Integral Membrane Protein II), a Class B Scavenger protein closely related to CD36, has recently been solved. Using this structure as a template, the 3D structure of human CD36 (hCD36) was modeled and predicted to exist as a homodimer (dimerization region amino acids 151-181). To test these predictions several mutations were introduced in order to break this secondary structure. The constructs were engineered as GFP fusions and transiently transfected into HeLa or COS-7 cell lines. Transfected constructs were tested for binding of oxLDL and PEs. Binding was quantified and normalized by enumerating only GFP expressing cells. Surface expression of the constructs was determined by immunofluorescence using an anti-hCD36 antibody and a proteinase K protection assay of intracellular proteins. Mutations introduced in this region abrogated binding of both ligands. Residues L158, L161 and in combination K164/K166 seemed to be crucial for maintaining the integrity of the binding site supporting the homodimer model theory. It has been believed that the CD36 binding site for PEs is similar to oxLDL. By studying the binding affinity of different highly conserved CD36 orthologs we found that bovine CD36 does not bind PEs but does bind oxLDL. Interestingly, residues L158, L161, K164 and K166 are highly conserved across orthologs. We hypothesized that a discrete highly polymorphic overlapping region (aa 146-156) might encode the observed differential PE binding. Here we show through detailed site directed mutational analysis that the binding sites for PEs and oxLDL are distinct. Further, ortholog swap analysis between bovine and hCD36 is being used to fine map the PE binding site by defining the minimal requirements to confer PE binding to bovine CD36 and conversely abrogate PE binding by hCD36, while preserving oxLDL binding.

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CHARACTERIZATION AND ANTIGENICITY OF *PLASMODIUM VIVAX* RHOPTRY-ASSOCIATED LEUCINE ZIPPER-LIKE PROTEIN 1 (PVRALP1), A NOVEL RHOPTRY NECK PROTEIN

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Rhoptry secreted proteins are associated with tight junction and parasitophorous vacuole formation during invasion of host targets cells and are sorted within rhoptry neck or bulb. We have identified blood-stage antigens of *Plasmodium vivax* likely to be highly immunogenic. Of these candidates, a novel protein PVX_096245, which is the ortholog of rhoptry-associated leucine zipper-like protein 1 (RALP1) from *P. falciparum*, was gained for detailed characterization. PvRALP1 contains a novel glutamate(Glu)/glycine(Gly)-rich domain that is conserved in other *Plasmodium* species. In present study, full-length without signal peptide (Ecto) as well as a Glu/Gly-rich domain (Tr) of recombinant PvRALP1 were expressed by using cell-free expression system. Sera screening experiments indicate that PvPvRALP1-Ecto and PvRALP1-Tr possess 58.9% and 55.4% in sensitivity and 95.0% and 92.5% in specificity. The PvRALP1 is localized in rhoptry neck; an apical organelle of the merozoite, and the localization of this protein is firstly defined in *P. vivax* . Of PvRALP1 immunogenicity, cytophilic antibodies were produced simultaneously. The present study suggests that PvRALP1 is immunogenic in humans during parasite infection and it may be a novel potential vaccine candidate in the blood stage of *vivax* parasite.

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PATTERNS OF GENE FLOW IN *PLASMODIUM VIVAX* POPULATION CURRENTLY CIRCULATING IN SRI LANKA - A COMPARATIVE GENETIC POPULATION BASED STUDY

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Epidemiological evidence of relatively unstable and low intensity malaria transmission due to successful elimination strategies lead Sri Lanka to achieve malaria pre-elimination status in the year 2008. Understanding the population genetic structure of current and previous local *Plasmodium vivax* isolates is important to (i) examine the degree of genetic isolation of these populations, and (ii) ascertain whether subsequent outbreaks would be due to residual transmission or due to introduction of new parasite strains to the parasite population, enabling population specific malaria control measures Sequences of *P. vivax* isolates that circulated locally, a decade ago was obtained from the Genebank (pvmsp3α: N=17; pvdbpII=100, pvmsp142= 95, pvcsp: N=60). PCR amplification and sequence analyses of these four polymorphic *loci* of *P. vivax* were carried out using 16 samples collected recently (2011-2012). Expected heterozygocity (He) and the genetic differentiation (Fst) was examined using DNasp 5.1 software, to draw comparison of current and previous population genetic structures. Low mean (He) in the current *P. vivax* population (He=0.76) compared with the previous population (He=0.93) was observed for all four genes indicating less gene diversity in the currently circulating isolates. However, the He of pvmsp-142 (0.962) current population was higher than that of the previous (0.978). Genetic differentiation (Fst) between the two test populations was highest in pvmsp3α (0.20719) followed by pvcsp (0.1271) indicating great differentiation between the two populations. PvdbpII (0.0793) and pvmsp-142 (0.0018) showed moderate and little genetic differentiations, respectively. Linkage disequilibrium was maintained across the current population except for pvmsp3α. A reasonable degree of overlap of amino acid haplotypes in these four proteins and not many novel a.a haplotypes were observed between current and previous populations. Thus these results for the first time in Sri Lanka suggest that new *P. vivax* variants may have been introduced to the island with simultaneous residual transmission of previously detected alleles. Further investigation is needed in order to ascertain the risk of re-introduction.

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HIGH RESOLUTION MELTING: AN ADAPTABLE AND DEPLOYABLE METHOD IN THE FIELD TO MONITOR *PLASMODIUM FALCIPARUM* GENETIC POLYMORPHISMS

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Understanding the genetic variation in malaria parasite populations and how selective pressures such as drug treatment regimes alter these patterns of genetic variation can be used to identify molecules responsible for changes in drug response, and to develop tools that can provide an early warning system for the emergence of drug resistance when new anti-malarial drug pressure is applied. These tools should be fast, sensitive, unambiguous, and cost-effective, and deployable in malaria endemic field sites. We have successfully deployed High Resolution Melting (HRM) technique in Senegal to analyze molecular four genes pfcrtK76T,