



Category: Clinical Genomics

# DNA sequence variation and determination of the putative *PvCSP* gene as potential vaccine target for *Plasmodium vivax* malaria in India

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## Abstract

Evolutionary genetic studies in genomes offer excellent opportunities to infer population structure and demographic history of species populations. However, such kinds of studies are very limited in malaria. Malaria is highly endemic in India and both of the causative agents of malaria, *Plasmodium vivax* and *Plasmodium falciparum* occur in almost equal proportion. The widespread distribution of *P. vivax* is attributing to socio-economic loss, and thereby increasing the public health concern. Therefore, it is important to understand the genetic features of *P. vivax* population in India. Comparative genomics of *P. falciparum* and *P. vivax* has revealed several syntenic chromosomal segments. One such 200 kb segment has been utilized to design several small DNA fragments from non-coding regions, and tested for 'putatively neutral' marker for inference of population structure and demography of *P. vivax*. Utilizing 126 *P. vivax* isolates collected from 10 different widespread geographic locations in India, it was found that two neutral DNA fragments (P10 and P17) showed fairly less nucleotide diversity in all the population samples of *P. vivax*. A sudden drop in diversity in putatively neutral genetic fragments indicates the role of positive natural selection under the hitchhiking model of molecular evolution. Evolutionary genetic studies in the regions surrounding P10 and P17 with functional validation might provide meaningful insights and help identify targets in *P. vivax* in India. The study can further extended to *P. falciparum* as it is syntenic to *P. vivax*. It was found that the neutral fragment P17 is flanked by putative circumsporozoite protein (*PvCSP*) gene. Since, CSP is a major surface protein of the infective stage of malaria parasite; it is believed that the *PvCSP* gene might be under a certain kind of selective pressure. The objective of this study is to obtain new DNA sequence information of the putative *PvCSP* gene in isolates from India and compare it with the estimated diversity of the non-coding DNA fragments located in-and around this gene for inference of natural selection. Effectiveness of putative *PvCSP* gene as a suitable vaccine candidate on the basis of genetic diversity in parasite populations can be evaluated.

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