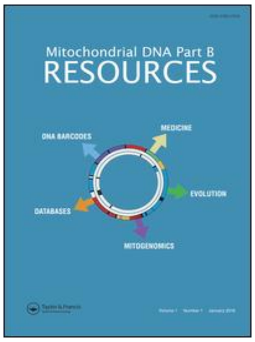

Taylor & Francis
Taylor & Francis Group

Mitochondrial DNA Part B
Resources

ISSN: (Print) 2380-2359 (Online) Journal homepage: https://www.tandfonline.com/loi/tmdn20

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

Jian-Guo Hu, Li-Fang Peng, Xin-Sheng Tang & Song Huang

To cite this article: Jian-Guo Hu, Li-Fang Peng, Xin-Sheng Tang & Song Huang (2019) The complete mitochondrial genome of *Takydromus septentrionalis* (Reptilia: Lacertidae), Mitochondrial DNA Part B, 4:2, 2193-2194, DOI: 10.1080/23802359.2019.1623123

To link to this article: https://doi.org/10.1080/23802359.2019.1623123

MITOCHONDRIAL DNA PART B
2019, VOL. 4, NO. 2, 2193–2194
https://doi.org/10.1080/23802359.2019.1623123

Taylor & Francis
Taylor & Francis Group

MITOGENOME ANNOUNCEMENT

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

Jian-Guo Hu[a], Li-Fang Peng[b], Xin-Sheng Tang[b] and Song Huang[b]

[a]School of Nursing, Anhui Sanlian University, Hefei, China; [b]College of Life and Environment Sciences, Huangshan University, Huangshan, China

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*.

ARTICLE HISTORY
Received 4 May 2019
Accepted 17 May 2019

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 Qiagin 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 positions of RNA genes were predicted by the MITOS (Bernt et al. 2013), and 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!input.action. 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

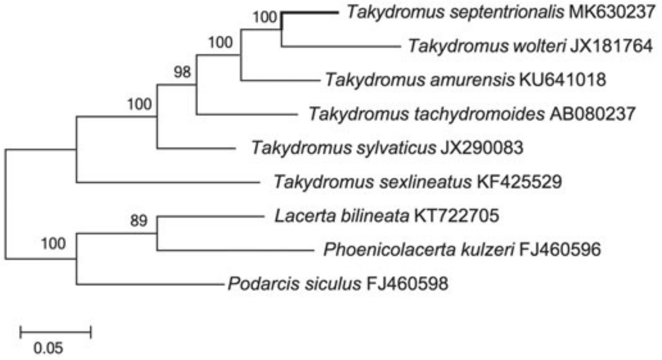

Figure 1. A maximum likelihood (ML) tree of *T. septentrionalis* in this study and 8 related species was constructed based on the dataset of the whole mitochondrial genome by online tool RAxML. The numbers above the branch meant bootstrap value. Bold black branches highlighted the study species and corresponding phylogenetic classification.

CONTACT Xin-Sheng Tang ✉ xstang@hsu.edu.cn College of Life and Environment Sciences, Huangshan University, Huangshan, 245041, China

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.

Funding

This project was funded by the Natural Science Research Project of Anhui Province Education Department [No. KJ2015ZD38], and National Natural Science Foundation of China [No. 31471968]. This research was funded by the Key Discipline of Ecology [zdxk201801] and Research Platform of Bioresource Institution [kypt201801], Huangshan University.

References

Arnold EN, Arribas O, Carranza S. 2007. Systematics of the Palaearctic and Oriental lizard tribe Lacertini (Squamata: Lacertidae: Lacertinae), with descriptions of eight new genera. Zootaxa. 1430:1–86.

Bernt M, Donath A, Juhling F, Externbrink F, Florentz C, Fritzsch G, Putz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69:313–319.

Boore JL. 1999. Animal mitochondrial genomes. Nucleic Acids Res. 27: 1767–1780.

Günther A. 1864. The reptiles of British India. London: Taylor & Francis; p. xxvii + 452.

Han JG, Ma HQ, Wang HJ, et al. 2007. A new record of *Takydromus septentrionalis* in Hebei province, China. Chin J Zool. 42:113–113.

Huang HY. 2002. A New Record of *Takydromus septentrionalis* in Guangdong province, China. Sichuan J Zool. 21:37–37.

Kumar S, Stecher G, Tamura K. 2016. MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Molecular Biology and Evolution. 33:1870–1874.

Lu YY, Zhang P, Wang XA, et al. 2000. A New Record of *Takydromus septentrionalis* in Shandong province, China. Sichuan J Zool. 19: 155–155.

Sorenson MD, Ast JC, Dimcheff DE, Yuri T, Mindell DP. 1999. Primers for a PCR-based approach to mitochondrial genome sequencing in birds and other vertebrates. Mol Phylogenet Evol. 12:105–114.

Uetz P, Hallermann J. 2019. August 2018 Takydromus 1 August 2018. The Reptile Database.

Zhao EM, Zhao KT, Zhou KY, et al. 1999. Fauna Sinica. Reptilia. Vol. 2. Beijing: Science Press.