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Genetic diversity in the *Plasmodium vivax* C-terminal 42 kDa region of merozoite surface protein-1(PvMSP-1p42) in Sri Lanka

Sajani Dias, Preethi Udagama-Randeniya*
Department of Zoology, Faculty of Science, University of Colombo, Sri Lanka

Proteolytic processing of *Plasmodium vivax* Merozoite Surface Protein-1 generates smaller fragments (i.e.19 and 42 kDa fragments) which play a vital role during merozoite invasion. The high polymorphism observed in PvMSP-1p42 fragment is maintained by positive selection. We investigated the sequence polymorphism occurring in PvMSP-1p42 (p33 and p19) of 95 *P. vivax* infected isolates from three study areas, two endemic for malaria, Anuradhapura (N=22) and Kataragama (N=36) and one non-endemic area, Colombo (N=37) and carried out population genetic analysis with previously published geographically different field isolates (i.*e.* India, Bangladesh, Thailand, Brazil). Nucleotide diversity (π) for MSP-1p42 and p33 was high and similar to those reported from other geographic areas while though conserved, comparatively higher π value was obtained for p19 from Sri Lanka. The difference between rates of non-synonymous (dN) to synonymous (dS) substitutions indicated positive selection acting on p42 and p33 whereas purifying selection was acting upon p19 in Sri Lankan isolates. McDonald-Kreitman test for neutrality using *P. cynomolgi* as the out group verified this fact. Linkage disequilibrium index (R^2) plotted against nucleotide distances indicated intragenic recombination contributing to the increased diversity observed in p42. Our 95 sequences were 100% similar at the p19 fragment to the Sal I strain while a hypervariable region was clustered in the p33 fragment with an excess of non-synonymous amino acid polymorphisms. Further, Sal I was the most frequent phenotype observed from the Sri Lankan isolates compared to Belem phenotype observed from Thailand and Brazil. We obtained 27 amino acid haplotypes of which all were recombinants of the Sal I and Belem strains. Of these, 19 were novel haplotypes reported for the first time in this study. The phylogenetic tree revealed local isolates clustered among those from different countries. The PvMSP-1p42 gene signifies high genetic diversity in our island where unstable malaria persists with low transmission. The highly conserved p19 fragment gives and insight for a vaccine strategy based against *P. vivax* infections in geographically endemic regions including Sri Lanka.

Key Words: Sri Lanka, *Plasmodium vivax*, Genetic Diversity, Merozoite Surface Protein-1, Evolutionary biology

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