Abstract

Shellfish allergy is one of the highest prevalence allergies in the world, accounting for 7.7% of the population including Indonesia. Thus, the development of T cell epitope and B cell epitope based vaccines play an important role in future prospects for alternative treatment for allergy. The vaccine aims to induce the immune system so it will not react towards the allergen though the body already went through sensitization. In this experiment, immunoinformatics methods were used to predict the T cell and B cell epitopes from Pen a 1 allergen, tropomyosin from *Penaeus aztecus*. T cell epitopes were obtained from NetCTLpan for HLA Class I binding peptide and NetMHCIIpan for HLA Class II binding peptide. As for B cell epitopes, three different servers that are complementary to each other were used; BepiPred 2.0, IEDB B Cell Epitope Prediction Tool, and ABCpred. T cell epitopes were analyzed further for their immunogenicity, IFN-gamma-inducing ability, cross-reactivity against human peptides, and conservancy in other tropomyosin sequences. The vaccine was then constructed using promiscuous T cell and B cell epitopes using beta-defensin as adjuvant and appropriate linkers. The vaccine construct has good population coverage and therefore potential to be developed as an allergen immunotherapy for the Indonesian population.

Keyword: shellfish allergy, multi epitope peptide-based vaccine, immunoinformatics, pen a 1, cytotoxic T cells, helper T cells