Complete mitogenome of the giant panda tick *Haemaphysalis longicornis* (Ixodida: Ixodidae) and its phylogenetic implications

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The giant panda (*Ailuropoda melanoleuca*) is a flagship species for wildlife conservation in the world (O’Brien et al. 1994; Wang et al. 2018). The ticks are common blood-feeding ectoparasites found in giant pandas and poses significant health burden to wild and captive populations. In the present study, the complete mitogenome of the giant panda tick *H. longicornis* was sequenced using Illumina sequencing technology. The entire mitogenome was 14,706 bp in length and encoded 37 genes including 13 protein-coding genes, 22 transfer RNAs and two ribosomal RNAs. Phylogeny showed that four isolates of *H. longicornis*, regardless of host origins or locations, clustered together and had a closer relationship with *Haemaphysalis恨tici* than other *Haemaphysalis* species among the subfamily Haemaphysalinae of Ixodidae. The cumulative mitochondrial DNA resources provide insights into genetic and phylogenetic studies of *Haemaphysalis* ticks.
and placed between tRNA-Leu and tRNA-Ile with a separation by tRNA-Val. The control region (also known as D-loop region) was located between tRNA-Leu and tRNA-Cys, similar to other Haemaphysalis ticks, suggesting its conservation and function in regulation of transcription and control of DNA replication (Clayton 1991).

Building on a concatenated amino acid sequences of 13 protein-coding genes from *H. longicornis* and 29 other ticks, the maximum-likelihood (ML)-based phylogeny demonstrated that four isolates of *H. longicornis*, regardless of host origins or locations, clustered together and shared a more close relationship to *Haemaphysalis hystricis* than to other *Haemaphysalis* ticks, with 100% bootstrap confidence (Figure 1), supporting their species validity in the subfamily Haemaphysalinae. In addition, the genera including Archaeocroton, Bothriocroton, Dermacentor, Rhipicephalus, Amblyomma and Aponomma were treated as monophyletic relationships with *Haemaphysalis* in the family Ixodidae, agreement with recent molecular studies (Burger et al. 2013; Geng et al. 2017; Tian et al. 2019; Liu et al. 2020). In summary, the *H. longicornis* mitogenome sequenced here provides novel insights into genetic and phylogenetic studies of this tick.

**Disclosure statement**

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**Data availability statement**

The data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov, reference number MT780294.

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