Next-generation sequencing yields a complete mitochondrial genome of the Asian Glass Lizard (Dopasia gracilis) from the Yungui Plateau in Southwest China

Bo Cai\textsuperscript{a,b,c}, Xianguang Guo\textsuperscript{a} and Jianping Jiang\textsuperscript{a}

\textsuperscript{a}Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu, China; \textsuperscript{b}Key Laboratory of Bio-resources and Eco-environment of Ministry of Education, College of Life Sciences, Sichuan University, Chengdu, China; \textsuperscript{c}Chengdu Institute of Biology, University of Chinese Academy of Sciences, Beijing, China

**ABSTRACT**

The Asian Glass Lizard, *Dopasia (Ophisaurus) gracilis*, has wide distribution in North India, Nepal, South China, and Indochina. In this study, a complete mitochondrial genome of *D. gracilis* from the Yungui Plateau in Southwest China was determined by next-generation sequencing. Similar to the typical mtDNA of vertebrates, the mitogenome was 17,133 bp in length and comprised the standard set of 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes, and 1 control region. The concatenated PCGs were used to conduct Bayesian phylogenetic analyses together with mitogenome data of Anguidae and related taxa in GenBank. The resulting phylogenetic tree confirmed the monophyly of Anguidae and Aguiniae as well as *D. gracilis*, respectively. The mitogenome reported here will contribute to the examination of phylogeographic structure for *D. gracilis* and understanding of mitochondrial DNA evolution in Anguidae.

**ARTICLE HISTORY**

Received 9 January 2020
Accepted 19 January 2020

**KEYWORDS**

Anguidae; Asian Glass Lizard; mitochondrial genome; next-generation sequencing; phylogenetic tree

The mitogenome of *D. gracilis* is 17,133 bp in length, comprising 13 protein-coding genes (PCGs), 22 tRNA genes, 2 rRNA genes, and 1 control region (CR or D-loop). The gene content, arrangement, and composition exhibited a typical vertebrate mitogenome feature. The majority of the genes in the mtDNA of *D. gracilis* was distributed on H-strand, except for the ND6 and eight tRNA genes (tRNA-Gln, Ala, Asn, Cys, Tyr, Ser\textsuperscript{UCN}, Glu, and Pro). In 13 PCGs, the shortest was ATP8 gene (168 bp) and the longest was ND5 gene (1824 bp). Twelve of 13 PCGs were initiated with the typical ATG codon, except for COX1 with GTG. Meanwhile, most PCGs were terminated with the typical TAA/TAG/AGG codons, except for COX2, COX3, ND3, and ND4 with the incomplete termination codon T. The 22 tRNA genes ranged in size from 61 bp in tRNA-Ser\textsuperscript{AGY} to 73 bp in tRNA-Leu\textsuperscript{JUR} and tRNA-Asn. The 12S rRNA, 16S rRNA, and D-loop were 948 bp, 1559 bp, and 1691 bp in length, respectively.

The concatenated PCGs of Anguidae available in GenBank and *Helodermia suspectum* (*Heloderma*idae) plus *Shinisaurus crocodilurus* (*Shinisauridae*) as outgroups were used to reconstruct the Bayesian phylogenetic tree for assessing mitochondrial sequence authenticity of *D. gracilis* and its phylogenetic placement. As shown in Figure 1, the monophyly of both Anguidae and Anguinae was recovered (Lavin and Girman 2019; and references therein). Two individuals of *D. gracilis* clustered together and formed sister taxon to all other
sampled congeners. The mitogenome sequence will provide fundamental data for further investigating the phylogeographic structure of *D. gracilis* along with exploring mitochondrial DNA evolution in Anguidae.

**Nucleotide sequence accession number**

The complete mitochondrial genome sequence of *Dopasia gracilis* has been assigned GenBank accession number MN661343.

**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.

**Funding**

This research was supported by Sichuan Science and Technology Plan Project [Grant No. 2019JDKP0016], the National Natural Science Foundation of China [Grant No. 31672270], and the National Key Research and Development Program of China [2017YFC0505202].

**References**

Bankevich A, Nurk S, Antipov D, Gurevich A, Dvorkin M, Kulikov AS, Lesin V, Nikolenko S, Pham S, Prijibelski A, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 19(5):455–477.

Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2):313–319.

Lavin BR, Girman DJ. 2019. Phylogenetic relationships and divergence dating in the Glass Lizards (Anguinae). Mol Phylogenet Evol. 133:128–140.

Nguyen TQ, Böhme W, Nguyen TT, Le QK, Pahl KR, Haus T, Ziegler T. 2011. Review of the genus *Dopasia* Gray, 1853 (Squamata: Anguidae) in the Indochina subregion. Zootaxa. 2894(1):58–68.

Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol. 61(3):539–542.

Tamura K, Stecher G, Peterson D, Filipski A, Kumar S. 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. Mol Biol Evol. 30(12):2725–2729.

Uetz P, Freed P, Hoşek J. 2019. The reptile database. [accessed 2019 Nov 9]. http://www.reptile-database.org.

Yan L. 2015. Analysis on the two complete mitochondrial genomes of Anguidae and the phylogenetic relationships of Squamata [Master Thesis]. Wuhu, Anhui province, China: Anhui Normal University [in Chinese with English abstract].