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The complete mitochondrial genome of *Takydromus septentrionalis* (Reptilia: Lacertidae)

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**ABSTRACT**

The complete mitochondrial genome sequence of *Takydromus septentrionalis* was determined by shotgun sequencing. The total length of mitogenome is 18,304 bp, and contains 13 protein-coding genes, 22 tRNA genes, 2 ribosome RNA genes, and 2 control regions. Most of the genes of *T. septentrionalis* were distributed on the H-strand, except for the ND6 subunit gene and eight tRNA genes which were encoded on the L-strand. The phylogenetic tree of *T. septentrionalis* and 8 other closely related species was reconstructed. The phylogenetic analyses based on these mitogenomes presented here will be useful for further insights on the evolutionary relationships of Takydromus.

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**KEYWORDS**

Mitogenome; *Takydromus septentrionalis*; phylogeny

The genus *Takydromus Daudin*, 1802 contains 22 known species (Arnold et al. 2007; Uetz and Hallermann 2019). *Takydromus septentrionalis* Günther, 1864 was described by Günther (1864). This species is a diurnal lizards and currently widely distributed in most of China (Zhao et al. 1999; Lu et al. 2000; Huang 2002; Han et al. 2007). In this research, we determined and described the mitogenome sequence of *T. septentrionalis* in order to obtain basic genetic information about this species.

The specimen of *T. septentrionalis* was collected from Jiulongfeng Nature Reserve, Huangshan, Anhui, China on May 28, 2017. It was preserved and deposited in the Museum of Huangshan University (Voucher numbers: HS17112). Total genomic DNA was extracted from liver using a Qiagen DNEasy blood and tissue extraction kit (Qiagen Inc., Valencia, CA, USA). The complete mitogenome sequence has been submitted to GenBank with accession number is MK630237.

The complete mitochondrial genome sequence of *T. septentrionalis* has been obtained from shotgun sequencing. The total length of the complete mitogenome of *T. septentrionalis* was sequenced to be 18,304 bp which consisted of 13 typical vertebrate protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes, and 2 control regions (D-loop). The base composition was 31.6% for A, 30.3% for T, 13.2% for G and 24.9% for C. The locations of protein-coding genes were identified by comparing with the homologous genes of other related species. Most of the *T. septentrionalis* mitochondrial genes are encoded on the H-strand except for the ND6 gene and eight tRNA genes, which are encoded on the L-strand. Among the mitochondrial protein-coding genes, the ATP8 was the shortest, while the ND5 was the longest. The gene order, contents and base composition are identical to those found in typical vertebrates (Boore 1999; Sorenson et al. 1999).

The phylogenetic tree of *T. septentrionalis* was constructed based on the complete mtDNA sequences with other 8 related species from GenBank by MEGA 7.0 (Kumar et al. 2016) using Maximum-likelihood (ML) methods. The ML tree (Figure 1) was reconstructed in [http://www.phylo.org/portal2/login](http://www.phylo.org/portal2/login). As shown in Figure 1, the *T. septentrionalis* was close to *T. wolteri*. The phylogenetic analysis result was consistent with the previous research with a high support. It indicated that our new determined mitogenome...
sequences could meet the demands and explain some evolution issues.

**Disclosure statement**

The authors declare that the study was conducted in the absence of any commercial or financial relationships that could be constructed as potential conflicts of interest.

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**References**


