Bioinformatics characterization of Plasmodium knowlesi apical membrane antigen 1 (PkAMA1) for multi-epitope vaccine design

ABSTRACT

Malaria caused by Plasmodium knowlesi species has become a public health concern, especially in Malaysia. Plasmodium knowlesi parasite which originates from the macaque species, infects human through the bite of the Anopheles mosquitoes. Research on malaria vaccine has been a continuous effort to eradicate the malaria infection, yet there is no vaccine against P. knowlesi malaria to date. Apical membrane antigen 1 (AMA1) is a unique surface protein of all apicomplexan parasites that plays a crucial role in parasite-host cell invasion and thus has been a long-standing malaria vaccine candidate. The selection of protective epitopes in silico has led to significant advances in the design of the vaccine. The present study aimed to employ bioinformatics tools to predict the potential immunogenic B- and T-cell epitopes in designing malaria vaccine targeting P. knowlesi AMA1 (PkAMA1). B-cell epitopes were predicted using four bioinformatics tools, i.e., BepiPred, ABCpred, BcePred, and IEDB servers whereas T-cell epitopes were predicted using two bioinformatics servers, i.e., NetMHCpan4.1 and NetMHCIIpan-4.0 targeting human major histocompatibility complex (MHC) class I and class II molecules, respectively. The antigenicity of the selected epitopes computed by both B- and T-cell predictors were further analyzed using the VaxiJen server. The results demonstrated that PkAMA1 protein encompasses multi antigenic regions that have the potential for the development of multi-epitope vaccine. Two B- and T-cell epitopes consensus regions, i.e., NSGIRIDLGEDAEVGNSKYRIPAGKCP (codons 28-54) and KTHAASFVIAEDQNTSY RHPAVYDEKNKT (codons 122-150) at domain I (DI) of PkAMA1 were reported. Advancement of bioinformatics in characterization of the target protein may facilitate vaccine development especially in vaccine design which is costly and cumbersome process. Thus, comprehensive B-cell and T-cell epitope prediction of PkAMA1 offers a promising pipeline for the development and design of multi-epitope vaccine against P. knowlesi.