

Prevalence of *Plasmodium vivax* VK210 and VK247 subtype in Myanmar

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Abstract

Background: *Plasmodium vivax* is divided into two subtypes, a dominant form, VK210 and a variant form, VK247. This division is dependent on the amino acid composition of the circumsporozoite (CS) protein. In this study, the prevalence of the VK247 variant form of *P. vivax* was investigated in Myanmar.

Methods: The existence of malaria parasites in blood samples was determined by microscopic examination, polymerase chain reaction (PCR) and DNA hybridization assays. To test for antibodies against *P. vivax* and *Plasmodium falciparum* in blood samples, an indirect immunofluorescence antibody test (IFAT) was performed using asexual blood antigens. An enzyme-linked immunosorbent assay with synthetic VK210 and VK247 antigens was carried out to discriminate between the *P. vivax* subtypes.

Results: By thick smear examination, 73 (n = 100) patients were single infected with *P. vivax*, one with *P. falciparum* and 13 with both species. By thin smear, 53 patients were single infected with *P. vivax*, eight with *only P. falciparum* and 16 with both. Most of the collected blood samples were shown to be *P. vivax* positive (n = 95) by PCR. All cases that were positive for *P. falciparum* by PCR (n = 43) were also positive for *P. vivax*. However, 52 cases were single infected with *P. vivax*. IFAT showed antibody titres from 1:32 to 1:4,096. Additionally, using specific antibodies for VK210 and VK247, ELISA showed that 12 patients had antibodies for only the VK210 subtype, 4 patients had only VK247 subtype antibodies and 21 patients had antibodies for both subtypes. Using a DNA hybridization test, 47 patients were infected with the VK210 type, one patient was infected with VK247 and 23 patients were infected with both subtypes.

Conclusions: The proportion of the VK247 subtype in Myanmar was 43.1% (n = 25) among 58 positive cases by serodiagnosis and 25.6% (n = 24) among 94 positive cases by genetic diagnosis. In both diagnostic methods, the infection status of malaria patients is highly diverse with respect to malaria species, and multiple clonal infections are prevalent in Myanmar. Therefore, the complexity of the infection should be considered carefully when diagnosing malaria in Myanmar.