

# **Genetic polymorphism and effect of natural selection at domain I of apical membrane antigen-1 (AMA-1) in *Plasmodium vivax* isolates from Myanmar**

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## **Abstract**

Malaria is endemic or hypoendemic in Myanmar and the country still contributes to the high level of malaria deaths in South-East Asia. Although information on the nature and extent of population diversity within malaria parasites in the country is essential not only for understanding the epidemic situation but also to establish a proper control strategy, very little data is currently available on the extent of genetic polymorphisms of the malaria parasites in Myanmar. In this study, we analyzed the genetic polymorphism and natural selection at domain I of the apical membrane antigen-1 (AMA-1) among *Plasmodium vivax* Myanmar isolates. A total of 34 distinguishable haplotypes were identified among the 76 isolates sequenced. Comparison with the previously available PvAMA-1 sequences in the GenBank database revealed that 21 of them were new haplotypes that have never been reported till date. The difference between the rate of nonsynonymous (dN) and synonymous (dS) mutations was positive (dN-dS, 0.013+/-0.005), suggesting the domain I is under positive natural selection. The Tajima's D statistics was found to be -0.74652, suggesting that the gene has evolved under population size expansion and/or positive selection. The minimum recombination events were also high, indicating that recombination may occur within the domain I resulting in allelic diversity of PvAMA-1. Our results collectively suggest that PvAMA-1 displays high genetic polymorphism among Myanmar *P. vivax* isolates with highly diversifying selection at domain I. These results have significant implications in understanding the nature of *P. vivax* population circulating in Myanmar as well as providing useful information for malaria vaccine development based on this antigen.