



NOTE

Parasitology

Detection of a *Babesia* sp. genotype closely related to marsupial-associated *Babesia* spp. in male *Haemaphysalis shimoga* from Sarawak, Malaysian Borneo

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ABSTRACT. In this study, *Babesia* screening was conducted in 55 rodents and 160 tick samples collected from primary forests and an oil palm plantation in Sarawak, Malaysian Borneo. PCR targeting the 18S ribosomal DNA revealed the presence of *Babesia* spp. DNA detected in two questing male *Haemaphysalis shimoga* ticks collected from the oil palm plantation. Sequence analysis revealed that both sequences were identical and had 98.6% identity to a *Babesia macropus* sequence obtained from Eastern grey kangaroos (*Macropus giganteus*) in Australia. Phylogenetic tree revealed clustering with marsupial-associated *Babesia* spp. in the *Babesia sensu stricto* clade. Whether or not *H. shimoga* is the competent vector and the importance of the *Babesia* sp. detected in this study warrants more investigation.

KEYWORDS: *Babesia*, *Haemaphysalis shimoga*, ixodid tick, rodent, Sarawak

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Babesia spp. are tick-borne protozoan parasites of the phylum Apicomplexa that infect erythrocytes of mammals and birds [33]. Since the discovery of *Babesia* species by Victor Babes in 1888 [1], over 100 *Babesia* spp. have been reported worldwide from a vast range of vertebrate hosts [15]. Furthermore, *Babesia* spp. are continuously being detected in new host species, including bears, badgers, kangaroos, and many more [3, 13, 27]. Recently updated phylogeny-based classification for piroplasmids designated *Babesia* spp. into *Babesia sensu stricto* (Clade X/(VI)), and *Babesia microti*-like (Clade I), Western clade (Clade III/(II)), and Peircei group (Clade V) collectively as *Babesia sensu lato* [15, 33]. Among the detected *Babesia* spp., *Babesia microti* is the main etiological agent for human babesiosis [20].

In the Southeast Asian region, there are several reports of *Babesia* spp. in humans, animals, and ticks. Two human cases inflicted by *B. microti* have been reported at the China-Myanmar border [40]. In addition, a previous study in Thailand reported a *Babesia* sp. detected in *Haemaphysalis lagrangei*, which was phylogenetically related to *Babesia* sp. KO1 from a human patient in Korea [39]. Dantrakool *et al.* [6] reported a *Babesia* sp. from *Bandicota indica* rats in Thailand, which morphologically resembled *B. microti*, but was closely related to *B. canis* in phylogenetic analysis. *Babesia bovis* and *B. bigemina*, the causative agents for bovine babesiosis, have been reported in Malaysia, Indonesia, Thailand, and Vietnam [4, 11, 23, 26, 31, 34]. Both *Babesia gibsoni* and *Babesia vogeli* have been detected in dogs from Malaysia and Thailand [8, 19, 30], while *B. vogeli* has been reported from the dogs in Cambodia [12, 14]. Additionally, *B. gibsoni* and *B. vogeli* were detected in *Rhipicephalus sanguineus* parasitizing dogs in Peninsular Malaysia [30]. Although several studies of *Babesia* spp. were conducted in Southeast Asian countries, knowledge of *Babesia* spp. in the region,

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