

High frequency of genetic diversity of *Plasmodium vivax* field isolates in Myanmar

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Abstract

Malaria is one of the most serious problems threatening human health in Myanmar. Although the morbidity and mortality rates due to malaria have been gradually declining, Myanmar still contributes to a large proportion of malarial death in the South-East Asia region. However, little is known about the nature and extent of genetic diversity of the malarial parasites circulating in Myanmar. In this study, we investigated the overall infection status of Plasmodium and the population diversity of *Plasmodium vivax* by analyzing three genetic markers, circumsporozoite protein (CSP), merozoite surface protein-1 (MSP-1), and merozoite surface protein-3 (MSP-3alpha), of *P. vivax* field isolates collected from infected individuals. In 349 blood samples collected from the individuals who exhibited clinical symptoms associated with malaria, 63.0% showed a positive result for malaria (220/349). *P. vivax* was detected in 58.2% (128/220) and *Plasmodium falciparum* was detected in 29.1% (64/220). Mixed infections with both parasites were detected in 12.7% (28/220). The 116 blood samples in which single infection of *P. vivax* was confirmed were selected and subjected to further genetic analysis. Genotyping of the CSP gene of *P. vivax* showed that VK210 type (98.3%, 114/116) is predominant in Myanmar, but a significant level of mixed infections of VK210 and VK247 types (24.1%, 28/116) was also identified. Sequence analyses of MSP-1 and MSP-3alpha genes revealed a large number of distinguishable alleles: 12 for MSP-1 and 25 for MSP-3alpha. These results collectively suggest that the *P. vivax* population in Myanmar is highly diverse and multiple clonal infections are prevalent in the country.