

Mitochondrial genome of the Guizhou snub-nosed monkey (*Rhinopithecus brelichi*)

FANGLEI SHI^{1,2*} BOSHI WANG^{2*} ZHIJIN LIU², & HUIJUAN PAN¹

¹College of Nature Conservation, Beijing Forestry University, Haidian, Beijing 100083, P.R. China, and ²Key laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, Chaoyang, Beijing 100101, P.R. China

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Abstract

The Guizhou snub-nosed monkey (*Rhinopithecus brelichi*) is an endangered species which is endemic to a small region in the fanjing mountain national nature reserve in Guizhou province, China. In this study, we determined the complete mitochondrial genome of *R. brelichi*. The results showed that the total length of the mitogenome was 16,548 bp and contained 13 protein-coding genes, 22 transfer RNA genes, two ribosomal RNA genes and one control region. Overall base composition of the complete mitochondrial DNA was 32.35% A, 29.28% T, 25.54% C and 12.83% G. All the genes in *R. brelichi* were distributed on the H-strand, except for the *ND6* subunit gene and eight tRNA genes which were encoded on the L-strand.

Keywords: *Rhinopithecus brelichi*, mitochondrion, genome

Rhinopithecus brelichi is categorized as an endangered species by the World Conservation Union (IUCN 2008), which comprises five distinct isolated species (Groves 2001; Geissmann et al. 2011). Three of the species are endemic to China (*Rhinopithecus roxellana*; *Rhinopithecus bieti*, and *Rhinopithecus brelichi*), while the other two species (*Rhinopithecus avunculus* and *Rhinopithecus strykeri*) are distributed in the northern Vietnam and the northeastern Myanmar, respectively. Presently, the complete mitochondrial (mt) genomes of *R. roxellanae*, *R. bieti*, and *R. avunculus* are available (Sterner et al. 2006; Yu et al. 2011). However, the information on the complete mtDNA genome of *R. brelichi* is lacking. In this study, the complete mtDNA of *R. brelichi* was amplified by long-range polymerase chain reaction with two primer pairs and sequenced by using 24 primers

(Supplementary Table I). Nucleotide sequences were deposited in GenBank (accession number JN540032). The complete mtDNA of *R. brelichi* (16,548 bp in length) had 13 protein-coding genes, 22 tRNA genes, two rRNA genes (12S rRNA and 16S rRNA), and one control region. Nine of the 13 protein-coding genes require ATG as the start codon, while *ND2*, *ND3*, and *ND5* utilize ATT, ATT, and ATA, respectively (Table I). Six of 13 protein-coding genes use TAA as stop codons. The *ND1* and *ND2* end with TAG, *ND6* stops with AGA, and four genes (*CO3*, *ND3*, *ND4*, and *CYTB*) use T as an incomplete stop codon, which is presumably completed as TAA by posttranscriptional polyadenylation (Anderson et al. 1981). The 22 tRNA genes range in size from 75 bp in tRNA^{Leu} (UUR) to 59 bp in tRNA^{Ser} (AGY). The 12S and 16S rRNA genes were 949 bp and 1565 bp, respectively. These

Correspondences: Z. Liu, 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: + 86 010 64807037. Fax: + 86 010 64807099. E-mail: liuzj@ioz.ac.cn
H. Pan, College of Nature Conservation, Beijing Forestry University, 35 Qinghua East Road, Haidian, Beijing 100083, P.R. China. Tel: + 86 010 62336065. Fax: + 86 010 62336724. E-mail: phjjanine@yahoo.com.cn

*These authors contributed equally to the paper.

Table I. Characteristics of the *R. brelichi* mitochondrial DNA genome.

Gene name	Coding strand	Start position	End position	Intergenic nucleotides	Overlapping nucleotides	Size (bp)	No. of codons	Start codon	Stop codon
tRNA ^{Phe}	H	1	71			71			
12S rRNA	H	72	1020			949			
tRNA ^{Val}	H	1021	1089			69			
16S rRNA	H	1090	2654			1565			
tRNA ^{Leu(UUR)}	H	2655	2729	2		75			
<i>ND1</i>	H	2732	3688		2	957	310	ATG	TAG
tRNA ^{Ile}	H	3687	3756		3	70			
tRNA ^{Gln}	L	3754	3825	1		72			
tRNA ^{Met}	H	3827	3894			68			
<i>ND2</i>	H	3895	4938		2	1044	336	ATT	TAG
tRNA ^{Trp}	H	4937	5004	7		68			
tRNA ^{Ala}	L	5012	5080	1		69			
tRNA ^{Asn}	L	5082	5154	1		73			
rep_origin	L	5156	5187		2	32			
tRNA ^{Cys}	L	5186	5253		1	68			
tRNA ^{Tyr}	L	5253	5318	1		66			
<i>CO1</i>	H	5320	6864		3	1545	500	ATG	TAA
tRNA ^{Ser(UCN)}	L	6862	6930	3		69			
tRNA ^{Asp}	H	6934	7001	1		68			
<i>CO2</i>	H	7003	7686	48		684	225	ATG	TAA
tRNA ^{Lys}	H	7735	7802	1		68			
<i>ATP8</i>	H	7804	7998		31	195	62	ATG	TAA
<i>ATP6</i>	H	7968	8648		1	681	224	ATG	TAA
<i>CO3</i>	H	8648	9431			784	250	ATG	T-
tRNA ^{Gly}	H	9432	9499			68			
<i>ND3</i>	H	9500	9845			346	111	ATT	T-
tRNA ^{Arg}	H	9846	9910			65			
<i>ND4L</i>	H	9911	10,207		7	297	98	ATG	TAA
<i>ND4</i>	H	10,201	11,578			1378	448	ATG	T-
tRNA ^{His}	H	11,579	11,646			68			
tRNA ^{Ser(AGY)}	H	11,647	11,705			59			
tRNA ^{Leu(CUN)}	H	11,706	11,776			71			
<i>ND5</i>	H	11,777	13,588			1812	593	ATA	TAA
<i>ND6</i>	L	13,589	14,113			525	159	ATG	AGA
tRNA ^{Glu}	L	14,114	14,182	4		69			
<i>Cytb</i>	H	14,187	15,321	6		1135	367	ATG	T-
tRNA ^{Thr}	H	15,328	15,392	2		65			
tRNA ^{Pro}	L	15,395	15,461			67			
D-loop	H	15,462	16,548			1087			

ribosomal subunit genes are located between the tRNA^{Phe} and tRNA^{Leu} (UUR) genes and are further separated by the tRNA^{Val} gene. The control region of the *R. brelichi* mtDNA is 1087 bp long and lies between the tRNA^{Pro} and tRNA^{Phe} genes. Mitochondrial genome sequences have been proven to be very useful for phylogenetic relationships at several taxonomic levels because of its maternal inheritance, small size, accelerated rate of mutation compared to that of the nuclear DNA, and little or no recombination (Brown et al. 1979; Ballard and Whitlock 2004). We expect the present study to provide a useful database for analyzing the phylogenetic relationship of *R. brelichi* and other snub-nosed monkeys.

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References

Anderson S, Bankier AT, Barrell BG, de Bruijn MHL, Coulson AR, Drouin J, Eperon IC, Nierlich DP, Roe BA, Sanger F, Schreier

- PH, Smith AJH, Staden R, Young IG. 1981 Sequence and organization of the human mitochondrial genome. *Nature* 290: 457–465.
- Ballard JWO, Whitlock MC. 2004. The incomplete natural history of mitochondria. *Mol Ecol* 13:729–744.
- Brown WM, George M, Wilson AC. 1979. Rapid evolution of animal mitochondrial DNA. *Proc Natl Acad Sci USA* 76: 1967–1971.
- Geissmann T, Lwin N, Aung SS, Aung TNN, Aung ZM, Hla TH. 2011. A new species of snub-nosed monkey, genus *Rhinopithecus* Milne-Edwards, 1872 (Primates, Colobinae), from northern Kachin state, northeastern Myanmar. *Am J Primatol* 73:96–107.
- Groves CP. 2001. *Primate taxonomy*. Washington, DC: Smithsonian Institution Press.
- IUCN. 2008. *IUCN Red List of Threatened Species*. IUCN, Gland: Switzerland. Available at <http://iucnredlist.org/> IUCN
- Sternner KN, Raam RL, Zhang YP, Stewart CB, Disotell TR. 2006. Mitochondrial data support an odd-nosed colobine clade. *Mol Phylogenet Evol* 40:1–7.
- Yu L, Wang XP, Ting N, Zhang YP. 2011. Mitogenomic analysis of Chinese snub-nosed monkeys: Evidence of positive selection in NADH dehydrogenase genes in high-altitude adaptation. *Mitochondrion* 11:497–503.