

Genetic diversity of the gene encoding apical membrane antigen 1 of the human malaria parasite, *Plasmodium falciparum*, in Thailand

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Abstract: Development of an effective vaccine is critically needed for prevention of the human malaria. The apical membrane antigen 1 (AMA-1) of the malaria parasite, *Plasmodium falciparum*, is a key vaccine candidate. The antigen is expressed at the apical end of the parasite and has a critical role in erythrocyte invasion. The gene encoding AMA-1 (*AMA-1* gene) has been studied in populations of *P. falciparum* worldwide, but the extent of sequence diversity of the *AMA-1* gene in *P. falciparum* in Thailand remains limited. Here, the *AMA-1* gene were amplified by PCR from genomic DNA of 65 isolates of *P. falciparum* collected from five endemic regions (Kanchanaburi, Mae Hong Son, Trad, Ranong, UbonRatchathani) across Thailand national borders and then sequenced. The analysis of 1,869 base pairs of *AMA-1* coding sequence of the *AMA-1* gene revealed 60 single nucleotide polymorphic sites (SNPs) which were predominately located in ectodomain-1 of AMA-1. The analysis also revealed 31 unique haplotypes, 11 of which were reported for the first time. Phylogenetic tree analysis of the 31 haplotypes implied that this gene formed a monophyletic clade. Consistently, population genetic difference indices (F_{st}) inferred the close genetic relationships among five populations of *P. falciparum* in Thailand. In conclusion, the present study reported novel sequences of *AMA-1* in Thailand, the information needed for further advancement of an AMA-1-based malaria vaccine.

Keywords: Apical membrane antigen1, *Plasmodium falciparum*, Genetic diversity, vaccine, antigen.

BS 019