

FULL LENGTH RESEARCH PAPER

Mitochondrial genome of the Chung-an ground lizard *Takydromus sylvaticus* (Reptilia: Lacertidae)Xin-Sheng Tang^{1*}, Jin-Min Chen^{1,2*}, and Song Huang^{1,3,4}¹College of Life and Environment Sciences, Huangshan University, Huangshan, Anhui, P.R. China, ²Laboratory for Conservation and Utilization of Bio-resources, Yunnan University, Kunming, Yunnan, P.R. China, ³State Key Laboratory of Genetic Resources and Evolution, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan, P.R. China, and ⁴Huangshan Institute of Ophiology, Huangshan, Anhui, P.R. China**Abstract**

The Chung-an ground lizard *Takydromus sylvaticus* is an endemic and long-lost reptile species in China. In this study, its mitochondrial genome (mitogenome) sequence was firstly determined by long PCR and primer walking methods. The genome is 17,838 bp long and contains 13 protein-coding genes, 22 transfer RNA genes, 2 ribosomal RNA genes and 2 main noncoding regions (the control region and the putative L-strand replication origin). The gene order and contents in the *T. sylvaticus* mitogenome is identical to that found in typical vertebrates, suggesting that it represents an ancestral arrangement. Within the control region, typical conserved domains and distinct repeat regions were identified.

KeywordsControl region, Lacertidae, mitochondrial genome, *Takydromus sylvaticus***History**Received 31 March 2013
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Although as of March 2013, 2016 complete mitochondrial genome (mitogenome) sequences of vertebrates have been determined, only eight complete mitogenome sequences of the diverse lizard family Lacertidae have been reported. The Chung-an ground lizard, *Takydromus sylvaticus* (Lacertidae), endemic to China, was first described in 1928 based on specimens from Chung-an County (or Wuyishan region), Fujian Province, China (Pope, 1928). After the first discovery, no other individual was reported for more than 70 years until Tang & Xiang (2002) rediscovered this poorly known species in Xiuning County, Anhui Province, China. Subsequently, fieldwork, molecular phylogeny and morphology of *T. sylvaticus* have been extensively studied (Le et al., 2009; Tang & Chen, 2006; Tang et al., 2007; Yang & Wang, 2010). In this article, we firstly described the mitogenome of *T. sylvaticus* in order to obtain basic genetic information about this long-lost species.

Because of long tandem duplications or heteroplasmy, some sections of tandem repeats in the control region (CR) cannot be completely sequenced. The nearly complete mitogenome of *T. sylvaticus* (Genbank accession number JX290083) was sequenced to be 17,838 bp which consisted of 13 typical

vertebrate protein-coding genes, 22 transfer RNA (tRNA) genes, 2 ribosomal RNA (rRNA) genes and 1 CR (Table 1). It has the typical vertebrate mitochondrial gene arrangement reviewed in Boore (1999). Most of the *T. sylvaticus* mitochondrial genes are encoded on the H-strand except for the *ND6* gene and eight tRNA genes, which are encoded on the L-strand (Table 1). The overall A + T content of the presented mitogenome is 60.3% (A = 31.1%; G = 13.7%; T = 29.2%; C = 26.0%), reflecting a typical sequence feature of the vertebrate mitogenome. All the 13 protein-coding genes initiate with an ATG start codon, except for *ND5*, which begin with ATA. Five genes (*ATP8*, *ATP6*, *ND4L*, *ND5* and *Cyt b*) use the most prevalent stop codon for vertebrates, TAA. Two protein-coding genes (*COI*, *ND6*) terminate with the stop codons AGG and AGA, respectively. The TAG and TNN (the incomplete stop codons, TA– and T–) as stop codons are observed in other protein-coding genes. The tRNA genes were interspersed among the mitogenome and ranged in size from 62 to 74 bp. In the WANCY cluster of tRNA genes, a 33 bp sequence located between *tRNA-Asn* and *tRNA-Cys* genes was considered as the putative L-strand replication origin, *O_L*. The rRNA genes, *12s* rRNA (950 bp) and *16s* rRNA (1529 bp), are located between the *tRNA-Phe* and *tRNA-Leu* (UUR) genes and separated by the *tRNA-Val* gene (Table 1). The major noncoding region, CR (2452 bp) in *T. sylvaticus* mitogenome was located between the *tRNA-Pro* and *tRNA-Phe* genes. The general organization of the CR is similar to the situation of other lizards (Böhme et al., 2007; Podnar et al., 2009; Rui et al., 2009). Two typical conserved domains were detected in *T. sylvaticus*, namely the conserved sequence blocks domains (CSB-1, CSB-2 and CSB-3) and the termination-associated sequence domains (TAS1 and TAS2). An array of tandem repeats and some repeat units are found in the CR.

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Table 1. Characteristics of the mitochondrial genome of *Takydromus sylvaticus*.

Gene/Region	Position 5'–3'	Size bp/aa	Codon		Anticodon	Spacer (+) or overlap (–)
			Start	Stop		
<i>tRNA-Phe</i>	1–73	73			GAA	
<i>12 S rRNA</i>	74–1023	950				
<i>tRNA-Val</i>	1024–1086	63			TAC	
<i>16 S rRNA</i>	1087–2615	1529				
<i>tRNA-Leu</i> (UUR)	2616–2688	73			TAA	
<i>ND1</i>	2689–3657	969 (322)	ATG	TAG		+3
<i>tRNA-Ile</i>	3661–3731	71			GAT	+1
<i>tRNA-Gln</i>	3733–3803 (L)	71			TTG	–1
<i>tRNA-Met</i>	3803–3870	68			CAT	
<i>ND2</i>	3871–4905	1035 (344)	ATG	TAG		–2
<i>tRNA-Trp</i>	4904–4977	74			TCA	+1
<i>tRNA-Ala</i>	4979–5046 (L)	68			TGC	+1
<i>tRNA-Asn</i>	5048–5120 (L)	73			GTT	+1
<i>O_L</i>	5154–5122	33				–3
<i>tRNA-Cys</i>	5152–5213 (L)	62			GCA	+5
<i>tRNA-Tyr</i>	5219–5289 (L)	71			GTA	+1
<i>COI</i>	5291–6835	1545 (514)	ATG	AGG		–5
<i>tRNA-Ser</i> (UCN)	6831–6901 (L)	71			TGA	+3
<i>tRNA-Asp</i>	6905–6971	67			GTC	
<i>COII</i>	6972–7659	688 (229)	ATG	T–		
<i>tRNA-Lys</i>	7660–7723	64			TTT	
<i>ATP8</i>	7724–7885	162 (53)	ATG	TAA		–10
<i>ATP6</i>	7876–8556	681 (226)	ATG	TAA		–1
<i>COIII</i>	8556–9339	784 (261)	ATG	T–		
<i>tRNA-Gly</i>	9340–9405	66			TCC	
<i>ND3</i>	9406–9751	346 (115)	ATG	T–		
<i>tRNA-Arg</i>	9752–9818	67			TCG	+4
<i>ND4L</i>	9823–10,119	297 (98)	ATG	TAA		–7
<i>ND4</i>	10,113–11,493	1381 (460)	ATG	T–		
<i>tRNA-His</i>	11,494–11,561	68			GTG	
<i>tRNA-Ser</i> (AGY)	11,562–11,627	66			GCT	–1
<i>tRNA-Leu</i> (CUN)	11,627–11,697	71			TAG	+3
<i>ND5</i>	11,701–13,524	1824 (607)	ATA	TAA		–5
<i>ND6</i>	13,520–14,035 (L)	516 (171)	ATG	AGA		
<i>tRNA-Glu</i>	14,036–14,104 (L)	69			TTC	+2
<i>Cytb</i>	14,107–15,249	1143 (380)	ATG	TAA		+2
<i>tRNA-Thr</i>	15,252–15,318	67			TGT	
<i>tRNA-Pro</i>	15,319–15,386 (L)	68			TGG	
Control region	15,387–17,838	2452				

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Declaration of interest

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