


MITOGENOME ANNOUNCEMENT

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## Complete mitochondrial genome and phylogenetic analysis of *Ixodes persulcatus* (taiga tick)

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### ABSTRACT

*Ixodes persulcatus* is a species of hard tick which is a predominant tick species that spreads a wide array of serious human and animal pathogens. Here, we first assemble the complete mitogenome of *I. persulcatus* of China. The total length of the mitogenome was 14,539 bp included 36 genes and with a mitogenome structure similar to other ticks. Phylogenetic tree was constructed based on the complete mitogenome of *I. persulcatus* and closely related 19 species ticks to assess their phylogenetic relationship and evolution. We also analyze the differences between the mitogenomes of *I. persulcatus* of Japan and China. The complete mitogenome data would be useful for further study of *I. persulcatus*.

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### KEYWORDS

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*Ixodes persulcatus* is a species of hard tick distributed from Europe through central and northern Asia to China and Japan, which is a predominant tick species that spreads a wide array of serious human and animal pathogens, including *Borrelia garinii*, which causes Lyme disease (Ai 1990; Cao et al. 2000), *Borrelia miyamotoi*, one of the relapsing fever borreliae, *Anaplasma phagocytophilum*, the causative agent of human granulocytic anaplasmosis (Cao et al. 2003). In addition to this information, *I. persulcatus* has recently drawn some attention as a vector for tick-borne encephalitis virus (Jääskeläinen et al. 2011), Babesia (Sun et al. 2008; Niu et al. 2016), and spotted fever group rickettsiae (Jia et al. 2013; Sun et al. 2015).

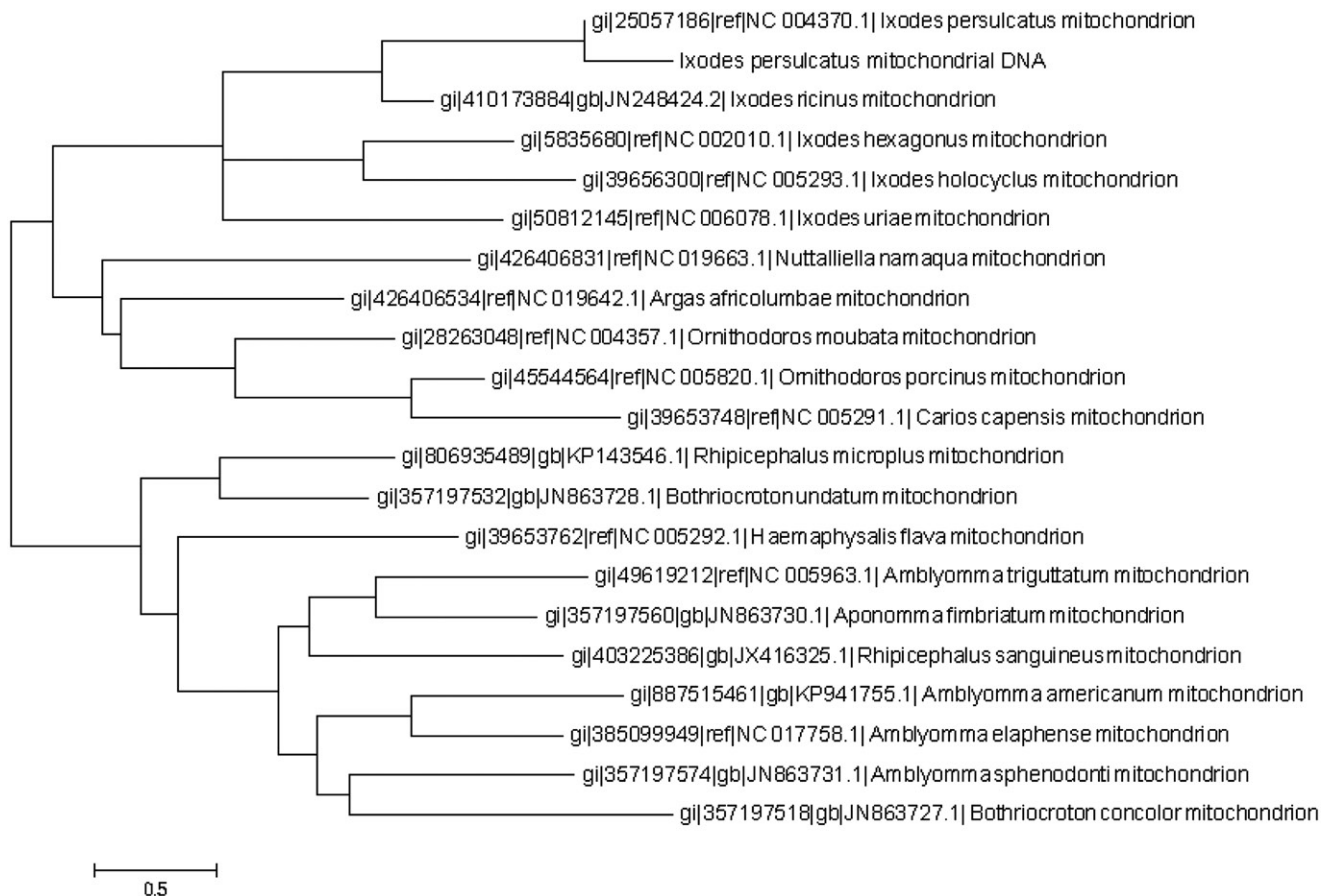
In this study, we first reported the complete mitogenome of *I. persulcatus* of China. A proportion of eggs, larvae, males, and females adults of ticks were collected in the forest region of Sui Fenhe, Hei Longjiang province, China. After morphological identification, the specimens were kept in the laboratory at  $-80^{\circ}\text{C}$  under the accession number SFH2714. The specimens were homogenized individually using metal beads and resuspended in phosphate-buffered saline (PBS); total genomic DNA was extracted using a Tiangen DNA extract kit (Tiangen Inc., Beijing, China) following the manufacturer's instructions. DNA was stored at  $-20^{\circ}\text{C}$ . The total length of its mitogenome was 14,539 bp, with a genome size similar to other ticks (Xu et al. 2014). The accurate annotated mitochondrial genome sequence was submitted to GenBank with accession number KU935457. The complete mitogenome has 13 protein-coding genes, 21 transfer RNA

genes, and 2 ribosomal RNA genes. The 12S and 16S rRNA genes were 718 bp and 1206 bp in length, respectively. The ribosomal subunit genes were located between the *tRNA-Leu* and *tRNA-Ile* genes and further separated by the *tRNA-Val* gene. The total base composition of the mitogenome is A (37.8%), T (39.55%), C (14.38%), and G (8.27%). Which shows AT bias, with the AT content of 77.35%. The percentage of GC (22.65%) was lower than AT rate, which was generally in accordance with other invertebrate mitochondrial genomes.

To further validate the new sequences, we used all of mitochondrial genome sequences published in Genbank of other tick species to construct the phylogenetic tree. These species were as follows: *Ixodes persulcatus*, *Ixodes ricinus*, *Ixodes hexagonus*, *Ixodes holocyclus*, *Ixodes uriae*, *Rhipicephalus microplus*, *Rhipicephalus sanguineus*, *Bothriocroton undatum*, *Bothriocroton concolor*, *Haemaphysalis flava*, *Amblyomma triggatum*, *Aponomma fimbriatum*, *Amblyomma americanum*, *Amblyomma elaphense*, *Amblyomma sphenodonti*, *Argas africolumbae*, *Carios capensis*, *Ornithodoros moubata*, *Ornithodoros porcinus*, and *Nuttalliella namaqua*. We used MEGA6 to produce the phylogenetic tree based on the maximum-likelihood method (Figure 1). The phylogenetic analysis results support that the mitochondrial DNAs of *Ixodes persulcatus* are more closely related to other species of *Ixodes* genus. Compared with the only other *I. persulcatus* mitogenome of Japan (Shao et al. 2005), there were 7 bases insertion, 7 bases deletion, and 31 bases substitution in the new *I. persulcatus* mitogenome of China we sequenced.

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**Figure 1.** Maximum-likelihood tree of complete mitogenomes of *I. persulcatus* and 19 other species. Inside of these parentheses are species with NCBI gi number, accession number and common name except *I. persulcatus* mitogenome we report.

## Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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