A-25: Allelic polymorphism of Merozoite surface antigenl of *Plasmodium vivax* (PvMSA1) in Sri Lankan parasite isolates

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Three allelic types of a variable portion of the PvMSA1 gene of *Plasmodium vivax* were defined previously. This was based on sequence analysis showing the presence of two alleles in this region, each displaying dimorphism in natural parasite isolates giving rise to 3 allelic types namely, B1/B2, S1/S2 and S1/B2

In the present study, DNA amplification by the Polymerase Chain Reaction (PCR) followed by oligonucleotide probing were used to characterize the allelic patterns of PvMSA1 in parasite isolates from *P. vivax* patients in Kataragama (a malaria endemic area) and Colombo (a non-endemic area). Four oligonucleotide probes to the far ends of the amplified fragments of each B1/B2 and S1/S2 of PvMSA1 were designed and used for probing.

The results showed the presence of a previously undescribed recombinant type, namely B1/S2. The distribution of the 4 allelic types were not significantly different in parasite isolates from Colombo and Kataragama. A high proportion of infections in both Kataragama (63%) and Colombo (50%) showed the presence of mixed genotypes (presence of more than one allelic type in a single infection).

This study suggests the prevalence of a high degree of genetic polymorphism in *P. vivax* parasite isolates in Sri Lanka, by the finding of 4 different allelic types, and their almost equal prevalence in parasite populations isolated from both areas. The results further show that the incidence of infections with mixed genotypes in Sri Lanka is higher than previously estimated using immunological markers. These estimates of mixed genotype infections are also higher than those reported from limited genetic studies carried out in Brazil.