

The complete mitochondrial genome of *Haemaphysalis concinna* (Ixodida: Ixodidae)

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ABSTRACT

The complete mitochondrial genome of *Haemaphysalis concinna* is reported for the first time in this study. Its entire mitogenome is 14,675 bp in length, contained 13 protein-coding genes, two ribosomal RNA genes, 22 transfer RNA genes, and two non-coding regions. Among the 13 protein-coding genes, apart from the *nad1*, *nad4*, *nad4L*, and *nad5* gene encoded on the L-strand, the remaining protein-coding genes were encoded on the H-strand. The phylogenetic analysis by Bayesian inference method shows that *Amblyomma sphenodonti* and *H. parva* formed one clade, while *H. concinna* and other species of genus *Haemaphysalis* formed the other clade, indicating that *H. concinna* belong to the genus *Haemaphysalis*.

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The obligate haematophagous ectoparasites *Haemaphysalis concinna* (Ixodida: Ixodidae) is widely distributed in China (Teng and Jiang 1991), Russia, Germany, as well as temperate Eurasia (Nosek 1971). These adult stages of *H. concinna* mainly parasitize on Artiodactyla, and accidentally attack humans that cause mechanical damage and transmit a great variety of pathogens (Mikryukova et al. 2014; Švehlová et al. 2014).

The adult of *H. concinna* was collected by swiping flags on vegetations from Seven peak national Forest Park (46.711100 N, 130.945300 E, 550 m at altitude), Huanan County Heilongjiang Province in Northeast China, on 12 April 2016. The individual tick was stored in the Department of Parasitology, Heilongjiang Bayi Agricultural University (specimen no. BYNKPL-160412), and DNA was extracted by TIANamp Genomic DNA Kit (TIANGEN, Beijing, China), and stored at -20°C until use. The entire mitochondrial genomic sequences were composed of two overlapping fragments, one fragment approximately 5.9 kb was amplified from *cox1* to *rml* using the primers CO1-J (5'-CCT GAT ATA GCA TT TCC TCG-3') and 16S-N (5'-CTG CTC AAT GAT TTT TAA ATT GCT GTG-3'), the other one fragment approximately 9.0 kb was amplified from *rml* to *cox1* using the primers 16S-J (5'-TTA CGC TGT TAT CCC TAG AGT ATT-3') and CO1-N (5'-GCT ATA TCA GGT GCA CCT-3').

The entire *H. concinna* mt genome was a typical circular DNA molecule with 14,675 bp in size (GenBank accession number NC_034785), which contained 13 protein-coding

genes (*cox1-3*, *nad1-6*, *nad4L*, *atp6*, *atp8*, and *cytb*), two ribosomal RNA (rRNA) genes, 22 transfer RNA (tRNA) genes, and two non-coding regions (NCRs). The protein-coding genes were transcribed in different directions, which were consistent with those of other ticks (Black and Roehrdanz 1998; Burger et al. 2014; Guo et al. 2016), but distinct from those of trematodes, cestodes, and nematodes (Yamasaki et al. 2012; Duan et al. 2015; Chang et al. 2016), which transcribed in the same directions. Among the 13 protein-coding genes, apart from the *nad1*, *nad4*, *nad4L*, and *nad5* gene encoded on the L-strand, the remaining protein-coding genes were encoded on the H-strand. The nucleotide compositions of the complete mtDNA sequence of *H. concinna* were biased towards A + T (77.96%), with T being the most favoured nucleotide (39.35%) and G was the least favoured (9.21%). The *H. concinna* mt genome encoded 3615 amino acids in total. The A + T content of protein-coding genes ranged from 71.02% (*cox1*) to 84.57% (*atp8*).

Based on the concatenated amino acid sequence dataset (13 protein-coding genes), phylogenetic analyses were performed using Bayesian inference (BI). The result showed that the tree was divided into two large branches: Prostriata and Metastricata (Figure 1). Within the metastricata, *H. concinna* and genus *Haemaphysalis* species clustered together with high statistical support (PP = 1), indicating that *H. concinna* belong to the genus *Haemaphysalis*. This study provides not only new mtDNA resource for phylogenetic studies, but also novel and useful genetic marker for further studies on species

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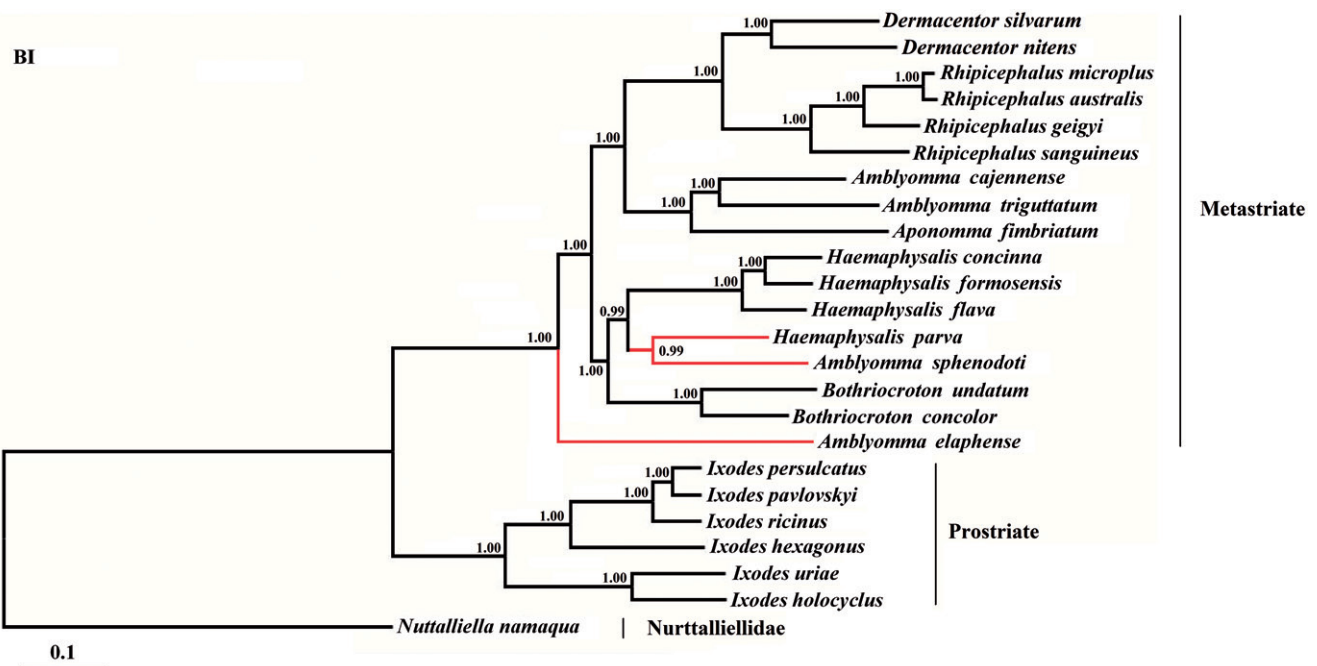


Figure 1. Phylogenetic relationships of *Haemaphysalis concinna* and other species based on mitochondrial sequence data. The concatenated amino acid sequences of 13 protein-coding genes were analysed with Bayesian inference (BI), using *Nuttalliellidae namaqua* (NC_019663) as an outgroup. All the species accession numbers in this study are listed as below: *Amblyomma triguttatum* NC_005963, *Amblyomma elaphense* NC_017758, *Amblyomma sphenodonti* NC_017745, *Amblyomma cajennense* NC_020333, *Aponomma fimbriatum* NC_017759, *Bothriocroton concolor* NC_017756, *Bothriocroton undatum* NC_017757, *Haemaphysalis flava* NC_005292, *Haemaphysalis formosensis* NC_020334, *Haemaphysalis parva* NC_020335, *Rhipicephalus sanguineus* NC_002074, *Rhipicephalus microplus* KP143546, *Rhipicephalus australis* NC_023348, *Rhipicephalus geigy* NC_023350, *Ixodes hexagonus* NC_002010, *Ixodes holocyclus* NC_005293, *Ixodes persulcatus* NC_004370, *Ixodes uriae* NC_006078, *Ixodes pavlovskyi* NC_023831, *Ixodes ricinus* NC_018369, *Dermacentor nitens* NC_023349, *Dermacentor silvarum* NC_026552, and *Nuttalliella namaqua* NC_019663.

identification, population genetics, and molecular epidemiology of the genus *Haemaphysalis* in ticks.

Disclosure statement

The authors declare no conflict of interest.

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