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Malaria parasites of long-tailed macaques in Sarawak, Malaysian Borneo: a novel species and demographic and evolutionary histories

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Abstract

Background: Non-human primates have long been identified to harbour different species of *Plasmodium*. Long-tailed macaques (*Macaca fascicularis*), in particular, are reservoirs for *P. knowlesi*, *P. inui*, *P. cynomolgi*, *P. coatneyi* and *P. fieldi*. A previous study conducted in Sarawak, Malaysian Borneo, however revealed that long-tailed macaques could potentially harbour novel species of *Plasmodium* based on sequences of small subunit ribosomal RNA and circumsporozoite genes. To further validate this finding, the mitochondrial genome and the apicoplast caseinolytic protease M genes of *Plasmodium* spp. were sequenced from 43 long-tailed macaque blood samples.

Results: Apart from several named species of malaria parasites, long-tailed macaques were found to be potentially infected with novel species of *Plasmodium*, namely one we refer to as "*P. inui*-like." This group of parasites bifurcated into two monophyletic clades indicating the presence of two distinct sub-populations. Further analyses, which relied on the assumption of strict co-phylogeny between hosts and parasites, estimated a population expansion event of between 150,000 to 250,000 years before present of one of these sub-populations that preceded that of the expansion of *P. knowlesi*. Furthermore, both sub-populations were found to have diverged from a common ancestor of *P. inui* approximately 1.5 million years ago. In addition, the phylogenetic analyses also demonstrated that long-tailed macaques are new hosts for *P. simiovale*.

Conclusions: Malaria infections of long-tailed macaques of Sarawak, Malaysian Borneo are complex and include a novel species of *Plasmodium* that is phylogenetically distinct from *P. inui*. These macaques are new natural hosts of *P. simiovale*, a species previously described only in toque monkeys (*Macaca sinica*) in Sri Lanka. The results suggest that ecological factors could affect the evolution of malaria parasites.

Keywords: Long-tailed macaque, *Macaca fascicularis*, *Plasmodium*, Population expansion

Background

Species in the genus *Plasmodium* (Apicomplexa: Haemosporida) are vector-borne blood parasites that infect a wide range of hosts, some of which cause the disease malaria [1] in humans. There are approximately 250 species of *Plasmodium* identified in mammals, birds and reptiles [2]. The number of *Plasmodium* species infecting non-human primates (apes, gibbons, New World Monkeys and Old World Monkeys) is estimated to be more than 30 [2] with non-human primates in Asia harbouring approximately 13 of these species [3]. Of these, six species (*P. knowlesi*, *P. inui*, *P. cynomolgi*, *P. fieldi*, *P. coatneyi* and *P. fragile*) infect two or more species of macaques (*M. fascicularis, M. nemestrina, M. mulatta, M. arctoides, M. cyclopsis, M. sinica, M. radiate* and *M. assamensis*) and silvered leaf monkeys (*Trachypithecus cristatus*) in nature [4]. *Plasmodium simiovale* is restricted to toque macaques (*M. sinica*) of Sri Lanka, while *P. fragile* has been identified in macaques (*M. mulatta* and *M. radiata*) in both India and Sri Lanka

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