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Research Article

Complete Mitochondrial Genome of a Karst-dwelling Gecko, *Gekko liboensis* (Zhou and Li, 1982)

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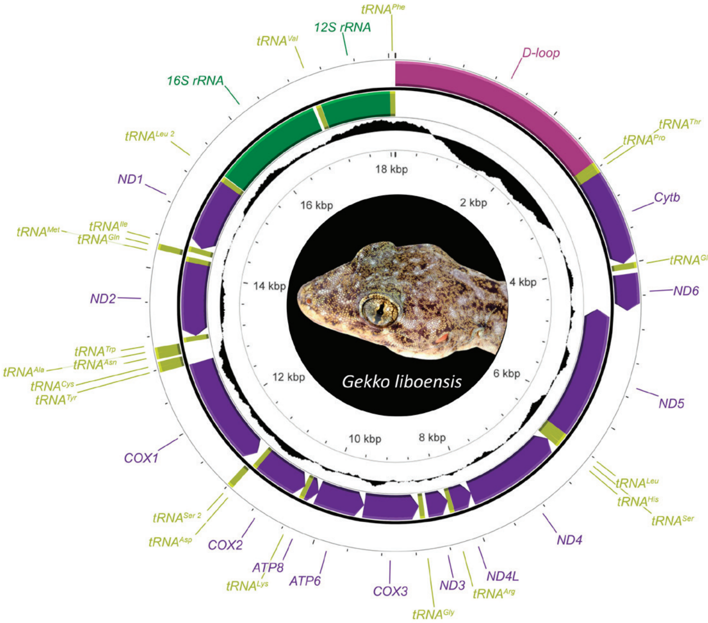
GRAPHICAL ABSTRACT



First complete mitogenome of the karst-endemic *Gekko liboensis*, providing insights into its phylogeny.

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ABSTRACT

Gekko liboensis is a karst-dwelling endemic species to China, with identification currently based solely on morphology. This study presents the first complete mitogenome of *G. liboensis*, collected from Libo, Guizhou, China. The genome is circular, spanning 18,079 bp, and contains 37 typical mitochondrial genes of the family Gekkonidae and one control region. Phylogenetic reconstructions, based on nine complete mitochondrial genomes and 25 concatenated *16S rRNA* and *ND2* sequences using Maximum Likelihood and Bayesian Inference methods, support the placement of *G. liboensis* within the subgenus *Japonigekko*, identifying *G. paucituberculatus* as its closest relative. These findings support previous morphological and phylogenetic studies within *Japonigekko* taxonomy. The newly obtained genomic data enhance our understanding of mitogenome structure and offer valuable insights into the genetic diversity and evolutionary background of *G. liboensis*. This study contributes to the growing genomic resources for gekkonid reptiles and aids future phylogenetic and conservation research.

Keywords: *Gekko* (*Japonigekko*) *liboensis*, Gekkonidae, mitogenome, phylogeny

1. INTRODUCTION

The genus *Gekko* Laurenti, 1768, belongs to the family Gekkonidae and is one of the most recognized gecko genera. It comprises a broadly spread group of nocturnal gekkonid lizards, currently encompassing approximately 90 known species classified into seven subgenera [1-2]. Among these, *Japonigekko* is the most diverse, with 21 species recorded in China [2], including four karst-dwelling species: *G. adleri* Nguyen et al. 2013, *G. kwangsiensis* Yang 2015, *G. liboensis* Zhou and Li 1982, and *G. paucituberculatus* Wang et al. 2024 [3].

Gekko liboensis, commonly known as the Libo Gecko, is endemic to China, occurring in Guizhou and Guangxi [4]. The species was originally described from a single female specimen collected in Libo, Guizhou [5]. In 1999, three additional specimens (two females and one juvenile) were reported [6]. However, due to its strong morphological similarity to *G. hokouensis* Pope, 1927, and the absence of male specimens, the taxonomic validity of *G. liboensis* remained uncertain for many years [7]. This uncertainty persisted until 2015, when Jono et al. (2015) confirmed its validity based on the morphological characteristics of 31 newly collected specimens from the type locality [4]. Despite these morphological studies, molecular data for the species remain unavailable, limiting further exploration of its genetic characteristics and molecular identification. This gap in knowledge restricts a deeper understanding of its phylogenetic relationships and evolutionary significance.

Currently, although 36 species have been described in the subgenus *Japonigekko* [2], only eight complete mitochondrial genomes, representing five species (*Gekko chinensis*, *G. japonicus*, *G. hokouensis*, *G. subpalmatus*, and *G. swinhonis*) [8-13], have been deposited in GenBank, none of which belong to karst-dwelling species. Here, by employing the next-generation sequencing technology, we present the first complete mitogenome of *G. liboensis*, marking the first mitogenome record for a karst-adapted species within *Japonigekko*. This study aims to enhance our understanding of the mitogenome structure, phylogenetic relationship, and taxonomic status of *G. liboensis*.

2. MATERIALS AND METHODS

2.1 Sampling and DNA Extraction

After morphological identification, based on characteristics such as a larger body size, the presence of one cloacal spur on each side, tubercles on the dorsal surface but absent on the limbs, and the absence of developed interdigital webbing [4-5], a voucher specimen of *Gekko liboensis* (SWU 0010068) was collected by hand from the Guizhou Maolan National Nature Reserve, Libo, Guizhou, China (25°15′26.3″N, 108°1′13.98″E; altitude 500 m a.s.l.). The specimen was preserved at Southwest University, Chongqing, China, while muscle tissue was isolated and preserved in 95% ethanol. Genomic DNA was extracted using the TIANamp Genomic DNA Kit (TIANGEN, Beijing, China).

2.2 Genome Sequencing and Annotation

A paired-end library with an insert size ranging from 300 to 800 bp was constructed and sequenced on the Illumina NovaSeq 6000 platform at Wuhan Benagen Technology Company Limited (Beijing, China) using paired-end 150-bp chemistry. The sequencing target depth for the sample was 25 ×.

The quality of the demultiplexed raw paired-end reads was evaluated using FastQC v0.12.0 (https://www.bioinformatics.babraham.ac.uk/projects/fastqc/). Reads were then processed using Trimmomatic v0.39 [14] to generate a cleaned dataset. This process involved trimming Illumina adapters, removing reads that fell below the quality threshold (sliding window set to 5:20), and discarding short cleaned reads (<50 bp) or those lacking either the forward or reverse pair. The cleaned reads were then assembled into the mitochondrial genome sequence using MitoFinder v1.4.2 [15], followed by annotation to generate the complete mitogenome sequence. A mitochondrial genome annotation file of the closely related species *Gekko swinhonis* (JQ906550) was downloaded from NCBI and used as a reference. Proksee [16], a specialized online genome visualization tool, was used to generate the circular mitogenome map of *G. liboensis*.

2.3 Phylogenetic Analysis

To analyze the phylogeny of *Gekko liboensis* within the subgenus *Japonigekko*, mitogenomes of five species and mitochondrial *16S rRNA* and *ND2* genes (concatenated into one contig for each species) of 16 species were downloaded from GenBank nucleotide database. *Gekko gecko*, belonging to the subgenus *Gekko* [1, 17], was used as the outgroup. In total, nine complete mitochondrial genomes, including *G. liboensis*, were used for mitogenome-based phylogenetic analysis, while 25 concatenated *16S rRNA* and *ND2* sequences were employed for mitochondrial gene based phylogenetic analysis (Supplementary Table S1). All sequences were assembled and aligned by MEGA X v10.1 [18].

Using the above two sets of genetic data, firstly, the Maximum Likelihood (ML) analyses were conducted on the IQ-TREE webserver [19-20], with the best-fitting substitution model and 10,000 ultrafast bootstrap replications (UFB) [21]. Strong support was assigned to nodes with UFB values greater than or equal to 95 [22]. Then Bayesian Inference (BI) analyses were conducted on the two mitochondrial gene sequences using MrBayes v3.2.7 [23]. The posterior probability distributions were generated using four incrementally heated Markov chains run for 20 million generations, with trees sampled every 1000 generations. After discarding the initial 25% of trees as burn-in, Bayesian posterior probabilities (BPPs) were estimated from the remaining sampled trees. Convergence was confirmed by a mean split frequency standard deviation below 0.01, effective sample sizes exceeding 200, and potential scale reduction factors approaching 1. BPP values of 0.95 or higher were regarded as providing significant support for the nodes [24-25]. Prior to phylogenetic analyses, PatitionFinder v2 [26] was used to determine the optimal nucleotide substitution model for *16S rRNA* and *ND2*.

3. RESULTS

3.1 Characteristics of *Gekko liboensis* Mitogenome

The whole mitochondrial genome of the *Gekko liboensis* is circular and has a total length of 18,079 bp (GenBank accession number PV066215). Its gene composition and arrangement pattern are consistent with those observed in other *Japonigekko* species [8-13]. The mitogenome contains the typical 37 genes: 13 protein-coding genes (PCGs), 22 tRNA genes, two rRNA genes, and a single control region (Figure 1). Among the PCGs, ten are initiated by the standard ATG start codon, while *ND2* starts with an ATT codon. The *ND6* and *ND3* genes begin with incomplete stop codons, G-- and A--, respectively. Seven PCGs (*ND6*, *ND4*, *ND4L*, *ATP6*, *ATP8*, *ND2* and *ND1*) terminate with a TAA stop codon, while three (*Cytb*, *ND3* and *COX2*) end in TAG and two (*ND5* and *COX1*) in AGA. The *COX3* gene, however, possesses an incomplete stop codon (A--) (Table 1).

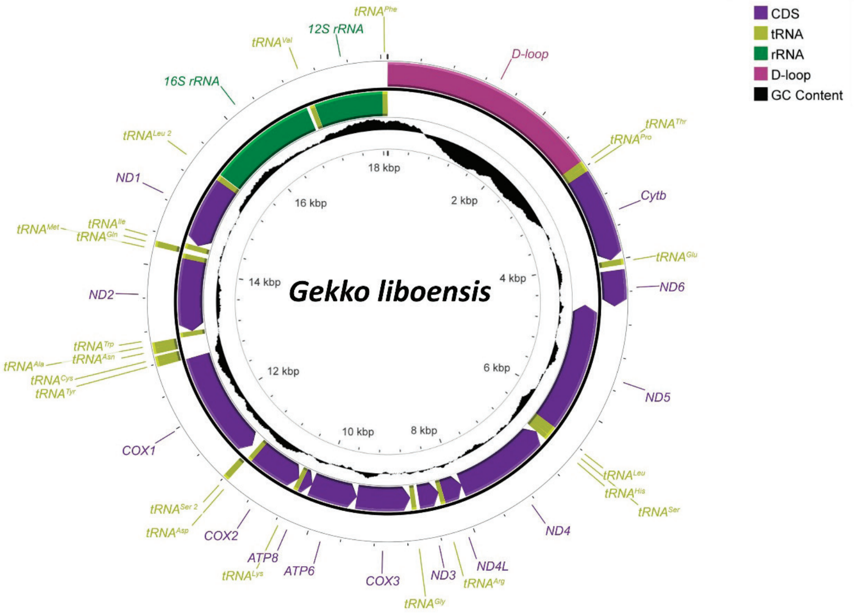

Figure 1. Circular map of *Gekko liboensis* mitochondrial genome. Different colors indicate different types of genes and regions. The black inner circle represents the GC content of the mitogenome.

Table 1. Characteristics of the mitochondrial genome of *Gekko liboensis.*

Gene/reginon	Start	End	Length(bp)	Spacer (+) Overlap (-)	Start codon	Stop codon
D-loop	1	2719	2719	1		
tRNA^{Pro}	2720	2789	70	1		
tRNA^{Thr}	2790	2858	69			
Cytb	2858	3997	1140	4	ATG	TAG
tRNA^{Glu}	4001	4072	72	57		
ND6	4129	4584	456	-15	G--	TAA
ND5	4569	6377	1809	2	ATG	AGA
tRNA^{Leu}	6379	6450	72	1		
tRNA^{Ser}	6451	6513	63	2		
tRNA^{His}	6515	6582	68	2		
ND4	6584	7942	1359	-6	ATG	TAA
ND4L	7936	8232	297	3	ATG	TAA
tRNA^{Arg}	8235	8298	64	-9		
ND3	8289	8591	303	49	A--	TAG
tRNA^{Gly}	8640	8706	67	2		
COX3	8708	9490	783		ATG	A--
ATP6	9490	10170	681	-9	ATG	TAA
ATP8	10161	10316	156	4	ATG	TAA
tRNA^{Lys}	10320	10385	66	-10		
COX2	10375	11073	699	1	ATG	TAG
tRNA^{Asp}	11074	11139	66	3		
tRNA$^{Ser\ 2}$	11142	11217	76	-6		
COX1	11211	12758	1548	5	ATG	AGA
tRNA^{Tyr}	12763	12825	63	2		
tRNA^{Cys}	12827	12891	65	30		
tRNA^{Asn}	12921	12993	73	1		
tRNA^{Ala}	12994	13062	69			
tRNA^{Trp}	13062	13128	67			
ND2	13128	14159	1032	1	ATT	TAA
tRNA^{Met}	14160	14228	69			
tRNA^{Gln}	14228	14299	72	-1		
tRNA^{Ile}	14298	14370	73	6		
ND1	14376	15338	963	1	ATG	TAA
tRNA$^{Leu\ 2}$	15339	15413	75	12		
16S rRNA	15425	16938	1514	46		
tRNA^{Val}	16984	17051	68	5		
12S rRNA	17056	18006	951	1		
tRNA^{Phe}	18007	18079	73			

On the heavy strand, the *ND6* gene along with eight tRNA genes (*tRNA*^{Pro}, *tRNA*^{Glu}, *tRNA*^{Ser}, *tRNA*^{Tyr}, *tRNA*^{Cys}, *tRNA*^{Asn}, *tRNA*^{Ala}, and *tRNA*^{Gln}) are located, while the other genes are encoded on the light strand. The *12S* and *16S rRNA* genes, which are 951 bp and 1514 bp in size, respectively, are positioned between the *rRNA*^{Phe} and *tRNA*^{Leu} genes, with the *tRNA*^{Val} gene serving as a separator. The length of tRNAs ranges from 63 to 76 bp. Moreover, the control region (*D-loop*), spanning 2719 bp, shows an A+T content of 62.9%. It is situated between the *tRNA*^{Phe} and *tRNA*^{Pro}. The overall base composition of the genome is as follows: 26.0% A, 31.8% T, 14.6% C, and 27.6% G, resulting in an A+T content of 57.8%, indicating a slight AT bias.

3.2 Phylogenetic Relationship

The outcome of the mitogenome-based phylogenetic analyses strongly support the placement of *Gekko liboensis* within the subgenus *Japonigekko* (Supplementary Figure S1). Due to the limited available data, the phylogenetic relationships between *G. liboensis* and other species cannot be reliably inferred from the currently published mitochondrial genome sequences.

The concatenated nucleotides dataset of *16S rRNA* and *ND2* genes is 1574 bp in length per species, with GTR + G identified as the best-fitting substitution model. Phylogenetic trees constructed using these sequences from 25 species reveal that *Gekko liboensis* is closely related to *G. paucituberculatus,* which subsequently groups with *G. kwangsiensis* (Figure 2). However, two inconsistencies are observed: 1.) the mitogenome of *G. hokouensis* (KT005801) clusters with the mitochondrial genes of *G. subpalmatus* (SYS r001762), instead of grouping with *G. hokouensis* (SYS r001290). and 2.) the mitogenome of *G. subpalmatus* (MK680534) groups with the mitochondrial genes of *G. cib* (SYS r000708), rather than with *G. subpalmatus* (SYS r001762). Aside from these discrepancies, the

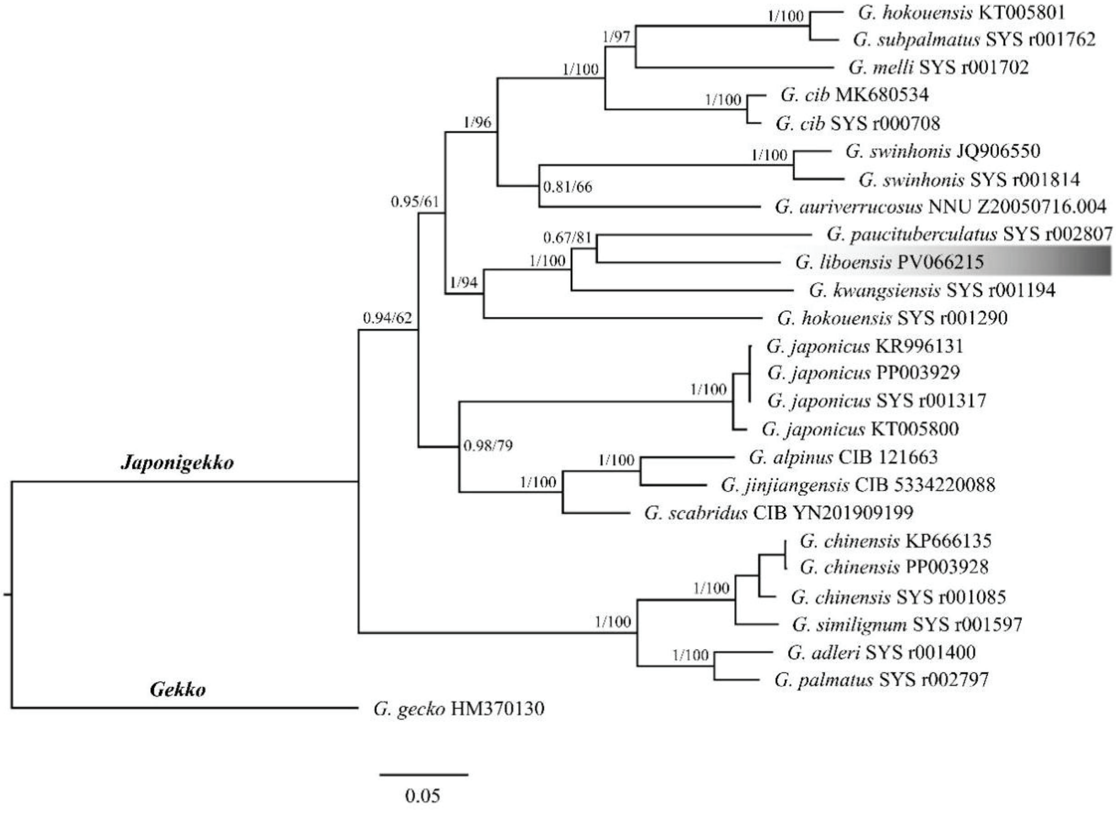

Figure 2. Bayesian Inference tree of the subgenus *Japonigekko* based on concatenated mitochondrial *16S rRNA* and *ND2* genes. Numbers before the slashes represent Bayesian posterior probabilities (BPP), while those after slashes denote ultrafast bootstrap replications (UFB). The scale bar represents 0.05 nucleotide substitutions per site.

phylogenetic relationships among other species within *Japonigekko* are consistent with previously reported phylogenies based on the same mitochondrial genes [3, 27].

4. DISCUSSION AND CONCLUSION

By employing next-generation sequencing technology, we have obtained and annotated the first complete mitochondrial genome of *Gekko liboensis*. Our findings reveal that the mitogenomic gene order and composition in Libo Gecko are identical to those of the five previously reported species within the subgenus *Japonigekko* [8-13], all of which were also included in the phylogenetic tree construction in our study. Furthermore, this study provides the first sequenced mitogenome of a karst-dwelling species within *Japonigekko*. This novel genomic data serves a valuable resource for future taxonomic and phylogenetic studies.

The phylogenetic analysis performed in this study, which integrated mitogenomes and nucleotides sequences of the *16S rRNA* and *ND2* genes, demonstrated that relationships within the *Japonigekko* group were largely consistent with earlier studies [3, 27-28]. However, two exceptions were observed in the mitochondrial genomes of *Gekko subpalmatus* (MK680534) and *G. hokouensis* (KT005801). The mitochondrial genome of *G. subpalmatus* (MK680534), reported by Luo et al. (2019), was based on a sample collected from Chengdu, Sichuan Province, China [12]. Following this study, Lyu et al. (2021) revealed that the *G. subpalmatus* complex comprises three evolutionarily distinct taxa. Among them, populations from Zhejiang in eastern China represent *G. subpalmatus*, while those from the Sichuan Basin in southwestern China have been identified as *G. cib* [29]. Therefore, based on these taxonomic revisions and our phylogenetic analyses, we consider that *G. subpalmatus* (MK680534) is *G. cib* (MK680534), and that the name change reflects a taxonomic update rather than the re-identification of a distinct species. For *G. hokouensis* (KT005801), the sample was collected from Luxi Island, Wenzhou, Zhejiang, China [10]. It is not geographically distinguishable from *G. subpalmatus*. In our phylogenetic analyses based on two mitochondrial genes, *G. hokouensis* samples did not cluster together. Instead, *G. hokouensis* (KT005801) formed a well-supported clade with *G. subpalmatus* (SYS r001762). In the absence of morphological data, this pattern may indicate either species misidentification or mitochondrial introgression, and further investigation is warranted.

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CONFLICT OF INTEREST STATEMENT

The authors declare that they hold no competing interests.

DECLARATION OF GENERATIVE AI IN PREPARATION OF MANUSCRIPT

During the preparation of this work, the authors used ChatGPT-4 to improve the readability and language of the manuscript. After using this tool, the authors reviewed and edited the content as necessary and take full responsibility for the publication’s content.

REFERENCES

[1] Wood P.L., Guo X.G., Travers S.L., Su Y.C., Olson K.V., Bauer A.M., et al., Parachute geckos free fall into synonymy: *Gekko* phylogeny, and a new subgeneric classification, inferred from thousands of ultraconserved elements. *Molecular Phylogenetics and Evolution*, 2020; **146**: 106731. DOI 10.1016/j.ympev.2020.106731.

[2] Uetz P., Freed P., Aguilar R., Reyes F., Kudera J. and Hošek J., The reptile database; Available at: http://www.reptile-database.org. [Accessed on 26 January 2025].

[3] Wang H.T., Qi S., Zhou D.Y. and Wang Y.Y., Description of a new karst-adapted species of the subgenus *Japonigekko* (Squamata: Gekkonidae: *Gekko*) from Guangxi, southern China. *Vertebrate Zoology*, 2024; **74**: 121-132. DOI 10.3897/vz.74.e113899.

[4] Jono T., Ding L., Kaito T., Tang Y.Z. and Toda M., Reevaluation of the taxonomic status of a poorly known gecko, *Gekko liboensis* (Reptilia: Squamata). *Asian Herpetological Research*, 2015; **6(3)**: 229-236. DOI 10.16373/j.cnki.ahr.150009.

[5] Zhou K.Y., Liu Y.Z. and Li D.J., Three new species of *Gekko* and remarks on *Gekko hokouensis* (Lacertiformes, Gekkonidae). *Acta Zootaxonomica Sinica*, 1982; **7(4)**: 438-446. DOI 10.5479/si.23317515.77.1.

[6] Zhao E., Zhao K. and Zhou K., *Fauna Sinica Reptilia*, *Vol. 2*, *Squamata Lacertilia,* Beijing, China: Science Press, 1999.

[7] Rösler H., Bauer A.M., Heinicke M.P., Greenbaum E., Jackman T., Nguyen T.Q., et al., Phylogeny, taxonomy, and zoogeography of the genus *Gekko* Laurenti, 1768 with the revalidation of *G. reevesii* Gray, 1831 (Sauria: Gekkonidae). *Zootaxa*, 2011; **2989**: 1-50. DOI 10.11646/zootaxa.2989.1.1.

[8] Li H.M., Zeng D.L., Guan Q.X., Qin P.S. and Qin X.M., Complete mitochondrial genome of *Gekko swinhonis* (Squamata, Gekkonidae). *Mitochondrial DNA*, 2013; **24(2)**: 86-88. DOI 10.3109/19401736.2012.717938.

[9] Hao S.L., Ping J. and Zhang Y.P., Complete mitochondrial genome of *Gekko chinensis* (Squamata, Gekkonidae). *Mitochondrial DNA Part A*, 2016a; **27(6)**: 4226-4227. DOI 10.3109/19401736.2015.1022751.

[10] Hao S.L., Yu D.N., Ping J., Zhou H.B. and Zhang Y.P., Complete mitochondrial genomes of two gecko species, *Gekko hokouensis* and *Gekko japonicus* (Squamata, Gekkonidae). *Mitochondrial DNA Part B*, 2016b; **1(1)**: 346-347. DOI 10.1080/23802359.2015.1137809.

[11] Kim I.H., Park J., Cheon K.S., Lee H.J., Kim J.K. and Park D., Complete mitochondrial genome of Schlegel's Japanese gecko *Gekko japonicus* (Squamata: Gekkonidae). *Mitochondrial DNA Part A*, 2016; **27(5)**: 3684-3686. DOI 10.3109/19401736.2015.1079855.

[12] Luo H.D., Huang A., Li B., Ni Q.Y., Yao Y.F., Xu H.L., et al., Complete mitochondrial genome of the webbed-toed gecko *Gekko subpalmatus* (Squamata: Gekkonidae). *Mitochondrial DNA Part B*, 2019; **4(1)**: 1725-1726. DOI 10.1080/23802359.2019.1610094.

[13] Zhan L.M., Chen Y.X., He J.Y., Guo Z.Q., Wu L., Storey K.B., et al., The phylogenetic relationships of major lizard families using mitochondrial genomes and selection pressure analyses in Anguimorpha. *International Journal of Molecular Sciences*, 2024; **25(15)**: 8464. DOI 10.3390/ijms25158464.

[14] Bolger A.M., Lohse M. and Usadel B., Trimmomatic: A flexible trimmer for Illumina sequence data. *Bioinformatics*, 2014; **30(15)**: 2114-2120. DOI 10.1093/bioinformatics/btu170.

[15] Allio R., Schomaker-Bastos A., Romiguier J., Prosdocimi F., Nabholz B. and Delsuc F., MitoFinder: Efficient automated large-scale extraction of mitogenomic data in target enrichment phylogenomics. *Molecular Ecology Resources*, 2020; **20(4)**: 892-905. DOI 10.1111/1755-0998.13160.

[16] Grant J.R., Enns E., Marinier E., Mandal A., Herman E.K., Chen C.Y., et al., Proksee: In-depth characterization and visualization of bacterial genomes. *Nucleic Acids Research*, 2023; **51(W1)**: W484-W492. DOI 10.1093/nar/gkad326.

[17] Qin X.M., Qian F., Zeng D.L., Liu X.C. and Li H.M., Complete mitochondrial genome of the red-spotted tokay gecko (*Gekko gecko*, Reptilia: Gekkonidae): Comparison of red- and black-spotted tokay geckos. *Mitochondrial DNA*, 2011; **22(5-6)**: 176-177. DOI 10.3109/19401736.2011.636440.

[18] Kumar S., Stecher G., Li M., Knyaz C. and Tamura K., MEGA X: Molecular evolutionary genetics analysis across computing platforms. *Molecular Biology and Evolution*, 2018; **35(6)**: 1547-1549. DOI 10.1093/molbev/msy096.

[19] Nguyen L.T., Schmidt H.A., von Haeseler A. and Minh B.Q., IQ-TREE: A fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution*, 2015; **32(1)**: 268-274. DOI 10.1093/molbev/msu300.

[20] Trifinopoulos J., Nguyen L.T., von Haeseler A. and Minh B.Q., W-IQ-TREE: A fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Research*, 2016; **44(W1)**: W232-W235. DOI 10.1093/nar/gkw256.

[21] Hoang D.T., Chernomor O., von Haeseler A., Minh B.Q. and Vinh L.S., UFBoot2: Improving

the ultrafast bootstrap approximation. *Molecular Biology and Evolution*, 2018; **35(2)**: 518-522. DOI 10.1093/molbev/msx281.

[22] Minh B.Q., Nguyen M.A.T. and von Haeseler A., Ultrafast approximation for phylogenetic bootstrap. *Molecular Biology and Evolution*, 2013; **30(5)**: 1188-1195. DOI 10.1093/molbev/mst024.

[23] Ronquist F., Teslenko M., van der Mark P., Ayres D.L., Darling A., Höhna S., et al., MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology*, 2012; **61(3)**: 539-542. DOI 10.1093/sysbio/sys029.

[24] Huelsenbeck J.P., Ronquist F., Nielsen R. and Bollback J.P., Bayesian inference of phylogeny and its impact on evolutionary biology. *Science*, 2001; **294(5550)**: 2310-2314. DOI 10.1126/science.1065.

[25] Wilcox T.P., Zwickl D.J., Heath T.A. and Hillis D.M., Phylogenetic relationships of the dwarf boas and a comparison of Bayesian and bootstrap measures of phylogenetic support. *Molecular Phylogenetics and Evolution*, 2002; **25(2)**: 361-371. DOI 10.1016/S1055-7903(02)00244-0.

[26] Lanfear R., Calcott B., Ho S.Y.W. and Guindon S., PartitionFinder: Combined selection of partitioning schemes and substitution models for phylogenetic analyses. *Molecular Biology and Evolution*, 2012; **29(6)**: 1695-1701. DOI 10.1093/molbev/mss020.

[27] Ma S., Shi S.C., Shen C., Chang L.M. and Jiang J.P., Discovery of a new species of the subgenus *Japonigekko* (Squamata, Gekkonidae, *Gekko*) from the Hengduan Mountains, southwestern China: The best *Japonigekko* mountaineer. *ZooKeys*, 2024; **1215**: 289-309. DOI 10.3897/zookeys.1215.125043.

[28] Hou Y.M., Shi S.C., Wang G., Shu G.C., Zheng P.Y., Qi Y., et al., A new species of the *Gekko japonicus* group (Squamata: Gekkonidae) from southwest China. *Asian Herpetological Research*, 2021; **12(1)**: 36-48. DOI 10.16373/j.cnki.ahr.200064.

[29] Lyu Z.T., Lin C.Y., Ren J.L., Jiang K., Zhang Y.P., Qi S., et al., Review of the *Gekko* (*Japonigekko*) *subpalmatus* complex (Squamata, Sauria, Gekkonidae), with description of a new species from China. *Zootaxa*, 2021; **4951(2)**: 236-258. DOI 10.11646/zootaxa.4951.2.2.