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MITOGENOME ANNOUNCEMENT

Complete mitochondrial genome of *Takydromus kuehnei* (Squamata: *Takydromus*) and its phylogenetic analysis

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ABSTRACT

We sequenced and annotated the complete mitochondrial genome (mitogenome) of *Takydromus kuehnei* Van Denburgh, 1909 (Squamata: *Takydromus*). This mitogenome was 17,224 bp long and encoded 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes, one non-coding regions of an L-strand replication origin and a displacement loop region. The overall nucleotide composition was 32.8% of A, 13.8% of G, 24.8% of T, and 30.5% of C. Phylogenetic analysis using maximum likelihood method validated the taxonomic status of *T. kuehnei*, exhibiting the close relationship with the species from the genus *Takydromus*.

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Squamata; *Takydromus kuehnei*; mitogenome; phylogenetic analysis

Takydromus kuehnei Van Denburgh, 1909 (Squamata: *Takydromus*) is a small lizard from family Lacertidae genera *Takydromus* and lives in secondary forest and grass, which was firstly found in Taiwan, China, and recently it was found in Wuyi mountain in Fujian, China and Zhejiang, China (Uetz et al. 2021). In this study, we sequenced the mitochondrial genome (mitogenome) of *T. kuehnei* (GenBank accession No. MZ435950).

The specimens of male *T. kuehnei* used in this study was collected in Quzhou, Zhejiang, China (29.45 N, 118.82 E) and its tail tissue was immediately stored in 75% ethanol at −20 °C. Then the lizard was released to sample site. The experimental procedures followed in this study complied with the animal welfare and research laws in China and were approved by the Ethics Committee of Lishui University (permit No. AREC-LSU202104001DGH). We used the Wizard® Genomic DNA Purification Kit (Promega, Madison, USA) to isolate the whole genomic DNA from tail tissues of each specimen according to the manufacturer's instructions. The extracted genomic DNA was stored in the Laboratory of Amphibian Diversity Investigation (contact person: Guo-Hua Ding, E-mail: guwoding@lsu.edu.cn) at Lishui University, and the Accession Number of the specimen was LSU20210413QLG001. The genomic DNA was sequenced using the Hiseq6000 platform (Illumina Inc., San Diego, CA, USA). The mitogenome of *Takydromus amurensis* (GenBank accession No. KU641018) was employed as the reference sequence (Park et al. 2016). We used the NOVO Plasty 3.7 (Dierckxsens et al. 2017) to assemble and MITOS Web Serve to annotate the mitogenome (Bernt et al. 2013).

We obtained the mitochondrial genome of *T. kuehnei* with 17,224 bp sequence. This mitogenome encoded 13 protein-coding genes (PCGs), 22 tRNAs, two rRNAs (*12S* and *16S*) and one non-coding regions of an L-strand replication origin and a displacement loop region (control region). The overall nucleotide composition was 32.8% of A, 13.8% of G, 24.8% of T, and 30.5% of C. The gene arrangement pattern and transcription directions were identical to previous studies in the suborder Sauria (Kim et al. 2016). Among the 13 PCGs, the *ATP8* was with the least nucleotides, while the *ND5* was with the most nucleotides. All PCGs initiated with ATG as a start codon, except for *APT6* gene, which began with GTG. Ten genes (*ND1*, *ND2*, *ND3*, *COI*, *ATP8*, *ATP6*, *ND4L*, *ND5*, *ND6*, and *Cytb*) ended with complete stop codons (TAA, AGA, and AGG), and the other genes ended with T or TA as the incomplete stop codons, which were presumably completed as TAA by post transcriptional polyadenylation (Anderson et al. 1981).

To validate the phylogenetic position of *T. kuehnei*, the phylogenetic tree was constructed using 13 mitochondrial PCGs, including six *Takydromus* species, and *Eremias vermiculata, Eremias dzungarica, Eremias brenchleyi,* and *Phrynocephalus putjatai* were used as out-group. The Bayesian Inference (BI) tree was constructed using MrBayes 3.2.6 under GTR + I + G + F (2,000,000 generations) with the initial 25% of sampled data discarded as burn-in, and maximum likelihood (ML) tree was constructed using IQ-TREE under the GTR + I+G4 + F model for 5000 ultrafast bootstraps in PhyloSuite v1.2.2 (Zhang et al. 2020). As shown in Figure 1, T. *kuehnei* was positioned near *T. sexlineatus*, and had a closer relationship with four species within the genus

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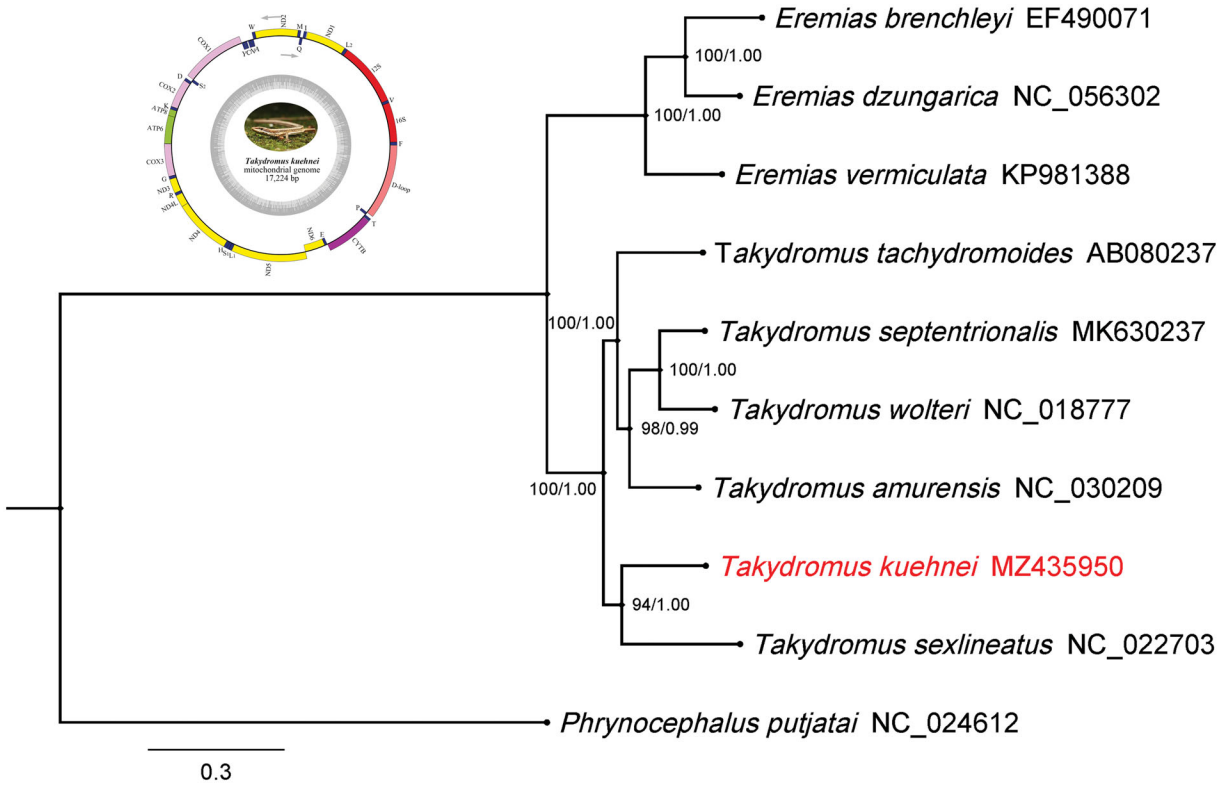

Figure 1. Phylogenetic tree obtained from BI and ML analysis based on 10 concatenated mitochondrial PCGs. Numbers on node are bootstrap values and bayesian posterior probability.

Takydromus, including *T. septentrionalis*, *T. wolteri*, *T. amurensis*, and *T. tachydromoides*. Meanwhile, the phylogenetic relationship of *T. kuehnei* is separated from the genus *Eremias*, and far away from *Phynocephalus putjatai* which is not the species of family Lacertiadae.

Author contributions

L.X.W and G.H.D were involved in the conception and design, analysis and interpretation of the data. G.H.D collected the sample. L.X.W. and K.N.L. wrote the original paper. G.H.D. finally approved the version to be published.

Disclosure statement

No potential conflict of interest was reported by the authors.

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov] under the accession no. MZ435950. The associated BioProject, BioSample, and SRA numbers are PRJNA636742, SAMN19899855, and SRR14933831, respectively.

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