The complete mitochondrial genome of a blue-tailed skink (*Plestiodon tunganus*) endemic to Sichuan Basin

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**ABSTRACT**

The complete mitochondrial genome of *Plestiodon tunganus* from its type locality (Pengba town, Luding County, China) was determined using polymerase chain reaction and directly sequenced with a primer walking method. The mitogenome is 17,263 bp in length and comprises the standard set of one control region, two rRNAs, 22 tRNAs plus 13 protein-coding genes (PCGs). The PCGs were used to perform Bayesian phylogenetic analyses together with other scincid lizards with mitogenome data in GenBank. The resulting phylogenetic tree showed that *P. tunganus* clustered in a branch close to the species from the same genus. The mitogenome of *P. tunganus* will provide fundamental data to explore mitochondrial genome evolution in skinks.

Blue-tailed skinks (genus *Plestiodon*) are a common component of the terrestrial herpetofauna throughout their range in East Asia and North and Middle America (Brandley et al. 2005, 2011, 2012). There are 10 described species of *Plestiodon* in China (Cai et al. 2015, Kurita et al. 2017). Among them, *P. tunganus* is endemic to the western region in Sichuan Basin (Zhao and Adler 1993). So far, little is known about the mitochondrial genome evolution in *Plestiodon* lizards, even in scincid lizards.

In this study, we report the whole mitochondrial DNA genome of *P. tunganus*, with voucher number MCB1021. The specimen was collected from the type locality of Pengba town (30.02559° N, 102.18163° E), Luding County, Sichuan Province, in China in August 2007. Its liver tissue was fixed with 95% ethanol and stored at –20°C in the herpetological collection at Chengdu Institute of Biology, Chinese Academy of Sciences. Total genomic DNA was extracted from liver tissue using a high-salt extraction protocol (Aljanabi and Martinez 1997). Published sequences of *P. egregious* (GenBank accession number AB016606), *P. chinensis* (Zhang et al. 2016) and *P. elegans* (Song et al. 2016) were used to design 16 pairs of primers. To obtain a sequence of the control region, we also designed some species-specific genome walking primers. Genes were annotated with the MITOS (Bernt et al. 2013) web server.

The mitochondrial genome of *P. tunganus* is 17,263 bp in length, with overall base composition of 24.5% (T), 29.5% (C), 30.4% (A) and 15.5% (G). Annotation of the mitogenome revealed 13 protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes, and one control region (CR or D-loop). The gene organization and order exhibited a typical vertebrate mitochondrial genome feature. Most genes are encoded on heavy strand except for ND6 and eight tRNA genes (tRNA-Gln, Ala, Asn, Cys, Tyr, Ser[UGA], Glu, and Pro). Most of the PCGs are initiated with the typical ATG codon, except for COX1 with GTT. Meanwhile, most PCGs are terminated with the typical AGA/AGG/TAA codons, except for COX2, COX3, ND3, and ND4 with the incomplete termination codon T. The 22 tRNA genes range in size from 66 bp in tRNA-Cys to 75 bp in tRNA-Phe and tRNA-Leu (UUA). The 12S rRNA, 16S rRNA, and D-loop are 950 bp, 1537 bp, and 2743 bp in size, respectively.

To evaluate mitochondrial sequence authenticity of *P. tunganus* and its phylogenetic placement, we performed a phylogenetic analysis using six complete mitochondrial genomes of the skinks (Squamata, Scincomorpha, Scincidae) as well as *Smaug warreni* (Squamata, Scincomorpha, Cordylidae) as the outgroup. We concatenated the PCGs and performed the Bayesian inference with MrBayes v.3.2.1 (Ronquist & Huelsenbeck 2003) with GTR þ Gamma substitution model. The resulting phylogenetic tree (Figure 1) indicated a close phylogenetic affinity of the four *Plestiodon* species, confirming previous findings (Brandley et al. 2011, 2012). The mitogenome sequence of *P. tunganus* will provide...
fundamental data to explore mitochondrial genome evolution in skinks.

Nucleotide sequence accession number

The complete mitochondrial genome sequence of *Plestiodon tunganus* has been assigned GenBank accession number MK37039.

Disclosure statement

No potential conflict of interest was reported by the authors. The authors alone are responsible for the content and writing of this article.

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