ABSTRACT

Cancer, the cause of the highest mortality number worldwide in 2020, had the majority of its deaths coming from low to middle income countries, which includes Indonesia. The importance of searching for cancer treatment therefore rose due to the high mortality number. Cancer vaccine is currently considered one of the most favorable approach among cancer therapies due to its high specificity, low toxicity, and ability to induce immunological memory. Therefore, this study adopted *in silico* immunoinformatics approach to design a cancer vaccine based on MAGE-A10 and NY-ESO-1, members of CTAs family known to be expressed in varieties of tumors. The epitopes of MAGE-A10 and NY-ESO-1 that are able to bind to selected HLA alleles of the Indonesian population were selected, clustered, and assembled with HBHA as adjuvant and linkers to construct the vaccine. The characteristics of the vaccine were then tested along with its cross-reactivity and was put through immune simulation. The vaccine's secondary and tertiary structure was also predicted and assessed. The resulting vaccine was immunogenic, non-allergenic, thermostable, may be able to cross-react with few other CTAs, would not disrupt gut immune homeostasis, and able to induce production of cytokines, antibodies, and immune cells such as CD4 and CD8 T cells, B cells, and NK cells. Immunological memory response may also be induced through the CD4 T memory cells. However, the protein model predicted was of unsatisfactory quality and may need structure refinement to obtain acceptable quality models first before further studies can be done.

Keywords: immunoinformatics, peptide-based cancer vaccine, MAGE-A10, NY-ESO-1, T cell epitopes.