

recombination between HVR-T1/T3 and HVRT6/T2, are reported for the first time from South America and Thailand, respectively. Intragenic recombination was a critical factor for the manifestation of a.a. haplotypes representing HVR-T3 to T7, and for the generation of H71-H89. In conclusion, under low transmission and unstable malaria conditions prevalent in the island, both interallelic and intragenic recombination appear to be critical for the origin of new PvMSP-1<sub>42</sub> amino acid haplotypes in local *P. vivax* populations.

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### **Phylogenetic relationship of *Plasmodium vivax* duffy binding protein gene between Sri Lankan and world wide isolates**

P. H. Premaratne<sup>1</sup>, B. R. Aravinda<sup>1</sup>, A. A. Escalante<sup>2</sup>, P. V. Udagama-Randeniya<sup>1</sup>

<sup>1</sup>Department of Zoology, Faculty of Science, University of Colombo, Colombo 03, Sri Lanka, <sup>2</sup>School of Life Sciences, Arizona State University, Tempe, AZ, USA.

Phylogenetic relationship of the region II of the *P. vivax* Duffy Binding Protein gene (*PvdbpII*), a prime vaccine candidate against blood stage of vivax malaria, was analysed between parasite isolates from Sri Lanka and from different geographical areas, worldwide. A gene tree was derived from the aligned nucleotide sequences of a 672 bp region, using the Neighbour-Joining method with 1000 bootstrap replicates, the Tamura's three-parameter distance model as implemented in the MEGA version 4.0 programme. One hundred and seventy five *PvdbpII* sequences found in the GenBank were compiled and compared to 100 Sri Lankan (SL) sequences. The worldwide sequences included those from the reference Salvador-I strain, single sequences each from Vietnam (VIAT), Indonesia (INDO) and India (INDI) and 13, 17, 30 and 111 sequences from South Korea (SK), Colombia (COL), Thailand (Thai) and Papua New Guinea (PNG), respectively.

Twenty three different groups in all were evident in the gene tree. SL isolates were grouped in 6 different clades (A-G). A majority of these concentrated amongst 3 different clades (A, B and C), with no clustering detected according to the sample collection sites within the country. A single clade (D), exclusively contained SL isolates, proving evidence for geographical isolation. Two other clades (A & F) contained isolates from SL in combination with THAI and SK, respectively. The close phylogeny of the SL sequences with world wide ones were more clearly evident in the gene tree by SL isolates grouping with those from PNG, THAI, COL, INDO and VIAT in clade B, and with those from PNG, THAI, COL and from INDI with the reference strain Sal-1 in clade E. Interestingly, both these groups lacked SK isolates. The Sri Lankan *PvdbpII* sequences thus appeared to represent a sample from the *PvdbpII* worldwide genetic diversity, rather than from any particular lineage.

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