

## **Incidence of malaria in the interior division of Sabah, Malaysian Borneo, based on nested PCR**

### **Abstract**

**Introduction.** Malaria is currently one of the most prevalent parasite-transmitted diseases caused by parasites of the genus *Plasmodium*. Misidentification of human malaria parasites especially *P. knowlesi* based on microscopic examination is very common. The objectives of this paper were to accurately identify the incidence of human malaria parasites in the interior division of Sabah, Malaysian Borneo, based on small subunit ribosomal RNA (ssrRNA) and to determine the misidentification rate in human malaria parasites. **Methods.** Nested PCR was used to detect the presence of human malaria parasites. A total of 243 blood spot samples from patients who had requested for blood film for malaria parasite (BFMP) analyses were used in this study. **Results.** Nested PCR findings showed that there was no *P. malariae* infection while the highest prevalent malaria parasite was *P. knowlesi*, followed by *P. vivax*, *P. falciparum*, and mixed infection. Only 69.5% of the 243 samples giving consistent nested PCR and microscopic results. **Conclusion.** The preliminary findings from molecular detection of malaria showed that *P. knowlesi* was the most prevalent *Plasmodium* species in the interior division of Sabah. The findings from this paper may provide a clearer picture on the actual transmission of different *Plasmodium* species in this region.