A-23: Genetic heterogeneity of Plasmodial genes in Sri Lankan isolates as detected by the Polymerase Chain Reaction

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Two plasmodial genes; PfMSA1 (MSA1: Merozoite Surface Antigen1) and PvMSA1 have been amplified by Polymerase Chain Reaction (PCR) from Sri Lankan isolates. In both genes, a polymorphic region was selected for PCR. In *P.falciparum*, a portion of PfMSA1 of 539 base paris (bp) and in P. vivax PvMSA1 of 651 bp was amplified. The results revealed that the amplified fragment of PvMSA1 existed as one of two different sizes. This includes the occurrence of both sizes of fragments (of 520 bp and 430 bp) (mixed genotype) in 11% of the isolates tested.

In *P.falciparum*, PCR was carried out in parasites isolated from patients with repeated recrudescence due to chloroquine resistance. Parasite DNA was extracted from the parasites at the primary infection and each subsequent recrudescence.

Among 14 primary parasite isolates 5 and 6 isolates (altogether 11) showed the existence of 1 of the 2 sized PCR fragments and the rest (3 isolates) both. In 7 of the 14 patients, parasites of the second and third recrudescence presented with the identical sized fragments(s) as did the parasites of the primary infection. In the other 7 patients however, the composition of the gene changed from the primary to recrudescent parasites in that the recrudescent parasites had either a different sized fragment to parasites of the primary infection or that while the primary parasites had only one genotype, the recrudescent population showed fragments of both lengths or vice versa.

Changing of the composition of PfMSA1 gene in primary and recrudescence parasite populations raises the question as to whether the drug pressure has any influence in selecting new genotypes in wild parasite populations, the prevalence of which were so low in the primary infections as not to be detected by PCR. Alternatively the recrudescent population was the result of selection following a mutation. If so, the mutation must always have been a switch between two alternative alleles. This has to be confirmed by DNA sequence analysis.