

***PLASMODIUM VIVAX*: GENETIC DIVERSITY AND MULTIPLE INFECTIONS IN MAE SOD, THAILAND**

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Knowledge about the population structure of *Plasmodium* parasites in malaria-endemic areas is essential for understanding the role of parasite diversity in malaria transmission and for designing and evaluating malaria vaccines. Using two polymorphic genetic markers, the merozoite surface protein-3a (MSP3a) and the circumsporozoite protein (CSP), we investigated the population diversity of *P. vivax* in Mae Sod, Thailand from April 2000 through June 2001. Genotyping of the parasites isolated from 90 malaria patients attending two local clinics by PCR and hybridization for two CSP genotypes, VK210 and VK247, revealed that the majority of the parasites (77%) were VK210 type. Equally intriguing is that among the VK247 parasites, only 3.3% occurred as single infections. Genotyping MSP3a locus by polymerase chain reaction/restriction fragment length polymorphism (PCR-RFLP) also indicated that *P. vivax* populations exhibited equally high levels of polymorphism as those from a hyperendemic region. Based on the length of PCR products, three major types of the MSP3a locus were distinguished with a frequency of 74.8, 18.7, and 6.5%, respectively. The 13 alleles distinguished by RFLP analysis did not show a significant seasonal difference in frequency. MSP3a analysis showed that 19.3% of patients has multiple infections, while genotyping the CSP gene identified 25.6% of the patients had multiple infections. The combination of the two molecular markers was more sensitive in detecting mixed infections than a single marker; the accumulative multiple infection rate from the two markers was 35.6%. Sequence comparisons of 9 clones further confirmed the genetic diversity of the parasite and also suggested that geographical isolation may also exist. Altogether, these results strongly indicate that *P. vivax* populations are highly diverse and multiple clonal infections are common in this malarial hypoendemic region of Thailand.

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