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Cover: Stripe-necked Mongoose *Urva vitticollis* in poster colours, adapted from photograph by Ashni Dhawale, by Pooja Ramdas Patil.



Phylogenetic insights on the delineation of Mysore and Malabar subspecies of the Grey Slender Loris *Loris lydekkerianus* in southern India

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Abstract: Slender lorises are a threatened genus of small and nocturnal strepsirrhine primates confined to India and Sri Lanka. The Grey Slender Loris *Loris lydekkerianus* is divided into several subspecies based on morphological variation and geographical distribution but not supported by molecular data. We investigated the phylogenetic divergence of two subspecies of the Grey Slender Loris in southern India: the Mysore Slender Loris *Loris lydekkerianus* ssp. *lydekkerianus* and the Malabar Slender Loris *Loris lydekkerianus* ssp. *malabaricus*. We generated whole genome shotgun sequence data and assembled the whole mitochondrial genomes of representative individuals from their distribution in southern India and compared them with publicly available mitogenomes of other lorises. We found that the Mysore and Malabar Slender Lorises vary by 2.09% in the COX1 and CYTB gene regions. Further, phylogenetic analysis of 13 protein-coding and two ribosomal RNA genes in the mitochondrial genome showed that the Mysore and Malabar Slender Lorises form distinct monophyletic clades that diverged about 1.049 million years ago, shortly after the divergence of Red Slender Loris *Loris tardigradus*. Considering this relatively high sequence variation and evolutionary divergence together with their already established morphological differences and geographically distinct habitats, we propose to recognize the Mysore and Malabar Slender Lorises as two distinct species *Loris lydekkerianus* and *Loris malabaricus*.

Keywords: Grey Slender Loris, Malabar Slender Loris, molecular dating, Mysore Slender Loris, phylogenetics.

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Author contributions: G.U. and H.N.K conceived the idea for this study and collected the samples. V.T. and S.M. analyzed the data and drafted the manuscript. All authors contributed to the revision of the manuscript and agreed to the final version of the manuscript.

For Tamil abstract see end of this article.

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INTRODUCTION

Slender lorises (genus *Loris*) are one of the two genera of extremely specialized nocturnal primates that inhabit India (Nekaris 2014). They belong to the family Lorisidae, which also includes Slow lorises, Pottos, and Angwantibos. Slender lorises are confined to India and Sri Lanka, where they inhabit dry to moist and lowland to montane forests (Singh et al. 2021). Slender lorises are characterized by their small size, long limbs, vestigial tail, large eyes, and slow locomotion. They are adapted for arboreal life, using their opposable thumbs and toes to grasp branches and their binocular vision to judge distances, visual acuity, precise hand-eye coordination and social communication. They feed mainly on insects but also consume fruits, flowers, gums, and other plant materials (Nekaris & Rasmussen 2003; Radhakrishna & Kumara 2010). They have a variety of vocalizations that may help them avoid predators and communicate with conspecifics (Radhakrishna & Singh 2002). Slender lorises are divided into two species: the Grey Slender Loris *Loris lydekkerianus* found in southern India and Sri Lanka and the Red Slender Loris *Loris tardigradus* found only in Sri Lanka (Groves 2001). Both species show high phenotypic variation in fur color, body size, and cranial morphology, leading to the recognition of several subspecies, most of which are refuted by molecular studies (Nijman et al. 2020). The Mysore Slender Loris *Loris lydekkerianus* ssp. *lydekkerianus* (Image 1) and the Malabar Slender Loris *Loris lydekkerianus* ssp. *malabaricus* (Image 2), which live in the dry and wet forests of the Eastern and Western Ghats, respectively, are the two subspecies that have been recognized thus far in southern India (Kumara et al. 2013). There are several regions in their distribution where slender lorises face serious threats to their existence such as habitat loss due to deforestation and urbanization, electrocution on live wires, road accidents, pet trade, and illegal poaching for traditional medicine and black magic (Dittus et al. 2022; Gnanaolivu et al. 2022). The IUCN Red List of Threatened Species classifies the Mysore Slender Loris (Kumara et al. 2022a) and Malabar Slender Loris (Kumara et al. 2022b) as 'Near Threatened' and they are listed under Schedule I of the Indian Wild Life (Protection) Act, 1972. Recently, Tamil Nadu became the first Indian state to notify a sanctuary for slender lorises spanning 118.06 km², which is crucial for protecting their habitat and ensuring the survival of this unique primate species (Government of Tamil Nadu 2022).

The Mysore and Malabar subspecies of the Grey Slender Loris were delineated based on their

morphological differences and geographic distribution (Groves 2001; Kumara et al. 2013). The Mysore Slender Loris is relatively larger (ca. 260 g) than Malabar Slender Loris (ca. 180 g) (Kumara et al. 2006). The Mysore Slender Loris has a grayish-brown coat and a prominent white stripe on its forehead, whereas the Malabar Slender Loris has a reddish-brown coat and a less distinct forehead stripe (Groves 2001; Kumara et al. 2006). The relative distribution of the two subspecies as well as their comparative densities and the extent of overlap between their distributions have been very well established (Kumara et al. 2013). The Mysore Slender Loris is found in the Eastern Ghats and eastern foothills of the southern Western Ghats, while the Malabar Slender Loris is confined to the western slope of the entire Western Ghats (Kumara et al. 2013). The Mysore Slender Loris prefers dry deciduous forests with moderate canopy cover and high tree density, while the Malabar Slender Loris prefers moist evergreen forests with high canopy cover and low tree density (Kumara et al. 2013). Their distributions overlap along the southern ridges of the Western Ghats, where hybridization may occur. While the diet of Mysore Slender Loris mostly consists of insects, plant material, and gum, the feeding behavior of the Malabar Slender Loris is not well studied (Radhakrishna & Kumara 2010). The reproductive biology and social system of the Mysore subspecies is influenced by factors such as seasonality, food availability, predation risk, and population density. It also has a seasonal breeding cycle that coincides with periods of high food availability (Radhakrishna & Singh 2004). No such information on the reproductive biology of the Malabar subspecies is available. Behavioral studies on lorises have always been more challenging than on relatively large, diurnal, and group-living primates such as macaques and langurs because they are nocturnal, small in size, and mostly semi-gregarious. Given the distinct habitat preferences and morphology of these two subspecies, understanding their evolutionary history and genetic differences is vital to address their conservation status and management issues.

Therefore, the main objective of this study is to investigate the phylogenetic relationship and genetic divergence between the Mysore and Malabar Slender Lorises in southern India. To achieve this, we sequenced and assembled the whole mitochondrial sequences from three representative samples. We aligned these sequences with the publicly available sequences of other lorises and constructed phylogenetic trees. We estimated the sequence divergence and divergence time between the two subspecies using phylogenetic analysis.



Image 1. Mysore Slender Loris *Loris lydekkerianus* ssp. *lydekkerianus*.



Image 2. Malabar Slender Loris *Loris lydekkerianus* ssp. *malabaricus*.

Our results support the morphological and geographical delineation of the Malabar and Mysore Slender Lorises and advocates for recognizing them as two distinct species. This study will contribute to the understanding of the biogeography and speciation processes of these threatened lorises and provide crucial insights for their conservation and management.

MATERIALS AND METHODS

Sample Collection, DNA extraction, and Sequencing

We followed the sample collection guidelines of the animal ethics committees of the CSIR-Centre for Cellular and Molecular Biology and Salim Ali Centre for Ornithology and Natural History. Necessary permissions for sample collection were obtained from the Central Zoo Authority of India, Ministry of Environment, Forests & Climate Change, Government of India, vide Ref. No. 9-2/2005-CZA(M) Vol III. Rescued lorises of known wild origin within the IUCN designated ranges (Figure 1) that were captive in Mysore and Hyderabad zoos were the sources of our samples. Blood samples were collected in EDTA vacutainers by qualified zoo veterinarians from three representative individuals of *Loris lydekkerianus* ssp. *lydekkerianus* (N = 2) and *Loris lydekkerianus* ssp. *malabaricus* (N = 1). We used the Qiagen DNeasy Blood and Tissue Kit to isolate the genomic DNA from the blood samples. We measured the quality and quantity of genomic DNA using Nanodrop and Qubit 4. We constructed whole genome libraries using the Truseq PCR-free library preparation kit according to Illumina's protocols. Briefly, 1 µg of genomic DNA was sheared to

approximately 350 bp using the Covaris ultrasonicator. The fragmented DNA was then end-repaired and blunt-end ligated with sequencing adapters containing unique dual indices from IDT. The library was then size-selected using SPRI beads and verified on the Agilent fragment analyzer. The cleaned-up libraries were finally quantified in qPCR using the standards and Illumina adapter-specific primers from the Roche library quantification kit. Libraries having good concentration were pooled along with other samples and sequenced on the Illumina Novaseq 6000 platform for 300 cycles in paired-end mode.

Mitochondrial genome assembly

We demultiplexed the base call files to separate the three samples with the dual-indexed barcodes using the BCL2FASTQ tool from Illumina. Raw reads were quality-filtered with a phred quality score threshold of 15 using FASTP v0.20 (Chen et al. 2018). We subsampled 10 million quality filtered reads to de novo assemble the circular mitochondrial genomes of all three samples using GetOrganelle v1.7.1 (Jin et al. 2020). We then annotated all the mitogenomes using MITOS2 (Bernt et al. 2013) with the Refseq 89 Metazoa reference mitochondrial database and the vertebrate mitochondrial genetic code. All the coding and non-coding genes were extracted from the mitochondrial genomes using the annotations.

Sequence and Phylogenetic analyses

We aligned the full-length COX1 and CYTB genes of lorises using Clustal Omega with the “distmat” flag and calculated the pairwise distances between the sequences (Sievers & Higgins 2021). To build the phylogeny, along

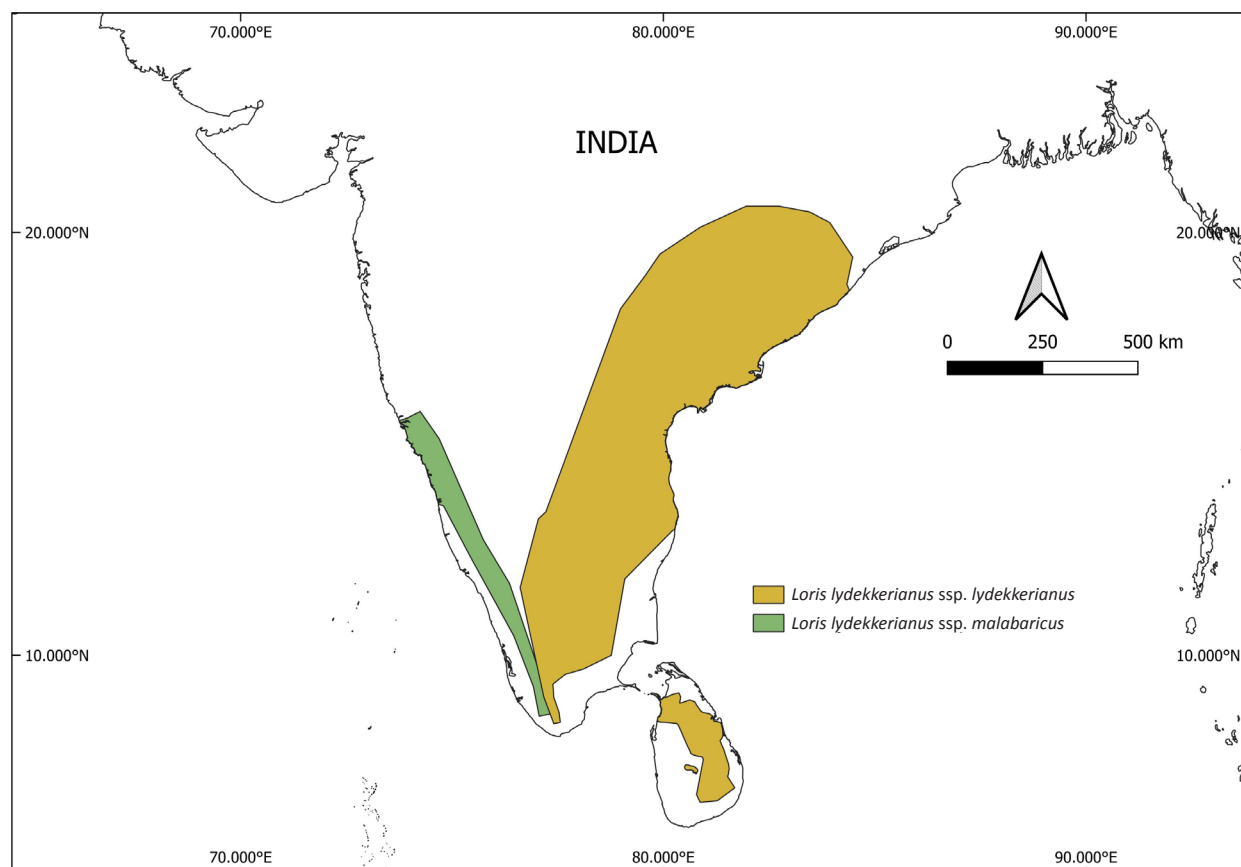


Figure 1. IUCN Red List distribution range of the Grey Slender Loris subspecies in southern India and Sri Lanka.

with our samples we used the NCBI RefSeq mitochondrial sequences from strepsirrhines namely, *Loris lydekkerianus*, *Loris tardigradus*, *Nycticebus coucang*, *Nycticebus bengalensis*, *Galago senegalensis*, and *Lemur catta*. We aligned the 13 protein-coding genes and two non-coding ribosomal RNA genes individually from the assembled mitochondrial genomes and reference sequences using the MUSCLE algorithm in MEGA7 (Kumar et al. 2016) and checked for the presence of any sequencing errors or frameshifts for codon position. We then concatenated all the gene alignments using MEGA7 (Kumar et al. 2016) and identified the optimum nucleotide substitution model for each partition based on the corrected Akaike information criterion (AICc) values using PartitionFinder2 (Lanfear et al. 2017) (Supplementary file 1). We built the maximum likelihood (ML) tree based using IQ-TREE (Minh et al. 2020) with 1000 times bootstrapping. The ML tree was visualized in Evolview v3 (Subramanian et al. 2019).

We utilized BEAST2.5 (Bouckaert et al. 2014) to create a divergence time tree using the same concatenated alignment of 13 coding and two non-coding genes from the complete mitochondrial genomes. We used

the same partitioning scheme and substitution models identified by PartitionFinder2. We then chose two fossil calibration points:

1) We calibrated the crown node of Galagos with 38 mya based on the age of the fossil *Saharagalago misrensis* (PaleoDB collection 67706) (Seiffert et al. 2003). We applied a normal distribution at 40 Mya (SD = 0.04; 95% range: 36–43)

2) We calibrated the crown node of Slow Lorises with 13.82 mya based on the age of the fossil *Nycticebus linglom* (PaleoDB collection 48126) (Harrison 2010). We applied a normal distribution at 14 Mya (SD = 0.05; 95% range: 9–17)

For all the partitions, we created a relaxed lognormal clock and employed a birth-death process using prior distributions. To get to the final tree, we ran for 40 million generation runs, sampling every 2,000th generation using TreeAnnotator (Helfrich et al. 2018) with a 10% burn-in. We verified that all the ESS values were over 200 in Tracer 1.7 (Rambaut et al. 2018) and visualized the tree in FigTree v1.4.4 (Rambaut 2014).

RESULTS

Phylogenetic analyses support the morphological and geographical delineation of Mysore & Malabar Slender Lorises

To investigate the genetic differences between the two subspecies of slender loris in southern India, we first assembled three new circular mitochondrial genomes with an average length of 16,771 bp from two samples of the Mysore Slender Loris *Loris lydekkerianus* ssp. *lydekkerianus* and one sample of Malabar Slender Loris *Loris lydekkerianus* ssp. *malabaricus*. We annotated the mitochondrial genomes along with published reference sequences and obtained the full-length sequences of 13 protein-coding genes and two ribosomal RNA genes. To check the variation in the nucleotide sequence within the *Loris* genus, we estimated the pairwise sequence similarity in the COX1 and CYTB regions spanning 2,682 bp between all six *Loris* samples (Table 1). We observed the highest average sequence variation of 2.82% (S.D. 0.16) between the four sequences of the Grey Slender Loris *Loris lydekkerianus* and the two sequences of the Red Slender Loris *Loris tardigradus* as they belong to two different species within the *Loris* genus. While there was no sequence variation found within the two sequences of Red Slender Loris, there was considerable variation within the four sequences of Grey Slender Loris contributed by the difference between the two subspecies. We found about 2.09% (S.D. 0.0) variation in the COX1 and CYTB sequences of the Mysore and Malabar Slender Lorises.

We then used phylogenetic analyses to understand the evolutionary relationships between the two subspecies. Along with our three samples, we included reference mitochondrial sequences from two species of slender lorises (*L. lydekkerianus*, *L. tardigradus*) and two species of slow lorises (*Nycticebus bengalensis*, *N. coucang*) along with galago and lemur as outgroups

(Figure 2). The phylogenetic tree recapitulates the broad evolutionary relationships of slender lorises with slow lorises and the outgroups. It reveals an interesting pattern within the clade of slender lorises where the Mysore Slender Loris *L.I. ssp. lydekkerianus* clusters with the reference sequence of Grey Slender Loris to form a monophyletic clade and the Malabar Slender Loris *L.I. ssp. malabaricus* forms a separate monophyletic clade with very strong statistical support. We noted that the Malabar Slender Loris appears more closely related to the Red Slender Loris *L. tardigradus*, albeit with a very small branch length (Figure 2). To estimate the divergence time between the two subspecies and other lorises, we constructed a fossil-calibrated Bayesian tree (Figure 3). Our results suggest that the split between the Grey Slender Loris *L. lydekkerianus* and Red Slender Loris *L. tardigradus* occurred approximately 1.087 million years ago (mya). This was immediately followed by diversification of the Mysore Slender Loris *L.I. ssp. lydekkerianus* and Malabar Slender Loris *L.I. ssp. malabaricus* at around 1.049 mya (Posterior probability = 1) (Figure 3).

DISCUSSION

Our results from the phylogenetic analyses based on the mitochondrial sequences show that the Mysore and Malabar Slender Lorises have significant genetic variation (2.09%) in the COX1 and CYTB genes and form distinct monophyletic clades in the phylogenetic tree that diverged a long time ago (1.049 mya), shortly after the divergence of Red Slender Loris from the Grey Slender Loris (1.087 mya). The observed sequence variation and divergence time between the Mysore and the Malabar Slender Lorises are surprisingly high, which is not very common between primate subspecies. Since they have been evolving independently for a

Table 1. Sequence distance matrix of the *Loris* genus based on full-length cytochrome b and cytochrome oxidase 1 genes.

Sample	<i>Loris tardigradus</i> -1	<i>Loris tardigradus</i> -2	<i>Loris lydekkerianus malabaricus</i>	<i>Loris lydekkerianus lydekkerianus</i> -1	<i>Loris lydekkerianus lydekkerianus</i> -2	<i>Loris lydekkerianus</i> -Ref
<i>Loris tardigradus</i> -1	-	0	2.58	2.82	2.95	2.9
<i>Loris tardigradus</i> -2	0	-	2.58	2.82	2.97	2.9
<i>Loris lydekkerianus malabaricus</i>	2.58	2.58	-	2.09	2.09	2.09
<i>Loris lydekkerianus lydekkerianus</i> -1	2.82	2.82	2.09	-	0.16	0.08
<i>Loris lydekkerianus lydekkerianus</i> -2	2.97	2.97	2.09	0.16	-	0.16
<i>Loris lydekkerianus</i> -Ref	2.9	2.9	2.09	0.08	0.16	-

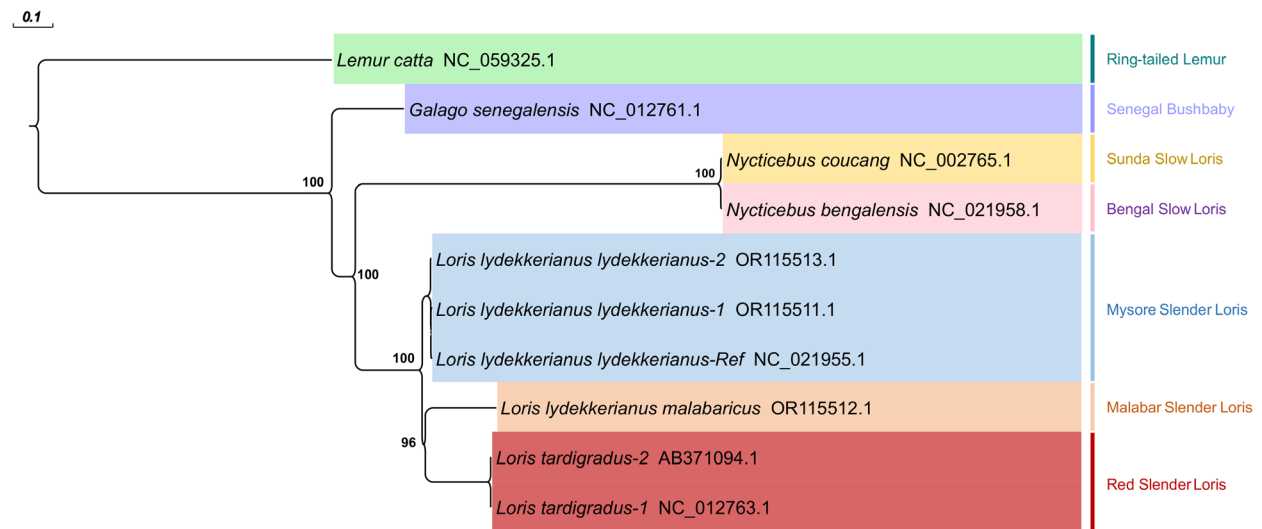


Figure 2. Maximum likelihood tree based on 13 protein-coding and two ribosomal RNA genes from whole mitochondrial genomes. The bootstrap values are denoted at the nodes.

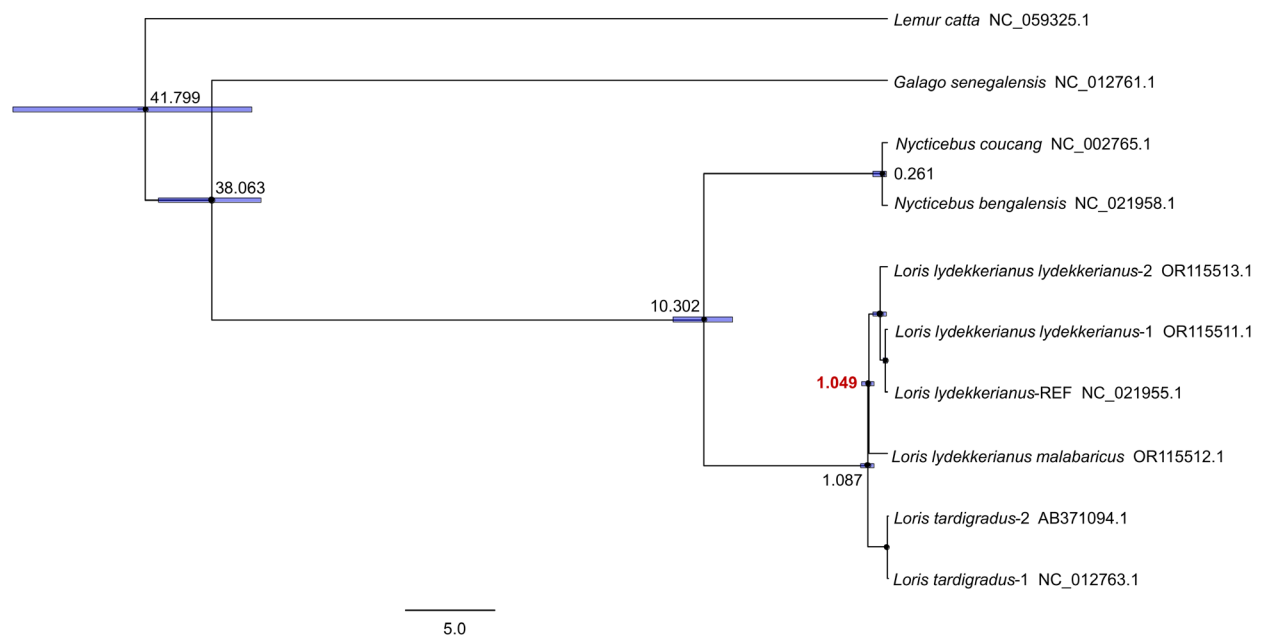


Figure 3. Fossil-calibrated Bayesian inference tree based on 13 protein-coding and two ribosomal RNA genes from whole mitochondrial genomes showing the divergence time estimates at the nodes in Mya. Bars indicate 95% CI.

long period comparable to the divergence time of their closest species (*Loris tardigradus*), the Mysore and Malabar Slender Loris deserve independent recognition. Moreover, they occupy a geographically different landscape and unique habitat, where the Malabar Slender Loris occupies the wet zone of the Western Ghats, while the Mysore Slender Loris occupies the dry habitat of the eastern slope of the Western Ghats, dry forests of the Deccan plateau and Eastern

Ghats (Kumara et al. 2006, 2009; 2013). They are also morphologically distinct, where the Malabar Slender Loris appears reddish in color and almost half the body size of the greyish colored Mysore Slender Loris (Kumara et al. 2006). Considering these significant differences in the morphological, geographical, and genetic factors, we propose to recognize the Mysore Slender Loris *Loris lydekkerianus* ssp. *lydekkerianus* and Malabar Slender Loris *Loris lydekkerianus* ssp. *malabaricus* as two distinct

species, *Loris lydekkerianus* and *Loris malabaricus*, respectively.

The divergence time estimates are supported by a number of molecular markers in the whole mitochondrial genome and is consistent with previous studies on the evolutionary history of this genus (Finstermeier et al. 2013). Several environmental, climatic, and geographical factors might have influenced the divergence of the Mysore and Malabar Slender Lorises about one million years ago. The mid-Pleistocene transition (1.25–0.7 Mya) was a time of dramatic climatic change and glaciation that influenced the environments and biogeography of Earth (Herbert 2023). The glaciation and interglaciation cycles affected the sea level, precipitation, temperature, vegetation, and habitat availability. The environmental conditions in India specifically during the Pleistocene were diverse and dynamic, ranging from deserts, tropical forests to grasslands (Morley & Morley 2022). The variability of monsoon coupled with expansion and contraction of forests due to glacial-interglacial cycles could have influenced availability of resources, fragmentation of habitats, and changes in forest cover promoting genetic differentiation and divergence of the Mysore and Malabar Slender Lorises.

Understanding the genetic structure and variation of species is crucial for the scientific management of threatened species and their eventual recovery. The findings of this study have important implications for the conservation and management of the slender lorises in India. With a clearer understanding of the genetic differences between the Mysore and Malabar Slender Lorises, it will be possible to more accurately identify and classify individual animals, which will in turn facilitate the development of an effective conservation breeding program. Such a program can be particularly beneficial for species like the slender loris that are threatened by habitat loss and fragmentation, and whose populations have been declining in recent years (Kumara et al. 2006, 2016).

The main drawback of this study is the limited sample size which we duly acknowledge. It is to be noted that the construction of whole mitochondrial genomes from WGS data for accurate molecular dating often requires good-quality DNA from animals of known geographic origin which is very difficult to obtain, especially for the Malabar Slender Loris. More samples from the Malabar Slender Loris could better resolve the phylogenetic tree and nuclear markers could also be used to confirm our findings and validate the species delimitation. Furthermore, sampling the individuals from the range edges and the overlapping ranges in the southern ridge of

Western Ghats would provide more statistical power to establish the monophyly and identify any hybridization. It would also be prudent to include samples of the Mysore subspecies from Sri Lanka in future studies to fully comprehend the diversity and understand the evolutionary history of the slender lorises throughout its geographical range. Comprehensive genome sequencing of all the subspecies of slender loris would also help to understand the genomic basis of morphological differences and their adaptations to respective niches.

In conclusion, this study provides the first molecular evidence for the genetic divergence and distinctiveness of the Mysore and Malabar Slender Lorises. The sequence analysis, phylogenetic analyses, and molecular dating suggest that the Mysore and Malabar Slender Lorises are genetically distinct and have been evolving independently for a significant period. The high level of genetic divergence between them highlights the importance of preserving their genetic diversity and underscores the need for more efforts to conserve them in the wild. By considering the significant differences in the morphological, geographical, and genetic factors, we recommend to elevate *L.l. ssp. lydekkerianus* and *L.l. ssp. malabaricus* to the species level. We propose to recognize them as two distinct species *Loris lydekkerianus* and *Loris malabaricus* as each of them represents a unique evolutionary lineage and deserves separate recognition and protection. We advocate for further studies to validate the species delimitation with larger sample sizes and recommend for separate conservation measures and management actions to preserve their unique genetic diversity in the wild and captivity.

Data Availability Statement

The three whole mitochondrial genome sequences generated in this study have been submitted to the NCBI database under the accessions OR115511, OR115512, and OR115513.

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Supplementary file 1. Partitioning scheme and nucleotide substitution model selection output from PartitionFinder2.

Best partitioning scheme

Scheme InL : -64454.10696411133

Scheme AICc : 129409.318896

Number of params : 246

Number of sites : 13594

Number of subsets : 33

Subset	Best Model	# sites	Partition names
1	GTR+I+X	622	NAD1_pos1, NAD4_pos3, ATP6_pos1
2	TRN+I+X	533	NAD1_pos2, ATP6_pos2
3	HKY+X	223	ATP6_pos3
4	HKY+X	132	ATP8_pos1, ATP8_pos2
5	GTR+X	317	ATP8_pos3, COX3_pos3
6	HKY+G+X	368	COB_pos1
7	GTR+I+X	368	COB_pos2
8	TRN+I+X	368	COB_pos3
9	GTR+G+X	496	COX1_pos1
10	HKY+G+X	496	COX1_pos2
11	HKY+G+X	496	COX1_pos3
12	K80	222	COX2_pos1
13	TRN+X	222	COX2_pos2
14	TRN+I+X	424	NAD3_pos1, NAD4_pos2, COX2_pos3
15	JC	251	COX3_pos1
16	HKY+X	251	COX3_pos2
17	HKY+X	310	NAD1_pos3
18	GTR+I+X	340	NAD2_pos1
19	HKY+I+X	340	NAD2_pos2
20	HKY+I+X	339	NAD2_pos3
21	TRN+I+X	111	NAD3_pos2
22	GTR+I+X	201	NAD4_pos1, NAD3_pos3
23	HKY+X	457	NAD4_pos1
24	HKY+X	456	NAD4_pos2
25	HKY+I+X	456	NAD4_pos3
26	HKY+I+X	596	NAD5_pos1
27	GTR+I+X	596	NAD5_pos2
28	HKY+I+X	596	NAD5_pos3
29	GTR+G+X	181	NAD6_pos1
30	HKY+I+X	180	NAD6_pos2
31	GTR+G+X	180	NAD6_pos3
32	GTR+G+X	1454	rns
33	GTR+I+X	1012	rnl

Tamil: மெலிந்த தேவாங்குகள், இந்தியா மற்றும் இலங்கையில் மட்டும் வாழும் இரவில் நடமாடுகிற சிறிய வகை ஈரமூக்கு கொண்ட முதனிகளில் ஒன்றான பேரினமாகும். இந்தப் பேரினம் தற்பொழுது அழிவுநிலைக்கு அச்சுறுத்தப்பட்டுள்ளது.. சாம்பல் நிற மெலிந்த தேவாங்கு (*Loris lydekkerianus*), உருவவியல் மாறுபாடு மற்றும் புவியியல் பரவல் ஆகியவற்றின் அடிப்படையில் பல துணை இனங்களாகப் பிரிக்கப்பட்டுள்ள போதும், இந்தப் பிரிவினை மூலக்கூறு சான்றுகளால் ஆதரிக்கப்படவில்லை. தென்னிந்தியாவில் வாழும் இந்த சாம்பல் நிற மெலிந்த தேவாங்குகளின் இரண்டு துணை இனங்கள்: அதாவது மைதூர் மெலிந்த தேவாங்கு (*Loris lydekkerianus* ssp. *lydekkerianus*) மற்றும் மலபார் மெலிந்த தேவாங்கு (*Loris lydekkerianus* ssp. *malabaricus*), பரிணாம வரலாற்றில் எப்பொழுது பிரிந்தன என்று ஆராய்ந்தோம். தென்னிந்தியாவில் வாழும் அவற்றின் புவியியல் தொகைகளில் இருந்து மாதிரிகள் எடுத்து, அவ்விலங்குகளின் முழு இழைமணி மரபணு தகவல்களை shotgun sequence எனப்படும் தகவல்களில் இருந்து ஒருங்கிணைத்து, பொது தரவுத்தளங்களில் கிடைக்கும் பிற தேவாங்குகளின் மரபணு தகவல்களுடன் ஒப்பிட்டோம். இதில் இருந்து மைதூர் மற்றும் மலபார் மெலிந்த தேவாங்குகளை ஒப்பிடுகையில், அவற்றின் இடையே COX1 மற்றும் CYTB மரபணு பகுதிகள் 2.09 சதவிகிதம் வேறுபடுவதை நாங்கள் கண்டறிந்தோம். மேலும், இழைமணி மரபணுவில் காணப்படும் 13 புரதங்கள் மற்றும் 2 ரைபோசோமல் RNAக்களைக் குறியிடக்கூடிய மரபணு தகவல்களை பகுப்பாய்வு செய்கையில், மைதூர் மற்றும் மலபார் மெலிந்த தேவாங்குகள், பரிணாம வரலாற்றில் சுமார் 10.49 இலட்சம் ஆண்டுகளுக்கு முன்பு பிரிந்தன என விளங்கியது. இது சிவப்பு மெலிந்த தேவாங்கு (*Loris tardigradus*) பிரிந்த சற்று காலத்திற்குப் பின் நிகழ்ந்த நிகழ்வாகும். மரபணு தகவல்களில் உள்ள மாற்றங்கள் மற்றும் பரிணாம வேறுபாடுகளை கருத்தில் கொண்டு, அவற்றுடன் ஏற்கனவே நிறுவப்பட்ட உருவ வேறுபாடுகள் மற்றும் புவியியல் ரீதியாக தனித்துவமான வாழ்விடங்களை சேர்க்கையில், மைதூர் மற்றும் மலபார் மெலிந்த தேவாங்குகளை *Loris lydekkerianus* மற்றும் *Loris malabaricus* என இரண்டு தனித்துவமான இனங்களாக அங்கீகரிக்க நாங்கள் முன்மொழிகிறோம்.



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