

011/A

Analysis of genetic polymorphism of *Plasmodium vivax* Duffy Binding Protein ligand domain of Sri Lankan isolates

P H Premaratne¹, Ramesh Aravinda¹, A Manamperi², P V Randeniya^{1*}

¹Department of Zoology, Faculty of Science, University of Colombo, Colombo

²Molecular Medicine Unit, Faculty of Medicine, University of Kelaniya, Ragama

Interaction of *Plasmodium vivax* Duffy Binding Protein region II (PvDBP_{II}) critical binding motif (CBM) with its erythrocyte receptor is critical for maintaining blood stage infections, rendering PvDBP a leading vaccine candidate. Since the efficacy of a vaccine based on a polymorphic antigen, such as PvDBP, is influenced by the local host immune response, characterization of the GD among local parasite strains is important in specific geographic settings. GD of the PvDBP_{II}-CBM was assessed for the first time among field isolates from Sri Lanka. Forty single clonal *P. vivax* infections identified from two malaria endemic areas (Anuradhapura and Kataragama) and from a non-endemic area (Colombo), were used to generate nucleotide sequence data of CBM of PvDBP_{II} (aa 285 to 521) by nested PCR amplification followed by direct sequencing.

Twenty dimorphic sites, 20 nucleotide polymorphisms and 15 haplotypes (haplotype diversity = 0.890) were identified at the CBM of PvDBP_{II} compared to Sal-1 sequence. Genetic polymorphism in terms of pair wise diversity (π) and Tamura's three parameter model (d) were calculated to be 0.00950 (S.D.=0.00072) and 0.00959 (S.D.= 0.00052), respectively, consistent with published data from world wide isolates. Eighteen non-synonymous(NS) and 02 synonymous(S) mutations were identified, and the ratio of NS (0.01086) to S (0.00458) mutation rates was significantly >1, suggesting that positive selection acts on the CBS of PvDBP_{II}. Residues essential for erythrocyte binding on PvDBP_{II}-CBM were conserved in these 40 isolates. Six polymorphic residues recorded in high frequencies in worldwide isolates were also present among Sri Lankan isolates. Polymorphisms occurring at higher frequencies than Papua New Guinea isolates, of three amino acid residues involved in resistance to binding inhibitory antibodies were also detected.

Thus, even under low and unstable transmission conditions prevalent in the island, relatively high allelic diversity and positive selection acting on CBM of PvDBP_{II}, possibly due to immune pressure were detected in Sri Lankan *P. vivax* field isolates.

Financial support by the National Science Foundation (Grant numbers NSF/SCH/2004/07 and NSF/RG/2005/HS/06) and the National Research Council (Grant numbers 05-34) is acknowledged.

*dappvr@yahoo.com

Tel: 011-2503399