

MITOGENOME ANNOUNCEMENT

Mitochondrial genome of Plateau zokor *Myospalax baileyi*

ZHIJIN LIU¹, YANGWEI LI², FANGLEI SHI^{1,3}, JIQI LU², MING LI¹, & ZHENLONG WANG²

¹Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, 1-5 Beixhenxi Road, Chaoyang, Beijing 100101, P.R. China, ²Department of Bio-Engineering, Zhengzhou University, Zhengzhou 450001, P.R. China, and ³College of Nature Conservation, Beijing Forestry University, 35 Qinghua East Road, Haidian, Beijing 100083, P.R. China

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Abstract

Plateau zokors *Myospalax baileyi* are subterranean rodents and endemic to the cold and hypoxic (2800–4300 m above sea level) climate of the farm, prairie, alpine prairie, and meadow habitats across the Tibetan plateau. The complete mitochondrial (mt) genome of *M. baileyi* has been determined. Our results showed that the total length of the mitogenome was 16,351 bp, and had a gene content of 13 protein coding, 22 tRNAs and 2 rRNAs. Except for the seven tRNA and Nd6 genes, all other mt genes are encoded on the heavy strand. The overall base composition of the heavy strand is 33.65% A, 29.65% T, 24.42% C, and 12.28% G, with an AT content of 63.3%.

Keywords: Mitochondrial, *Myospalax baileyi*, genome

Plateau zokors *Myospalax baileyi* are subterranean rodents and endemic to the cold and hypoxic (2800–4300 m above sea level) climate of the farm, prairie, alpine prairie, and meadow habitats across the Tibetan plateau (Smith and Foggin 1999). The genus *Myospalax* comprises *M. fontanieri*, *M. cansus*, *M. baileyi*, *M. rothschildi*, *M. smithi*, and *M. rufescens* (Carleton and Musser 1984). Until now, no complete mitochondrial (mt) genome sequence in genus *Myospalax* is available.

In this study, we determined the complete mt genome of *M. baileyi* with a GenBank accession number JN540033. The complete mtDNA of *M. baileyi* was amplified using two primer pairs of long-range PCRs and sequenced using 30 primers (Supplemental Table I). The complete mt genome (16,531 bp in length) consists of 13 protein coding, 22 tRNA genes and 2 rRNA genes, and a displacement loop (D-loop) locus (Table I). The overall nucleotide composition of the heavy strand is 33.65% A, 29.65% T, 24.42% C, and 12.28% G. For 11 of the 13

protein-coding genes, the start codon is ATG. The nicotinamide adenine dinucleotide dehydrogenase subunit 1 (ND1) gene starts with GTC, and the ND2 gene starts with ATT. Six of the 13 protein-coding genes use TAA as the stop codon. The ND1, ND2, and ND6 were stopped with TAG, and the ND4 and ND5 were stopped with TGT and TGA. Cytochrome oxidase subunit 3 (Cox3) appears to use a template-encoded CAT codon, and cytochrome *b* gene (Cytb) appears to use a template-encoded AAA codon. The 12S and 16S ribosomal RNA genes are 952 and 1563 bp long, respectively. The tRNA genes vary from 60 to 75 bp in length and employ the anticodons typical of vertebrate mt-tRNAs. In our study, the noncoding control region (D-loop) of the *M. baileyi* mtDNA is 933 bp long (Table I).

Mitochondria generate energy by oxidative phosphorylation and play important roles in oxygen usage and energy metabolism (Xu et al. 2007; Luo et al. 2008). Hence, the mt genome represents a particular

Correspondence: Z. Wang, Department of Bio-Engineering, Zhengzhou University, Zhengzhou 450001, P.R. China. Tel: + 86 371 67780989. Fax: + 86 371 67783235. E-mail: wzl@zzu.edu.cn; M. Li, Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, 1-5 Beixhenxi Road, Chaoyang, Beijing 100101, P.R. China. Tel: + 86 10 64807037. Fax: + 86 10 64807099. E-mail: lim@ioz.ac.cn

Table I. Characteristics of the mt genome of *M. baileyi*.

Locus	From	To	Length (bp)	Codon		Intergenic nucleotides*	Strand†
				Start	Stop		
tRNA ^{phe}	1	67	67				H
12SrRNA	68	1019	952				H
tRNA ^{val}	1020	1085	66				H
16SrRNA	1086	2648	1563				H
tRNA ^{leu}	2650	2724	75			1	H
ND1	2726	3682	957	GTG	TAG	1	H
tRNA ^{Ile}	3681	3749	69			-2	H
tRNA ^{Gln}	3747	3817	71			-3	L
tRNA ^{Met}	3821	3890	70			3	H
ND2	3891	4934	1044	ATT	TAG		H
tRNA ^{Trp}	4933	5001	69			-2	H
tRNA ^{Ala}	5004	5072	69			2	L
tRNA ^{Asn}	5073	5145	73				L
Rep-origin	5146	5182	37				H
tRNA ^{Cys}	5183	5248	66				L
tRNA ^{tyr}	5250	5316	67			1	L
COX1	5318	6862	1545	ATG	TAA	1	H
tRNA ^{Ser}	6860	6928	69			-3	L
tRNA ^{Asp}	6931	6999	69			2	H
COX2	7001	7684	684	ATG	TAA	1	H
tRNA ^{Lys}	7686	7749	64			1	H
ATP8	7753	7956	204	ATG	TAA	3	H
ATP6	7914	8594	681	ATG	TAA	-43	H
COX3	8594	9377	784	ATG	CAT	-1	H
tRNA ^{Gly}	9378	9446	69				H
ND3	9447	9794	348	ATA	TAA		H
tRNA ^{Arg}	9797	9865	69			2	H
ND4L	9866	10162	297	ATG	TAA		H
ND4	10156	11535	1380	ATG	TGT	-7	H
tRNA ^{His}	11534	11600	67			-2	H
tRNA ^{Ser}	11601	11660	60				H
tRNA ^{leu}	11661	11730	70				H
ND5	11722	13560	1839	ATG	TGA	-9	H
ND6	13544	14068	525	ATG	TAG	-17	L
tRNA ^{Glu}	14069	14137	69				L
Cytb	14142	15284	1143	ATG	TAA	4	H
tRNA ^{Thr}	15286	15353	68			1	H
tRNA ^{Pro}	15354	15418	65				L
D-Loop	15419	16351	933				H

* Numbers correspond to the nucleotides separating different genes. Negative numbers indicate overlapping nucleotides between adjacent genes; † H and L indicate genes transcribed on the heavy and light strands, respectively.

useful genetic marker for investigating the molecular basis of organismal adaptation to high altitude environments (Wallace 2007). Comparative analyses of complete mt genomes can therefore reveal unusual selection pressures acting at the molecular level for organisms living at high altitude (Xu et al. 2007; Luo et al. 2008). We expect the present study to contribute to the comparative analyses of complete mt genomes of the genus *Myospalax*.

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