



Mitochondrial DNA

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MITOGENOME ANNOUNCEMENT

**Complete mitochondrial genome of the crested black macaque
(*Macaca nigra*)**Li-Na Du^{1,2}, Fang-Lei Shi³, Zhi-Jin Liu³, and Qi-Hai Zhou^{1,2}¹Guangxi Key Laboratory of Rare and Endangered Animal Ecology, Guangxi Normal University, Guilin, China, ²College of Life Science, Guangxi Normal University, Guilin, China, and ³Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing, China**Abstract**

The complete mitochondrial sequence of the crested black macaque (*Macaca nigra*) has been determined by mapping the raw data to previously published mitochondrial assemblies of the corresponding species. The total sequence length is 16,564 bp and includes 13 protein-coding genes, 2 ribosomal RNA genes, 22 transfer RNA genes and 1 D-loop control region. The base composition of mtDNA genome is 31.76% A, 25.27% T, 30.17% C, and 12.80% G, with an AT content of 57.03%. The arrangement of genes in *M. nigra* is identical to that of *M. mulatta*. All genes are encoded on the heavy strand with the exception of ND6 and eight tRNA genes. The mitochondrial genome of *M. nigra* presented here will contribute to a better understanding of the population genetics, help to protect its genetic diversity and resolve phylogenetic relationships within the family.

KeywordsMitochondrial genome, *Macaca nigra***History**

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The crested black macaque (*Macaca nigra*) belongs to genus *Macaca* (Colobinae: Cercopithecidae). It is endemic to a small geographic area of the eastern tip of Sulawesi's northern peninsula and all populations of *M. nigra* are threatened by hunting in the last few decades (Rosenbaum et al., 1998). This species is categorized as critically endangered (CR) in the IUCN Red List of Threatened Species (IUCN, 2014).

In this study, the complete mitochondrial genome sequence of the crested black macaque has been reported for the first time. We assembled the mitochondrial genome (mtDNA) of *M. nigra* with paired-end reads with length of 125 bp. We captured reads from the mitochondrial genome by mapping the raw data to previously published mitochondrial assemblies of the corresponding species. The mapping was carried out using mrFAST (Alkan et al., 2009) with paired-end mode and 6% of divergence. We removed low-quality reads when at least one of both paired-ends had a median Phred quality score lower than 32. The mtDNA sequence was annotated in comparison with the complete mitochondrial genomes of *M. mulatta* (Liedigk et al., 2014). The accession numbers of the GenBank for *M. nigra* mtDNA is KP072068. The complete mtDNA sequence (16,564 bp in length) consists of 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and one

D-loop control region (Table 1). All genes are encoded on the heavy strand with the exception of ND6 and eight tRNA genes (tRNA-Gln, tRNA-Ala, tRNA-Asn, tRNA-Cys, tRNA-Tyr, tRNA-Ser, tRNA-Glu and tRNA-Pro). For 11 of the 13 protein-coding genes, the start codon is ATG, while ND2 and ND3 utilize ATT. With regards to stop codons, six genes (COX1, COX2, ATP6, ATP8, ND4L and ND5) use TAA, ND6 uses AGG, and six genes (ND1, ND2, ND3, ND4, COX3 and CYTB) have an incomplete stop codon T, which were presumably completed as TAA by posttranscriptional polyadenylation (Anderson et al., 1981). The 12S and 16S ribosomal RNA genes are 947 bp and 1557 bp long, respectively. The tRNA genes are various from 59 bp to 75 bp. In our study, the D-loop control region of the *M. nigra* mtDNA is 1086 bp long and is located between the tRNA-Pro and tRNA-Phe genes (Table 1). We did not find repeat sequences in the D-loop control region. The mitochondrial genome have been proved to be very useful for phylogenetic relationships at several taxonomic levels, mainly because of its maternal inheritance, its small size, an accelerated rate of mutation compared to that of the nuclear DNA, and little or no recombination (Ballard & Whitlock 2004; Brown et al., 1979). We expect these results will provide relevant information for *M. nigra* comparative studies in the future.

Table1. Characteristics of *M. nigra* mitochondrial DNA genome.

Gene name	Coding strand	Start position	End position	Space (–) overlap (+)	Length(bp)	Start codon	Stop codon
tRNA-Phe	H	1	72		72		
12S rRNA	H	73	1019		947		
tRNA-Val	H	1020	1088		69		
16S rRNA	H	1089	2645		1557		
tRNA-Leu(UUR)	H	2648	2722	–2	75		
ND1	H	2725	3679	–2	955	ATG	T––
tRNA-Ile	H	3680	3748		69		
tRNA-Gln	L	3746	3817	+3	72		
tRNA-Met	H	3819	3886	–1	68		
ND2	H	3887	4928		1042	ATT	T––
tRNA-Trp	H	4929	4995		67		
tRNA-Ala	L	5003	5071	–7	69		
tRNA-Asn	L	5073	5145	–1	73		
rep_origin	L	5147	5179	–1	33		
tRNA-Cys	L	5178	5246	+2	69		
tRNA-Tyr	L	5246	5310	+1	65		
COX1	H	5315	6859	–4	1545	ATG	TAA
tRNA-Ser(UCN)	L	6855	6926	+5	72		
tRNA-Asp	H	6928	6995	–1	68		
COX2	H	6997	7680	–1	684	ATG	TAA
tRNA-Lys	H	7756	7819	–75	64		
ATP8	H	7821	8027	–1	207	ATG	TAA
ATP6	H	7982	8662	+46	681	ATG	TAA
COX3	H	8662	9445	+1	784	ATG	T––
tRNA-Gly	H	9446	9513		68		
ND3	H	9514	9859		346	ATT	T––
tRNA-Arg	H	9860	9924		65		
ND4L	H	9925	10,221		297	ATG	TAA
ND4	H	10,215	11,592	+7	1378	ATG	T––
tRNA-His	H	11,593	11,661		69		
tRNA-Ser(AGY)	H	11,662	11,720		59		
tRNA-Leu(CUN)	H	11,721	11,791		71		
ND5	H	11,798	13,603	–6	1806	ATG	TAA
ND6	L	13,604	14,131		528	ATG	AGG
tRNA-Glu	L	14,132	14,200		69		
CYTb	H	14,205	15,345	–4	1141	ATG	T––
tRNA-Thr	H	15,346	15,409		64		
tRNA-Pro	L	15,411	15,478	–1	68		
D-loop	H	15,479	16,564		1086		

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Declaration of interest

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of the paper. This project was supported by Supported by Guangxi Key Laboratory of Rare and Endangered Animal Ecology, Guangxi Normal University (1402k005) and the Natural Science Foundation of China (No. 31471989, 31172122).

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