

Genetic Diversity and Antibody Response to Merozoite Surface Protein (MSP1) of *P. falciparum* in Districts of Assam

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Abstract—Malaria is a major global health issue with 300 to 500 million clinical infections and more than a million deaths reported each year. According to World Health Organization (WHO) there were 212 million new cases of malaria in 2015 with an estimated 429 000 malaria deaths (range 235 000–639 000) worldwide. Malaria is endemic in the north east region of India especially Assam with nearly 65% of the total population of the state estimated to be living in high-risk areas. The major cause of malaria infection in Assam is the species *Plasmodium falciparum* which accounts for 58–68% of the cases and the remainder are due to *P. vivax*.

A relation between transmission intensity and *Plasmodium falciparum* diversity has been suggested. We have examined fragment size polymorphism of merozoite surface protein (MSP1) in districts of Assam. Polymorphism as well as distribution of alleles was seen to be transmission season related. We also looked at immune response to the antigenic variants of MSP1 fragment and crude antigen. The variant response was significantly higher at the site where MSP1 alleles MAD20 and RO33 were found to vary with transmission season. The implications of this finding will be discussed.