

Genetic polymorphism of merozoite surface protein-1 and merozoite surface protein-2 in *Plasmodium falciparum* field isolates from Myanmar

Jung-Mi Kang, Sung-Ung Moon, Jung-Yeon Kim, Shin-Hyeong Cho, Khin Lin, Woon-Mok Sohn, Tong-Soo Kim and Byoung-Kuk Na

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Abstract

Background: Merozoite surface protein-1 (MSP-1) and MSP-2 of *Plasmodium falciparum* are potential vaccine candidate antigens for malaria vaccine development. However, extensive genetic polymorphism of the antigens in field isolates of *P. falciparum* represents a major obstacle for the development of an effective vaccine. In this study, genetic polymorphism of MSP-1 and MSP-2 among *P. falciparum* field isolates from Myanmar was analysed.

Methods: A total of 63 *P. falciparum* infected blood samples, which were collected from patients attending a regional hospital in Mandalay Division, Myanmar, were used in this study. The regions flanking the highly polymorphic characters, block 2 for MSP-1 and block 3 for MSP-2, were genotyped by allele-specific nested-PCR to analyse the population diversity of the parasite. Sequence analysis of the polymorphic regions of MSP-1 and MSP-2 was also conducted to identify allelic diversity in the parasite population

Results: Diverse allelic polymorphism of MSP-1 and MSP-2 was identified in *P. falciparum* isolates from Myanmar and most of the infections were determined to be mixed infections. Sequence analysis of MSP-1 block 2 revealed that 14 different alleles for MSP-1 (5 for K1 type and 9 for MAD20 type) were identified. For MSP-2 block 3, a total of 22 alleles (7 for FC27 type and 15 for 3D7 type) were identified.

Conclusion: Extensive genetic polymorphism with diverse allele types was identified in MSP-1 and MSP-2 in *P. falciparum* field isolates from Myanmar. A high level of mixed infections was also observed, as was a high degree of multiplicity of infection.