

## Detection of parasites in salivary glands and its possibilities

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Concerted control measures have considerably reduced the burden of malaria in Vietnam, and the parasites are now mostly restricted to forested rural areas. Malaria and forest activity is a well-known association in Southeast Asia, and many studies reported forest activity as a strong risk factor for malaria. Therefore, this is considered to be 'forest malaria'. However, actual conditions of the transmission of malaria parasites in the forest are unclear. In order to investigate how and which parasites mosquitoes carry in the forest, we collected mosquito samples and analyzed malaria parasites using PCR. By analysis of sporozoite positive salivary glands, human malaria parasites and *P. knowlesi* were detected in the samples. *P. knowlesi* were found as single infections and mixed with human malaria parasites: with *P. vivax*, one with *P. falciparum*, and *P. vivax* and *P. falciparum*. The results suggest that *Anopheles dirus* harbors *P. knowlesi* in a considerably high rate, and bites monkeys as frequently as humans. To get detailed information from the mosquitos regarding transmission of forest malaria, we analyzed gametocytes related genes. We targeted region 3 of *pfg377* and *pvs25* as indicators for *P. falciparum* and *P. vivax*, respectively. Two allelic types of *pfg377* region 3 were detected in sporozoites from *P. falciparum* infected mosquito salivary glands. Similarly, two alleles of *pvs25* were also detected in samples from *P. vivax* infected mosquitoes. The proportion of these allelic types identified in samples derived from sporozoite-infected mosquito salivary glands was comparable to that observed for blood sample derived gametocytes. The distribution of detected *pvs25* alleles had local specificity. These results suggest a characteristic of transmission of forest malaria.