Molecular and Morphological Detection of Plasmodium Species in Wild Macaques in Selangor, Malaysia

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Abstract

Malaria is a serious global health problem, and rapid, accurate diagnosis is required to control the disease. A number of methods have been developed in recent years for diagnosing this disease, including polymerase chain reaction (PCR)-based technique that detect specific nucleic acid sequences, and microscopic examination of thin blood films that remains the most widely and commonly used method. In this study, blood samples were collected from 125 wild macaques consisting of 18 *Macaca nemestrina* and 107 *M. fasicularis* from various areas of Selangor. Giemsa-stained thin blood films (TBF) were prepared, and PCR using *Plasmodium* genus-specific primers for initial amplification and nested species-specific primers for *Plasmodium knowlesi* was conducted on all the blood samples. The prevalence of *Plasmodium* by TBF was 1.9% in *M. fasicularis* and 27.8% in *M. nemestrina*. The molecular prevalence of *Plasmodium* was 64.5% in *M. fasicularis* and 100% in *M. nemestrina.* When *P. knowlesi*-specific PCR was carried out, the prevalence in *M. nemestrina* was 5.6%, whereas in *M. fasicularis* it was 23.3%. These results indicate that the local wild macaques harbor a high rate of infection of *Plasmodium*. In addition, the prevalence of *P. knowlesi*, the zoonotic malaria parasite is higher than previously assumed. This warrants further investigation as these macaques may be potential reservoirs of human malaria in Malaysia.

Keywords: polymerase chain reaction (PCR), thin blood films, *Plasmodium knowlesi, Macaca nemestrina*, *Macaca fasicularis.*