The complete mitochondrial genome of *Asymblepharus himalayanus* (Scincidae; Sauria) and its phylogenetic position within Scincidae

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**ABSTRACT**

The complete mitochondrial genome of *Asymblepharus himalayanus*, has been determined for the first time by sanger sequencing. The overall length of the mitogenome is 17,304 bp and contains 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes, and a putative control region. The total base composition is 31.2% for A, 27.0% for T, 14.4% for G, and 27.4% for C. The phylogenetic tree with the whole mitochondrial genome sequence of *A. himalayanus* together with 10 other related species belonging to the family Scincidae was reconstructed, in order to prove the validity of the mitogenome of *A. himalayanus*. Phylogenetic analysis indicated that *A. himalayanus* was not nested within *Scincella*, and further corroborated this species does not belong to the genus of *Scincella*. The results of blastx searches against the amino acid sequences of the annotated proteins of other related mitochondrial genomes found in the NCBI RefSeq. A postprocessing step detects the start and stop codons, duplicates, and hits belonging to the same transcript (Bernt et al. 2013).

The complete mitochondrial genome (Genbank accession number: MN885892) of *A. himalayanus* was sequenced to be 17,304 bp which consisted of 13 typical vertebrate protein-coding genes (PCGs), 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes and one control region. The base composition was 31.2% for A, 27.0% for T, 14.4% for G, and 27.4% for C. Complete mitogenome was encoded on the H-strand except for the ND6 gene and eight tRNA genes, which were encoded on the L-strand. The 22 tRNA genes ranged in size from 66 to 75 bp. Among the mitochondrial protein-coding genes, the ATP8 was the shortest, while the ND5 was the longest. The 12 s rRNA (949 bp) and 16 s rRNA (1495 bp), were located between the tRNA-Phe and tRNA-Leu genes and separated by the tRNA-Val gene. The gene order, contents and base composition were identical to those found in typical vertebrates (Boore 1999; Sorensen et al. 1999).

In order to help clarifying its phylogenetic position, we used the whole mitochondrial genome sequences of *A. himalayanus* and other 10 related species to perform a phylogenetic analysis. These species were as follows: *Scincella reevesii*, *Tropidophorus vandenburghi*, *S. modesta*, *Tropidophorus hangman*, *Scincus scincus*, *Plestiodon egregious*, *Sphenomorphus indicus*, *Isopachys gyldenstolpei*, *Aeuchosaurus chinensis* (outgroup). We aligned these sequences using MAFFT 7.307 (Kato et al. 2019). Maximum likelihood (ML)
methods was used to reconstruct phylogenetic tree (Figure 1) in http://www.phylo.org/portal2/login!input.action. Phylogenetic analysis indicated that *A. himalayanus* was sister to the groups of *Tropidophorus hangman*, *Isopachys gyldenstolpei*, and *Scincella spp.*., not nested within *Scincella*. We further corroborated this species does not belong to the genus *Scincella*. Given the limited genetic data used, our results did not provide enough resolution regarding phylogenetic relationships between the genera *Scincella* and *Asymblepharus*. The species division of intra-genera and the relationships with other genera are still unclear, more specimens and molecular data are needed in the future.

**Disclosure statement**

No potential conflict of interest was reported by the author(s).

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**Data availability statement**

The complete mitochondrial genome sequence and annotation of *A. himalayanus* that support the findings of this study are available in GenBank of NCBI at [https://www.ncbi.nlm.nih.gov] under the accession NO. MN885892.

**References**

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.

Boore JL. 1999. Animal mitochondrial genomes. Nucleic Acids Res. 27(8): 1767–1780.

Cai B, Wang YZ, Chen YW, Li JT. 2015. A revised taxonomy for Chinese reptiles. Biodiver Sci. 23(3):365–382.

Che J, Jiang K, Yan F, Zhang YP. 2020. Amphibians and reptiles in Tibet: diversity and evolution. Beijing: Science Press. p. 553–577.

Katoh K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform. 20(4):1160–1166.

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(2):105–114.

Wang K, Ren JL, Chen HM, Lyu ZT, Guo XG, Jiang K, Chen JM, Li JT, Guo P, Wang YY, et al. 2020. The updated checklists of amphibians and reptiles of China. Biodiv Sci. 28(2):189–218.