ABSTRACT

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Study Program : Bioinformatics
Title : Structural and Immunogenicity Analysis of P41, P48/45, and P230 Protein of *Plasmodium sp.* as a Potential Vaccine Target Candidate Against Malaria Infection
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The development of antimalaria vaccines hindered by genetic diversity that possessed by *Plasmodium sp.,* which makes the proposed antigen have a low efficacy towards non-vaccine strain. Previously, we have shown P41, P48/45, and P230 protein from 6-Cysteine shared by *Plasmodium sp.* and could be used for cross-species antimalaria vaccines. Two different approaches are known as ancestral, and consensus sequence reconstruction were used in this study to validate the efficacy of P41, P48/45, and P230 as cross-species vaccine candidate. Phylogenetic and time tree reconstruction was conducted to determine the relationship of 6-Cysteine proteins and help the sequence reconstruction. The structural prediction was made by using the psipred and Rosetta program. The characteristic of proteins was analyzed by assessing hydrophobicity, Post-Translational Modification sites, and molecular docking simulation. Meanwhile, the immunogenicity score for B-cell, T-cell, and MHC was determined using an immunoinformatic approach. The result suggests that ancestral sequences are more stable with a higher number of epitopes. The conserved epitopes between ancestral and consensus which consist of specific modifications and located in binding sites were located in all target proteins. The presence of conserved epitopes might indicating greater efficacy possess by 6-Cysteine proteins. Thus, this study provides detailed insight into P41, P48/45, and P230 efficacy for the cross-species antimalaria vaccine.

Keywords: malaria; vaccine; 6-Cysteine; protein structure; Immunogenicity