

Diversity and natural selection of *Merozoite surface protein-1* in three species of human malaria parasites: Contribution from South-East Asian isolates

ABSTRACT

The present study aimed to examine the genetic diversity of human malaria parasites (i.e., *P. falciparum*, *P. vivax* and *P. knowlesi*) in Malaysia and southern Thailand targeting the 19-kDa C-terminal region of Merozoite Surface Protein-1 (MSP-1₁₉). This region is essential for the recognition and invasion of erythrocytes and it is considered one of the leading candidates for asexual blood stage vaccines. However, the genetic data of MSP-1₁₉ among human malaria parasites in Malaysia is limited and there is also a need to update the current sequence diversity of this gene region among the Thailand isolates. In this study, genomic DNA was extracted from 384 microscopy-positive blood samples collected from patients who attended the hospitals or clinics in Malaysia and malaria clinics in Thailand from the year 2008 to 2016. The MSP-1₁₉ was amplified using PCR followed by bidirectional sequencing. DNA sequences identified in the present study were subjected to Median-joining network analysis with sequences of MSP-1₁₉ obtained from GenBank. DNA sequence analysis revealed that PfMSP-1₁₉ of Malaysian and Thailand isolates was not genetically conserved as high number of haplotypes were detected and positive selection was prevalent in PfMSP-1₁₉, hence questioning its suitability to be used as a vaccine candidate. A novel haplotype (Q/TNG/L) was also detected in Thailand *P. falciparum* isolate. In contrast, PvMSP-1₁₉ was highly conserved, however for the first time, a non-synonymous substitution (A1657S) was reported among Malaysian isolates. As for PkMSP-1₁₉, the presence of purifying selection and low nucleotide diversity indicated that it might be a potential vaccine target for *P. knowlesi*.