RESEARCH ARTICLE
doi: 10.2306/scienceasia1513-1874.2026.087

ScienceAsia 52 (5): 2026: ID 2026087: **1–8**

Comparison of *MC1R* expression differences and mitochondrial genome analysis between albino and wild-type *Eothenomys eleusis*

Juan Zhang[a], **Yuan Mu**[b], **Hao Zhang**[a,*], **Wanlong Zhu**[a,*]

[a] School of Life Sciences, Yunnan Normal University, Kunming 650500 China
[b] Institute of Eastern-Himalaya Biodiversity Research, Dali University, Dali 671003 China

*Corresponding authors, e-mail: 3971@ynnu.edu.cn, zwl_8307@163.com

Received 22 Sep 2025, Accepted 23 Sep 2026
Available online 18 Oct 2026

ABSTRACT: To investigate the survival and adaptive evolution of albino individuals in *Eothenomys eleusis*, this study measured differences in the expression levels of the *MC1R* (melanocortin 1 receptor) gene between albino and wild-type individuals using RT-qPCR technology. Furthermore, high-throughput sequencing technology was employed to perform a comparative analysis of the mitochondrial genome sequences of both types. The results showed that the expression level of the *MC1R* gene in albino *E. eleusis* was significantly lower than that in the wild-type. Compared to the wild-type, the third most abundant codon in albino *E. eleusis* was AUA ($n > 170$), and it contained one of the least abundant codon CGG ($n < 5$). A mutation from GC to AU was found in the dihydrouridine loop structure of the albino *trnP* gene, which could destabilize the gene's secondary structure, thereby affecting the translation efficiency and mitochondrial energy metabolism. Additionally, the sequence lengths of the albino *rrnL* gene and control region OH were 1 bp and 31 bp missing, respectively, while the intergenic spacer between the *trnP* gene and the next gene increased by 31 bp. Notably, the missing sequence fragment in the OH exactly matched the increased sequence in the *trnP* gene spacer region, indicating a physical positional shift. This shift might also disrupted mitochondrial energy metabolism. Therefore, these findings provided a unique perspective for studying the survival ability and adaptive evolution of albino individuals in other species.

KEYWORDS: *Eothenomys eleusis*, albino-type, *MC1R* gene, mitochondrial genome, gene difference phenomena

INTRODUCTION

Small mammals actively adapt to environmental stresses, such as diurnal temperature variations and seasonal changes, by regulating their morphological and physiological traits [1]. Animal coat color is an important morphological, genetic and evolutionary feature. Its albinism phenomenon was caused by gene mutations, which affected the synthesis of melanin and the survival and adaptation of species by the coordinated regulation of multiple genes [2, 3]. The *MC1R* (melanocortin 1 receptor) gene was one of the most extensively studied key regulatory for coat color genes in mammals, primarily expressed in hair follicles and skin melanocytes [4, 5]. This gene mainly participated in regulating the type and amount of melanin, affecting the synthesis of eumelanin (black or brown) or pheomelanin (white, red, or yellow). Specifically, the lower the expression levels of the *MC1R* gene, the lighter the animal's coat color [4, 6]. Currently, research on albino species both domestically and internationally, mainly focuses on the polymorphisms of the *MC1R* gene, expression levels, and coat color phenotypes. For example, the experiment of Wang et al [7] demonstrated that the *MC1R* gene was expressed in the skin tissues of Tan sheep with different coat colors, and showed significant differences between groups. Jia et al [4] found that *MC1R* and other genes related to coat color had multiple variation sites in four Chinese local rabbits with different coat colors, and these sites exhibited low to moderate polymorphism. Dimov et al [8] studied native Bulgarian sheep breeds and showed that the deletion of the dominant E^D allele in the *MC1R* gene was associated with the appearance of "spotted" or white phenotypes. However, the genetic basis of adaptive evolution of albinism still needed to be further explored.

Adaptive regulation of energy metabolism was one of the important physiological strategies for animals to cope with environmental changes [9, 10]. Mitochondrial genome (mtDNA) was a crucial component of the genetic material in eukaryotic cells, carrying 13 protein-coding genes (PCGs: *nad1–6*, *nad4l*, *cox1–3*, *atp6* and *atp8*), 22 tRNA genes, 2 rRNA genes and a control region, all of which participated in the process of cell energy metabolism, especially oxidative phosphorylation [11, 12]. Specifically, the products encoded by the PCGs, such as NADH dehydrogenase, cytochrome c oxidase (*COX*) and ATP synthase, were essential for the electron transport chain (ETC) and ATP synthesis [13]. tRNA genes transport specific amino acids to ribosomes to promote the assembly of mitochondrial proteins. rRNA genes, including *rrnl* (16S rRNA) and *rrnS* (12S rRNA), form part of the mitochondrial ribosomes, and were involved in the translation of mitochondrial mRNA [14]. The control

region mainly regulates the replication and transcription of mitochondrial genes, ensuring the accuracy of gene expression and maintaining the stability of function [15]. Notably, mutations in these genes could enhanced reactive oxygen species ROS and reduced ATP synthesis, resulting in excessive oxidative stress, thereby affecting the survival and adaptation of species [16]. Furthermore, based on its maternal inheritance, high mutation rate and rapid evolution, the genome had become an important molecular marker for studying vertebrate phylogeny, species evolution, and adaptability [17]. Therefore, using mitochondrial genome mutations as molecular evidence, it was particularly necessary to conduct in-depth research on the occurrence of albinism in species and its adaptive evolutionary mechanisms.

Eothenomys eleusis (Thomas, 1911) belonged to the family Cricetidae and the genus *Eothenomys*. This vole is a small rodent, endemic species to China, widely distributed in the subtropical regions of southwest and southern China, inhabiting areas with an altitude of 1,000–3,000 m [18]. Most existing research had focused on the morphology, distribution and taxonomic evolution of *E. eleusis*. For example, Zhang et al [19] described in detail the morphological characteristics of albino *E. eleusis*, including the skull and appearance. Lopatin et al [20] and Wang et al [18] confirmed fossil and distribution records of *E. eleusis* in Tham Hai Cave in Vietnam and the Sichuan region, respectively. Zhu et al [21] and Zhang et al [22] preliminarily revealed the mitochondrial genome features of wild-type *E. eleusis* from Guizhou and albino-type *E. eleusis* from Yunnan, respectively. However, there were limited research on the expression level of the *MC1R* gene in wild albino *E. eleusis* and comparative studies of their mitochondrial genomes with those of the wild-type. Therefore, this study raised two questions: (1) Is there a difference in the expression level of the coat color gene *MC1R* between albino and wild-type *E. eleusis*, which affected its survival? (2) Compared to the wild-type, are there differences in the general characteristics of the mitochondrial genome of the albino-type (such as nucleotide composition and bias, codon preference, secondary structure of tRNA genes, etc.)? And are these differences related to the energy metabolism of species?

MATERIALS AND METHODS

Animal collection

This study captured samples of albino and wild-type *E. eleusis* in farmland and surrounding areas of shrubs in Mile City, Yunnan Province (103°24.40′ E, 24°31.24′ N, Fig. S1), China. Skin (1 cm^2) and liver (0.5 g) tissue samples were collected from each sample and quickly placed in a low temperature environment of −80 °C, and properly stored in the Physiological Ecology Research Group of the School of Life Sciences, Yunnan Normal University, China. For further research, these skin and liver samples were sent to Shanghai Personalized Bio Technology Co., China where the skin tissue was utilized for expression level analysis of *MC1R* gene, and the liver tissue was used for sequencing, analysis, and comparative studies of mitochondrial genome.

Expression level of the *MC1R* gene

According to the research by Han et al [6], primers for the target gene and reference gene were designed based on the conserved regions of the *Rattus norvegicus MC1R* gene sequence (Table S1) to detect the expression levels of the *MC1R* gene in skin samples from albino ($n = 2$) and wild-type *E. eleusis* ($n = 6$). The main procedures were as follows: first, total RNA was extracted from the samples using the Trizol method [23]. After confirming RNA quality by 1% agarose gel electrophoresis, it was used as a template to reverse transcribe the first strand of cDNA, and then the cDNA template was amplified by utilizing a real-time fluorescence quantitative instrument (LightCycler 480 II, Roche, Basel, Switzerland), and the fluorescence signal was detected. Next, perform qPCR reaction according to the instructions of AceQ qPCR SYBR Green Master Mix. To ensure the reliability of the experimental results, blank samples were included as negative controls for each reaction, and each sample was run in triplicate. Subsequently, the relative expression levels of the target gene were calculated using the $2^{-\Delta\Delta Ct}$ method [24].

Extraction and sequencing of mitochondrial genome

Based on the improved CTAB method, total DNA was extracted from liver samples of albino ($n = 2$) and wild-type ($n = 6$) *E. eleusis*, respectively. After passing the quality inspection, the Whole Genome Shotgun (WGS) strategy was first employed to construct DNA libraries with an insertion fragment length of 400 bp. Then, paired-end sequencing of these libraries was performed on the Illumina NovaSeq platform. Secondly, a series of software were used for quality assessment, sequences assembly, and genome annotation of the sequencing data, including Fastp [25], SPAdes [26], GetOrganelle [27], and Pilon [28] to obtain the final complete mitochondrial genomes. Finally, the genomes of the two individuals were uploaded to NCBI, receiving the corresponding GenBank accession numbers (albino-type: PP475794; wild-type: PP999024).

Statistical analysis

The expression data of the *MC1R* gene were analyzed and plotted using SPSS 22.0 and GraphPad Prism 9.5 software, and all data followed a normal distribution. Independent sample *t*-test was employed to assess homogeneity of variance and significance analysis for

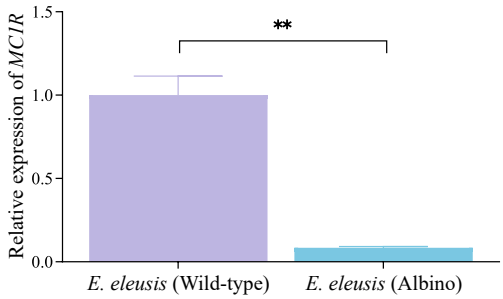


Fig. 1 The difference in expression levels of *MC1R* gene between albino and wild-type *E. eleusis*. Note: **, $p < 0.01$.

intergroup comparisons. Gene expression levels were expressed as mean ± SEM, with $p < 0.05$ indicating significant difference and $p < 0.01$ indicating extremely significant difference. The mitochondrial genome sequences were functionally annotated employing MITOS [29] to examine the predicted tRNA structures, and then compared with erroneous tRNA genes using NCBI's Blastn tool. Finally, based on PhyloSuite [30], the nucleotide composition, PCGs, and codon preferences of the genome were analyzed and compared to reveal the differences between albino and wild-type *E. eleusis* at the mitochondrial genome level.

RESULTS

Differential expression levels of *MC1R* gene

This study successfully amplified a conserved fragment of approximately 200 bp of the gene. The RT-qPCR results demonstrated that the *MC1R* gene was expressed in the skin tissues of both types, but there were differences in expression. Specifically, the expression levels of the *MC1R* gene in the albino-type and the wild-type were 0.08 ± 0.003 and 1.00 ± 0.046, respectively. Further statistical analysis revealed that the expression level of the *MC1R* gene in the albino-type was significantly lower than that in wild-type ($p < 0.01$, Fig. 1), which may be closely related to the decrease in melanin synthesis in the skin of albino-type.

Analysis and comparison of mitochondrial genomes

Nucleotide composition and bias

The mitochondrial genome lengths of the albino and wild-type *E. eleusis* are 16,347 bp and 16,348 bp, respectively, both containing 37 genes (13 PCGs, 22 tRNA genes, 2 rRNA genes) and one control region (OL, OH). When analyzing the nucleotide composition and bias of the mitochondrial genome, the base content of the albino-type whole genome was ranked as A (32.98%) > C (27.38%) > T (26.21%) > G (13.43%), with A + T content accounting for 59.19% and G + C content accounting for 40.81%. The base content ranking of the wild-type whole genome was similar to that of the albino-type, showing only differences in decimal fractions (Fig. 2). Meanwhile, the AT_skew or GC_skew of individual protein-coding genes and rRNA genes also showed only differences in decimal fractions.

Protein coding genes and codon preference

Using PhyloSuite to calculate and analyze the relative synonymous codon usage (RSCU) of 13 PCGs in albino and wild-type *E. eleusis*. The results showed that, except for 18 codons (such as CUC, AUU, and UCU), there were numerical differences in the rest of the codons between the two types. Furthermore, except for the codons AGA* and AGG* ($n = 0$) that did not encode Arg, the highest number of codons used in the albino-type were CUA (Leu1), AUC (Ile), and AUA (Met) ($n > 170$), while the lowest were UAG (*), CAG (Gln), and CGG (Arg) ($n < 5$). In contrast, the highest number of codons used in wild-type were CUA, AUC, and UUC (Phe), while the lowest were UAG and CAG (Fig. 3, Table 1).

RNA genes and control regions

In both the albino and wild-type *E. eleusis*, a comparison of the predicted tRNA secondary structures revealed that the *trnP* (Proline) gene exhibited the standard "cloverleaf" structure, but some base pairs within this structure contained U-G mismatches, which did not conform to the classical Watson-Crick pairing rules. Additionally, on the dihydrouracil loop (*D-loop*), the albino-type had an AU (T) pair replacing the GC pair found in wild-type, indicating the presence of a base mutation at this site (Fig. 4A,B). Furthermore, the *rrnL* gene and control region OH sequence length of albino-type was 1 bp (A) and 31 bp (TTTCGTCCACACGACTATCCCTGCCCCAT) shorter than those of wild-type, respectively, while the intergenic spacer sequence length between the *trnP* gene and the next gene (*trnF* gene) was 31 bp (TTTCGTCCACACGACTATCCCTGCCCCAT) longer than that of wild-type (Fig. 5).

DISCUSSION

Expression and regulation of *MC1R* gene

The coat color change of animals plays an important role in reproduction and survival, including aspects such as predation, courtship, avoidance of natural enemies, and resistance to ultraviolet radiation. This change was mainly regulated by the ratio and distribution pattern of eumelanin and pheomelanin, reflecting significant adaptive evolution [2, 31]. Among them, the *MC1R* gene encoded a G protein-coupled receptor that could bind to α-melanocyte-stimulating hormone (α-MSH) and adrenocorticotropic hormone (ACTH), activating adenylate cyclase on the cell membrane, promoting the conversion of adenosine triphosphate (ATP) to cyclic adenosine monophosphate (cAMP), further activated tyrosine kinase, and tyrosine kinase



Fig. 2 The nucleotide composition of the albino and wild-type *E. eleusis*.

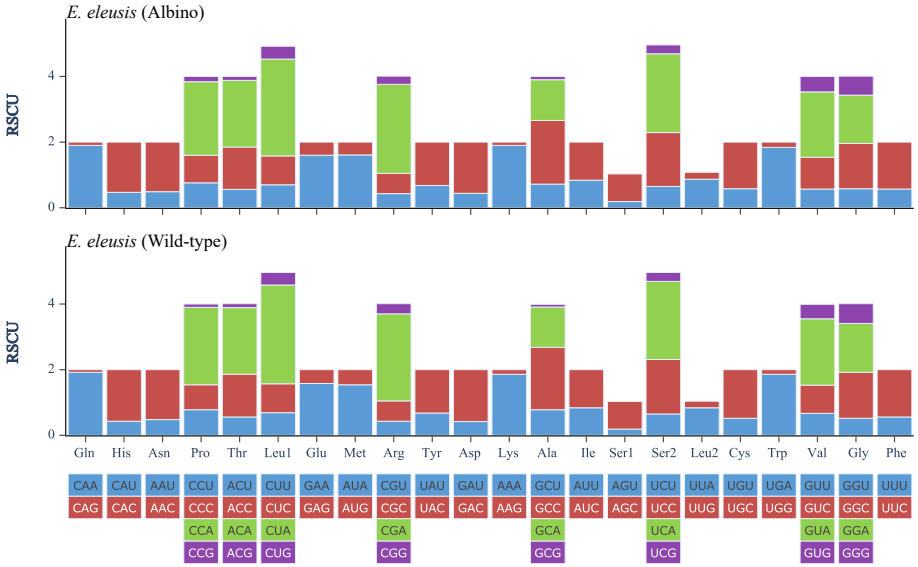


Fig. 3 Comparison of relative synonymous codon usage rates (RSCU) between the albino and wild-type *E. eleusis*.

reactivated tyrosine, thereby regulating the synthesis of eumelanin and pheomelanin, ultimately affecting the coat color changes of animals [32]. Previous studies had shown that differential expression of the *MC1R* gene typically led to changes in coat color in most animals. For example, Li et al [24] found that the *MC1R* gene was closely associated with coat color variation in cashmere goats, with significantly lower expression level in white cashmere goats than in black cashmere goats. Studies on different coat colors in species such as rabbits, Tan sheep, and guinea pigs confirmed that the expression levels of *MC1R* gene in dark-colored individuals were significantly higher than those in light-colored individuals [4, 7, 33]. The results of this study showed that the *MC1R* gene expression level in albino *E. eleusis* was the lowest and significantly lower than that of wild-type, consistent with the previous research findings. Additionally, compared to large and medium-sized species such as the albino *Panthera tigris tigris* [34], *Ursus thibetanus* [35], and *Ailuropoda melanoleuca* [2], *E. eleusis*, as one of the primary consumers of small mammals, was located at the bottom of the food chain. Its albinism was particularly prominent in farmlands and shrubs, making it easily exposed to the view of natural enemies, and consequently significantly increasing its survival risk in the natural environment. Therefore, this study further confirmed that the lightening of animal coat color phenotypes induced by low expression of the *MC1R* gene could affect their survival adaptability, es-

Table 1 The number of codons used in albino and wild-type *E. eleusis*. Note: * indicates a stop codon. AGA* and AGG* indicate that these two codons do not encode Arg in the mitochondrial genetic code and are considered stop codons.

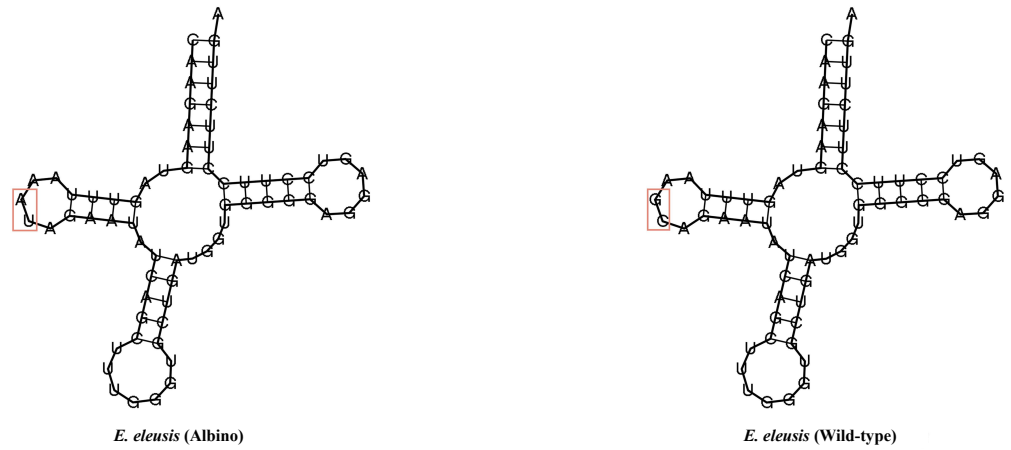
Amino acid	Codon	Count		Amino acid	Codon	Count	
		E. eleusis (Albino)	*E. eleusis* (Wild-type)			*E. eleusis* (Albino)	*E. eleusis* (Wild-type)
Phe	UUU	68	67	Tyr	UAU	43	43
	UUC	169	171		UAC	84	84
Leu2	UUA	85	82	*	UAA	9	9
	UUG	20	19		UAG	1	1
Leu1	CUU	68	67	His	CAU	23	21
	CUC	86	86		CAC	74	76
	CUA	288	293	Gln	CAA	73	74
	CUG	38	37		CAG	4	3
Ile	AUU	158	158	Asn	AAU	41	40
	AUC	219	218		AAC	126	127
Met	AUA	180	169	Lys	AAA	98	96
	AUG	43	51		AAG	5	7
Val	GUU	24	29	Asp	GAU	16	15
	GUC	41	37		GAC	57	57
	GUA	84	87	Glu	GAA	76	76
	GUG	20	19		GAG	19	20
Ser2	UCU	31	31	Cys	UGU	9	8
	UCC	78	79		UGC	22	23
	UCA	114	113	Trp	UGA	95	96
	UCG	13	13		UGG	8	7
Pro	CCU	38	39	Arg	CGU	7	7
	CCC	42	38		CGC	10	10
	CCA	112	118		CGA	44	43
	CCG	8	5		CGG	4	5
Thr	ACU	43	43	Ser1	AGU	9	9
	ACC	99	100		AGC	40	40
	ACA	155	156	Arg	AGA*	0	0
	ACG	9	9		AGG*	0	0
Ala	GCU	45	49	Gly	GGU	31	28
	GCC	122	119		GGC	74	75
	GCA	78	77		GGA	79	80
	GCG	6	5		GGG	31	32

pecially for prey species in the wild (non-light-colored environment).

Comparison of mitochondrial genomes features

To cope with diverse living environments, animals typically evolve corresponding adaptive strategies to meet their own survival needs, especially in terms of energy metabolism [36]. Mitochondria is the energy factory of animal cells, capable of producing up to 95% of ATP through oxidative phosphorylation, serving as the primary energy source for cellular respiration [12]. Given the central role of mitochondria in energy metabolism, their genomes have also become an important focus for studying animal survival and adaptive evolution. The results of this study indicated that compared to the wild-type *E. eleusis*, there was a mutation in the *D-loop* structure of the albino *trnP* gene from base GC to AU. Due to the fact that the structural stability of DNA or RNA was mainly determined by the number of hydrogen bonds between base pairs, with GC base pairs having three hydrogen bonds and AU base pairs having only two hydrogen bonds [37], this mutation may lead to reduced stability of the secondary structure of the *trnP* gene. The stability of the secondary structure was crucial for tRNA function, and decreased stability caused by base mutations may weaken the recognition and binding ability of tRNA structure, thereby interfering with the translation efficiency of mitochondrial genome and ultimately affecting the species' energy metabolism process [16, 38]. Notably, a decrease in energy metabolism levels might further lead to a weakening of species activity and be detrimental to survival [11]. Additionally, preliminary findings based on sequencing data indicate that the missing sequence fragment in the control region OH of the albino-type was completely consistent with the

A



B

Score		E value	Identities	Gaps	Strand
115 bits (62)		0.00	66/68 (97.06 %)	0/68 (0 %)	Plus/Plus
E. eleusis (Albino)	1	CAAGAAGTAGTTTAAATAGAATATCAGCTTTGGGTGCTGATGGTGGGGGAGGAGTCCTTC			60
E. eleusis (Wild-type)	1	CAAGAAGTAGTTTAAGCAGAATATCAGCTTTGGGTGCTGATGGTGGGGGAGGAGTCCTTC			60
E. eleusis (Albino)	61	CTTCTTGA			68
E. eleusis (Wild-type)	61	CTTCTTGA			68

Fig. 4 Comparison of the secondary structure and base sequence of *trnP* gene between the albino and wild-type *E. eleusis*. A: The secondary structure of *trnP* gene; B: Comparison of base sequences of *trnP* genes based on Blastn.

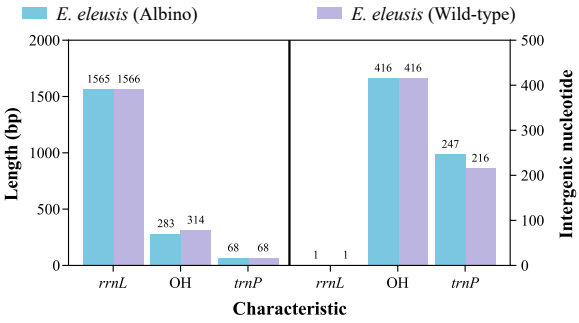


Fig. 5 Comparative analysis of mitochondrial genome composition between the albino and wild-type *E. eleusis*. Note: Length, sequence length; Intergenic nucleotide, the length of the intergenic sequence between this gene and the next gene.

sequence increased in the intergenic spacer region of the *trnP* gene, indicating the possible physical position shift phenomenon. Meanwhile, this phenomenon will be independently validated in subsequent PCR studies. Given that the control region was 2–5 times larger than other genes in the mitochondrial genome, was the most active, and exhibited high variability [39, 40], this observed movement phenomenon was likely due to variations in this region. Meanwhile, Pastukh et al [15] and Xing et al [13] indicated that the control region contains fundamental elements such as promoters and terminators, which play a crucial regulatory role in the replication and transcription of the mitochondrial genome, thereby maintaining the stability of mitochondrial energy metabolism. Therefore, this movement phenomenon might affect the species' energy metabolism, providing new clues for a deeper understanding of the genetic variation and adaptive evolution of mitochondrial genomes in albino species.

CONCLUSION

In summary, this study confirmed that the expression of the *MC1R* gene in albino *E. eleusis* was significantly lower than that in the wild-type, resulting in a lighter coat color and subsequently affecting the species' survival in natural environments. Further mitochondrial genome analysis revealed that the AU base mutation of *trnP* gene in albino mitochondrial genome, causing instability in the gene's secondary structure, which may impact mitochondrial translation efficiency and energy metabolism in the species. Therefore, the results of this study provided a reference for further understanding of the survival and adaptive evolution of albino individuals in other species. However, future research was still needed to further verify the correlation between coat color gene expression regulation and phenotype, as well as energy metabolism and species adaptive evolution.

Appendix A. Supplementary data

Supplementary data associated with this article can be found at https://dx.doi.org/10.2306/scienceasia1513-1874.2026.087. The gene organization and size of the mitochondrial genome were published in the *Indian J Anim Res*, with the DOI: 10.18805/IJAR.BF-1882.

Acknowledgements: This work was financially supported by the National Natural Scientific Foundation of China (32560262), Yunnan Fundamental Research Projects (202401AS070039).

REFERENCES

1. Guan ZH, Ma CY, Fei HL, Huang B, Ning WH, Ni QY, Jiang XL, Fan PF (2018) Ecology and social system of northern gibbons living in cold seasonal forests. *Zool Res* **39**, 255–265.
2. Guan D, Sun S, Song L, Zhao P, Nie Y, Huang X, Zhou W, Yan L, et al (2024) Taking a color photo: a homozygous 25-bp deletion in *Bace2* may cause brown-and-white coat color in giant pandas. *Proc Natl Acad Sci USA* **121**, e2317430121.
3. Li LX, Huang JX, Chen YL, Ran RS (2025) Disruption of mc1r disturbs skin pigmentation in *Xenopus tropicalis*. *Pigment Cell Melanoma Res* **38**, e70033.
4. Jia XB, Ding P, Chen SY, Zhao SK, Wang J, Lai AJ (2021) Analysis of *MC1R*, *MITF*, *TYR*, *TYRP1*, and *MLPH* genes polymorphism in four rabbit breeds with different coat colors. *Animals* **11**, 81.
5. Yan X, Terai Y, Widayati KA, Itoigawa A, Purba LHPS, Fahri F, Suryobroto B, Imai H (2022) Functional divergence of the pigmentation gene melanocortin-1 receptor (*MC1R*) in six endemic *Macaca* species on Sulawesi Island. *Sci Rep* **12**, 7593.
6. Han CY, Jia T, Wang Y, Wang ZK, Zhu WL, Zhang H (2022) Comparative on the expression of *MC1R* gene and the contents of *UCP1*, *Hb* and *Mb* of *Eothenomys miletus* at different altitudes from Hengduan Mountain region in winter. *Acta Theriol Sin* **42**, 69–75.
7. Wang XW, Fan Y, Ma XM, Ma LN, Yue CJ, Wang J, Zhao ZW, Ma Q (2020) Quantitative analysis of mRNA expression of Tan sheep coat color candidate genes *MC1R* and *TCF25*. *Acta Agric Zhejiangensis* **32**, 1351–1356.
8. Dimov D, Kostova M, Vuchkov A, Dimitrova I, Kalaydzhiev G, Staykova G, Iliev M, Bozhilova M (2025) Genetic polymorphisms in Agouti signaling protein (*ASIP*) and melanocortin 1 receptor (*MC1R*) genes and their association with coat color in native Bulgarian sheep breeds. *Small Rumin Res* **249**, 107517.
9. Wang DH (2011) Some progress in mammalian physiological ecology in China. *Acta Theriol Sin* **31**, 15–19.
10. Zhang XY, Sukhchuluun G, Bo TB, Chi QS, Yang JJ, Chen B, Zhang L, Wang DH (2018) Correction to: Huddling remodels gut microbiota to reduce energy requirements in a small mammal species during cold exposure. *Microbiome* **6**, 126.
11. Harrington JS, Ryter SW, Plataki M, Price DR, Choi AMK (2023) Mitochondria in health, disease, and aging. *Physiol Rev* **103**, 2349–2422.
12. Moura PJ, Oliveira JP, Urbano MA (2025) Mitochondria: An overview of their origin, genome, architecture, and dynamics. *Biochim Biophys Acta Mol Basis Dis 1871*, 167803.
13. Xing BP, Lin LY, Wu Q (2025) Application of mitochondrial genomes to species identification and evolution. *Electron J Biotechnol* **76**, 39–48.
14. D'Souza AR, Minczuk M (2018) Mitochondrial transcription and translation: Overview. *Essays Biochem* **62**, 309–320.
15. Pastukh VM, Gorodnya OM, Gillespie MN, Ruchko MV (2016) Regulation of mitochondrial genome replication by hypoxia: The role of DNA oxidation in *D-loop* region. *Free Radic Biol Med* **96**, 78–88.
16. Hahn A, Zuryn S (2019) Mitochondrial genome (mtDNA) mutations that generate reactive oxygen species. *Antioxidants* **8**, 392.
17. Ghosh A, Tyagi K, Dubey AK, Sweet AD, Singha D, Goswami P, Kumar V (2024) Purifying selection drove the adaptation of mitochondrial genes along with correlation of gene rearrangements and evolutionary rates in two subfamilies of Whitefly (Insecta: Hemiptera). *Funct Integr Genomics* **24**, 121.
18. Wang XM, Liu M, Zhao SP, Liu YX, Wang X, Chen SD, Liu SY (2024) Determination of classification and distribution of *Eothenomys eleusis* (Thomas, 1911) from Sichuan Province. *Chin J Zool* **59**, 210–216.
19. Zhang W, Zhu WL (2024) The albino *Eothenomys eleusis* was first discovered in Mile, Yunnan Province. *Sichuan J Zool* **43**, 347.
20. Zhang J, Mu Y, Zhu WL, Yang XM (2025) A rare mitochondrial genome of albino *Eothenomys eleusis* Thomas 1911 (Cricetidae: Arvicolinae) from Southeastern Yunnan, China and its phylogenetic analysis. *Indian J Anim Res* **59**, 560–567.
21. Lopatin AV (2023) The first record of *Eothenomys* (Arvicolinae, Cricetidae, Rodentia) from the pleistocene of Vietnam. *Dokl Biol Sci* **508**, 63–66.
22. Zhu L, Bi ZD, Qian HA, Mei XF, Zhao JY, Zhao XX, Chen H, Zhang JS, et al (2023) Sequencing and analysis of the complete mitochondrial genome of *Eothenomys eleusis* Thomas 1911 from China and its phylogenetic analysis. *Mitochondrial DNA Part B* **8**, 493–496.
23. Wu SJ, Zhao L, Huang JQ, Li YJ, Zhang Q, Pan YC, Wang XL, Liu Z (2021) Cloning, sequencing and expression analysis of *mc1r* gene in different developmental stages and tissues of rainbow trout *Oncorhynchus mykiss*. *Chin J Zool* **56**, 746–755.
24. Li JP, Chen W, Wu SF, Ma T, Jiang HZ, Zhang QL (2019) Differential expression of *MC1R* gene in Liaoning Cashmere goats with different coat colors. *Anim Biotechnol* **30**, 273–278.
25. Chen S, Zhou YQ, Chen YR, Gu J (2018) Fastp: An ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics* **34**, i884–i890.
26. Prjibelski A, Antipov D, Meleshko D, Lapidus A, Korobeynikov A (2020) Using SPAdes *de novo* assembler. *Curr Protoc Bioinf* **70**, e102.
27. Jin JJ, Yu WB, Yang JB, Song Y, dePamphilis CW, Yi TS, Li DZ (2020) GetOrganelle: A fast and versatile toolkit for accurate de novo assembly of organelle genomes. *Genome Bio* **21**, 241.
28. Walker JB, Abeel T, Shea T, Priest M, Abouelliel A, Sakthikumar S, Cuomo AC, Zeng QD, et al (2014) Pilon: An integrated tool for comprehensive microbial variant detection and genome assembly improvement. *Plos One* **9**, e112963.

29. Bernt M, Donath A, Jühling F, Externbrink F, Florentz C, Fritzsch G, Pütz J, Middendorf M, et al (2013) MITOS: Improved *de novo* metazoan mitochondrial genome annotation. *Mol Phylogenet Evol* **69**, 313–319.
30. Zhang D, Gao FL, Jakovlić I, Zou H, Zhang J, Li WX, Wang GT (2020) PhyloSuite: An integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. *Mol Ecol Resour* **20**, 348–355.
31. Hu YB, Wang XP, Xu YC, Yang H, Tong ZY, Tian R, Xu SH, Yu L, et al (2023) Molecular mechanisms of adaptive evolution in wild animals and plants. *Sci China Life Sci* **66**, 453–495.
32. Upadhyay PR, Swope VB, Starner RJ, Koikov L, Abdel-Malek ZA (2024) Journey through the spectacular landscape of melanocortin 1 receptor. *Pigment Cell Melanoma Res* **37**, 667–680.
33. Tang YG, Feng YX, Zhong M, Wei Z, Wang L, Liu DW (2025) Polymorphism and tissue expression analysis of *TYR* and *MC1R* genes in *Guinea Pigs* with different coat-color phenotypes. *Lab Anim Comp Med* **45**, 21–29.
34. Xu X, Dong GX, Schmidt-Küntzel A, Zhang XL, Zhuang Y, Fang R, Sun X, Hu XS, et al (2017) The genetics of tiger pelage color variations. *Cell Res* **27**, 954–957.
35. Ma GF, Yu HL, Jiang HZ, Du JH, Xiong JY, Sun ZP, Tu SQ (2021) First record of albino muntjac (*Muntiacus reevesi*) by camera traps in Shennongjia national park. *Chin J Wildl* **42**, 277–280.
36. Wu L, Tong Y, Ayivi Sam PG, Storey KB, Zhang JY, Yu DN (2022) The complete mitochondrial genomes of three Sphenomorphinae species (Squamata: Scincidae) and the selective pressure analysis on mitochondrial genomes of limbless *Isopachys gyldenstolpei*. *Animals* **12**, 2015.
37. Majumder S, Coupe S, Fakhri N, Jain A (2025) Sequence-encoded intermolecular base pairing modulates fluidity in DNA and RNA condensates. *Nat Commun* **16**, 4258.
38. Hatakeyama H, Katayama A, Komaki H, Nishino I, Goto YI (2015) Molecular pathomechanisms and cell-type-specific disease phenotypes of MELAS caused by mutant mitochondrial tRNA (Trp). *Acta Neuropathol Commun* **3**, 52.
39. Liu LY, Peng Z, Zhou JW, Chen DX, Wang KF, Lin SY, Li Q, Gui L (2025) Structural characterization and phylogenetic analysis of mitochondrial DNA *D-loop* region of *Acrossocheilus*. *Hunan Agric Sci* **15**, 81–86. [in Chinese]
40. Luo M, Yang W, Bai L, Zhang L, Huang JW, Cao YH, Xie YH, Tong LP, Zhang HB, et al (2024) Artificial intelligence for life sciences: A comprehensive guide and future trends. *Innov Life* **2**, 100105.

Appendix A. Supplementary data

Table S1 Relevant information on primers.

Primer	Primer sequence (5′–3′)		Amplification product length (bp)
MC1R	F: CTCCACGGACTGCTTCCTAC	R: GAGTGCAGGTTGCGGTTTTT	200
Housekeeping genes	F: GAAGGTCGGTGTGAACGGAT	R: CCCATTTGATGTTAGCGGGAT	250

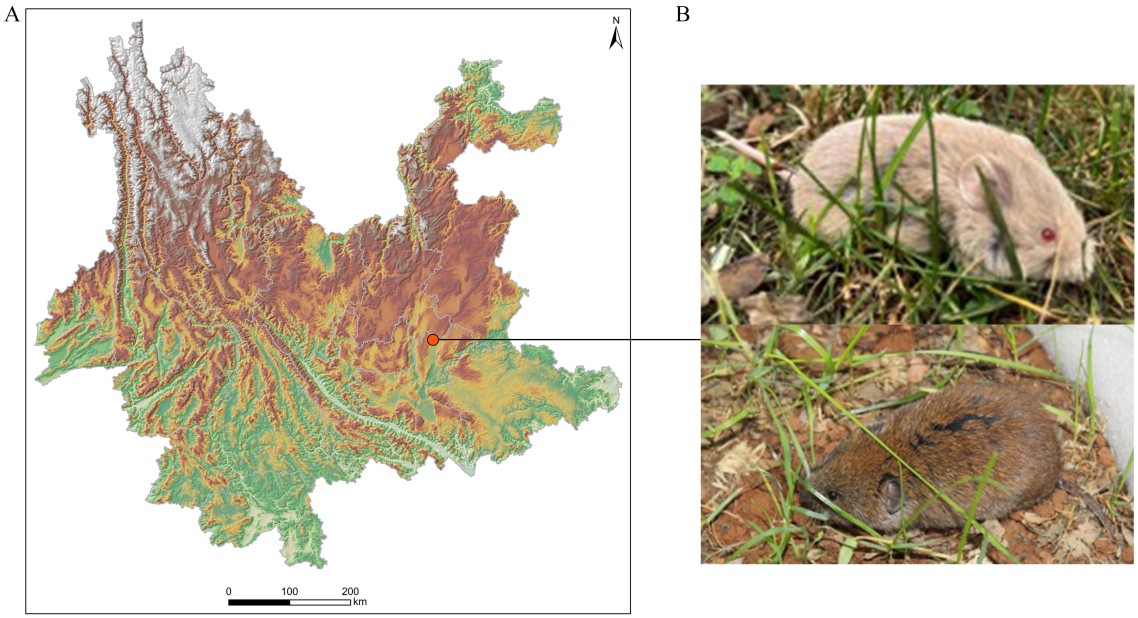


Fig. S1 Animal sample collection. A: Sampling points; B: Photos of albino and wild-type *E. eleusis* (from top to bottom).