ABSTRACT

This thesis focused on malaria vaccinology and employed reverse vaccinology (RV) and molecular techniques to predict potential candidate vaccine epitope against *P. falciparum*. RV is fundamentally an *in silico* method that predicts vaccine candidates from an entire organism's proteome, enabling the identification of a greater number of putative vaccine candidates (PVC) in a realistically shorter time when compared to conventional vaccinology approaches. Several computation methods were utilised to predict potential vaccine candidates *for P. falciparum.* The need to control *P. falciparum* is urgent because over 229million people are infected worldwide and about 400,000 were killed in 2019. It is also clearly documented that the only clinically recommended vaccine against Plasmoduim infection, RTS, S vaccine (Mosquirix), offers suboptimal (50%) protection to clinical infection which wanes within six months. One of the predicted PVCs by RV was synthesised as recombinant protein vaccine and tested in rabbits. The predicted PVC produced antibodies in the immune response that recognised the native protein prepared from plasmodium parasite protein lysate probed in a Western blot analysis. Finally, these antibodies also showed significant inhibition of merozoite invasion of erythrocytes in *in-vitro* invasion inhibition assay (IIA). In summary, this thesis has identified and partially characterized a potential vaccine candidate. Further testing of this protein is recommended to determine its vaccine potential which can be used to facilitate the rapid formulation of novel subunit vaccines.