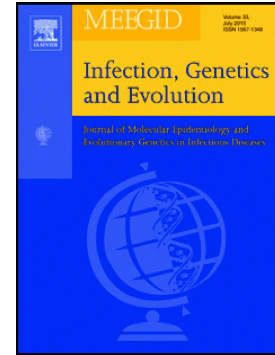


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Genetic diversity of the *Plasmodium vivax* multidrug resistance 1 gene in Thai parasite populations

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ABSTRACT

Plasmodium vivax resistance to chloroquine (CQ) was first reported over 60 years ago. Here we analyzed sequence variations in the multidrug resistance 1 gene (*Pvmdr1*), a putative molecular marker for *P. vivax* CQ resistance, in field isolates collected from three sites in Thailand during 2013-2016. Several single nucleotide polymorphisms previously implicated in reduced CQ sensitivity were found. These genetic variations encode amino acids in the two nucleotide-binding domains as well as the transmembrane domains of the protein. The high level of genetic diversity of *Pvmdr1* provides insights into the evolutionary history of this gene. Specifically, there was little evidence of positive selection at amino acid F1076L in global isolates to be promoted as a possible marker for CQ resistance. Population genetic analysis clearly divided the parasites into eastern and western populations, which is consistent with their geographical separation by the central malaria-free area of Thailand. With CQ-primaquine remaining as the frontline treatment for vivax malaria in all regions of Thailand, such a population subdivision could be shaped and affected by the current drugs for *P. falciparum* since mixed *P. falciparum*/*P. vivax* infections often occur in this region.

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