

EVALUATION OF GENETIC VARIABILITY AND ITS POTENTIAL IMPACT ON THE ANTIGENICITY OF B-CELL EPITOPES OF THE PV41 AND PVGAMA PROTEIN IN BRAZILIAN ISOLATES OF *PLASMODIUM VIVAX*

Ana Luiza Carneiro Alencar¹, Cinthia Magalhães Rodolphi¹, Isabela Ferreira Soares¹, Lana Bitencourt Chaves¹, Daiana de Souza Perce-da-Silva⁶, Dalma Maria Banic², Paulo Renato Rivas Totino³, Ricardo Luiz Dantas Machado⁵, Lilian Rose Pratt-Riccio³, Cláudio Tadeu Daniel-Ribeiro³, Rodrigo Nunes Rodrigues da Silva⁴, Josué da Costa Lima-Junior¹.

¹Laboratory of Immunoparasitology, Oswaldo Cruz Institute, Rio de Janeiro, RJ, Brazil;

²Laboratory of Clinical Immunology, Oswaldo Cruz Institute, Rio de Janeiro, RJ, Brazil;

³Laboratory for Malaria Research, Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, Brazil;

⁴Laboratory of Hantaviruses and Rickettsioses, Oswaldo Cruz Institute, Fiocruz, Rio de Janeiro, Brazil. ⁵Center for Microorganism Research, Biomedical Institute, Fluminense Federal University (UFF), Niterói, RJ, Brazil, ⁶University of Medicine of Petrópolis (FMP/UNIFASE), Petrópolis, RJ, Brazil.

Plasmodium vivax merozoite surface proteins have been considered promising blood-stage vaccine candidates because of their roles in erythrocyte invasion and their recognition by naturally acquired immune responses. Among these, Pv41 and PvGAMA have emerged as relevant targets, although they appear to differ in their degree of genetic conservation, an important factor for vaccine design. Because antigen polymorphism may compromise immune recognition and reduce vaccine efficacy, evaluating the genetic diversity of these candidates in endemic settings is essential. In Brazil, where *P. vivax* predominates and transmission is concentrated in the Amazon region, population-based analyses of vaccine candidate genes are particularly important to determine whether local parasite diversity may affect predicted antigenicity and epitope conservation. The aim of this study was to investigate the genetic variability of Pv41 and PvGAMA by sequencing their genes in 72 clinical isolates from the Brazilian Amazon. Additionally, immunoinformatic tools were used to predict B-cell linear epitopes on Pv41 and PvGAMA, as well as to explore the potential impact of single nucleotide polymorphisms (SNPs) on B-cell epitope antigenicity. Fifteen non-synonymous substitutions were identified in Pv41, with allele frequencies ranging from 3% to 11%. Five sequences were predicted as B-cell epitopes. Of the detected SNPs, only the A509T mutation resulted in an alteration (H170L), which reduced the epitope antigenicity score. In contrast, only two non-synonymous SNPs were found in PvGAMA: T269C (L89P) and G875A (R292K). Neither variant overlapped the predicted epitopes, indicating minimal impact on antigenicity. Overall, these results demonstrate that Pv41 exhibits greater polymorphism and may necessitate multivalent vaccine strategies or designs that target conserved epitopes. In contrast, the stable profile of PvGAMA suggests its potential as a reliable component in future *P. vivax* vaccines.