a successful binding, and the immune simmulation result indicated capability of the vaccine to elicit CTL, HTL, B cell, and dendritic cell responses. Overall, the vaccine constructed showed a promising result and can be used for candidate as COVID-19 vaccine. However, further wet-lab validation is required before application of the vaccine.

Keywords : Epitope, Indonesia, In silico, Vaccine, SARS-CoV-2