

ABSTRACT

Heterogeneity in host response and parasite diversity of *Plasmodium falciparum* contributes to complexity of disease and pose a challenge to vaccine development. A role for NK cell receptors in modulating the innate and adaptive responses has been suggested. We have studied the KR gene profile and diversity of MSP1 locus.

In the present work, the KIR gene polymorphism study was carried out among the North East Indian population. This is the first reported work on KIR gene polymorphism in this region. Here a panel of people were analyzed for 2DL1, 2DL2, 2DL3, 2DL4, 2DL5, 3DL1, 3DL2, 3DL3, 2DS2, 2DS3, 2DS4 and 2DS5 genes. All the participants have different KIR genotypes, that share features with both North Indian and austro-aboriginal population.

We have studied the genetic composition of *P. falciparum* at the MSP1 locus in a region endemic for malaria. Block 2 of MSP1 was amplified using allele specific primers and the amplicons were sized on 2% agarose gel. MAD20 was detected at lowest frequency (55%), while RO33 had the highest frequency (80%). Multiplicity of infection was 2.1, indicating high transmission rate. The distinct MSP1 diversity noted in the studied population could be related to the immune pressure or drug pressure or both.