GENETIC DIVERSITY AND INSIGHTS INTO *PLASMODIUM VIVAX* BINDING AND IMMUNE EVASION FROM THE 3D STRUCTURE OF THE DUFFY-BINDING PROTEIN

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Plasmodium vivax is the human malaria species with a most widely world distribution and is highly endemic in Brazilian Amazon region. The establishing of the disease in the host depends on the merozoite invasion of new blood cells and in *P. vivax*, this invasion is exclusively mediated by interaction of Duffy-binding protein (DBP) to the cognate erythrocyte receptor. The current investigation undertakes a comprehensive analysis of genetic diversity at the binding domain of DBP (DBPII) from different Brazilian populations using DNA sequencing and the identification of polymorphic residues in the structure of the protein. We report genetic diversity varying between Brazilian regions, which may reflect differences of transmission intensity, geographic isolation and possible divergent selection between populations. Interpopulation comparisons of genetic divergence revealed that the *dbpII* haplotype repertoire in Brazilian regions overlap only slightly. We also find that meiotic recombination seems not to play an important role in generating haplotype diversity at this locus. Mapping of diversity onto a 3D structural model of the protein indicates that some polymorphisms lie near the binding site and may have functional importance for erythrocyte binding, while others may be likely to bear epitopes for antibody recognition.

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