ABSTRACT

Plasmodium falciparum antigenic diversity and polymorphism confuses the issue of antimalarial vaccine development. MSP-2 is a highly polymorphic genetic marker that is highly discriminatory for characterizing *Plasmodium falciparum* field isolates. Genetic diversity of isolates obtained from symptomatic patients residing in Kondoli, Assam was analyzed by an allele specific polymerase chain reaction and sizing of the amplified products using 2% agarose gel electrophoresis. Of 20 isolates, 5% had only FC27- type alleles, 10% had only IC1-type alleles and 60% had multiple parasite populations with both alleles. 11 alleles of Fc and 9 of IC were noted in our study. Clone multiplicity of 3.15 was noted in our study indicating a large number of circulating clones. Diversity index of 0.98 for FC and 0.84 for IC1 emphasise the high diversity of MSP2 in the parasite population .

The pathogenic manifestations during malaria crisis have been attributed to proinflammatory cytokines, such as Tumor necrosis factor (TNF-α), released by T cells and macrophages in response to malaria parasite. High IFN-γ production as part of a Th1-driven immune response has been associated with a more favorable outcome. These proinflammatory cytokines were analysed by western blotting in samples from Kondoli, Assam. Frequency of TNF- α was observed to be higher in the presence of the antigen expressed TNF- α and this might be due to the antigenic stimulation by the MSP-1 antigen employed in the study. Only 10% of the isolates, cultured in the absence as well as in the presence of the antigen expressed IFN- α and IFN- γ. The most predominant proinflammatory cytokine was TNF- α. However, correlation of the levels of these proinflammatory cytokines with the clinical outcome of the disease were inconclusive because of small sample size.