

The first studies of small mammals of the Cham Chu and Bac Me Nature Reserves, north-eastern Vietnam

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ABSTRACT. Field surveys of mammals in two protected areas of the north-eastern limestone region of Vietnam, the Cham Chu (Tuyen Quang Province) and Bac Me (Ha Giang Province) Nature Reserves were conducted in 2018 and 2019. Thirty-five species of small mammals were recorded based both on field observations and on morphological and/or molecular evidence, as follows: one Scandentia species, four Eulipotyphla species, 14 Chiroptera species, and 16 Rodentia species. New records of *Aselliscus dongbacanus* and *Chiromyscus thomasi* in north-eastern Vietnam have been confirmed. Interestingly, the mole specimens collected during this study resemble *Euroscaptor orlovi* morphologically but significantly differ from it genetically. The present study has revealed that Chiroptera (38.9%) and Rodentia (47.2%) are the dominant groups in terms of their species diversity. Yet, the number of bat species is much lower as compared to that revealed by the previous study conducted in the same region (16 vs. 35). Although a couple of abundant species — *Aselliscus dongbacanus* (40 of 176 specimens) and *Hipposideros cf. larvatus* (37 of 176 specimens) — have been found during the present survey, other common species, such as *Callosciurus inornatus* and *Rhizomys pruinosus*, were very scarce, suggesting the occurrence of a severe anthropogenic pressure on small mammal fauna. More studies to assess a conservation status of and anthropogenic threats to small mammals are needed to protect them from serious population decline in the future.

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Первые исследования мелких млекопитающих в заповедниках Чамчу и Бакме, северо-восточный Вьетнам

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РЕЗЮМЕ. Полевые исследования на двух охраняемых территориях в северо-восточном карстовом регионе Вьетнама, в заповеднике Чамчу (провинция Туенкуанг) и заповеднике Бакме (провинция

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Хазанг) были проведены в 2018 и 2019 годах. На основании данных полевых наблюдений, морфологических и генетических исследований зарегистрировано 35 видов мелких млекопитающих, включающих один вид Scandentia, четыре вида Eulipotyphla, 14 видов Chiroptera и 16 видов Rodentia. Подтверждены новые находки *Aselliscus dongbacanus* и *Chiromyscus thomasi* на северо-востоке Вьетнама. Интересно, что экземпляры кротов, собранные в ходе этого исследования, морфологически напоминают *Euroscaptor orlovi*, но генетически они значительно отличаются от этого вида. Результаты наших исследований свидетельствуют, что доминирующими группами по видовому составу являются Chiroptera (38.9%) и Rodentia (47.2%). Однако количество отмеченных видов летучих мышей было намного меньше по сравнению с предыдущими исследованиями, проведенным в этом же регионе (16 против 35). Хотя было отмечено несколько многочисленных видов — *Aselliscus dongbacanus* (40 из 176 экз.) и *Hipposideros cf. larvatus* (37 из 176 экз.) — другие обычные виды, такие как *Callosciurus inornatus* и *Rhizomys pruinosus*, были очень редки, что свидетельствует о серьезном антропогенном давлении на фауну мелких млекопитающих. Необходимы дополнительные исследования по оценке уровня сохранности и антропогенной опасности для мелких млекопитающих с тем, чтобы в будущем предотвратить серьезное снижение их численности.

КЛЮЧЕВЫЕ СЛОВА: чеклист, северо-восточный Вьетнам, карстовый район, Чамчу, Бакме.

Introduction

Vietnam is situated in the Indochina Peninsula, harbouring a very high diversity of forest mammals. To date, over 331 mammal (sub)species have been recognized in the country (Nguyen Quang Truong *et al.*, 2020), compared to 500 mammal species found in the Indochina Peninsula (Francis, 2019). In terms of species richness and endemism, Vietnam is commonly recognized as a biodiversity hotspot not only in SE Asia but also in the world (Tordoff *et al.*, 2007, 2012). However, the mammal fauna of Vietnam has experienced a steep decline in recent decades. Specifically, the Javan rhinoceros *Rhinoceros sondaicus annamiticus* became extinct from Vietnam in 2011 (Brook *et al.*, 2011, 2012; Ellis & Talukdar, 2020) and more than 60 species are currently listed as vulnerable or a higher category in the IUCN Red List (IUCN, 2020), although the country's forest cover has moderately raised from 37% in 2006 (1970/QĐ/BNN-KL) to 41.9% in 2019 (1423/QĐ-BNN-TCLN). The overexploitation resulted from poaching is regarded as the most severe threat to mammals and other vertebrates in Vietnam (Gray *et al.*, 2018).

The north-eastern limestone region of Vietnam contains large karst outcrops surrounded by hills and low mountains consisting of soil (Sterling & Hurley, 2005; Sterling *et al.*, 2006). Karst towers form an extensive but highly dissected plateau (Sterling *et al.*, 2006). The region possesses one of the highest concentrations of endemic species (Clements *et al.*, 2006). There are several remarkable mammals that are endemic to the northeast region, including the Tonkin snub-nosed monkey *Rhinopithecus avunculus* (Le Khac Quyet *et al.*, 2020; IUCN, 2020), the Daovantien's limestone rat *Tonkinomys daovantieni* (Musser *et al.*, 2006) and the Cao-vit black crested gibbon *Nomascus nasutus* (Rawson *et al.*, 2020; IUCN, 2020).

The field surveys conducted in Tuyen Quang and Ha Giang Provinces between 1998 and 2011 have recorded 68 small mammal species, consisting of one Scandentia, 10 Eulipotyphla, 35 Chiroptera and 22 Rodentia (Nguyen

Truong Son *et al.*, 2011). A number of new endemic small mammal species in this karst area, such as *Tonkinomys daovantieni* (Musser *et al.*, 2006), *Aselliscus dongbacanus* (Vuong Tan Tu *et al.*, 2015), *Euroscaptor orlovi* and *E. kuznetsovi* (Zemlemerova *et al.*, 2016), continues to be discovered. Yet, the small mammal fauna of north-eastern Vietnam has been studied in some protected areas: viz., the Huu Lien Nature Reserve (NR) (Lang Son Province) (Lunde *et al.*, 2007), the Ba Be National Park (NP) (Bac Kan Province) (Nguyen Truong Son & Vu Dinh Thong, 2008), the Tay Con Linh NR (Ha Giang Province) (Lunde *et al.*, 2003; Nguyen Truong Son *et al.*, 2017) and the Na Hang NR (Tuyen Quang Province) (Nguyen Truong Son & Vu Dinh Thong, 2008).

To better understand the small mammal fauna of north-eastern Vietnam, field surveys were conducted in the Cham Chu (Tuyen Quang Province) and Bac Me (Ha Giang Province) Nature Reserves in 2018 and 2019. During the surveys tree shrew, bats, rodents, shrews and moles were recorded. Species were identified on the basis of both morphological and genetic characters. In the present paper, the first list of small mammals recorded from these reserves is provided for the first time.

Material and methods

Field surveys were conducted in Nam Nuong, Phu Luu and Cao Duong hamlets (Cham Chu NR), and in Khau Ca Forest and Lung Cang hamlet (Bac Me NR and its vicinity). The Cham Chu NR is located in Tuyen Quang Province covering the area of 15262.3 ha; the Bac Me NR covers the area of 9042.5 ha in Ha Giang Province. Both protected areas are situated in the limestone karst region of north-eastern Vietnam, and are mainly covered with the secondary montane evergreen forest consisting of both broad-leaved and coniferous trees (Sterling *et al.*, 2006). The elevations range from 100 to 850 m above sea level. Of the study sites, Cao Duong hamlet lies at the highest elevations between 600 and 850 m, whereas at Phu Luu hamlet lies lower, at the elevations of 100 to 550 m. These sites were selected

in the areas with a complex limestone terrain, including caves, lowland mountains, torrent streams and high waterfalls (Fig. 1).

The field surveys were conducted in the Cham Chu NR in August 2018 and April 2019, and in the Bac Me NR in May and October 2019 (Tab. 1).

During the survey, different methods were used to collect small mammals: viz., Sherman box traps, Tomahawk traps, mole-traps, mist nets and harp trap at daytime and nighttime following the methods recommended by

the Animal Care and Use Guidelines of the American Society of Mammalogists (Sikes *et al.*, 2016). Three types of the Sherman live-traps (3 × 3 × 10 cm; 5 × 5 × 18 cm; 7 × 7 × 30 cm) were employed to catch medium and small-sized rodents and shrews. Tomahawk (15 × 15 × 45 cm) and local cage traps were used to capture large-sized rodents and squirrels. Cassava, crisps, pineapples and peanuts were chosen as bait. Peanut butter was mixed with baits to enhance the flavor or aroma. Baits were changed every day after checking the traps.

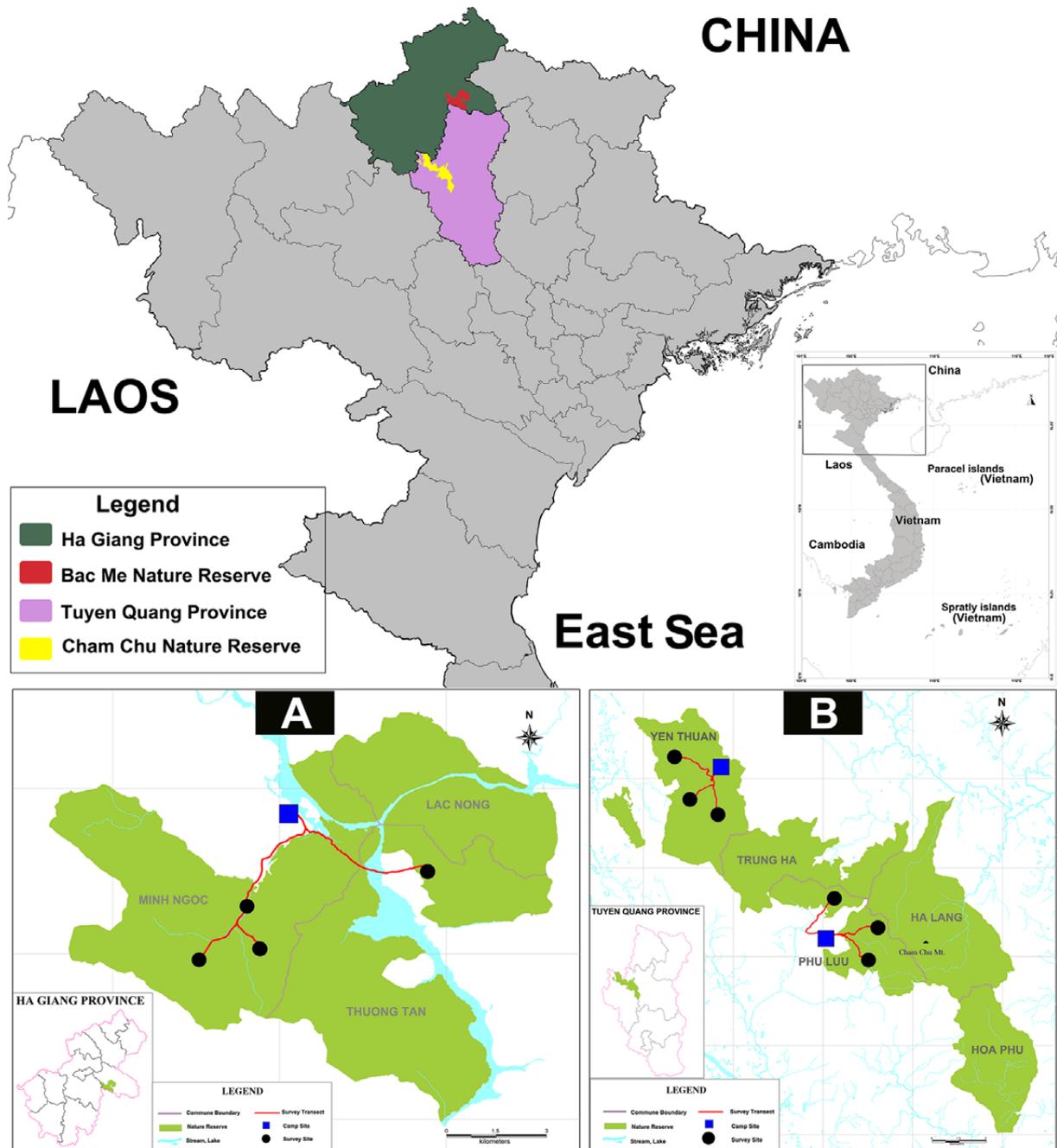


Fig. 1. Geographic locations of the Cham Chu (A) and Bac Me (B) NRs and the survey transects (red lines).

Table 1. Total survey efforts in the study areas: D.O. — daytime observation (hours); MN — mist nets (m²/n/h); H — harp trap (m²/n/h); M — mole-traps (trap nights); S & C — Sherman and cage traps (trap nights); N.O. — nighttime observations (hours); *n* — number of captured specimens.

Site	Date of survey	D.O.	MN	H	M	S & C	N.O.	<i>n</i>
Cham Chu NR	24–31.10.2018	22	810	189	16	252	8.25	30
	13–19.04.2019	14	1161	162	42	315	25.5	58
	Total efforts	36	1971	351	58	567	33.75	86
Bac Me NR and surrounding area	24–31.05.2019	17.5	864	162	15	210	8.75	48
	14–21.10.2019	24.5	1512	162	16	204	22.75	49
	Total efforts	42	2376	324	31	414	31.5	90
Total		78	4347	675	89	981	65.25	176

Different types of mist nets (2 × 3 m, 6 × 3 m and 12 × 4 m) and harp trap (1.5 × 1.5 m) were used to capture live bats. These traps were set across trails, over streams, inside and at forest edges, and at cave entrances, in accordance with the published recommendations by Kunz & Parsons (2009). Japanese hand-made traps and Talpex traps were set up on the trails where mole tunnels were observed. The total survey efforts are shown in Table 1.

Specimen photos were taken to record pelage features in detail. Several external characters, including the head and body length (HB), the tail length (TL), the hind foot length (HF), the ear length (E), the forearm length (FA) (for bats) and the greatest skull length (GL), were measured with a digital caliper (Mitutoyo NTD12-15PMX, Kawasaki, Japan) to an accuracy of 0.01 mm. Body mass (BW) in grams were measured following the standard methods.

The morphological descriptions of Csorba *et al.* (2003), Kruskop (2013), Wilson *et al.* (2016, 2017, 2018), Francis (2019) and Wilson & Mittermeier (2019) were used for a morphological analysis in the present study. Besides, for a morphological comparison, we have also obtained data from the following papers: viz., Balakirev *et al.* (2014), Zemlemerova *et al.* (2016), Vuong Tan Tu *et al.* (2015), Nguyen Truong Son *et al.* (2015). The nomenclature of mammals followed Wilson *et al.* (2016, 2017, 2018) and Wilson & Mittermeier (2019), unless stated otherwise.

By using the DNA barcoding, we have been able to identify 26 specimens belonging to the groups with a complicated morphological variation (Tab. 3). We took liver or wing membrane punch (for bats) tissue samples from 26 specimens and stored them in 70% ethanol for a further verification of the species identification by means of the DNA barcoding method. Two mitochondrial genes, cytochrome *b* (*cytb*) and cytochrome *c* oxidase subunit I (COI) were amplified and sequenced using the primers L14724-H15149 for *cytb* and partial tRNA-Thr from Irwin *et al.* (1991) and the primers VF1d-VR1d for COI from Ivanova *et al.* (2006). Tissue samples were extracted using the DNeasy blood and tissue kit, Qiagen (Hilden, Germany). Extracted DNA from fresh tissue was

amplified by the DreamTaq PCR mastermix, Thermo Fisher Scientific (Vilnius, Lithuania). The PCR volume consisted of 21 µl (10 µl of mastermix, 5 µl of water, 2 µl of each primer at 10 pmol/µl, and 2 µl of DNA or higher depending on a DNA quantity in the final extraction solution). The PCR conditions were: 95°C for 5 min to activate the taq; with 40 cycles at 95°C for 30 s, 50°C for 45 s, 72°C for 60 s; and the final extension at 72°C for 6 min. PCR products were subjected to electrophoresis through the 1% 135 agarose gel, 1st BASE (Selangor, Malaysia). Gels were stained for 10 min in 1X TBE buffer at 2 pg/ml of ethidium-bromide and visualized under UV light. Successful amplifications were purified to eliminate PCR components using the GeneJET™ PCR Purification Kit, Thermo Fisher Scientific (Vilnius, Lithuania). Purified PCR products were sent to Macrogen Inc. (Seoul, South Korea) for sequencing. The 140 sequences generated in this study were aligned with one another using the De Novo Assemble function in the program Geneious v.7.1.8 (Kearse *et al.*, 2012). Then they were compared with other sequences using the Basic Local Alignment Search Tool (BLAST) in GenBank (NCBI).

A phylogenetic tree was constructed to recover phylogenetic relationships of complex groups, for instance, *Niviventer–Chiromyscus*, by employing the Bayesian inference as implemented in MrBayes v.3.2.7 (Ronquist *et al.*, 2012). The final matrix contained 1164 aligned characters of 16 taxa. Two outgroups selected were *Mus musculus* (LC325158) and *Apodemus draco* (HQ333255). We used the optimal model for nucleotide evolution as determined by jModeltest 2.1.4 (Darriba *et al.*, 2012) with parameters estimated by MrBayes v.3.2.7. Two simultaneous analyses with four Markov chains (one cold and three heated) were run for 10 million generations with a random starting tree and trees were sampled every 1000 generations. The cutoff point for the burn-in function was set to 5 in the Bayesian analyses, as -lnL scores reached stationarity after 5000 generations in both runs. Posterior probability values for major clades in the final majority rule consensus tree were provided.

Results

In total, we collected 176 specimens, which were assigned to 35 small mammal species of 13 families in four orders: viz., 23 species in the Cham Chu NR and 23

species in the Bac Me NR (Tab. 2). Fifty five individuals were released back to the wild after taking measurements and photos. According to the recent IUCN Red List (IUCN, 2020), all recorded species listed as Least Concern, and only *Belomys pearsonii* — as Data Deficient.

Table 2. Species of small mammals documented in the Cham Chu and Bac Me NRs during the field surveys in 2018 and 2019. Numbers denote the quantity of individuals captured; O — observed; * — identification confirmed by the DNA analysis.

No.	Scientific name	Cham Chu NR	Bac Me NR	Comments
1	<i>Tupaia belangeri</i>	–	2	common species
2	<i>Crocidura tanakae</i> *	1	2	
3	<i>Suncus murinus</i>	O	O	common species
4	<i>Chimarrogale himalayica</i> *	1	–	
5	<i>Euroscaptor cf. orlovi</i> *	6	2	
6	<i>Cynopterus sphinx</i> *	12	4	common species
7	<i>Macroglossus sobrinus</i>	2	–	
8	<i>Rhinolophus microglobosus</i>	–	5	
9	<i>Rhinolophus pearsonii</i>	2	1	
10	<i>Rhinolophus pusillus</i> *	–	1	
11	<i>Rhinolophus rex</i>	2	–	
12	<i>Rhinolophus thomasi</i>	2	–	
13	<i>Rhinolophus affinis</i> *	–	1	
14	<i>Aselliscus dongbacanus</i> *	20	20	common species
15	<i>Hipposideros armiger</i> *	2	12	common species
16	<i>Hipposideros cf. larvatus</i>	17	20	common species
17	<i>Hipposideros gentilis</i>	–	2	
18	<i>Lyroderma lyra</i>	4	–	
19	<i>Myotis chinensis</i> *	1	–	
20	<i>Belomys pearsonii</i>	–	1	
21	<i>Callosciurus erythraeus</i>	2	4	common species
22	<i>Callosciurus inornatus</i> *	–	2	common species
23	<i>Tamiops maritimus</i>	–	1	
24	<i>Rhizomys pruinosus</i> *	1	–	common species
25	<i>Berylmys bowersi</i>	–	1	
26	<i>Chiropodomys gliroides</i>	1	–	
27	<i>Chiromyscus thomasi</i> *	1	–	
28	<i>Chiromyscus langbianis</i> *	1	4	
29	<i>Leopoldamys edwardsi</i>	1	–	
30	<i>Maxomys surifer</i>	1	–	
31	<i>Mus pahari</i>	–	1	
32	<i>Niviventer fulvescens</i> *	2	1	
33	<i>Rattus andamanensis</i>	–	3	
34	<i>Rattus nitidus</i>	4	–	
35	<i>Atherurus macrourus</i>	–	O	

Key small mammal species

ORDER SCANDENTIA
Family TUPAIIDAE*Tupaia belangeri* (Wagner, 1841)

This is a common species in Vietnam known from various habitat types such as primary and secondary, evergreen and deciduous forests in limestone mountains, from the sea level up to high elevations (Molur *et al.*, 2005). Only two specimens were collected in the secondary forest in limestone mountains at the altitude of 620 m a.s.l. in Khu Ca Forest, the Bac Me NR.

ORDER EULIPOTYPHLA
Family SORICIDAE*Crocidura tanakae* Kuroda, 1938

C. tanakae is widespread in China and Vietnam (Bannikova *et al.*, 2011; Li *et al.*, 2019). This species was first reported from Tuyen Quang based on the same specimen collected during our field surveys (Bui Tuan Hai *et al.*, 2019). We obtained one specimen from the Cham Chu NR: HB is 69.3 mm, TL is 53.8 mm, and GL is 20.64 mm. The *cytb* sequence of this specimen is 98.8% similar to that of *C. tanakae* from Longmen, Guangdong, China (Tab. 3).

Chimarrogale himalayica (Gray, 1842)

The Himalayan water shrew *C. himalayica* is widespread in south China and north Vietnam (Abramov *et al.*, 2017). A single specimen collected during our survey from the Cham Chu NR was the first record of this species from Tuyen Quang Province (Bui Tuan Hai *et al.*, 2019). This specimen has HB = 122.25 mm, TL = 86.13 mm, and GL = 26.19 mm. Abramov *et al.* (2017) reported just four specimens of *C. himalayica* in northern Vietnam collected from 2013 to 2015. Scanty records of this species are evidence that the species is rare in Vietnam and its conservation status needs to be assessed.

Family TALPIDAE

Euroscaptor cf. *orlovi* Zemlemerova, Bannikova,
Lebedev, Rozhnov, Abramov, 2016

Euroscaptor orlovi was first described from Sa Pa District (Lao Cai Province, north-western Vietnam) (Zemlemerova *et al.*, 2016). To date, in Vietnam, this species has been known to occur in Lao Cai Province only. Eight specimens were collected in the Cham Chu and Bac Me NRs during our surveys.

Our specimens have the same body size as those of *E. orlovi* and *E. kuznetsovi* and the tail shape as that of *E. orlovi* (Zemlemerova *et al.*, 2016), while differ from other *Euroscaptor* species in the pelage colour and tooth structure. HB is 129.71 (120.71–137.62) mm, TL is 14.82 (8.93–19.28) mm, tail ratio is 7.4–18.3%, and GL is 33.25 (32.4–33.71) mm. Several specimens from Phu Luu (the Cham Chu NR) have a remarkable dark orange in neck and adjacent forearm by secretion

(Fig. 2). The molecular analysis showed that sequences from the studied specimens were at least 4.8% divergent from other *Euroscaptor* species based on the complete *cytb* gene (Tab. 4). Recent studies suggested that both *E. orlovi* and *E. kuznetsovi* inhabit high elevations (1900–2330 m and 700–1300 m a.s.l., respectively). However, our specimens were collected from lower elevations, 200 m (Phu Luu) to 700 m (Cao Duong) a.s.l. In our opinion, the taxonomic status and distribution of *Euroscaptor* moles in northern Vietnam are in need of re-evaluation. Bui Tuan Hai *et al.* (2019, 2020b), whose results were partly based on the collection from Tuyen Quang and Ha Giang provinces, hypothesized that Red River seems to be a biogeographic boundary between *E. kuznetsovi* and *E. orlovi*.

ORDER CHIROPTERA
Family PTEROPODIDAE*Cynopterus sphinx* (Vahl, 1797)

This is a medium-sized bat (FA = 67.47–71.06 mm; GL = 29.96–32.44 mm) with the short muzzle that is characterized by white margins on ears and pale wing digits. Sixteen individuals were captured using mist nets, of which 14 were from the Cham Chu NR and four from the Bac Me NR. They were collected from the orange plantation near the Phu Luu Commune and along a small stream in the secondary forest at the elevations of 300–600 m a.s.l. in the Bac Me NR. Some juvenile females were collected without moms in October during both fieldwork trips.

Taxonomic remarks: There are three species of the genus *Cynopterus* recorded from Vietnam: *C. sphinx*, *C. brachyotis* and *C. horsfieldi* (Kruskop, 2013), of which the former is most common. These species are similar in morphology and sometimes difficult to distinguish in the field. Yet, they can be easily separated by mitochondrial data (Bumrungsri & Racey, 2005; Francis *et al.*, 2010). Besides, *C. sphinx* can be distinguished from *C. brachyotis* by its size. For *C. sphinx* and *C. horsfieldi*, the shape and size of lower premolars are reported as a diagnostic feature (Lekagul & McNeely, 1988; Kruskop, 2013; Dao Nhan Loi *et al.*, 2017). To confirm a significant difference in their size, shape and a biogeographic variation of cranial characters, more samples are to be examined in future studies.

Macroglossus sobrinus Andersen, 1911

This is a small nectarivorous bat characterized by the elongated, slender muzzle and a very long tongue. Two females (FA = 47.35–49.22 mm; GL = 30.47–30.51 mm) were captured by a mist net along a stream and near the orange plantation at the Cham Chu NR (22.12667° N, 105.02972° E, 134 m a.s.l.).

Taxonomic remarks: The genus *Macroglossus* contains two species recorded from Vietnam. Morphologically, *M. sobrinus* is usually larger than *M. minimus* (Francis, 2019). They are distributed in lowland areas with mixed forest habitats, especially in the secondary plant formations with banana growth and mixed natural

Table 3. Results of molecular identification based on *cytb* and COI fragments.

Voucher No.	Species	Locality	GenBank No.		Similarity	Reference
			<i>cytb</i>	COI		
NTS.2019.04.40	<i>Crociodura tanakae</i>	Cao Duong	MW046275		98.82%	Li <i>et al.</i> , 2019
C.CHU.18.22	<i>Euroscaptor cf. orlovi</i>	Phu Luu	MW046264		94.21%	Zemlemerova <i>et al.</i> , 2016
C.CHU.18.31	<i>Euroscaptor cf. orlovi</i>	Phu Luu	MW046265		94.67%	Zemlemerova <i>et al.</i> , 2016
C.CHU.18.32	<i>Euroscaptor cf. orlovi</i>	Phu Luu	MW046266		94.39%	Zemlemerova <i>et al.</i> , 2016
NTS.2019.04.38	<i>Euroscaptor cf. orlovi</i>	Cao Duong	MW046267		95.08%	Zemlemerova <i>et al.</i> , 2016
NTS.2019.04.48	<i>Euroscaptor cf. orlovi</i>	Cao Duong	MW046268		94.61%	Zemlemerova <i>et al.</i> , 2016
NTS.2019.04.50	<i>Euroscaptor cf. orlovi</i>	Cao Duong	MW046269		94.99%	Zemlemerova <i>et al.</i> , 2016
NTS.2019.04.56	<i>Euroscaptor cf. orlovi</i>	Cao Duong	MW046270		94.47%	Zemlemerova <i>et al.</i> , 2016
NTS.2019.04.57	<i>Euroscaptor cf. orlovi</i>	Cao Duong	MW046271		94.38%	Zemlemerova <i>et al.</i> , 2016
C.CHU.18.11	<i>Cynopterus sphinx</i>	Phu Luu		MW039079	99.71%	Arai, 2019
C.CHU.18.14	<i>Cynopterus sphinx</i>	Phu Luu	MW046263		99.65%	Hassanin <i>et al.</i> , 2020
NTS 2019.04.07	<i>Aseliscus dongbacanus</i>	Cao Duong		MW039080	99.26%	Arai, 2019
NTS 2019.04.08	<i>Aseliscus dongbacanus</i>	Cao Duong		MW039081	99.26%	Arai, 2019
NTS 2019.10.09	<i>Aseliscus dongbacanus</i>	Cao Duong		MW039082	99.26%	Arai, 2019
NTS.2019.10.32	<i>Rhinolophus pusillus</i>	Lung Cang	MW046278		99.06%	Shi <i>et al.</i> , 2016
C.CHU.18.10	<i>Rhinolophus affinis</i>	Phu Luu		MW039078	98.29%	Mao <i>et al.</i> , 2019
BM 2019.05.09	<i>Rhinolophus affinis</i>	Khau Ca	MW046259		98.29%	Mao <i>et al.</i> , 2019
BM 2019.05.25	<i>Hipposideros armiger</i>	Khau Ca	MW046261		99.55%	Lin <i>et al.</i> , 2014
BM.2019.05.07	<i>Hipposideros cf. larvatus</i>	Khau Ca	MW046260		99.29%	Li <i>et al.</i> , 2007
NTS.2019.04.37	<i>Myotis chinensis</i>	Cao Duong	MW046274		98.12%	Guo <i>et al.</i> , 2013
NTS 2019.10.45	<i>Callosciurus inornatus</i>	Lung Cang	MW046276		99.53%	Oshida <i>et al.</i> , 2011
NTS.2019.04.58	<i>Rhizomys pruinosus</i>	Cao Duong	MW046277		99.29%	Steppan & Schenk, 2017
C.CHU.18.01	<i>Chiromyscus thomasi</i>	Phu Luu	MW046262		99.35 %	Balakirev <i>et al.</i> , 2014
NTS 2019.10.37	<i>Chiromyscus langbianis</i>	Cao Duong	MW046279		98.65%	Pages <i>et al.</i> , 2010
NTS 2019.04.31	<i>Niviventer fulvescens</i>	Cao Duong	MW046272		99.82%	Zhang <i>et al.</i> , 2016
NTS 2019.10.38	<i>Niviventer fulvescens</i>	Lung Cang	MW046273		99.82%	Zhang <i>et al.</i> , 2016

Table 4. Pairwise genetic distance of *Euroscaptor* spp. based on a fragment of *cytb* gene.

	1	2	3	4	5	6	7	8	9
1 C.CHU.18.22	–								
2 NTS.2019.04.38	0.840	–							
3 <i>E. orlovi</i> SIK0821	5.789	4.827	–						
4 <i>E. klossi</i> SIK0673	9.123	8.648	7.982	–					
5 <i>E. kuznetsovi</i> SIK0865	6.316	6.047	5.614	7.895	–				
6 <i>E. longirostris</i> KIZ0905172	8.860	9.010	7.807	8.596	7.105	–			
7 <i>E. malayana</i> SIK0550	8.421	8.169	7.807	8.596	7.105	8.158	–		
8 <i>E. parvidens ngoclinhensis</i> SIK0858	13.772	13.191	13.070	13.246	12.544	12.456	13.509	–	
9 <i>E. subanura</i> SIK0938	16.316	15.761	15.877	15.702	14.737	15.439	14.825	15.526	–



Fig. 2. Coloration of neck and adjacent forearms, and tail shape of two specimens of *Euroscaptor* cf. *orlovi* from the Cham Chu NR. Photographed by Bui Tuan Hai.

forest. In Vietnam, *M. minimus* has been recorded from two localities in southern Vietnam only, while *M. sobrinus* has been documented from all the northern, central and southern regions of the country. In Vietnam, the two species are distinguishable by the size, nostril shape and mandible symphyse (Kruskop, 2013; Hoang Trung Thanh *et al.*, 2019), but are indistinguishable by their mitochondrial DNA (Francis *et al.*, 2010; Abramov *et al.*, 2018), probably due to an ancient interbreed event.

Family RHINOLOPHIDAE

Rhinolophus microglobosus Csorba, Jenkins, 1998

This is medium sized horseshoe bat, FA = 44.89 mm (44.04–45.27 mm), GL = 19.32 mm (18.61–20.10 mm), similar to *R. stheno*, but with a smaller skull size and a wider postorbital constriction (Kruskop, 2013; Francis, 2019).

Three females and two males were collected during the field surveys. All five individuals were harp-trapped



Fig. 3. *Rhinolophus microglobosus*. Photographed by Nguyen Truong Son.

at a cave's entrance near the Bac Me NR (Fig. 3). The colony size was estimated to be about 35–40 individuals.

Taxonomic remarks: This bat was originally described and for some time treated as a subspecies of *R. stheno* (Csorba & Jenkins, 1998; Simmons, 2005). However, it has been demonstrated to be distinct based on generally smaller body and skull sizes and a higher call frequency, yet being found sympatrically with *R. stheno* s. str. (Soisook *et al.*, 2008).

Rhinolophus pearsonii Horsfield, 1851

This is a medium to large horseshoe bat with FA 49–55 mm (Francis, 2019). Two females and one male were captured by a mist net set up on small tracks near caves at the Phu Luu Hamlet (22.2104° N, 105.0582° E, 220–230 m a.s.l.) in October, 2018 and the Cao Duong Hamlet (22.2948° N, 104.9885° E, 664 m a.s.l.) in April, 2019. The specimens have FA = 53.82–54.66 mm, GL = 24.43–25.89 mm.

Taxonomic remarks: This species has a wide range, occurring from Nepal, India, Bangladesh and Bhutan to southeast China, Laos, Myanmar, Thailand, Vietnam, and Peninsular Malaysia (Francis, 2019). In Vietnam, *R. pearsonii* is widespread across the country and quite common at middle elevations with limestone outcrops (Kruskop, 2013). Another species of the same species group in Vietnamese fauna is *R. yunnanensis* Dobson, 1872, which is morphologically similar but somewhat larger (Yoshiyuki, 1990; Srinivasulu *et al.*, 2010). However, reliable records of the Yunnan horseshoe bat in Vietnam are still not known (Dang Ngoc Can *et al.*, 2008; Kruskop, 2013). At the same time, the high genetic diversity within *R. pearsonii* suggests its taxonomic heterogeneity (Francis *et al.*, 2010). Therefore, the

taxonomy of this species group, including Vietnamese populations, requires further study.

Rhinolophus pusillus Temminck, 1834

This small-sized bat is widespread in Vietnam (Kruskop, 2013). One male was captured by a harp trap at a cave in the mountainous forest habitat near the Bac Me NR (FA = 36.91 mm, GL = 13.57 mm), where some other species were also observed, such as *Hipposideros cf. larvatus* and *Aselliscus dongbacanus*.

Taxonomic remarks: This species is widespread in SE Asia, southern and south-western China, being recorded from 200–1370 m a.s.l. (Fukui, 2019). Yet, the taxonomy of pygmy horseshoe bats from the “*pusillus*” species complex remains problematic (Abramov & Kruskop, 2012). In Vietnam, four species of the “*pusillus*” species group have been reported: viz., *R. subbadius*, *R. pusillus*, *R. lepidus* and *R. acuminatus* (Dang Ngoc Can *et al.*, 2008; Kruskop, 2013). Of these, *R. acuminatus* is well distinguishable by the relatively large size, while identification of other species may cause certain problems (e.g. Abramov & Kruskop, 2012). *R. pusillus* is supposed to be a common species that is distributed in both primary and secondary forest habitats across the country, while *R. lepidus* is known mainly from the Central Highlands and southern Vietnam (Wu *et al.*, 2012; Kruskop, 2013; Hoang Trung Thanh, 2018). In Vietnam, in order to clarify the taxonomic status of local forms of *R. pusillus* and *R. lepidus* further sampling is needed.

Rhinolophus rex G.M. Allen 1923

This is a medium-sized bat (FA = 53–57 mm) with enormous ears (Francis, 2019). One male (FA = 55.36 mm, GL = 22.13 mm) and one pregnant female (FA = 54.75 mm, GL = 21.40 mm) were collected by a harp trap near a cave in the Cham Chu NR (22.2948° N, 104.9885° E, 664 m a.s.l.) in April, 2019 (Fig. 4).



Fig. 4. *Rhinolophus rex*. Photographed by Nguyen Truong Son.

Rhinolophus thomasi Andersen, 1905

We collected three individuals (two males from the Cham Chu NR, one female from the Bac Me NR) and identified them on the basis of their morphology with FA = 45.56 mm, GL = 46.26–48.06 mm. The obtained fragment of *cytb* was compared with the sequences available from GenBank using the BLAST tool and the sequence is 97.7% similar to *R. sinicus* (GenBank accession no. KP257597, Sun *et al.*, 2016), 99.1% to *R. thomasi* (GenBank accession no. EU434943, Sun *et al.*, 2009), and 98.3% to *R. affinis* (GenBank accession no. MK976912, Mao *et al.*, 2019).

Taxonomic remarks: Despite Dang Ngoc Can *et al.* (2008) arguing that this is a widespread Vietnamese species, Kruskop (2013) demonstrated that the species remains poorly known and occurs in the Phong Nha–Ke Bang NP only. In its natural history, the species is similar to *R. sinicus*. Nguyen Truong Son *et al.* (2010, 2011), Dang Huy Phuong & Nguyen Truong Son (2011), and Dang Huy Phuong *et al.* (2013) suggested that the species is mostly recorded from limestone areas. Recently, there is no unambiguous decision on a species affiliation of this taxon in Vietnam.

Family HIPPOSIDERIDAE

Aselliscus dongbacanus Vuong, Csorba, Görföl, Arai, Nguyen, Hoang, Hasanin, 2015

This is a small leaf-nosed bat (mean FA = 42.25 mm, mean GL = 15.39 mm) that in its size and external morphology is very close to the widespread *A. stoliczkanus* (Vuong Tan Tu *et al.*, 2015), from which it differs primarily in the longer canines. Our specimens were captured at limestone caves in both Bac Me and Cham Chu NRs. Forty individuals were caught by a harp trap at the sites surrounded by forest in the Bac Me area (22.8512° N, 105.1796° E, 737 m a.s.l.) and in Cham Chu (22.2948° N, 104.9885° E, 664 m a.s.l.). This species was found together with other leaf-nosed bats, *Hipposideros armiger* and *H. cf. larvatus*. According to our estimation, a species' colony size in the surveyed caves was 300 to 400 individuals. This species was described in 2015 from the limestone area of the Ba Be NP in Bac Kan Province, north-eastern Vietnam and was also reported from Tuyen Quang, Ha Giang and Cao Bang Provinces (Vuong Tan Tu *et al.*, 2015). The closely related *A. stoliczkanus* has been recorded from north-western and central Vietnam and Laos, Thailand, Myanmar (Francis, 2019); the ranges of two species are likely to be separated by the Red River valley.

Hipposideros armiger (Hodgson, 1835)

It is the largest Asian *Hipposideros* species with FA up to 98.9 mm and GL up to 32.01 mm (Vu Dinh Thong *et al.*, 2012). Morphologically, it is highly similar to the recently described *H. griffini* (see Vu Dinh Thong *et al.*, 2012), from which it mainly differs in larger skull measurements. Fourteen individuals (FA = 86.57–96.58 mm, GL = 31.11–32.91 mm) were collected from caves in the Bac Me and Cham Chu NRs, where other bat species,

such as *A. dongbacanus* and *H. cf. larvatus*, were also found. Few individuals were also collected using mist nets outside the caves and other study sites. In the Bac Me NR, they roosted in high and large cavities on the ceiling of a limestone cave. The colony size was estimated to be of some 200 individuals. The colony size in the Cham Chu NR was smaller. Some pregnant females were collected in May in the Bac Me NR.

Taxonomic remarks: Analysis of complete *cytb* gene and partial D-loop have shown that *H. armiger* differs from the closely related *H. griffini* by 5.3–5.4% (Vu Dinh Thong *et al.*, 2012). However, recent results in nuclear genes have shown no significant deviation between these species (Yusefovich *et al.*, 2020). This result together with uncertain morphological difference and unclear border of distribution areas of both species suggests the need for the further and more wide-scale studies.

Hipposideros cf. larvatus (Horsfield, 1823)

Thirty-five individuals of this medium-size leaf-nosed bat were captured (FA = 55.10–61.50 mm, GL = 21.91–23.39 mm), composing about 28.7% of all bats captures during the field work in both sites. These bats were observed in larger limestone caves with high ceilings. The colony in the Bac Me NR was estimated to be 100–200 individuals. They concentrated in small groups in different positions and co-occupied the cave with other species, including *H. armiger*, *A. dongbacanus* and *H. gentilis*. This species alongside with *A. dongbacanus* was found to be the most abundant bat in this area, occurring almost in all studied habitats. Some collected males captured in the Bac Me NR in October possessed a well-developed frontal gland behind the posterior noseleaf (Fig. 5).



Fig. 5. *Hipposideros cf. larvatus*. Photographed by Nguyen Truong Son.

Taxonomic remarks: The *H. larvatus* species complex has a vast distribution across SE Asia (Francis, 2019) and, in particular, throughout Vietnam (Kruskop, 2013). The taxonomic structure and species delimitations within this complex are highly tangled and insufficiently studied (Thabah *et al.*, 2006; Kruskop, 2015). In the latter study, it was shown that there are at least four species in this complex in the Vietnam, and most probably none of them belongs to “true” *H. larvatus*. A smaller form inhabiting northern Vietnam differs genetically from *H. larvatus* from southern Thailand, as well as from *H. grandis*, and sometimes is referred to as *H. cf. poutensis* (Yusefovich *et al.*, 2020). *H. poutensis* was described from Hainan Island (Allen, 2006); comparative material from there is needed to clarify the matter. Until such a comparison is undertaken, we have designated the studied morphotype as *H. cf. larvatus*.

Hipposideros gentilis K. Andersen, 1918

This is a small sized bat with FA about 40.69 mm (39.2–42.17 mm) and large rounded ears. Two specimens were captured in the Bac Me NR by mist nets, one in a karst cave in May and another, a juvenile female in October 2019.

Taxonomic remarks: This species was previously considered within *H. pomona*. However, it was shown that specimens of *H. pomona* from the type locality (SW India) and those from the remaining range differ significantly in morphology, and the two forms should be regarded as different species (Srinivasulu & Srinivasulu, 2018). “*H. gentilis* K. Andersen, 1918” represents the valid name for the second form. Its intraspecies structure is complicated, containing few highly divergent mitochondrial lineages of an uncertain taxonomic status



Fig. 6. *Lyroderma lyra*. Photographed by Ly Ngoc Tu.

(Francis *et al.*, 2010; Zhao *et al.*, 2015). However, it was shown that all these lineages at least form a monophyletic group (Yusefovich *et al.*, 2020).

Family MEGADERMATIDAE

Lyroderma lyra E. Geoffroy, 1810

Until recently, this large species of the false vampire bats was considered within the genus *Megaderma*. However, both genetics and morphology support its distinct generic status (Soisook *et al.*, 2015).

During the field survey, four females were captured in Loong Booc Cave (22.2296° N, 105.0489° E, 293 m a.s.l.) at Cham Chu NR with FA = 68.8–71.76 mm, GL = 29.64–31.14 mm (Fig. 6).

Family VESPERTILIONIDAE

Myotis chinensis (Tomes, 1857)

It is the largest *Myotis* species in SE Asia (Francis, 2019). In Vietnam, records include the Hoang Lien NP (Lao Cai Province), the Ba Be NP (Bac Kan Province), the Na Hang NR (Tuyen Quang Province), the Huu Lien NR (Lang Son Province), the Cuc Phuong NP (Ninh Binh Province), the Xuan Son NP (Phu Tho Province), the Pu Mat NP (Nghe An Province) and the Phong Nha–Ke Bang NP (Quang Binh Province) (Bates *et al.*, 1999; Hendrichsen *et al.*, 2001; Nguyen Truong Son *et al.*, 2002; Dang Ngoc Can *et al.*, 2008). Despite having a wide range, the population status of this species in Vietnam has not been accurately assessed.

During the field survey, an adult male (FA = 66.26 mm, GL = 24.17 mm) was collected (Fig. 7). The animal was captured by a mist net set up across a stream nearby a cave (22.2948° N, 104.9883° E, 664 m a.s.l.) at the late night. To date, the species in northern and central Vietnam has only been recorded from near cave entrances in limestone habitats with the presence of rivers or streams (Bates *et al.*, 1999, 2001; present paper).



Fig. 7. *Myotis chinensis*. Photographed by Nguyen Truong Son.

ORDER RODENTIA
Family SPALACIDAE

Rhizomys pruinosus (Blyth, 1851)

The hoary bamboo rat is a common and widespread species in Vietnam (Francis, 2019; Dang Huy Huynh *et al.*, 2008). Its preferred habitat is a hilly bamboo forest mixed up with scrub and grass (Lunde & Nguyen Truong Son, 2001). This species is often hunted for food by local people (Aplin & Molur, 2016).

During our surveys, one specimen of *R. pruinosus* was collected by the local trapper in the Cham Chu NR. The external body measurements of this species are as follows: BW = 1300 g, HB = 320 mm, TL = 140 mm, HF = 57.54 mm, and E = 22.82 mm. Based on the external morphology data by Francis (2019), a significant difference in the tail length of the studied specimen (140 mm vs. 100–120 mm) has been recorded. Besides, its fur colour is greyish brown, with many long guard hairs, and more specifically with a white blaze on the forehead (from the top of the nose to the forehead). The cheek fur is lighter (Fig. 8). However, a molecular analysis shows that the specimen indeed belongs to *R. pruinosus* (Tab. 3).

Family SCIURIDAE

Belomys pearsonii (Gray, 1842)

This widespread species is distributed throughout northern to southern Vietnam, such as Ha Giang, Lao Cai, Quang Binh, Dong Nai, Ba Ria–Vung Tau Provinces (Dang Ngoc Can *et al.*, 2008; Oshida *et al.*, 2015). This species can only be found in the areas of high-quality forests with tall canopies that allow animals to hover. But currently, the information about the records and distribution of this species are still deficient due to a relatively small number of individuals in nature.

One adult female was caught by using a local trap in a limestone forest habitat of the Bac Me NR, 22.85278° N, 105.15417° E, 630 m a.s.l. in 27 May 2019. This is a small flying squirrel with BW = 200 g; HB = 185 mm, TL = 165 mm, HF = 27.75 mm, HF = 34.73 mm, and E = 20.99 mm.

Taxonomic remarks: Thorington *et al.* (2012) recognized four subspecies of *B. pearsonii*: *pearsonii*, *blandus*, *kaleensis*, and *trichotis*. Based on the specimens from Vietnam, Oshida *et al.* (2015) showed a significant genetic variation within *B. pearsonii*, with a pairwise distance of the complete *cytb* sequences being greater than 11% among the populations from northern and central Vietnam. A further study on the external, craniodental and bacular morphology of the *Belomys* species is needed to identify clear diagnostic characters.

Family MURIDAE

Chiromyscus thomasi

Balakirev, Abramov, Rozhnov, 2014

C. thomasi was suggested to occur from north-western (Son La, Lao Cai Provinces) to central Vietnam (Kon Tum and Nghe An Provinces) (Balakirev *et al.*, 2014).



Fig. 8. *Rhizomys pruinosus* from the Cham Chu NR. Photographed by Nguyen Truong Son.

This species was recently found in Dien Bien Province in 2019 (the specimen deposited in the Institute of Ecology and Biological Resource, Vietnam Academy of Science and Technology).

During the present survey, a single female was collected in the Cham Chu NR at 255 m a.s.l. HB length of this specimen is 180 mm, TL = 250 mm. Balakirev *et al.* (2014) reported this species to have HB = 145–180 mm and a relatively short tail (200–231 mm). GL of the Cham Chu specimen is 44.58 mm against 41–43 mm in specimens from Son La Province (Balakirev *et al.*, 2014). Genetically, this specimen is close to the holotype of *C. thomasi* from Son La (Tab. 3).

The find of this species in the Cham Chu NR enlarges the known species range in northern Vietnam. Thus, this species occurs on both sides of Red River.

Chiromyscus langbianis (Robinson, Kloss, 1922)

C. langbianis is a common species distributed throughout Vietnam (Dang Ngoc Can *et al.*, 2008). We collected five specimens during the field surveys, one from the Cham Chu NR and four from the Bac Me NR. The specimens were captured by cage traps baited by cassava. This rat has a medium size (HB = 140–190 mm) with a long monochrome black tail (TL = 180–220 mm). The specimen NTS 2019.10.37 from Ha Giang Province, which is in the *Niviventer* clade (Fig. 9), was identified genetically as *C. langbianis*.

Taxonomic remarks: *Niviventer–Chiromyscus* s. lato is a complex group. A taxonomic status of the Lang Bian rat is still controversial. Balakirev *et al.* (2014) placed *Niviventer langbianis* to the genus *Chiromyscus* based on molecular data. In our tree, the monophyly of *Niviventer*, including *C. langbianis*, is not supported with high confidence (Bayesian posterior probability, PP = 71%). However, independent clades within the genus are significantly corroborated (PP ≥ 98%) as is the genus *Chiromyscus* (PP = 100%). More data, both from mitochondrial and nuclear genes, are needed to clarify the relationships in this group.

Niviventer fulvescens (Gray, 1874)

N. fulvescens is a widespread and common species in SE Asia (Balakirev *et al.*, 2011; Francis, 2019). This

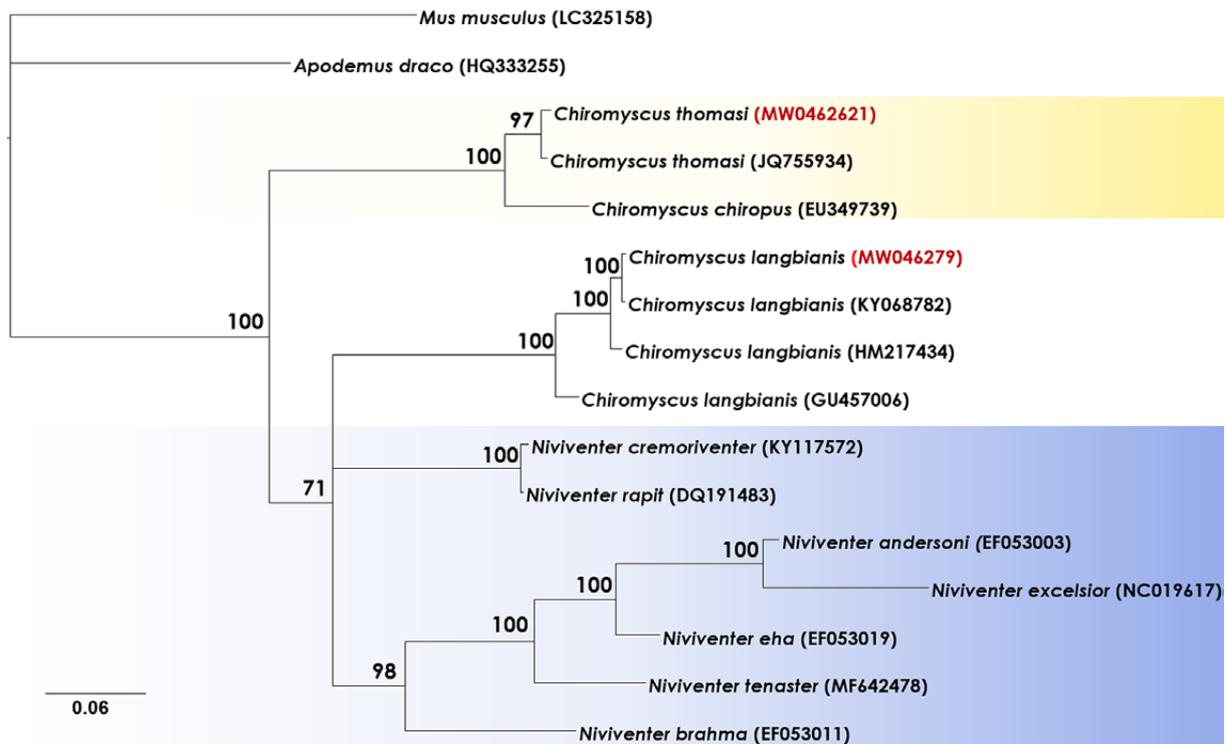


Fig. 9. The phylogenetic relationships in *Niviventer*–*Chiromyscus*, as reconstructed by the MrBayes based on *cytb* and partial tRNA-Thr data using GTR+I+G model. Numbers above branches correspond to Bayesian posterior probabilities.

species is usually caught by cage-traps set up on trees along streams.

During the field survey, we collected three specimens of this species. Among them, one was subadult and could not be identified with confidence. We decided to use the DNA barcoding approach to determine its taxonomic status. Our sequence data confirmed that the specimen indeed belongs to *N. fulvescens* (Tab. 3).

Conclusion

Based on the results of our field surveys, the studied sites of the Cham Chu and Bac Me NRs account for one Scandentia species, four Eulipotyphla species, 14 Chiroptera species and 17 Rodentia species. However, many species documented in Tuyen Quang and Ha Giang by Nguyen Truong Son *et al.* (2011) could not be confirmed during our surveys, including *Blarinella griselda*, *Chodsigoa caovansunga*, *Chodsigoa parca*, *Scaptonyx fuscicaudus*, *Mogera latouchei*, *Hipposideros gentilis*, *Leopoldamys* spp.

Our study shows a greater number of species in the surveyed sites than that recorded from the Huu Lien NR in Lang Son Province (21 species) (Lunde *et al.*, 2007). However, the number of bat species is lower than that documented in the Ba Be NP (27 species) and the Na Hang NR (45 species) (Nguyen Truong Son & Vu Dinh Thong, 2008). These regions share some common species: viz., *Suncus murinus*, *Cynopterus sphinx*,

Rhinolophus pearsonii, *R. pusillus*, *R. microglobosus*, *Hipposideros armiger*, *H. cf. larvatus*, *Aselliscus dongbacanus*, *Rhizomys pruinosus*, *Callosciurus erythraeus*, *C. inornatus* and *Rattus andamanensis*.

We were able to capture only one individual of *Belomys pearsonii* in the Chau Ca Forest. This flying squirrel is regarded as an indicator of a forest quality (Kato *et al.*, 2011). IUCN (2020) listed it as Data Deficient, whereas the Vietnam Red Data Book (2007) accessed it as a Critically Endangered species.

Based on both molecular and morphological evidence, the new records of *Aselliscus dongbacanus* and *Chiromyscus thomasi* in north-eastern Vietnam have been confirmed. Besides, although external characters and skull morphology of all the collected mole specimens being similar to those of *Euroscaptor orlovi*, they are significantly different genetically. Therefore, future studies on the mole population should be conducted to clarify the taxonomic status of the studied population.

Some species are considered rare because the number of specimens encountered were fewer than 10, although the survey efforts were high. The total survey effort for the bat was 4374 m²n/h mist nest and 675 m²n/h harp trap. However, we could only collect single specimens of several bat species, including *Rhinolophus pusillus*, *R. affinis* and *Myotis chinensis*. The total survey effort for rodents is 981 trap nights, but for some species, only a single specimen was collected: e.g., *Berylmys bowersi* and *Chiropodomys gliroides*. Moreover, several

common species did not yield many specimens: viz., *Callosciurus inornatus* (two specimens collected in the Bac Me NR), *Rhizomys pruinosus* (only one specimen from Cao Duong, the Cham Chu NR). We did not record any information on the mammal occurrence in the areas close to anthropogenic places, rice lands and orange plantations. However, we observed many individuals of these species in local houses. The situation suggests that the surveyed sites are heavily impacted by human activities, such as orange production, agricultural expansion, forest loss, mining, and especially by a high level of poaching. The species considered in this study warrant further investigation to verify their conservation status and assess possible anthropogenic threats.

Based on the present survey, the dominant mammal groups in terms of species diversity are Chiroptera (40%) and Rodentia (45.7%). However, the number of bat species is much lower, as compared to the earlier study conducted in the same region (16 vs. 35) (Nguyen Truong Son *et al.*, 2011). We have also documented a couple of abundant species, such as *Aselliscus dongbacanus* (40 of 176 specimens) and *Hipposideros cf. larvatus* (37 of 176 specimens). Other common species include *Suncus murinus*, *Aselliscus dongbacanus*, *Hipposideros armiger*, *H. cf. larvatus*, *Callosciurus erythraeus*, *C. inornatus* and *Rhizomys pruinosus*.

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