

**Genetic diversity of *Plasmodium falciparum* isolates from Mannar District**

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The epidemiology of malaria results from the interaction of gene pools of parasites, humans and mosquito vectors. Knowledge of the diversity of the parasite population in a given area as well as that of the human and mosquito hosts forms the foundation for understanding the mechanisms underlying the pathology, acquisition of immunity, spread of drug resistance and the conditions of transmission of malaria. In this study, we attempted to determine the extent of genetic diversity of *P. falciparum* isolates in a selected region of the Northern Province. Two polymorphic domains of the genes of two *P. falciparum* proteins, merozoite surface protein 1 (PfMSP-1) block 2, and merozoite surface protein 2 (PfMSP-2) and one conserved region of PfMSP-1 (block 17) were amplified using Polymerase Chain Reaction (PCR) technique and the genetic variants were determined based on size polymorphism detected by polyacrylamide gel electrophoresis.

Among 55 *P. falciparum* infected samples, 3 size variants of PfMSP-1 block 2 (490, 550 & 560bp) and 2 size variants of each of PfMSP-1 block 17 (300 & 310bp) and PfMSP-2 (800 & 805bp) were detected. When combinations of all three domains were analyzed, only 9 genetic variants were detected in this parasite population. 38.2% of the 55 blood samples had infections with more than one genetic variant indicating a high occurrence of mixed variant infections. Overall, the 55 blood samples had a maximum of 96 possible distinct infections, showing a considerable genetic diversity within the *P. falciparum* population in this study area. PfMSP-1 block 17, which is considered a leading vaccine candidate against falciparum malaria, has found to be highly conserved among the Sri Lankan isolates. However, we found 2 size variants (approximately 10bp difference) of PfMSP-1 block 17 with 91% predominance of 300bp variant. Further, more, PfMSP-1 block 2 and PfMSP-2 were found to be highly polymorphic and therefore may play an important role in determining the genetic variation in *P. falciparum* population in this area.

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