UNIVERSITI TEKNOLOGI MARA

IN SILICO IDENTIFICATION OF *PLASMODIUM FALCIPARUM* MEROZOITE MEMBRANE PROTEINS; A STUDY OF MALARIA VACCINOLOGY

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TABLE OF CONTENTS

ABSTRACT

Malaria is a serious infectious disease that has contributes to high rate of mortality throughout the world. It is spread by *Anopheles* mosquitoes, which have been prior infected by *Plasmodium* parasites such as *Plasmodium falciparum*, *Plasmodium vivax, Plasmodium ovale,* and *Plasmodium malariae.* The current scenarios of malaria are that the antimalarial drugs cannot provide sufficient treatment, and the vaccines available also could not give full protection. Therefore, this study is aim at using *in silico* software to analyze protein sequence whether it could be a candidate to produce an effective vaccine. The analysis of the Pf7 protein sequence of *Plasmodium falciparum* shows that this protein consists of 264 amino acids, with grand average of hydropathicity (GRAVY) value of -0.824. The negative value indicates that this protein is hydrophilic. This protein is located extracellularly and secondary structure prediction shows that it consists of 46.8% coil, 23.8% sheet, 19.0% turns, and 16.9% helix. For antigen epitope prediction, the result shows that subsequence "FFIFVTFNI" has high probability as promiscuous binder. As the conclusion, results obtained from all of the analyses conducted for this Pf7 protein can act as preliminary information in designing actual candidate vaccine in the future.

CHAPTER 1

INTRODUCTION

1.1 Background

Malaria is a disease spread by female *Anopheles* mosquitoes that have been prior infected by *Plasmodium* parasite. There are four species of malaria parasites that can infect humans via mosquito transmission, which are *Plasmodium falciparum, Plasmodium vivax, Plasmodium ovale,* and *Plasmodium malariae* (Birkholtz *et al.*, 2006).

The death rate of malaria is estimated to be 1 to 2 million people each year (Birkholtz *et al.*, 2006). And now *Plasmodium falciparum* has shown to develop resistance to the earlier first-line antimalarials such as chloroquine and sulfadoxine/pyrimethamine, and it has reached critically high levels in many malaria-endemic regions (Ekland & Fidock, 2008). Thus, these events have made it clear that this disease need effective preventions and treatments.

As malaria is the most serious parasitic disease in Africa, thus there is a pressing need for its vaccines (Scorza *et al.*, 2008). But the aim of developing a safe and efficacious malaria vaccine has remained elusive for the past 80 years (Guinovart & Alonso, 2007).