DOI: https://doi.org/10.3897/arphapreprints.e96249

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ARPHA Preprints Author-formatted, not peer-reviewed document posted on 17/10/2022 DOI: https://doi.org/10.3897/arphapreprints.e96249

A new species of *Tupaia* (Mammalia, Scandentia, Tupaiidae) from northeastern Vietnam

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Abstract

There are 19 currently recognized species of treeshrews in the genus *Tupaia* (Tupaiidae, Scandentia) with a majority of the taxa found in Southeast Asia. During our surveys in northeastern Vietnam, nine new specimens of *Tupaia* were collected from five different localities, including Lang Son and Ha Giang provinces and Cat Ba Island, Hai Phong City. Our molecular analysis reveals that the new population diverges from its closest congeners by at least 11.2% based on a fragment of the mitochondrial COI gene and 10.1% based on a fragment of the mitochondrial cytochrome *b* (cyt *b*) gene. The distinction of the newly discovered population is also supported by significant differences compared to other species based on morphological analysis. As a result,

a new species, *Tupaia danghuyhuynhi* **sp. nov.**, was described based on morphological and molecular evidence.

Key words: Indochina, morphology, phylogenetic relationships, species complex, treeshrews, *Tupaia danghuyhuynhi* **sp. nov.**

Introduction

Treeshrews of the family Tupaiidae are terrestrial, arboreal, and scansorial small mammals, which can be found throughout much of tropical South and Southeast Asia. The family contains three genera and 22 species, occurring primarily in southeastern and southern Asia. Except for *Tupaia nicobarica*, a species endemic to Nicobar Island in the Indian Ocean, most species are distributed in the mainland Southeast Asia and on islands of the Sunda Shelf with 18 of 19 *Tupaia* and two of *Dendrogale* found in the region (Hawkins 2018). To date, four species of the two genera, namely *Dendrogale murina*, *Tupaia minor*, *T. belangeri*, and *T. glis*, have been recorded in mainland Southeast Asia (Hawkins 2018; Francis 2019). Of all the species in the genus *Tupaia* known from the Indomalayan region, only *T. belangeri* and *D. murina* have been reported from Vietnam (Corbet and Hill 1992; Hawkins 2018; Francis 2019).

Tupaiids form a diverse and complex group with a high number of species and subspecies (Helgen 2005; Hawkins 2018). Broad geographic variations in their pelage and external features result in enormous taxonomic confusions. Although treeshrew studies were sporadic in the past, over the last two decades, research on this group has progressed to a more advanced stage with several studies addressing treeshrew molecular phylogenetics (Schmitz et al. 2000; Roberts et al. 2009, 2011; Francis 2019), behavioral ecology (Emmons 2000), and morphology (Sargis 2000, 2013a). In addition, taxonomic boundaries within species complexes of *Tupaia* has been investigated using different approaches, such as hand skeleton comparison, geometric morphometrics, and craniometrical analysis (Endo et al. 1999; Sargis et al. 2013a, 2013b, 2014a, 2014b, 2017, 2018, 2021; Woodman et al. 2020). More than two decades have passed since the first study on the complete mitochondrial genome of *Tupai belangeri* was published (Schmitz et al. 2000), more recent molecular studies have employed both mitochondrial and nuclear genomes to recover phylogenetic relationships and divergence dates between species in the genus (Olson et al. 2004, 2005; Roberts et al. 2009, 2011). In the analyses, *T. belangeri* is shown to be a sister taxon to *T. glis*. The two species occupy mainland Southeast Asia and are closely related to the narrowly distributed group of *T. chrysogaster* – *T. longipes* (Roberts et al. 2011).

Vietnam is situated in the Indochina Peninsular, Southeast Asia. The country makes up an important part of the Indo – Burma Biodiversity Hotspot and is characterized by numerous endemic and highly threatened species (Mittermeier et al. 2011; Tordoff et al. 2012). The country also harbors globally significant diversity of mammals (Sterling et al. 2006). In addition, many new non-volant small mammals species and subspecies have been discovered in Vietnam in recent years, e.g., *Laonastes aenigmanus* (Jenkins et al. 2005; Nguyen et al. 2012), *Saxatilomys paulinae* (Musser et al. 2005), *Chodsigoa caovansunga* (Lunde et al. 2003) *Tonkinnomys daovantieni* (Musser et al. 2006), *Crocidura zaitsevi* (Jenkins et al. 2007), *Crocidura phuquocensis* (Abramov et al. 2008), *Crocidura phanluongi* (Jenkins et al. 2009), *Crocidura sapaensis* (Jenkins et al. 2013), *Callosciurus honkhoaiensis* (Nguyen et al. 2018), and *Callosciurus finlaysonii honngheensis* (Vu et al. 2021).

During our fieldwork in northeastern Vietnam, we collected a number of specimens assigned to *Tupaia*. However, based on a detailed examination of the specimens, the population is shown to be distinct genetically and morphologically from other existing congeners. In this study, we describe the population as a new species of *Tupaia* on the basis of integrative evidence with descriptions of the external, size, and formula characters and provide some notes on its ecological behavior.

Materials and methods

Sampling. The studies were conducted in several protected areas in northeastern Vietnam, including Cham Chu Nature Reserve (NR) (Tuyen Quang Province), Bac Me NR (Ha Giang Province), Huu Lien NR (Lang Son Province), and Cat Ba National Park (Hai Phong City). (Fig. 1). This region is well known for its unique limestone karst ecosystem, diverse topography, and biodiversity values. This type of habitat is ideal for mammals in general and for small mammals in particular.

Figure 1. Map showing collection sites of *Tupaia danghuyhuynhi* **sp. nov.** in northeastern Vietnam (Source: Yale University Press)

During three years from 2019 to 2021, a total of eight specimens was collected from northeastern Vietnam. We deployed cage traps (15 cm x 15 cm x 25 cm) on ground and in trees following methods approved by the American Society of Mammalogists (Sikes et al. 2016). Collected specimens consisted of five females (field numbers NTS.2020.151, NTS.2021.126, and NTS.2021.127 collected in Cat Ba NP; BM.2019.05.22 and NTS.2019.10.48 collected in Bac Me and Cham Chu NRs) and three males (NTS.2020.255 and NTS.2020.256 of Huu Lien NR; NTS.2020.160 of Cat Ba NP) and we also examined a specimen (ID: Motokawa 553) collected in Tam Dao NP (Vinh Phuc Province) in 2013. All newly collected specimens were deposited in the Department of Vertebrate Zoology, Institute of Ecology and Biological Resources (IEBR), Vietnam Academy of Science and Technology (VAST), Hanoi, Vietnam.

*Molecular data and phylogenetic analyses***.** Six new samples of *Tupaia*, three from Hai Phong, two from Lang Son, and one from Ha Giang, were sequenced. Sequences from other species of *Tupaia* were downloaded from GenBank. We selected *Dendrogale melanura*, *Dendrogale murina*, and *Phodopus sungorus* as outgroups.

We used Le et al. 2006 protocols for DNA extraction, amplification, and sequencing. Three fragments of mitochondrial genes were sequenced for the new samples, including cytochrome b (cyt *b*), cytochrome c oxidase subunit 1 (COI), and 16S ribosomal RNA (16S). Three pairs of primers were used for amplification, i.e., AR–BR for 16S (Palumbi et al. 1991), L14058 – H15298 for cyt *b* (Chen et al. 2011), and BatL5310–R6036R for COI (Robin et al. 2007). After sequences were aligned using Clustal X v2 (Thompson et al. 1997), data were analyzed using Bayesian Inference (BI), as implemented in MrBayes v3.2 (Ronquist et al. 2012) and maximum likelihood (ML) analyses as implemented in IQ-TREE v1.6.8 (Nguyen et al. 2015). Settings for the BI analysis followed Le et al. (2006), except that the number of generations in the Bayesian analysis was increased to 1×10^7. The optimal models of nucleotide evolution for BI and ML were selected by jModelTest v2.1.4 (Darriba et al. 2012). Nodal support was evaluated by posterior probabilities (PP) in MrBayes and ultrafast bootstrap (UFB) with 10,000 replications in IQ-TREE. We regarded PP and UFB values of ≥ 95% as strong support and values of < 95% as weak support (Ronquist et al. 2012; Minh et al. 2013). We ran three separate analyses with cyt *b*, COI, and combined data consisting of four genes: Cyt *b*, COI, 12S, and 16S to determine the phylogenetic relationship of the new population with regard to other species of the genus. The optimal models for nucleotide evolution were set to TVM+I+G, TVM +G, and GTR+G as selected by jModelTest, for cyt *b*, COI, and the combined data, respectively. In BI, the cutoff point for burn - in function was set to 10, 7, and 10 as - ln*L* scores reached stationarity after 10,000, 7,000, and 10,000 generations in both runs for cyt *b*, COI, and combined data analyses, respectively. The uncorrected pairwise distances between operational taxonomic units were calculated in PAUP*4.0b10 for cyt *b* and COI datasets (Swofford, 2001).

Morphological analyses. To determine specimen age, we used the method based on tooth eruption described in published literature, and sexual maturation such as pregnancy and lactation of females, and development of sexual organs during the breeding season of males (Slaughter et al. 1974; Shigehara, 1980; Woodman et al. 2020). However, we found a difference between juvenile and adult specimens based on orbital growth. Out of nine specimens, two with voucher numbers NTS 2020.151 and NTS.2020.160 were juvenile, two, NTS 2021.126 and NTS 2021.127, were adult due to nursing and pregnancy and the remaining five were identified as adult based on teeth structure and complete development of orbit.

Measurements in millimeters (mm) were taken by digital caliper Mitutoyo model NTD12 – 15PMX, Mitutoyo Corp., Kawasaki, Japan to the nearest 0.01 mm (Endo et al. 1999, 2000a, b, 2017, 2021; Gao et al. 2017 and Wible 2011). External measurements consisted of Head and body length (HB), tail length (TL), hind foot length (HF), ear length (E) in millimeters (mm) and body mass (BW) in grams (g).

Skull characters: In total 23 skull characters were measured, including: Profile length (PL), Condylobosal length (CL), Short lateral facial length (SL), Length if incisive foramen (LIF), Length of rostrum (LR), Greatest breadth of upper first incisor I1 (GBFI1), Minimum distance of upper first incisor I1 (MLFI1), Zygomatic width (ZW), Least breadth between the orbits (LBO), Greatest neurocranium (GNB), Median palatal length (MPL), Length from Basion to Staphylion (LBS), Greatest palatal breadth (GPB), Dental length (DL), Length of auditory bulla (LAB), Greatest mastoid breadth (GMB), Minimum distance of auditory bulla (MLA), Height from Akrokranion to Basion (HAB), Length from the condyle (LC), Length of angular process (LA), Length from the Infradentale to aboral of the alveolus (LIA), Height of the vertical ramus (HR), Height of the mandible at M1(HM) (Fig. 2).

Figure 2. Skull measurements in the genus *Tupaia*.

Results

Table 3. Molecular sequences used in this study

Phylogenetic analyses. The cyt *b* matrix consisted of 1171 aligned characters with 29 sequences of 28 ingroup and one outgroup taxa (Table 3). The COI matrix included 650 aligned characters with 41 sequences of 28 ingroup and one outgroup taxa. The final four gene matrix contained 3319 aligned characters with 52 sequences of 48 ingroup and four outgroup taxa. The new population was either placed as a sister taxon to purported *Tupaia belangeri* as shown in the analyses using cyt *b* and COI with high statistical nodal values from at least one analysis (Fig. 3A and 3B), or to *T. longipes* + *T. chrysogaster* as determined by the phylogenetic estimation using the combined data with low support (Supplementary data). Genetically, the new population is significantly divergent from other congeners by at least 11.2% based on a fragment of the COI gene and 10.1% based on a fragment of the cyt *b* gene (uncorrected *p* – distance) (Table 4, 5).

Figure 3 (A, B). Maximum likehood phylogenetic trees based on A – COI gene, B – cyt *b* gene. Numbers above branches are Bayesian posterior probabilities and ML ultrafast bootstrap, respectively.

Table 4. Percentages of uncorrected pairwise distance between the new population and closely related species based on 650 aligned characters of a COI fragment

Table 5. Percentages of uncorrected pairwise distance between the new population and closely related species based on 1171 aligned characters of a cyt *b* fragment

In all analyses, the population from northeastern Vietnam forms a monophyletic lineage with perfect nodal support values from BI and ML analyses (Fig. 3A, B, and Supplementary data). Based on the molecular evidence and morphological distinction (see below), we recognize the population from northeastern Vietnam as a new species of *Tupaia*, which is formally described below.

Taxonomic account

***Tupaia danghuyhuynhi* sp. nov.**

Suggested valid name: Dong Bac's treeshrews and Vietnamese name: Đồi đông bắc

Photographs and measurements of the *Tupaia danghuyhuynhi* are shown in Fig. 4, and Table 1 respectively.

Holotype. IEBR – M – 8098 (field number NTS.2021.126). Dried skin, skull extracted and tissue samples of an adult female collected by Son Truong Nguyen and Tu Ngoc Ly in May 2020 in Cat Ba NP. The holotype specimen stored at Department of Vertebrate Zoology, IEBR, VAST, Ha Noi, Vietnam.

Holotype measurements. External measurement (in mm) of the holotype: HB 182, TL 145, HF 41.05, E 10.92; Wt 130 g.

Cranial measurement (in mm) of the holotype: PL 48.28, CL 41.95, SL 19.70, LIF 4.34, LR 15.80, GBFI1 2.69, MLFI1 1.54, ZW 23.97, LBO 13.95, GNB 19.47, MPL 25.33, LBS 16.82, GPB 14.83, DL 25.03, LAB 8.62, GMB 17.16, MLA 3.32, HAB 5.65. Mandible measurements (in mm): LC 32.30, LA 31.59, LIA 27.03, HR 12.49, HM 3.77.

Paratypes. Dried skin, cleaned skull and tissue sample of 03 males IEBR – M – 5047 (field number: Motokawa 553); IEBR – M – 7977 (field number: NTS.2020.255); and IEBR – M – 7978 (field number: NTS.2020.256) and 03 females IEBR – M – 8099 (field number: NTS.2021.127); IEBR – M – 7624 (field number: BM.2019.05.22); IEBR – M – 7737 (field number: NTS.2019.10.48) were deposited at the Department of Vertebrate Zoology, The IEBR, Hanoi, Vietnam.

Etymology. The name "danghuyhuynhi" of this treeshrew is used in recognition of Prof. Dr. Dang Huy Huynh's contributions to biodiversity research and conservation in Vietnam.

Type locality. Cat Ba NP, Hai Phong City, northeast of Vietnam (Fig. 1).

Dianogsis. *Tupaia danghuyhuynhi* can be distinguished from other members of the genus *Tupaia* by having an overall smaller skull than those of *T. belangeri belangeri*, *T. b. chinensis*, and others *Tupaia* found in Southeast Asia (Table 1). Its high dome-shaped skull also differs from those with lower braincases of other *Tupaia* species. Molars of this species are quite small, creating large tooth gaps. Esspecially, the gap of upper incisor I1 is relatively wider. Its external characters similar to those of *T. belangeri* but the average body size is significantly smaller.

Description of holotype. *External characters*: The specimen from Cat Ba Island has the featured head of *Tupaia* with long, pointed muzzle and no hairs. Without face marking around eyes. Ears were non-hair with burlywood coloration (or darker) on both sides. Dorsal pelage was light brown and the hair showed agouti: light gray at the base, darker in the middle, and golden brown at the top. This structure was simpler with the young hairs, consisting of only 2 bands: silver, gray at the base and darkening at the top. This coat tends to turn daker orange in older individuals. Ventral was wheat color without agouti: its hair sometime mixed with several black hairs, almost appeared in bolder region between under part and upper part. The abdominal skin was usually thin with a dark yellow layer of fat, creating a more golden feel for the belly hair in some individuals who are pregnant or nursing. The foot was skinny with rather long hindfoot and similar coloration to the dorsum and ventrum in both sides. The tail was thin with light brown and lacked hairs in the under part. In the upper part, its hair had agouti consisting of three light brown bands and three dark bands, light band at base and ended by short dark band, the light band near the tip browner. This species belongs to the *Tupaia belangeri* group - sensu lato Lyon, 1913 with the pairs of mammae. The head and body length, tail length, hind foot length, ear length, and body weight were 182 – 210 mm, 145 – 168 mm, 10.92 – 15.18 mm, 39.73 – 46.85 mm, 130 – 200 g, respectively (Table 1). Reproductive endocrinology of *T. danghhuyhuynhi* was similar to that of *T. belangeri* with a penis without bone.

Skull characters: There was almost no sexual dimorphism between male and female individuals. In dorsum view: the skull was small with a relatively slender, short, and thin rostrum. The nasal sutures were almost fused and difficult to determine where is beginning or end point of the nasal bone. The infraorbital foramen quite small. The ridges less developed and converged to the low weak sagittal crest in a V-shape, the interparietal was a low and blunt shape. In ventral view, incisive foramen relatively large compared to the overall size of the skull with a high rate of LIF/CL. The dental formula of this species identical to those of the Tupaiidae as described by Lyon, 1913: incisors $\frac{2}{3}$, canines $\frac{1}{1}$, premolars $\frac{3}{3}$, molars $\frac{3}{3}$ (Fig. 5, 6). However, the dental structure of *Tupaia danghuyhuynhi* was slender and sharp, making the gap between upper incisor I1 wider than that in *T. belangeri* (anterior view in Fig 5). The entotympanic auditory bullas quite high and

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thick, making the distance between these two auditory bullae relatively close. In left lateral view: *T. danghuyhuynhi* had a high brain case with frontal highly convex. This species had a relatively narrow zygomatic with an orifice guttate. The zygomaticofacial foramen in medium size and had a teardrop shape that gradually shrinks towards the snout. In this species, the location of the connection between postorbital process of frontal and frontal process of jugal is also an important character in determining the maturity. Due to the transformation from cartilaginous bone to full-fledged bone, the more mature individuals are, the more complete this character is. In adult individuals, this skeletal system of *T. danghuyhuynhi* was relatively thin and weak. In comparison skull measurements, the result shows *T. danghuyhuynhi* significantly smaller than *T. belangeri* (Table 1).

Figure 5. Skull holotype of *Tupaia danghuyhuynhi* collected in Cat Ba NP

Figure 6. The formular of *Tupaia danghuyhuynhi* collected in Cat Ba NP

Distribution. *Tupaia danghuyhuynhi* presently known only from northeastern Vietnam (Fig. 1).

Comparison. We compared the pelage color of *Tupaia danghuyhuynhi* with those of 19 *Tupaia* species (*T. glis* Diard, 1820; *T. belangeri* Wagner, 1841*; T. minor* Gunther, 1876; *T. nicobarica* Zelebor, 1869; *T. ferruginea* Raffles, 1821; *T. chrysogater* G. S. Miller, 1903*; T. discolor* Lyon, 1906; *T. javanica* Horsfield, 1822*; T. hypochrysa* Thomas, 1895*; T. tana* Raffles, 1821; *T. longipes* Thomas, 1893; *T. gracilis* Thomas, 1893; *T. montana* Thomas, 1892; *T. dorsalis* Schlegel, 1857; *T. picta* Thomas, 1892; *T. salatana* Lyon, 1913; *T. splendidula* Gray, 1865; *T. everetti* Thomas, 1892; *T. palawanensis* Thomas, 1894) currently recorded in the genus *Tupaia* (Hawkins 2018). We also synthesized and compared *T. danghuyhuynhi* with two subspecies *T. belangeri belangeri* Wagner, 1841 (Distributed in South of Myanmar) and *T. belangeri chinensis* Anderson, 1879 (Distributed in China, Thailand and Vietnam) (Table 2). The comparative analysis shows that *T. danghuyhuynhi* is distinct from any other *Tupaia* species known to science. The fur morphology was similar to that of the subspecies *Tupaia belangeri chinensis*, but *T. danghuyhuynhi* had a quite smaller body. In addition, *T. danghuyhuynhi* even though the new population is sympatric with *T. b. belangeri*, molecular results revealed a significant genetic distance between the two taxa (Table 4 and 5).

Discussion. Recent studies have recorded *Tupaia belangeri belangeri* in Vietnam (Hawkins 2018; Francis 2019). However, Endo et al. (2021) through a multivariate analysis suggested the treeshrews from southern Vietnam exhibit distinct morphological characteristics compared to other populations from Thailand, Laos, and Malaysia. Based on the skull morphology, the authors confirm that populations from southern Vietnam and southern and western Thailand in the *Tupaia glis-belangeri* complex differs substantially. However, factors driving the morphological differentiations have not been identified. In this study, molecular and morphological evidence clearly demonstrates that the population from northeastern Vietnam constitutes a new species. The previous hypothesis regarding geographical barriers (Oshida et al. 2001, 2011, 2013, 2016; Nguyen et al. 2018, Bui et al. 2020; Ly et al. 2021) also being considered in this study. We attempted to gather specimens of this species from northwestern of Vietnam by conducting surveys in Son La, Dien Bien, and Hoa Binh provinces. However, to date we have not been able to obtain any specimens of this species.

Compared with other groups in the mainland, the new species is closely related to the *T. belangeri* - *T. glis* group. Further studies on the distribution of the new species in Indochina region will shed light on this issue. Addition of data on the *T. belangeri* - *T. glis* and *T. chrysogaster* - *T. longipes* groups in the regions is crucial to clarify issues related to taxonomy, phylogeny, and biogeography of the genus.

Contrary to Bergman's law, this species demonstrates that, despite occurring in a region with supposedly colder climate than areas where other *Tupaia* species are distributed, this species has a smaller body size compared to other members of *Tupaia* (Sargis et al. 2018).

Ecological notes. *The phenomenon of shedding hair*. This phenomenon usually occurs at a specific point in a wild animal's life cycle, such as seasonal pelage change before or after breeding and molting in reptiles. The timing of this change varies between species (John 1970). Shedding hair was recorded in one specimen collected from Cat Ba NP (Female Holotype: IEBR – M – 8098 (NTS.2021.126) in May 2021. This specimen was just going through a breeding period. The replacement of dorsal hairs is a manifestation of this changing process. Old hairs were replaced by young, short, soft, pale black hairs.

Breeding. According to Collins et al. 1982, the reproduction of *Tupaia* species primarily takes place in the winter. Local environmental factors appear to regulate reproductive function so that the greatest number of births occurs during the dry season, i.e., from November to the following February, when the seminiferous tubules are spermatogenetically active. According to Lyon 1913, the number of embryos is dependent on the mammae common of that species. We suggest that the trapped pregnant individual of *T. danghuyhuynhi* has 3 + 3 mammae with only three of offspring produced.

Diet. Ecological research on members of *Tupaia* has provided detailed information on their diets and feeding behaviors (Cantor 1846; Lyon 1913; Harrison 1954; Davis 1962; D'Souza 1972; Langham 1982). The species are omnivores, feeding on both fruit and insects. The baits we used to trap this species consisted of cassava, potato, banana, pineapple and sometimes replaced with dried fish. Traps were set primarily in secondary limestone forests, a common type of forest habitat in northern Vietnam.

Activity patterns. This species has a relatively similar behavior pattern to tree squirrels, as they are usually active in both evening and early morning. They are active throughout the day, promptly leaving nests early in the morning at daylight and returning to a sleep site at sunset.

Acknowledgements

This research was generously funded by the NEF Bio-ecological Nature Conservation Project in Mountainous Region of Northern Vietnam. Additional funding was provided by the Program of Developing Basic Sciences in Chemistry, Life Sciences, Earth Sciences and Marine Sciences, Vietnam Academy of Science and Technology (KHCBSS.02/20–22). We are grateful to the director and Department of Vertebrate Zoology from IEBR (VAST) and Cham Chu NR (Tuyen Quang Province), Bac Me NR (Ha Giang Province), Huu Lien NR (Lang Son Province), and Cat Ba National Park (Hai Phong City) from Vietnam for their support for our field survey and specimens. Thanks to Yale University Press for providing access to the map.

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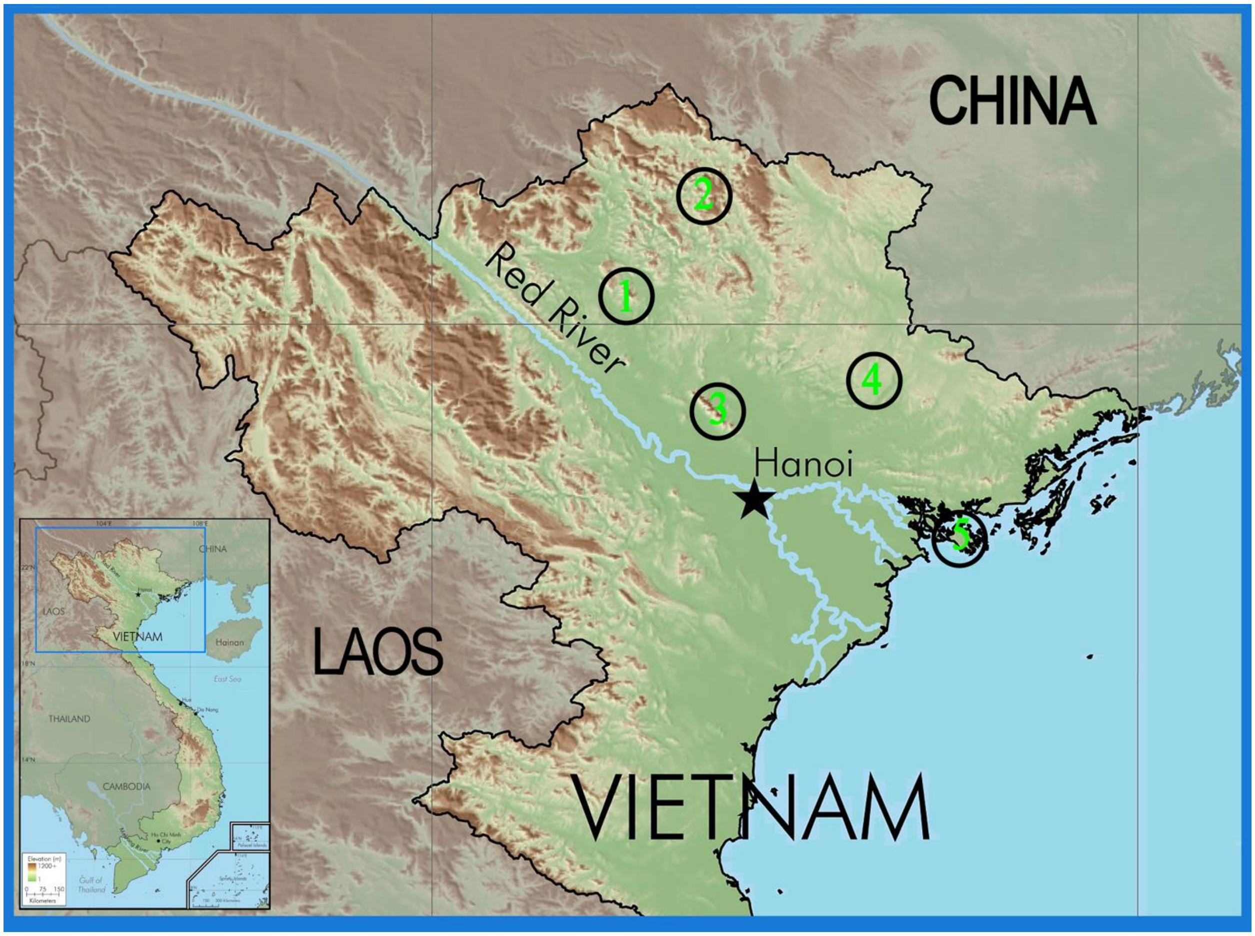

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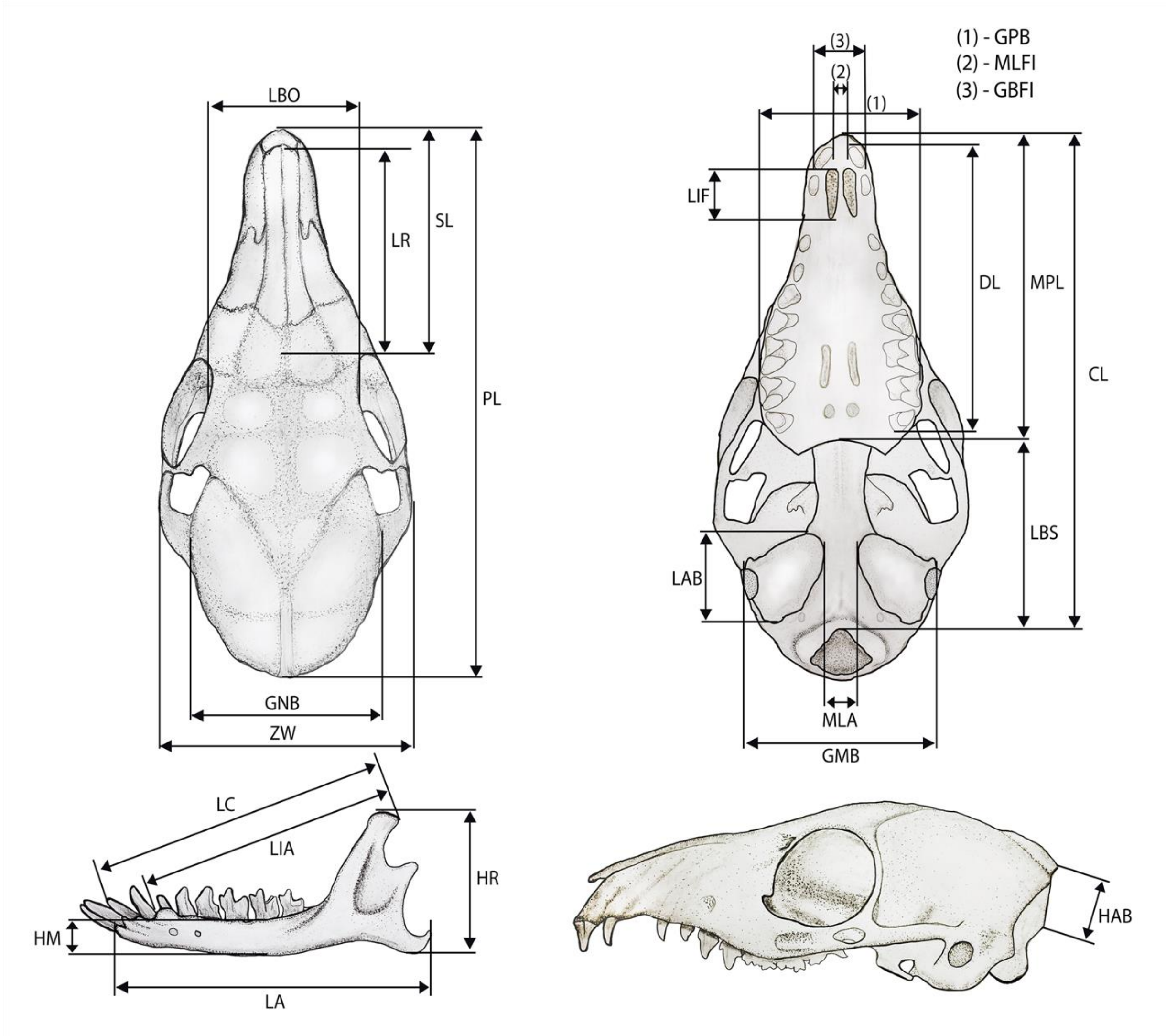


Figure 3A. Maximum likehood phylogenetic trees derived from COI gene

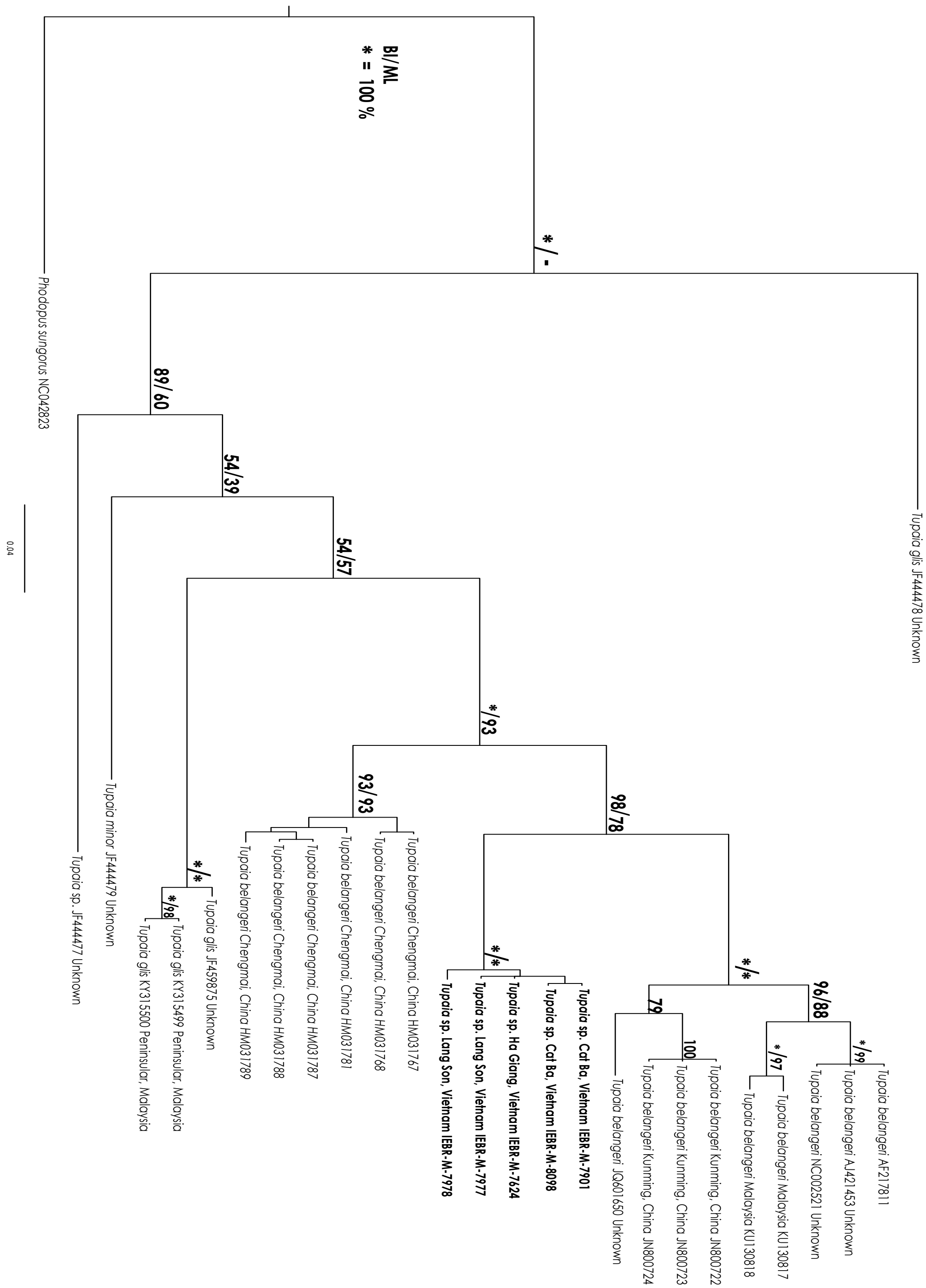
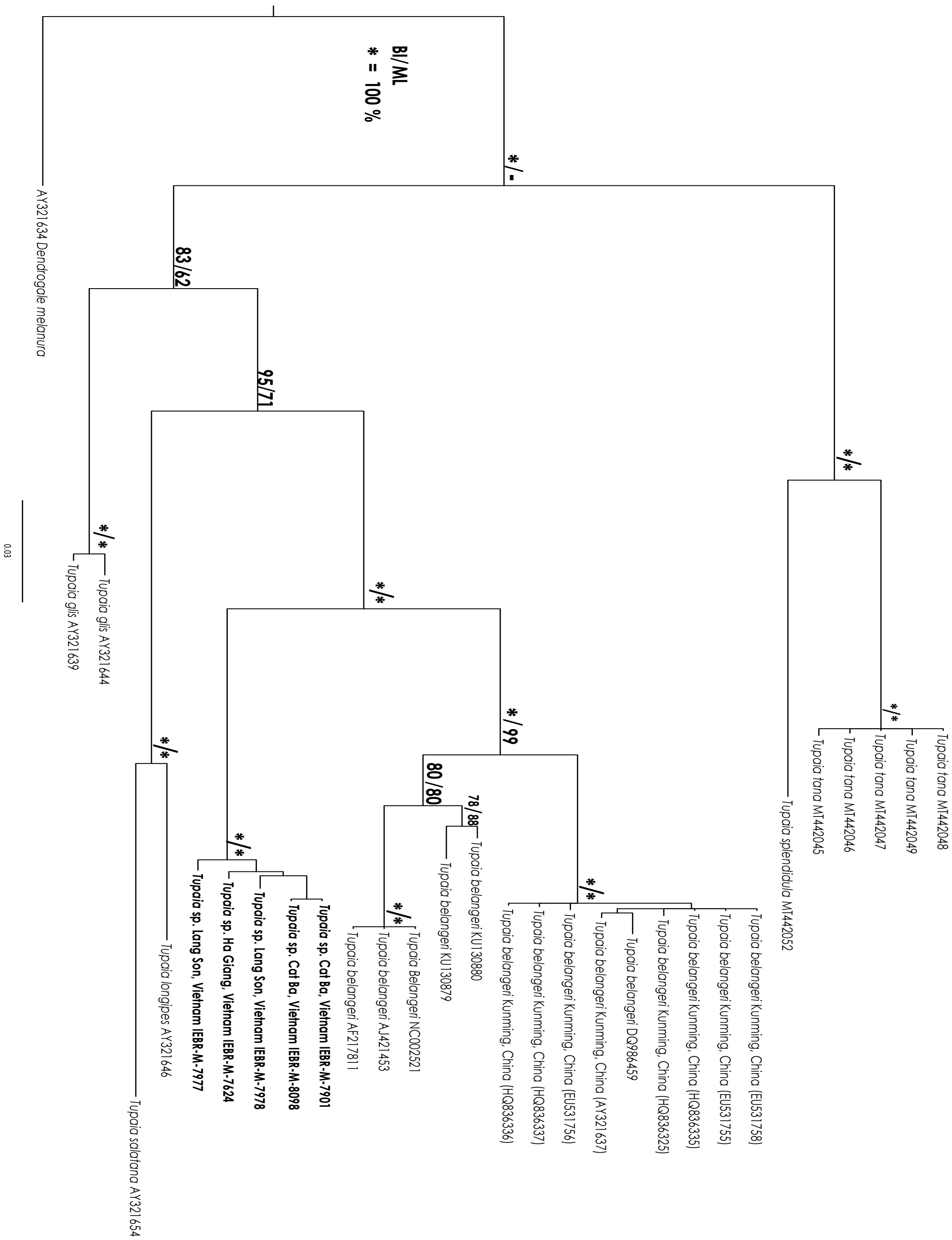


Figure 3B. Maximum likehood phylogenetic trees derived from Cyt b gene



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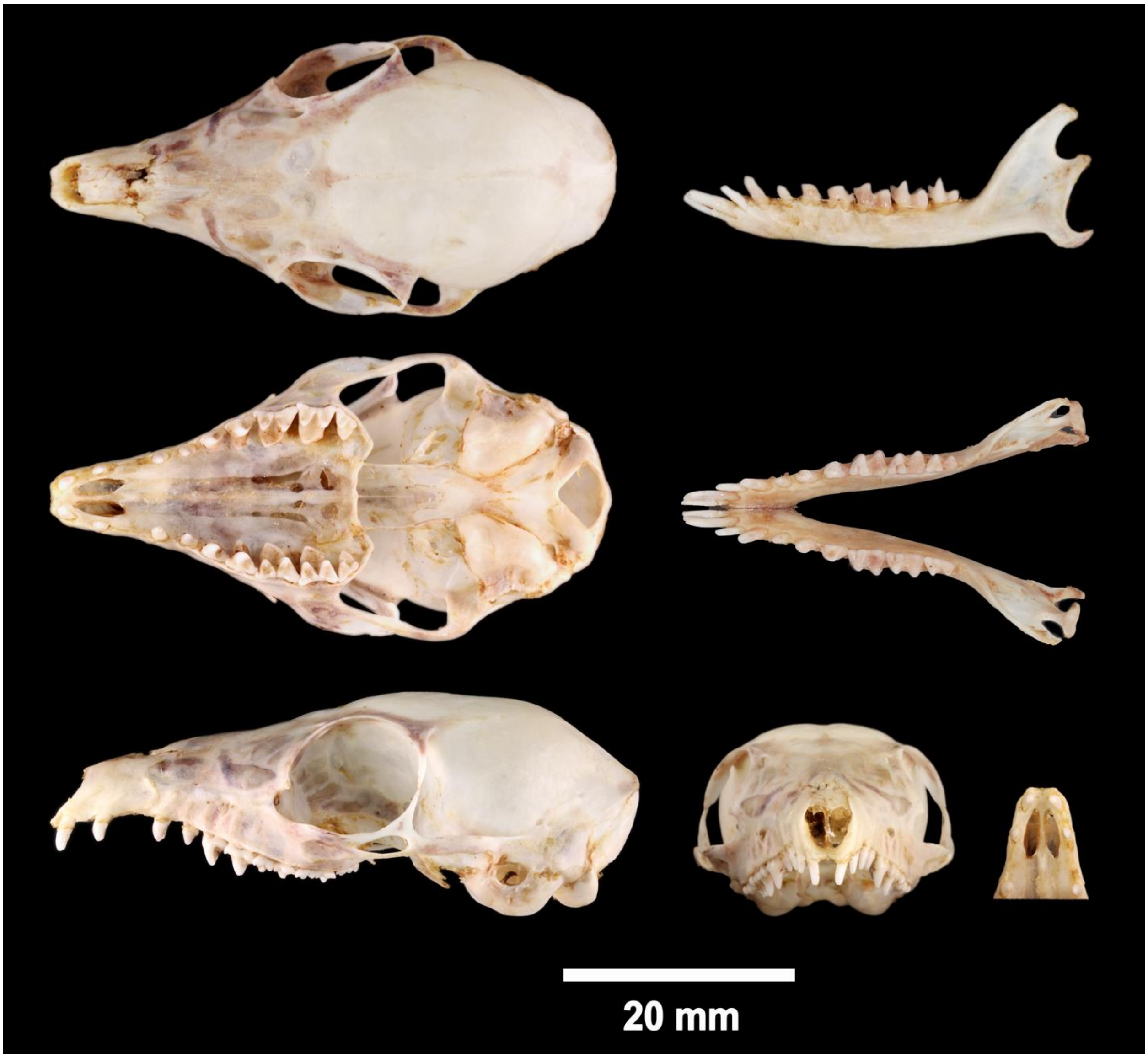

565 **Figure 6.** The fomular of *Tupaia danghuyhuynhi* collected in Cat Ba NP

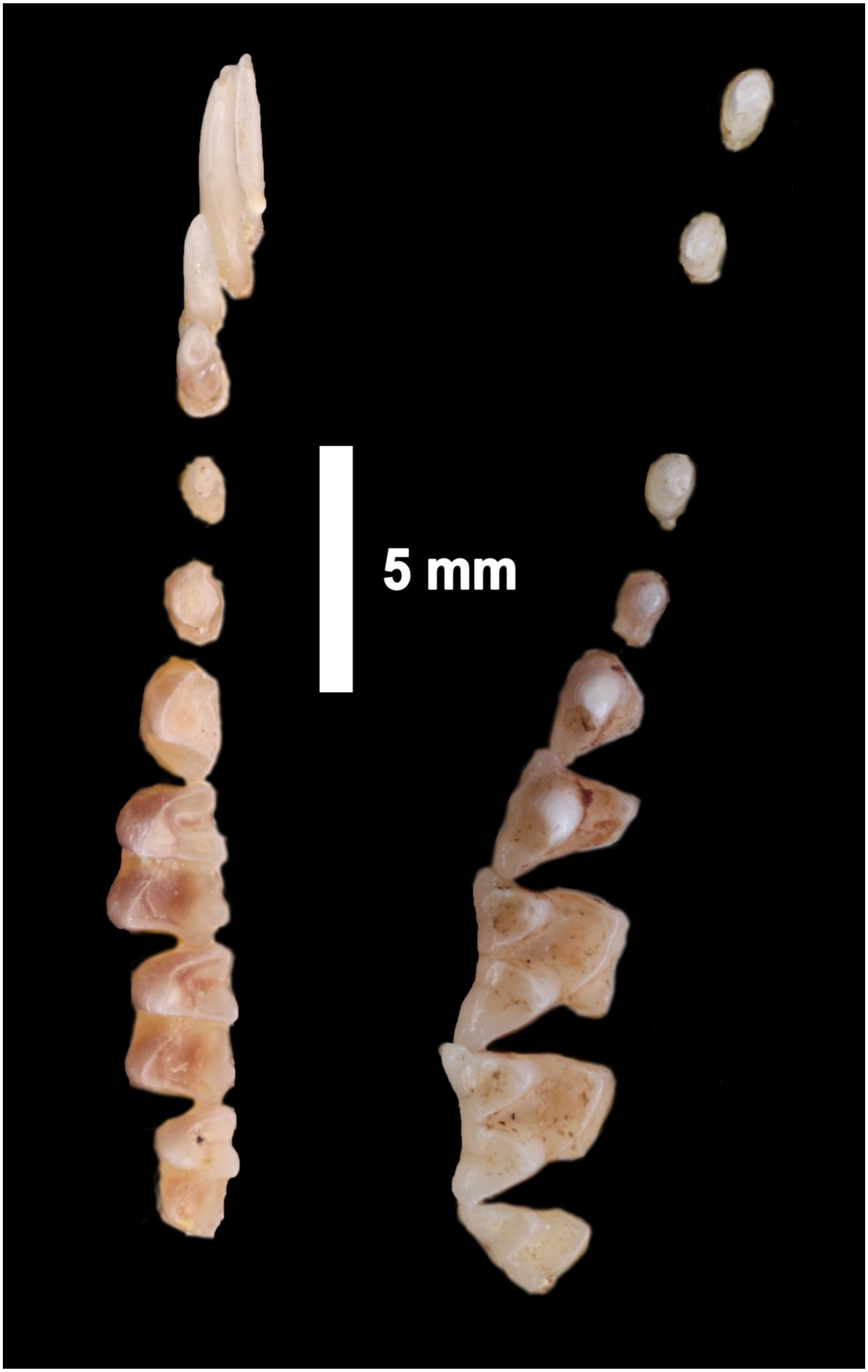

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Table 1. Comparision of external and skull measurements of *T. danghuyhuynhi* with *T. belangeri* (Examine data from Endo et al., 2021)

Characters	***Tupaia danghuyhuynhi***					**Male - *Tupaia belangeri***			**Female - *Tupaia belangeri***		
	n	**Mean**	**SD**	**Min**	**Max**	**n**	**Mean**	**SD**	**n**	**Mean**	**SD**
External											
HB	5	191,20	11,63	182,00	210,00	160 - 230					
TL	5	156,60	8,65	145,00	168,00	150 - 200					
E	5	12,90	1,70	10,92	15,18	15 - 20					
HF	5	43,73	3,14	39,73	46,85	38 - 45					
Wt	5	166,00	27,02	130,00	200,00	160 - 200					
Skulls						*Following: Wilson 2017*					
PL	7	45,39	1,81	48,28	52,83	22	52,57	1,07	38	51.81	1.14
CL	7	39,39	1,47	41,95	46,15	22	45,59	1,06	38	44.98	1.04
SL	7	19,48	1,33	19,70	23,16	22	23,02	0,96	38	22.49	0.73
LIF	7	4,70	0,25	4,13	4,77	22	-	-	38	-	-
LR	7	16,53	1,28	15,80	19,19	22	-	-	38	-	-
GBFI	7	3,98	0,63	2,69	4,22	22	-	-	38	-	-
MLF1	7	2,59	0,40	1,54	2,64	22	-	-	38	-	-
ZW	7	22,83	0,88	23,97	26,56	22	26,34	0,87	38	25.34	0.89
LBO	7	13,17	0,46	13,61	14,97	22	15,85	0,67	38	14.38	0.54
GNB	7	18,17	0,23	19,47	20,14	22	19,67	0,30	38	19.70	0.45
MPL	7	24,12	0,92	25,33	27,71	22	28,18	0,81	38	27.32	0.72
LBS	7	16,39	0,66	16,82	18,48	22	17,72	0,54	38	17.54	0.54
GPB	7	15,01	0,84	14,83	17,15	22	16,39	0,53	38	16.38	0.50
DL	7	23,45	0,70	24,85	26,91	22	27,64	0,62	38	27.74	0.79
LAB	7	9,14	0,54	8,62	10,18	22	-	-	38	-	-
GMB	7	16,66	0,51	17,16	18,60	22	21,01	0,58	38	20.74	0.47
MLA	7	3,83	0,38	2,83	3,94	22	-	-	38	-	-
HAB	7	6,45	0,55	5,64	7,03	22	12,51	0,42	38	12.22	0.35
LC	7	30,35	1,00	32,30	34,61	22	36,02	1,03	38	35.10	0.86
LA	7	30,68	1,61	31,59	35,83	22	36,14	1,12	38	35.22	0.89
LIA	7	25,83	0,94	27,03	29,33	22	22,61	0,68	38	22.23	0.64
HR	7	12,54	0,64	12,49	14,51	22	14,33	0,84	38	13.81	0.52
HM	7	4,42	0,33	3,52	4,45	22	3,91	0,39	38	3.74	0.25
						Following: Endo et al., 2021					

573 **Table 2.** Comparision pelage characters in the genus *Tupaia*

Genus	Species	Recorded region	Pelage characters of distinct with *Tupaia danghuyhuynhi*	Sources
Tupaia	*danghuyhuynhi*	Northeast Vietnam	Quite small body, agouti brown dorsum (Light and dark banding on each hair), wheat ventral	
	glis	Malay Peninsular and some Islands around	Agouti brown dorsum (Light and dark banding on each hair), reddish tail	Diard, 1820
	belangeri belangeri	South Myanmar	Agouti brown dorsum (Light and dark banding on each hair), buff venter	Wagner, 1841
	belangeri chinensis	China, Thailand and Vietnam	Agouti brown dorsum (Light and dark banding on each hair), buff venter	Anderson, 1879
	minor	Wide distributed in Sumatra and Borneo and Malay Peninsula	Large body, almost invariably light brown, some subspecies having darker colored in tail	Gunther, 1876
	nicobarica	Nicobar Island	Anterior one-half lighter brown agouti and posterior one - half nearly solid black. Fur is longer than many other Tupaia sp. Tail is longer also and fluffy	Zelebor, 1869
	ferruginea	Sumatra and Tanahbala in Batu Island	Relatively similar to *T. glis* but tail shorter and underpart gray or tan. Fur slight gray tint, with reddish wash along midsection.	Raffles, 1821
	chrysogater	Sipora, Pagai and Mentawai islands	Dorsum is uniform brown, with tinges of red and venter tan hue. Diagnostic is light fur markking on shoulder.	G. S. Miller, 1903
	discolor	Banka island, belong to SE of Sumatra	Medium size, Anterior one-half reddish and posterior one - half very gray. Tail fur is wider at base and shortens towards tip.	Lyon, 1906
	javanica	West Sumatra, Nias Island, Java, and Bali.	Slender, uniform agouti-brown pelage, tail fur thick, venter is tan and rostrum is short.	Horsfield, 1822
	hypochrysa	West Java	Body large and long tail. Dorsum is brown - agouti. Under part are tan or ange.	Thomas, 1895
	tana	Wide distributed in Sumatra and Borneo	Large body and very long rostrum. Has there dark line run across anterior part of dorsum.	Raffles, 1821
	longipes	North Borneo lowlands to Rayan and Kayan rivers	Medium body with relatively long hindfeet, dorsum is brown agouti, venter is lighter ivory-tan.	Thomas, 1893
	gracilis	Borneo, except center highland and Southest	Dorsum is gray to brown agouti, venter pale white to ivory. Relatively similar to *T. minnor*	Thomas, 1893
	montana	Central highland of Borneo	Medium body with plush brown fur and faint agouti banding. Venter is tan to gray. Short tail and sometime occurred marking on shoulder.	Thomas, 1892
	dorsalis	Endemic in West, Center and East Borneo	Medium body with dark brown to black striped from nape to neck to base of tail.	Schlegel, 1857
	picta	Endemic in Borneo	Relatively similar to *T. dorsalis* in external morphology but longer and leaner.	Thomas, 1892

	salatana	Endemic in Borneo, South of Rajang and Kayan rivers.	Relatively similar to *T. longipes* but the fur more reddish and shoulder marking appered more red	Lyon, 1913
	splendidula	Almost in Borneo and some Islands around	Pelage variation exists among subspecies. Shoulder markings are present and most subspecies have variable colored faces.	Gray, 1865
	everetti	Endemic in Mindanao Island	Uniformly brownish, venter is orange to red. Exists lighter marking on shoulder.	Thomas, 1892

576 **Table 3.** DNA samples list of the genus *Tupaia*

Table 3. GenBank accession numbers and associated voucer/laboratory numbers of ingroup taxa used in this study

Species name	GenBank Number cyt b	GenBank Number COI	GenBank Number 12S	GenBank Number 16S	Voucher/Lab number	Reference	Locality
Tupaia glis	-	JF444478	-	-	-	-	-
Tupaia glis	-	JF459875	-	-	ROM:113061	-	-
Tupaia glis	-	KY315499	-	-	MZF00986	-	-
Tupaia glis	-	KY315500	-	-	MZF00894	-	-
Tupaia glis	AY321644	-	-	-	Tglis5071	-	-
Tupaia glis	AY321639	-	-	-	Tglis4995	-	-
Tupaia glis	-	-	AY862174	JF795307	MVZ 192180	Roberts et al. 2011	Sumatera Utara (Sumatra), Indonesia
Tupaia glis	-	-	AY862175	JF795308	MVZ 192184	Roberts et al. 2011	Aceh (Sumatra), Indonesia
Tupaia belangeri	NC002521	NC002521	NC002521	NC002521	NC002521	Schmitz et. 2000	-
Tupaia belangeri	AF217811	AF217811	AF217811	AF217811	AJ421453	Schmitz et. 2000	-
Tupaia belangeri	AJ421453	AJ421453	AJ421453	AJ421453	AJ421453	Arnason et al. 2002	-
Tupaia belangeri	JN800722	JN800722	JN800722	JN800722	H1	Xu et.al. 2012	Kunming, China
Tupaia belangeri	JN800723	JN800723	JN800723	JN800723	H1-HD	Xu et.al. 2012	Kunming, China
Tupaia belangeri	JN800724	JN800724	JN800724	JN800724	H5	Xu et.al. 2012	Kunming, China
Tupaia belangeri		JQ601650			-	-	-
Tupaia belangeri	-	HM031767	-	-	-	Lu et.al. 2012	Chengmai, China
Tupaia belangeri	-	HM031768	-	-	-	Lu et.al. 2012	Chengmai, China
Tupaia belangeri	-	HM031781	-	-	-	Lu et.al. 2012	Chengmai, China
Tupaia belangeri	-	HM031787	-	-	-	Lu et.al. 2012	Chengmai, China
Tupaia belangeri	-	HM031788	-	-	-	Lu et.al. 2012	Chengmai, China
Tupaia belangeri	-	HM031789	-	-	-	Lu et.al. 2012	Chengmai, China
Tupaia belangeri	EU531755	-	-	-	LG8	Jia et al. 2008	Kunming, China
Tupaia belangeri	EU531756	-	-	-	LG9	Jia et al. 2008	Kunming, China
Tupaia belangeri	EU531758	-	-	-	LQ11	Jia et al. 2008	Kunming, China
Tupaia belangeri	HQ836325	-	-	-	H10_TS208	Chen et al. 2011	Kunming, China
Tupaia belangeri	HQ836335	-	-	-	H4_N2	Chen et al. 2011	Kunming, China
Tupaia belangeri	HQ836336	-	-	-	H5_N22	Chen et al. 2011	Kunming, China
Tupaia belangeri	HQ836337	-	-	-	H5_T84	Chen et al. 2011	Kunming, China
Tupaia belangeri	DQ986459	-	-	-	A1	-	-
Tupaia belangeri	AY321637	-	-	-	Tchin5078	-	-
Tupaia belangeri	KU130879	KU130817	-	-	126.2	-	-
Tupaia belangeri	KU130880	KU130818	-	-	126.3	-	-
Tupaia belangeri	-	-	AY862170	JF795297	FMNH 165412	Roberts et al. 2011	Malaysia, Sabah (Borneo)
Tupaia belangeri	-	-	AY862171	JF795299	USNM 583857	Roberts et al. 2011	Mon – Myanmar
Tupaia belangeri	-	-	JF795300	JF795300	UAM 102606	Roberts et al. 2011	Cambodia
Tupaia belangeri	-	-	JF795301	JF795301	UAM 102607	Roberts et al. 2011	Cambodia
Tupaia belangeri	-	-	JF795303	JF795303	USNM 583793	Roberts et al. 2011	Bago – Myanmar
Tupaia minor	-	JF444479	-	-	ROM:102255	-	-
Tupaia minor	-	-	JF795313	JF795313	USNZ 109751	Roberts et al. 2011	-
Tupaia minor	-	-	JF795314	JF795314	USNZ 109988	Roberts et al. 2011	
Tupaia tana	MT442045	MT442045	MT442045	MT442045	BOR010	Parker et.al. 2020	Borneo, Malaysia
Tupaia tana	MT442046	MT442046	MT442046	MT442046	BOR050	Parker et.al. 2020	Borneo, Malaysia

Tupaia tana	MT442047	MT442047	MT442047	MT442047	BOR016	Parker et.al. 2020	Borneo, Malaysia
Tupaia tana	MT442048	MT442048	MT442048	MT442048	BOR038	Parker et.al. 2020	Borneo, Malaysia
Tupaia tana	MT442049	MT442049	MT442049	MT442049	BOR056	Parker et.al. 2020	Borneo, Malaysia
Tupaia tana	-	-	AY862182	JF795321.	MVZ 192193	Roberts et al. 2011	Aceh (Sumatra), Indonesia
Tupaia tana	-	-	AY862183	JF795322	JS M11	Roberts et al. 2011	Malaysia, Sabah (Borneo)
Tupaia splendidula	MT442052	MT442052	MT442052	MT442052	UMMZ174 429	Parker et.al. 2020	Borneo, Malaysia
Tupaia splendidula	-	-	JF795320	JF795320	UMMZ 174428	Roberts et al. 2011	Indonesia, Kalimantan Barat (Borneo)
Tupaia splendidula	-	-	AY862181	JF795319	UMMZ 174429	Roberts et al. 2011	Indonesia, Kalimantan Barat (Borneo)
Tupaia salatana	AY321654	-	-	-	Tsal5326	-	-
Tupaia montana	-	-	JF795315	JF795315	USNM 449964	Roberts et al. 2011	Malaysia, Sabah (Borneo)
Tupaia palawanensis	-	-	AY862180	JF795317	FMNH 168969	Roberts et al. 2011	Philippines, Palawan (Palawan)
Tupaia moellendorffi	-	-	JF795312	JF795312	USNM 477838	Roberts et al. 2011	Philippines Palawan (Culion)
Tupaia javanica	-	-	AY862177	JF795310	FMNH 47118	Roberts et al. 2011	Indonesia, Jawa Tengah (Java)
Tupaia nicobarica	-	-	AY862179	JF795316	USNM 111753	Roberts et al. 2011	India, Little Nicobar Island
Tupaia gracilis	-	-	AY862176	JF795309	USNZ 109023	Roberts et al. 2011	Sabah (Borneo), Malaysia
Tupaia dorsalis	-	-	AY862173	JF795305	UMMZ 174427	Roberts et al. 2011	Indonesia, Kalimantan Barat (Borneo)
Tupaia dorsalis	-	-	JF795306	JF795306	UMMZ 174651	Roberts et al. 2011	Indonesia, Kalimantan Barat (Borneo)
Tupaia longipes	-	-	AY862178	JF795311	JS M02b	Roberts et al. 2011	Sabah (Borneo), Malaysia
Tupaia chrysogaster	-	-	JF795304	JF795304	USNM 121577	Roberts et al. 2011	Sumatera Barat (Pagai Selatan), Indonesia
Tupaia sp.	-	JF444477	-	-	ROM:10212 3	-	-
Urogale everetti	-	-	AY862184	JF795323	FMNH1477 81	Roberts et al. 2011	Philippines, Bukidnon
Dendrogale murina	-	-	JF795295	JF795295	UAM 102608	Roberts et al. 2011	Cambodia, Koh Kong (Cardamom Mts.)
Dendrogale murina	-	-	JF795294	JF795294	UAM 103000	Roberts et al. 2011	Cambodia, Mondulkiri
Tupaia sp. nov.	xxx xxx	xxx xxx	-	xxx xxx	IEBR – M – 7901	This study	Cat Ba, Hai Phong, Vietnam
Tupaia sp. nov.	xxx xxx	xxx xxx	-	-	IEBR – M – 7935	This study	Cat Ba, Hai Phong, Vietnam
Tupaia sp. nov.	-	-	-	xxx xxx	IEBR – M – 8098	This study	Cat Ba, Hai Phong, Vietnam
Tupaia sp. nov.	xxx xxx	xxx xxx	-	xxx xxx	IEBR – M – 7624	This study	Bac Me, Ha Giang, Vietnam
Tupaia sp. nov.	xxx xxx	xxx xxx	-	xxx xxx	IEBR – M – 7977	This study	Huu Lien, Lang Son, Vietnam
Tupaia sp. nov.	xxx xxx	xxx xxx	-	xxx xxx	IEBR – M – 7978	This study	Huu Lien, Lang Son, Vietnam

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Table 4. Genetic distance between *Tupaia* species based on the mitochondrial COI gene

		1	2	3	4	5	6	7	8	9	10	11	12	13
1	**NC042823 *Phodopus sungorus***	-												
2	**AF217811 *Tupaia belangeri***	18.97	-											
3	**AJ421453 *Tupaia belangeri***	18.97	0	-										
4	**JN800722 *Tupaia belangeri***	19.58	6	6	-									
5	**JN800723 *Tupaia belangeri***	19.58	6	6	0	-								
6	**JN800724 *Tupaia belangeri***	19.58	6	6	0	0	-							
7	**NC 2521 *Tupaia belangeri***	18.97	0	0	6	6	6	-						
8	**HM031767 *Tupaia belangeri***	18.52	13.23	13.23	12.92	12.92	12.92	13.23	-					
9	**HM031768 *Tupaia belangeri***	18.52	13.23	13.23	12.92	12.92	12.92	13.23	0	-				
10	**HM031781 *Tupaia belangeri***	18.52	13.08	13.08	13.08	13.08	13.08	13.08	1.23	1.23	-			
11	**HM031787 *Tupaia belangeri***	18.52	13.08	13.08	13.54	13.54	13.54	13.08	1.54	1.54	0.62	-		
12	**HM031788 *Tupaia belangeri***	18.52	13.08	13.08	13.54	13.54	13.54	13.08	1.54	1.54	0.62	0	-	
13	**HM031789 *Tupaia belangeri***	18.21	13.54	13.54	13.69	13.69	13.69	13.54	1.69	1.69	0.77	0.77	0.77	-
14	**JQ601650 *Tupaia belangeri***	19.67	6.51	6.51	5.25	5.25	5.25	6.51	12.24	12.24	12.08	11.92	11.92	12.71
15	**KU130817 *Tupaia belangeri***	19.51	5.38	5.38	6.74	6.74	6.74	5.38	12.44	12.44	12.28	12.95	12.95	12.94
16	**KU130818 *Tupaia belangeri***	19.69	5.06	5.06	6.75	6.75	6.75	5.06	13.13	13.13	12.96	13.63	13.63	13.62
17	**JF444478 *Tupaia glis***	17.21	18.6	18.6	19.59	19.59	19.59	18.6	17.1	17.1	17.45	16.94	16.94	17.44
18	**JF459875 *Tupaia glis***	21.48	19.23	19.23	18.8	18.8	18.8	19.23	16.55	16.55	16.7	17.17	17.17	17.17
19	**KY315499 *Tupaia glis***	20.11	18.46	18.46	18.46	18.46	18.46	18.46	16.92	16.92	16.77	16.92	16.92	16.92
20	**KY315500 *Tupaia glis***	20.71	18.5	18.5	18.46	18.46	18.46	18.5	15.69	15.69	15.65	15.86	15.86	16.21
21	**JF444479 *Tupaia minor***	19.35	17.55	17.55	18.4	18.4	18.4	17.55	16.9	16.9	17.24	16.9	16.9	16.9
22	**JF444477 *Tupaia* sp.**	22.02	21.01	21.01	18.91	18.91	18.91	21.01	18.79	18.79	18.8	18.64	18.64	18.97
23	**Tb1 *Tupaia* sp. CatBa**	**18.07**	**12.92**	**12.92**	**12**	**12**	**12**	**12.92**	**11.85**	**11.85**	**11.23**	**11.54**	**11.54**	**11.39**
24	**Tb6 *Tupaia* sp. HaGiang**	**18.54**	**13**	**13**	**11.72**	**11.72**	**11.72**	**13**	**11.9**	**11.9**	**11.27**	**11.59**	**11.59**	**11.75**
25	**Tb7 *Tupaia* sp. LangSon**	**18.38**	**12.92**	**12.92**	**12**	**12**	**12**	**12.92**	**11.85**	**11.85**	**11.23**	**11.54**	**11.54**	**11.69**
26	**Tb14 *Tupaia* sp. LangSon**	**18.38**	**12.92**	**12.92**	**11.69**	**11.69**	**11.69**	**12.92**	**11.85**	**11.85**	**11.23**	**11.54**	**11.54**	**11.69**
27	**Tb18 *Tupaia* sp. Cat Ba**	**18.07**	**12.92**	**12.92**	**12**	**12**	**12**	**12.92**	**11.85**	**11.85**	**11.23**	**11.54**	**11.54**	**11.39**

		14	**15**	**16**	**17**	**18**	**19**	**20**	**21**	**22**	**23**	**24**	**25**	**26**	**27**
14	**JQ601650 *Tupaia belangeri***	-													
15	**KU130817 *Tupaia belangeri***	7.43	-												
16	**KU130818 *Tupaia belangeri***	7.77	1.35	-											
17	**JF444478 *Tupaia glis***	18.83	19.57	19.91	-										
18	**JF459875 *Tupaia glis***	18.14	18.03	17.87	20.67	-									
19	**KY315499 *Tupaia glis***	18.16	18.39	18.05	20.49	2.08	-								
20	**KY315500 *Tupaia glis***	17	17.46	17.69	19.33	1.89	0	-							
21	**JF444479 *Tupaia minor***	16.78	17.8	17.97	17.27	17.79	18.26	16.54	-						
22	**JF444477 *Tupaia* sp.**	19.14	20.34	20.52	18.29	20.72	20.6	20.88	19.68	-					
23	**Tb1 *Tupaia* sp. CatBa**	**12.26**	**12.97**	**13.14**	**18.29**	**18.48**	**18**	**18.31**	**18.57**	**18.25**	**-**				
24	**Tb6 *Tupaia* sp. HaGiang**	**12.14**	**12.9**	**13.08**	**18.33**	**18.28**	**17.79**	**18.07**	**18.43**	**18.15**	**0.31**	**-**			
25	**Tb7 *Tupaia* sp. LangSon**	**11.95**	**12.64**	**12.81**	**18.12**	**18.16**	**17.69**	**17.9**	**18.57**	**18.6**	**0.92**	**0.64**	**-**		
26	**Tb14 *Tupaia* sp. LangSon**	**11.94**	**12.64**	**12.81**	**18.29**	**18.32**	**17.85**	**18.12**	**18.57**	**18.09**	**0.31**	**0**	**0.62**	**-**	
27	**Tb18 *Tupaia* sp. Cat Ba**	**12.26**	**12.97**	**13.14**	**18.29**	**18.48**	**18**	**18.31**	**18.57**	**18.25**	**0**	**0.31**	**0.92**	**0.31**	**-**

Table 5. Genetic distance between *Tupaia* species based on the mitochondrial Cyt *b* gene

		1	2	3	4	5	6	7	8	9	10	11	12
1	**AY321634 *Dendrogale melanura***	-											
2	**EU531758 *Tupaia belangeri***	16.53	-										
3	**EU531756 *Tupaia belangeri***	16.44	0.27	-									
4	**EU531755 *Tupaia belangeri***	16.53	0	0.27	-								
5	**HQ836337 *Tupaia belangeri***	16.62	0.27	0.18	0.27	-							
6	**HQ836336 *Tupaia belangeri***	16.71	0.18	0.27	0.18	0.09	-						
7	**HQ836335 *Tupaia belangeri***	16.53	0	0.27	0	0.27	0.18	-					
8	**HQ836325 *Tupaia belangeri***	16.53	0.18	0.44	0.18	0.44	0.36	0.18	-				
9	**DQ986459 *Tupaia belangeri***	16.62	0.71	0.8	0.71	0.98	0.89	0.71	0.89	-			
10	**KU130880 *Tupaia belangeri***	16.67	5.22	5.2	5.22	5.2	4.95	5.22	5.43	6.05	-		
11	**KU130879 *Tupaia belangeri***	16.45	5.97	5.94	5.97	5.94	5.69	5.97	6.17	6.78	1.24	-	
12	**NC2521 *Tupaia belangeri***	16.33	8.26	8.17	8.26	8.17	8.08	8.26	8.35	8.61	3.23	3.99	-
13	**AJ421453 *Tupaia belangeri***	16.33	8.26	8.17	8.26	8.17	8.08	8.26	8.35	8.61	3.23	3.99	0
14	**AF217811 *Tupaia belangeri***	16.33	8.26	8.17	8.26	8.17	8.08	8.26	8.35	8.61	3.23	3.99	0
15	**AY321637 *Tupaia chinensis***	16.53	0.18	0.44	0.18	0.44	0.36	0.18	0.36	0.71	5.47	6.22	8.43
16	**AY321646 *Tupaia longipes***	17.51	15.29	15.38	15.29	15.38	15.29	15.29	15.38	15.56	13.82	13.57	16.42
17	**AY321644 *Tupaia glis***	12.36	15.73	15.64	15.73	15.64	15.73	15.73	15.73	16.18	15.24	15.02	15.62
18	**AY321639 *Tupaia glis***	11.91	15.38	15.29	15.38	15.29	15.38	15.38	15.38	15.82	14.76	14.54	15.36
19	**MT442048 *Tupaia tana***	14.72	17.04	17.04	17.04	17.04	17.04	17.04	17.04	17.4	15.7	15.44	16.26
20	**MT442049 *Tupaia tana***	14.71	17.12	17.11	17.12	17.11	17.11	17.12	17.12	17.47	15.7	15.44	16.24
21	**MT442047 *Tupaia tana***	14.71	17.03	17.03	17.03	17.03	17.03	17.03	17.03	17.39	15.71	15.45	16.33
22	**MT442046 *Tupaia tana***	14.8	17.12	17.12	17.12	17.12	17.12	17.12	17.12	17.47	15.95	15.7	16.41
23	**MT442045 *Tupaia tana***	14.89	17.12	17.11	17.12	17.11	17.11	17.12	17.12	17.47	15.71	15.45	16.24
24	**AY321654 *Tupaia salatana***	18.04	17.24	17.07	17.24	17.07	17.07	17.24	17.33	17.51	17.02	17.75	17.67
25	**MT442052 *Tupaia splendidula***	16.15	16.87	16.69	16.87	16.69	16.69	16.87	16.87	17.05	14.65	14.89	16.28
26	**Tb1 *Tupaia* sp. Cat Ba**	**17.04**	**12.68**	**12.59**	**12.68**	**12.59**	**12.51**	**12.68**	**12.68**	**12.77**	**11.11**	**10.87**	**12.57**
27	**Tb6 *Tupaia* sp. Ha Giang**	**16.77**	**12.34**	**12.25**	**12.34**	**12.25**	**12.16**	**12.34**	**12.34**	**12.61**	**10.35**	**10.11**	**11.91**
28	**Tb7 *Tupaia* sp. Lang Son**	**16.95**	**12.15**	**12.06**	**12.15**	**12.06**	**11.97**	**12.15**	**12.15**	**12.42**	**10.62**	**10.38**	**12.3**
29	**Tb14 *Tupaia* sp. Lang Son**	**16.77**	**11.97**	**11.88**	**11.97**	**11.88**	**11.79**	**11.97**	**11.97**	**12.24**	**10.6**	**10.36**	**12.06**
30	**Tb18 *Tupaia* sp. Cat Ba**	**17.03**	**12.68**	**12.59**	**12.68**	**12.59**	**12.51**	**12.68**	**12.68**	**12.77**	**11.11**	**10.87**	**12.59**

		13	14	15	16	17	18	19	20	21	22	23	24
13	AJ421453 *Tupaia belangeri*	-											
14	AF217811 *Tupaia belangeri*	0	-										
15	AY321637 *Tupaia chinensis*	8.43	8.43	-									
16	AY321646 *Tupaia longipes*	16.42	16.42	15.38	-								
17	AY321644 *Tupaia glis*	15.62	15.62	15.82	16.8	-							
18	AY321639 *Tupaia glis*	15.36	15.36	15.47	16.62	0.8	-						
19	MT442048 *Tupaia tana*	16.26	16.26	17.22	15.44	15.98	15.63	-					
20	MT442049 *Tupaia tana*	16.24	16.24	17.29	15.6	15.88	15.52	0.17	-				
21	MT442047 *Tupaia tana*	16.33	16.33	17.2	15.42	16.06	15.7	0	0.17	-			
22	MT442046 *Tupaia tana*	16.41	16.41	17.29	15.51	16.15	15.79	0.09	0.26	0.09	-		
23	MT442045 *Tupaia tana*	16.24	16.24	17.29	15.51	16.15	15.79	0.17	0.35	0.17	0.26	-	
24	AY321654 *Tupaia salatana*	17.67	17.67	17.33	11.47	15.91	15.73	17.31	17.3	17.3	17.39	17.38	-
25	MT442052 *Tupaia splendidula*	16.28	16.28	17.05	17.03	16.6	16.34	12.38	12.54	12.45	12.54	12.45	19.7
26	Tb1 *Tupaia* sp. Cat Ba	**12.57**	**12.57**	**12.77**	**15.53**	**15.45**	**15.62**	**15.65**	**15.72**	**15.72**	**15.8**	**15.8**	**18.29**
27	Tb6 *Tupaia* sp. Ha Giang	**11.91**	**11.91**	**12.43**	**15.63**	**15.01**	**15.18**	**15.35**	**15.42**	**15.42**	**15.51**	**15.51**	**18.21**
28	Tb7 *Tupaia* sp. Lang Son	**12.3**	**12.3**	**12.23**	**15.34**	**15**	**15.18**	**15.3**	**15.37**	**15.37**	**15.45**	**15.45**	**18.37**
29	Tb14 *Tupaia* sp. Lang Son	**12.06**	**12.06**	**12.06**	**15.35**	**15.18**	**15.35**	**15.14**	**15.21**	**15.21**	**15.3**	**15.3**	**18.38**
30	Tb18 *Tupaia* sp. Cat Ba	**12.59**	**12.59**	**12.77**	**15.53**	**15.44**	**15.62**	**15.68**	**15.75**	**15.75**	**15.84**	**15.84**	**18.3**

		25	26	27	28	29	30
25	MT442052 *Tupaia splendidula*	-					
26	Tb1 *Tupaia* sp. Cat Ba	**17.4**	-				
27	Tb6 *Tupaia* sp. Ha Giang	**16.92**	**0.95**	-			
28	Tb7 *Tupaia* sp. Lang Son	**16.79**	**1.03**	**0.6**	-		
29	Tb14 *Tupaia* sp. Lang Son	**16.62**	**1.29**	**0.69**	**0.94**	-	
30	Tb18 *Tupaia* sp. Cat Ba	**17.42**	**0**	**0.95**	**1.03**	**1.29**	-