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SHORT COMMUNICATION

Natural transmission of *Plasmodium knowlesi* to humans by *Anopheles latens* in Sarawak, Malaysia

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Summary Four species of malaria parasites are known to infect humans. A fifth species, *Plasmodium knowlesi*, has been reported to infect humans in Malaysian Borneo. Here we report for the first time the incrimination of *Anopheles latens* as the vector of *P. knowlesi* among humans and monkeys in Sarawak, Malaysia.

1. Introduction

Malaria remains a public health problem in many countries in Southeast Asia. Besides the four species of *Plasmodium* that commonly cause malaria in humans, simian malarias such as *Plasmodium inui*, *P. cynomolgi* and *P. knowlesi* can also cause malaria in humans (Garnham, 1966). These simian malaria infections were acquired by humans through blood passage or in laboratory settings through mosquito bites (Garnham, 1966). Naturally-acquired cases of *P. knowlesi* in humans were thought to be extremely rare, as previously there had been only two reports of such cases, both in peninsular Malaysia (Chin et al., 1965; Yap et al., 1971). However, a large number of human *P. knowlesi* cases have recently been reported in Kapit, Sarawak, Malaysian Borneo by Singh et al. (2004). Cases are also being reported from peninsular Malaysia (I. Vythilingam et al., unpublished data). *Plasmodium knowlesi* has also been detected in a patient who had spent time in a forested area on the Thai–Myanmar border (Jongwutiwes et al., 2004). Thus, it is essential to identify the mosquito vectors responsible to determine the dynamics of *P. knowlesi* transmission to humans. Studies were therefore initiated to determine the vectors of monkey malaria in different areas in Kapit, Sarawak.

2. Methods

2.1. Mosquito collection

Mosquitoes attracted to humans and monkeys were collected and dissected. When sporozoites or oocysts were encountered, they were preserved in absolute ethanol. DNA was extracted using the Qiagen DNeasy tissue® kit (Qiagen, Hilden, Germany) and samples were analysed by means of a nested PCR-based assay (Singh et al., 2004).

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