

***P. vivax* MALARIA IN MAE SOD, THAILAND: PARASITE DIVERSITY AND MULTIPLE INFECTION**

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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-3 α (MSP3 α) and the circumsporozoite protein (CSP), we investigated the population diversity of *P. vivax* in Mae Sod, Thailand from April 2000 through June 2001. Parasites isolated from 50 malaria patients attending two local clinics showed a high level of polymorphism at the MSP3 α locus as revealed by polymerase chain reaction/restriction fragment length polymorphism (PCR-RFLP) and direct sequencing. Based on the length of PCR products, three major types of the MSP3 α locus were distinguished with a frequency of 70, 24, and 6%, respectively. These major types were further divided into at least 13 alleles by RFLP analysis. MSP3 α analysis also showed that 9 of the 50 patients had multiple infections. Genotyping of the parasites by PCR and hybridization for two known CSP genotypes, VK210 and VK247, revealed that the majority of the parasites (75%) were VK210 type. Equally intriguing is that among the VK247 parasites, only 3% occurred as single infections. Multiple infections were also easily identified by CSP typing, accounting for 28% of the patients. Altogether, our results strongly indicated that infections with multiple *P. vivax* clones were common in malaria endemic regions of Thailand.

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