

Short Communication

The Complete Mitochondrial Genome of Leopard Cat, *Prionailurus bengalensis euptilurus* (Carnivora: Felidae)Feng Gao^{1*} and Jinping Zhang²¹Beijing Wildlife Rescue & Rehabilitation Center, China.²Jiangsu Key Laboratory for Biodiversity and Biotechnology, College of Life Sciences, Nanjing Normal University, Nanjing, 210023, China

ABSTRACT

The full-length of the mitochondrial (mt) genome of leopard cat (*Prionailurus bengalensis euptilurus*) was first determined in this study and consisted of a 17,246bp fragment, including 13 protein-coding genes, two rRNA genes, 22 tRNA genes, a control region (CR), and an origin of L-strand replication (OLR). The total base composition of the heavy strand was A, 33.05%; G, 13.52%; C, 25.94%; and T, 27.49%, with a slight AT bias of 60.54%. The complete mitochondrial data of *P. b. euptilurus* may provide an important for further phylogenetic and taxonomic analyses of Genus *Prionailurus* species.

Article Information

Received 28 July 2024

Revised 25 August 2024

Accepted 08 September 2024

Available online 03 March 2025
(early access)

Published 31 December 2025

Authors' Contribution

FG conceived this project, performed the extraction of the mitochondrial genomic DNA, coordinated the genome sequencing, performed the data analyses and wrote the initial manuscript draft. JZ mainly constructed the phylogenetic tree and involved in the revision of the paper. All authors read and approved the final version.

Key words

Leopard cat, Mitochondrial genome, *Prionailurus bengalensis euptilurus*

The Asian leopard cat (Felidae: *Prionailurus bengalensis* Kerr, 1792) occurs in forests from South Asia through East Asia to the Russian Far East, and from Southeast Asia to western Indonesia and the Philippines (Nowell and Jackson 1996). Leopard cat (*Prionailurus bengalensis*) is a small wild cat and widely distributed in Asia. The name of leopard cat is derived from the leopard-like spots prevalent in all subspecies, but its relationship with the leopard seems very distant. There are 12 leopard cat subspecies, which differ largely in appearance (Wilson and Mittermeier, 2009). It is widely distributed in China, living in the mountain broad-leaved forest, mixed forest, copse and so on. It is mainly active at night, and can occasionally see activities during the day. It is good at climbing. Its diet includes grass rabbits, rats, squirrels, birds, frogs, lizards, insects and a few fruits (Chen *et al.*, 2002).

Since 2002, it has been listed as least concern by IUCN as it is widely distributed but threatened by habitat loss and hunting in parts of its range (Sanderson *et al.*, 2008; Shuai-Tan *et al.*, 2015).

In order to better protect the leopard cat China classified the leopard cat as a National Grade II protected wild animal in 2021.

However, the molecular data of this species mainly focus on the samples collected from Japan, Korean, and some islands of Southeast Asian (Park, 2011; Tamada *et al.*, 2006), as well as molecular data for this species are mainly concentrated in samples collected from Japan, Korea, some islands in Southeast Asia, and Sichuan, China (Park, 2011; Tamada *et al.*, 2006; Shuai-Tan *et al.*, 2015), and the ocelot genome in Beijing and North China has not yet been sequenced. In this study, the complete sequence of the *euptilurus* was determined to obtain additional molecular information available for phylogenetic and taxonomic analyses in the future. In this study, combined with data from GenBank, we sequenced the mitotic whole genome of *P. bengalensis* from northern China and constructed its relatives to other ocelots.

Materials and methods

This sample was obtained from Cuihu Wetland Park (116°11'26.52"E, 40°6'25.08"N), Haidian District, Beijing,

* Corresponding author: radio6182000@163.com
0030-9923/2026/0001-0485 \$ 9.00/0



Copyright 2026 by the authors. Licensee Zoological Society of Pakistan.

This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

China. On the night of December 13, 2021, Blood samples are stored in the Animal Hospital of Beijing Wildlife Rescue Center. Sample number is 2021121301 and the email address of the collection director is bwrrc@126.com. the leopard cat was hit by a car in Cuihu Wetland Park and was saved by Beijing Wildlife Rescue Center. We employed polymerase chain reaction (PCR) methods to amplify the complete of the *P. b. chinensis* with the PCR primers designed by ourselves. A previous published sequence (NC_016189) of Amur leopard cat was used to design these primers for PCR-amplification and a template for gene annotation.

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov>; <https://www.ncbi.nlm.nih.gov/>) under the accession no. OR282482.

Results

The full-length of *P. b. euphilurus* mitogenome consists of a 17,246 bp fragment and the gene content of the mitogenome is identical to most of other vertebrates (Table I). The base composition of mitochondrial genome, protein-coding gene and rRNA gene were calculated respectively. The creation of circos was used to map the whole mitochondrial genome, and the results were shown in (Fig. 1).

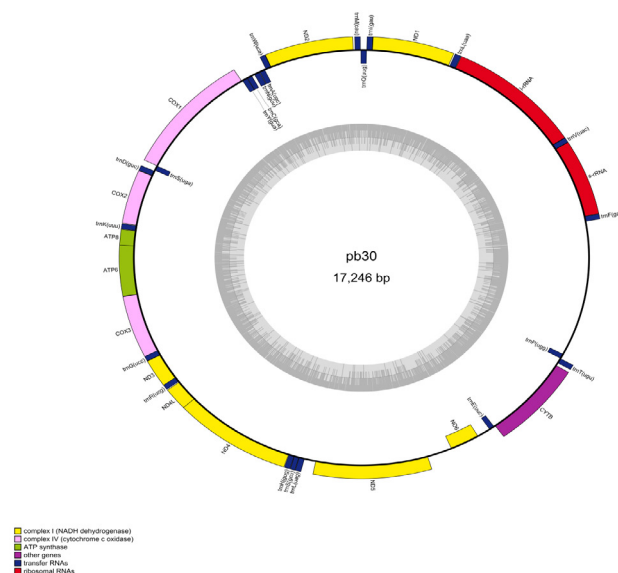


Fig. 1. Mitochondrial complete genome circle.

Note: From outside to inside are: genome structure chart, coverage of reads on genome, GC content.

It contains 13 protein-coding genes, 22 tRNAs, two rRNAs, one control region, and an origin of L-strand

Table I. Characteristics of the mitochondrial genome of *Prionailurus bengalensis euphilurus*.

Gene	Position		Length (bp)	Codon		Intergenic nucleo- tides ^b	Str- and
	From	To		Start	Stop ^a		
<i>tRNAPhe</i>	1	70	70			0	H
<i>12S rRNA</i>	71	1030	960			0	H
<i>tRNAVal</i>	1028	1095	68				H
<i>16S rRNA</i>	1094	2666	1573				H
<i>tRNALeu</i> (UUR)	3148	3222	75			+2	H
<i>nd1</i>	2754	3701	948	ATG	TA-	0	H
<i>tRNAIle</i>	3701	3769	69			-3	H
<i>tRNAGln</i>	3767	3840	74			+1	L
<i>tRNAMet</i>	4322	4390	69			0	H
<i>nd2</i>	3929	4954	1026	ATG	T--		H
<i>tRNATrp</i>	5433	5500	68			14+	H
<i>tRNAAla</i>	5035	5103	69			+1	L
<i>tRNAAsn</i>	5105	5177	73			0	L
<i>OriL</i>	5178	5210	33			0	L
<i>tRNACys</i>	5691	5755	65				L
<i>tRNATyr</i>	5756	5342	67			+1	L
<i>cox1</i>	5350	6888	1539	ATG	TAA	-3	H
<i>tRNASer</i> (UCN)	7366	7434	69			+6	L
<i>tRNAAsp</i>	6961	7029	69			0	H
<i>cox2</i>	7030	7713	684	ATG	TAA	+3	H
<i>tRNALys</i>	7717	7785	69			+1	H
<i>atp8</i>	7787	7990	204	ATG	TAA	-43	H
<i>atp6</i>	7948	8628	681	ATG	TAA	-1	H
<i>cox3</i>	8628	9462	835	ATG	T--	0	H
<i>tRNAGly</i>	9412	9480	69			0	H
<i>nd3</i>	9478	9837	360	ATA	TA-	0	H
<i>tRNAArg</i>	9828	9896	69			0	H
<i>nd4l</i>	9903	10193	291	ATG	TAA	-7	H
<i>nd4</i>	10187	11562	1376	ATG	A--	0	H
<i>tRNAHis</i>	11565	11633	69			0	H
<i>tRNASer</i> (AGY)	11634	11692	59			0	H
<i>tRNALeu</i> (CUN)	11693	11762	70			0	H
<i>nd5</i>	12378	13746	1369	ATA	TAA	+4	H
<i>nd6</i>	13567	13932	366	ATG	TAA	0	L
<i>tRNAGlu</i>	14095	14163	69			+3	L
<i>cytb</i>	14176	15271	1096	ATG	AGA	0	H
<i>tRNAThr</i>	15307	15375	69			0	H
<i>tRNAPro</i>	15376	15442	67			0	L
Control region	15443	17246	1804				H

^aT-- and TA- represent incomplete stop codons. ^bNumbers correspond to the nucleotides separating adjacent genes. Negative numbers indicate overlapping nucleotides.

replication (OLR). The total base composition of the heavy strand was A, 33.05%; G, 13.52%; C, 25.94%; and T, 27.49%, with a slight AT bias of 60.54%. All 13 protein-coding genes share the start codon ATG, except for ND4 and ND5, which start with ATA. Twelve out of 13 protein-coding genes are encoded on the heavy strand, while ND6 is encoded on the light strand. As in other mammals, most protein-coding genes share the typical termination codon TAA (COXI, COXII, ATPase8, ATPase 6, ND4L, ND5, and ND6), while Cytb terminates with AGA. In particular, incomplete stop codons are found in ND1 (TA-) and ND2, ND3, ND4, COX3 (T-). The length of 22 tRNAs ranges from 59 to 75 bp. The two ribosomal RNAs, 12S rRNA (960 bp) and 16S rRNA (1573 bp), are located between tRNAPhe and tRNA^{Leu}(UUR) and separated by tRNA^{Val}. Additionally, it is also important to note that the L-strand replication origin (OL) (33 bp in length) is located within the WANCY region containing five tRNA genes (tRNA^{Trp}, tRNA^{Ala}, tRNA^{Asn}, tRNA^{Cys}, and tRNA^{Tyr}) as in the most vertebrates (Seutin *et al.*, 1994).

The other non-coding region, the control region (1804 bp in length), is bound by tRNA^{Pro} and tRNA^{Phe}. It is expected that the complete mitogenomic data of *P. b. euphilurus* could provide an important data set for further phylogenetic and taxonomic analyses of Genus *Prionailurus* species.

Discussion

We downloaded the sequences of another 11 ocelots from NCBI to construct the phylogenetic tree, the phylogenetic tree reveals that *Prionailurus viverrinus* nests in the *P. bengalensis* ontogenetic population, close to *Prionailurus bengalensis euphilurus*, its Accession ID are JN392459 and NC016189, the similarity is 48 percent (Fig. 2). It is necessary to further examine the monophyly of *P. bengalensis* and taxonomy of the species *P. viverrinus* using more samples and/or morphological and molecular data.

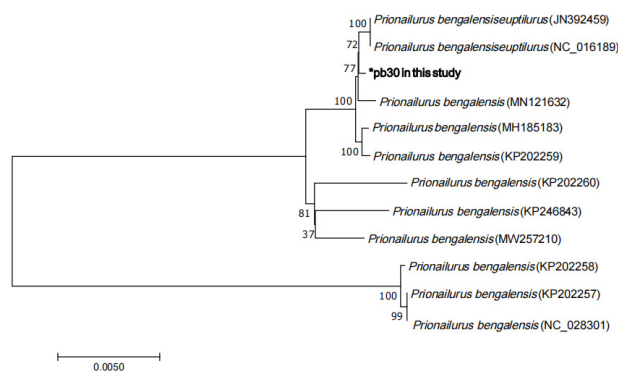


Fig. 2. Phylogenetic tree of *Prionailurus bengalensis* based on 13 protein-coding genes.

DECLARATIONS

Funding

This research was supported by a financial project of Beijing terrestrial wildlife rescue breeding daily operation and maintenance project, its number is 11000022T000000430317.

Animal ethics declaration

The experiment was approved by Beijing Municipal Bureau of Landscape and Afforestation in advance, passed the review of animal ethics, and was in line with the Wildlife Protection Law of the People's Republic of China.

Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov>) (<https://www.ncbi.nlm.nih.gov/>) under the accession OR282482. The associated **BioProject**, **SRA**, and **Bio-Sample** numbers are PRJCA022082, CRA014553, and PRJCA022082, respectively.

Statement of conflict of interest

The author report that they have no conflicts of interest. Author Solely responsible for the content and writing of the paper. This research was supported by a financial project of Beijing terrestrial wildlife rescue breeding daily operation and maintenance project, its number is 11000022T000000430317.

References

- Andrew, T. and Smith, Y.X., 2009. *A guide to the mammals of China*. Hunan Education Press.
- Chen, W., Gao, W. and Fu, B.Q., 2002. *Zoology of Beijing*. China Forestry Publishing Press, Beijing.
- Nowell, K. and Jackson, P., 1996. *Wild cats: Status survey and conservation action plan*. IUCN, Switzerland.
- Park, Y.C., 2011. *Mitochond. DNA*, **22**: 89–90. <https://doi.org/10.3109/19401736.2011.624607>
- Seutin, G., Lang, B.F., Mindell, D.P. and Morais, R., 1994. *Mol. Biol. Evol.*, **11**: 329–341.
- Shuai-Tan, Jie-Tian, X., Fang-Dong, Z., Que-Kun, P. and Rui, P., 2015. *Mitochond. DNA early online*, **1–2**: 1940–1736.
- Tamada, T., Siriaronrat, B., Subramaniam, V., Hamachi, M., Lin, L.K., Oshida, T., Rerkamnuaychoke, W. and Masuda, R., 2006. *Zool. Sci.*, **25**: 154–163. <https://doi.org/10.2108/zsj.25.154>

Wilson, D.E. and Mittermeier, R.A., 2009. *Handbook of the mammals of the world*. Vol 1: Carnivores. Lynx Edicions, Barcelona, Spain.

Zhang, J.J., Liang, Y.L. and Ren, Z.M., 2019. *Mitochond. DNA B*, 4: 3072-3074. <https://doi.org/10.1080/23802359.2019.1666678>