

P4.09 Malaria pathogenesis and vaccines

P4.09.01

Comparison of population structure of *Plasmodium vivax* currently circulating in Sri Lanka and of that a decade ago based on diversity of four selected antigen encoding loci

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As Sri Lanka achieved malaria pre-elimination status in 2008, understanding 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.

Sequences of four polymorphic antigen encoding loci of *P. vivax* isolates collected a decade ago were retrieved from the Genbank (pvmsp3 α : N=17; pvdbp, pvmsp1 and pvcsp: N=30). PCR amplification and sequencing of these four loci were carried out using 16 isolates collected recently (2011-2012). DNasp 5.1 software was used to examine the expected heterozygosity (He) and the genetic differentiation (Fst), to draw comparison of current and previous population genetic structures.

Low mean He in the current *P. vivax* population (He=0.76) compared with previous population (He=0.92) was observed for all four genes. Genetic differentiation amongst the two test populations was highest in pvmsp3 α (Fst=0.20719), moderate in pvdbp (Fst=0.06785) and was absent in pvmsp1 and pvcsp (Fst= - 0.02876, Fst= - 0.01103). Though a low degree of overlap of amino acid haplotypes of these four proteins was observed between current and previous populations, most current haplotypes were novel. Thus these results suggest the possibility that new *P. vivax* variants have been introduced to the island; however, residual transmission of alleles that were not previously detected cannot be ruled out.

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