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A new shrew mole species of the genus *Uropsilus* (Eulipotyphla: Talpidae) from northwestern Vietnam

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Abstract

A new medium-sized shrew mole species of the genus *Uropsilus* from Mount Fansipan, Hoang Lien National Park, Lao Cai Province, northwestern Vietnam is described based on morphological and molecular differences. *Uropsilus fansipanensis* **sp. nov.** is distinguished from the other *Uropsilus* species by the combination of the following features: the dorsum is lightly reddish-brown and venter is dark gray; the dark gray tail is long and slender, with a scattered white base and short bristle hairs; orbital process is oriented upwards posteriorly; lacrimal foramen is well developed and much larger than infraorbital foramen; the lower first premolar is approximately the same size as the lower third premolar. Genetic distances in terms of mitochondrial cytochrome *b* from other *Uropsilus* species presented pairwise divergences from 8.63 to 20.70%. To date, the new species is known to exist only in the type locality of Mt. Fansipan, a wet and cold temperate climate area with an upper montane forest at an elevation of approximately 2900 m, forming the southernmost distribution of the genus *Uropsilus*.

Key words: Uropsilinae, taxonomy, Mt. Fansipan, Hoang Lien Son range

Introduction

Shrew moles of subfamily Uropsilinae Dobson, 1883 are classified as family Talpidae, order Eulipotyphla, class Mammalia, and are endemic to central and southern China and adjacent Myanmar (Hoffmann 1984; Wan *et al*. 2013; Kryštufek & Motokawa 2018; Hu *et al*. 2021). The subfamily Uropsilinae currently comprises of a single genus, *Uropsilus* Milne-Edwards 1872 (Kryštufek & Motokawa 2018). Kryštufek & Motokawa (2018) suggested that the genus *Uropsilus* occurs at high altitudes, from 1550 to 4600 m above sea level (asl.). Hu *et al*. (2021) mentioned that *Uropsilus* inhabits mountain forests and shrub grasslands and found a shrew mole population from an altitude of 1064 to 1273 m asl. in eastern China. This genus has not yet been recorded in Vietnam.

Milne-Edwards (1872) described *U. soricipes* from Baoxing, Sichuan (originally Moupin), which is the type species of the genus *Uropsilus* and possesses 34 teeth and dental formula I 2/1, C 1/1, P 3/3, M 3/3 = 34 representing number of incisors (I), canines (C), premolars (P), molars (M) in each side of upper and lower dentition. Subsequently, Thomas (1912) described two new shrew mole species, differing in the presence or absence of one or two antemolars from *U. soricipes* and established two new monotypic genera with two new species *Rhynchonax andersoni* Thomas, 1911 (I 2/2, C 1/1, P 4/3, M 3/3 = 38) from Mount Emei (originally Omi-san), Sichuan and *Nasillus gracilis* Thomas, 1911 (I 2/1, C 1/1, P 4/4, M 3/3 = 38) from Mount Jinfo (originally Chin-fu-san) in Nanchuan, Chongqing. Thus, discrimination among genera was based on differences in the dental formula. Later, Thomas (1922) described *N. investigator* from the Kui-chiang-Salween divide at 28°N, 11000 feet (= 3353 m)

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altitude, Yunnan. Allen (1923) described *R. andersoni nivatus* from Yulong Snow Mountain (originally Ssu-shan), Lijiang, Yunnan, and *R. andersoni atronates* from Mu-cheng, Salween drainage, Yunnan. These two names were described as subspecies of *R. andersoni*, but they were later treated as conspecific with *N. gracilis* (e.g., Hoffman 1984; Corbet & Hill 1992; Hutterer 1993, 2005; Wan *et al*. 2013), because their dental formula is that of *Nasillus* (I 2/1, C 1/1, P 4/4, M 3/3 = 38).

Ellerman & Morrison-Scott (1951), Cranbrook (1960), Corbet & Hill (1980), and Honacki *et al*. (1982) considered that *Rhynchonax* and *Nasillus* are junior synonyms of *Uropsilus* and that *Uropsilus* is a monotypic genus consisting of one species (*U. soricipes*) with five subspecies (*U. s. soricipes*, *U. s. gracilis*, *U. s. investigator*, *U. s. andersoni*, and *U. s. nivatus*), while Gureev (1979) defended the view that shrew mole consists of three genera and four species (*U. soricipes*, *Nasillus gracilis*, *N. investigator*, and *Rhynchonax andersoni*). Hoffmann (1984) reviewed shrew moles by examining almost all holotypes and the majority of extant specimens in North American and European museums, and recognized three species (*U. soricipes*, *U. gracilis*, and *U. andersoni*) in a single genus *Uropsilus* and considered *investigator*, *nivatus*, and *atronates* to be junior synonyms of *U. gracilis*. Corbet & Hill (1992) and Hutterer (1993) followed this view. Hutterer (2005) separated *U. investigator* from *U. gracilis* based on their morphological differences and sympatric distribution, and consequently recognized four species in the genus *Uropsilus* (*U. soricipes*, *U. gracilis, U. investigator*, and *U. andersoni*). Hoffmann & Lunde (2013) followed this classification and recognized four species distributed in China.

Liu *et al*. (2013) described a new species *U. aequodonenia* from the Luoji Shan Scenic Area, Puge County, Sichuan, China. The species was suggested to be closely related to *U. andersoni*, while it possesses a distinct dental formula (I 2/2, C 1/1, P 3/3, M 3/3 = 36) that is different from the other *Uropsilus* species. Based on molecular approaches, Wan *et al*. (2013) reconstructed a robust phylogeny and found cryptic diversity in *Uropsilus*, and determined seven distinct species (*U. soricipes*, *U. gracilis, U. investigator*, *U. andersoni*, *U. aequodonenia*, *U. nivatus* and *U. atronates*), as well as five putative and undescribed species. Wan *et al*. (2018) regenerated gene trees with additional specimens illustrating 15 distinct clades and explained that the diversification of shrew moles in the mountains of Southwest China is largely cryptic owing to niche conservatism and complex topography.

In consideration of Wan *et al*. (2013), Kryštufek & Motokawa (2018), and Burgin *et al*. (2020), seven shrew mole species are recognized in the genus *Uropsilus*: *U. soricipes*, *U. gracilis*, *U. investigator*, *U. andersoni*, *U. aequodonenia*, *U. nivatus*, and *U. atronates*; although the taxonomic statuses of species in Myanmar are unclear. Wan (2015) described six names as new species from China, but the PhD thesis (Wan 2015) is not regarded as published within the meaning of the International Code of Zoological Nomenclature (amended Article 8.1 and 9.12: ICZN 1999, 2012). The six species-group names introduced by Wan (2015), i.e., *U.* "robustus", *U.* "qinlingensis", *U.* "wulingensis", *U.* "binchuanensis", *U.* "jingdongensis", and *U.* "parva" are thus deemed to be unavailable. Hu *et al*. (2021) described a new species, *U. dabieshanensis* from the Dabie Mountains, Anhui, as the easternmost distribution of the genus based on morphological and molecular characteristics. Therefore, the genus *Uropsilus* currently includes eight species. In addition, Hu *et al*. (2021) indicated five names (*U.* "qinlingensis", *U.* "wulingensis", *U.* "binchuanensis", *U.* "jingdongensis", and *U.* "parva") of Wan (2015) and another name *U.* "rubustus" in the molecular phylogenetic trees, but these six names are not accompanied by a description or definition, and are not available following Article 13 of the International Code of Zoological Nomenclature (ICZN 1999).

To the west of the Red River, the Hoang Lien Son Range of northwestern Vietnam is at the end of the southeastern extension of the Himalayan mountains (Tordoff *et al*. 1999; Sterling *et al*. 2006) and Mt. Fansipan, with an altitude of 3143 m asl., is the highest mountain in this range. The Hoang Lien Son Range has risen approximately 65 million years ago and continues to rise till the current day (Sterling *et al*. 2006). Above 3000 m on Mt. Fansipan, the climate is temperate with freezing temperatures during December and January, and possesses around three snowfall days per year (Sterling *et al*. 2006; Bain & Hurley 2011). The mountainous areas in northern Vietnam, close to the Vietnam–China border, host a number of Eulipotyphla species that might also be found in southwestern China and are interesting in zoogeography (Saito *et al*. 2021).

During our recent fieldwork on Mt. Fansipan, Hoang Lien National Park, Lao Cai province, northwestern Vietnam, two shrew moles were collected. Molecular analyses and morphological examination showed that these specimens represent an undescribed species of the genus *Uropsilus*, which is distinct from the currently known eight species. In the present study, we describe a new species of the genus *Uropsilus* in Vietnam.

Material and methods

Sampling. A field survey on small mammals was conducted from April 30 to May 6, 2022, on Mt. Fansipan, along a trail from 2200 m to 2950 m (Hoang Lien National Park, Lao Cai Province). The first shrew mole (field number, Motokawa 837) was collected using a Sherman live trap (7.5 × 7.5 × 24 cm) at 22°18.804 N and 103°45.92 E, at an altitude of 2821 m. The second (field number, Motokawa 914) was trapped by pitfall (plastic cup of height 150 mm × diameter 95 mm) at 22°18.783 N and 103°45.92 E, at an altitude of 2840 m.

Specimen examination. Photographing and measurements of the total length (TL), tail length (T), ear length (E), forefoot length (FF1 and FF2, without and with claws, respectively), hindfoot length (HF1 and HF2, without and with claws, respectively), and body mass (Wt) were made. Head-body length (HB) was calculated by subtracting T from TL. The specimens were fixed in 70% ethanol. The liver samples were preserved separately in 99% ethanol. Skulls were separated from the body and cleaned. Twelve cranial and dental measurements were taken from each specimen following Thomas (1912), Allen (1923), Hoffmann (1984), and Hu *et al*. (2021): profile length (PL), from the most anterior point of upper incisor to the most posterior point of the skull; basal length (BL), from the tip of the premaxilla to the posterior margin of the occipital condyles; palatal length (MPL), from the anterior tip of the first incisor to the posterior tip of the palate; greatest neurocranium breadth (GNB), zygomatic breadth (ZB), greatest breadth of snout (GBSn), least breadth between orbits (LBO), braincase height (BH), upper tooth row length including first incisor (UTRL), greatest width across the upper second molars (M2–M2), length of mandible not including first incisor (LM), and mandibular tooth row length including first incisor (MTRL). All measurements were taken using digital calipers to the nearest 0.01 mm. The specimens were deposited at the Department of Vertebrate Zoology, Institute of Ecology and Biological Resources (IEBR), Vietnam Academy of Science and Technology, Hanoi. In addition, we examined five specimens of four *Uropsilus* species deposited in the Natural History Museum, London: *U. soricipes* BMNH 1911.9.8.12; *U. gracilis* BMNH 1911.9.8.13 (holotype); *U. investigator* BMNH 1922.9.1.16 (holotype); *U. andersoni* BMNH 1911.2.1.30 and 31. We also referred to photographs in Liu *et al.* (2013), Wan (2015), and Hu *et al.* (2021) for non-metric morphological characters of *U. aequodonenia*, *U. nivatus*, *U. atronates*, and *U. dabieshanensis*.

Molecular data and phylogenetic analyses. DNA was extracted from tissues preserved in 99% ethanol using the DNeasy® Blood & Tissue DNA kit (Qiagen, Hilden, Germany), following the manufacturer's protocol. Polymerase chain reaction (PCR) was performed to amplify partial fragments of mitochondrial DNA of cytochrome *b* (cyt*b*) and nuclear DNA of recombination activating genes 1 and 2 (RAG1 and RAG2). These genes were amplified using the 2× Taq plus PCR Master Mix kit (Biosharp, Anhui, China). The primers used were SoriR (5'-TGACATGAAAAATCATCGTTG-3') and SoriF (5'-CCATCTCTGGTTTACAAGAC-3') for cyt*b* (Bui *et al*. 2020a); Rag1F1851 (5'-ACATGGAAGAAGACATCTTGGAAGG-3') and Rag1R2486 (5'-AATGTCACAGTGAAGGGCATCTATGGAAGG- 3') for RAG1 (Sato *et al*. 2004); RAG2-F220 (5'-GATTCCTGCTAYCTYCCTCCTCT-3') and RAG2-R995 (5'-CCCATGTTGCTTCCAAACCATA-3') for RAG2 (Teeling *et al*. 2000). Fragments of these sequences were amplified under the following PCR conditions: 94°C for 5 min; 40 cycles at 94°C for 30 s, 52°C for 30 s, and 72 °C for 2 min; followed by a final extension step at 72°C for 7 min for cyt*b*; and 95°C for 5 min; 35 cycles at 95°C for 30 s, 56.8–61.6°C for 45 s, and 72°C for 1 min; 72°C for 10 min for RAG1 and RAG2. The PCR products were purified and sequenced by 1st BASE (Selangor, Malaysia). The sequences obtained were deposited in GenBank (accession number: OQ509373, OQ509374 (cyt*b*); OQ509371, OQ509372 (RAG1); OQ512024, OQ512025 (RAG2), Appendix 1). We also used GenBank sequences from 107 individuals of other taxa (Appendix 1).

Chromas Pro software (Technelysium Pty Ltd., Tewantin, Australia) and MEGA 11 (Tamura *et al*. 2021) were used to edit and align sequences. Alignment was performed using MUSCLE in MEGA 11 (Tamura *et al*. 2021) using the default settings. The sequences were then assembled by eye to manually confirm the correct sequence alignment. The lengths were 1140 bp for cyt*b*, 1010 bp for RAG1, and 751 bp for RAG2; the concatenated sequences yielded 2901 bp. Of these, 503 were variable, and 465 were parsimony informative. We used maximum likelihood (ML) and Bayesian inference (BI) methods to conduct phylogenetic analyses of concatenated cyt*b*, RAG1, and RAG2 fragment datasets. The ML and BI analyses produced topologies with log-likelihoods of −13113.89 and −13123.36, respectively. The optimum substitution models for both analyses were selected based on the corrected Akaike information criterion (AIC; Sugiura 1978) using Kakusan 4 (Tanabe 2011). The best-fit models for partition cyt*b,* RAG1, and RAG2 were GTR+G, HKY85+G, and GTR+G, respectively, for ML and BI analyses. The ML phylogenetic tree was constructed using IQ-TREE (Nguyen *et al*. 2015) with maximum likelihood bootstrap support (MLBS) evaluated by ultrafast bootstrap approximation with 1000 replicates (Hoang *et al*. 2018). The BI tree and Bayesian posterior probabilities (PP) were estimated using MrBayes v.3.2.7a (Ronquist & Huelsenbeck 2012). BI analyses were run with four Markov Chain Monte Carlo analyses for 10 million generations, with trees sampled every 100 generations. The runs were stopped when the average standard deviation of the split frequencies was below 0.01. The convergence of the runs and the effective sample size were checked using Tracer version 1.7.1 (Rambaut *et al*. 2018). The first 25% of sampled trees were discarded as burn-in. The remaining trees were summarized, and a 50% consensus tree was generated. The ML and BI trees were visualized in Figtree 1.4.4 (Rambaut 2018) and were represented using Adobe Illustrator (Adobe Inc. 2022).

Pairwise comparisons of uncorrected sequence divergences (*p*-distance) were calculated for cyt*b* fragments in MEGA 11 (Tamura *et al*. 2021) with variance estimated via bootstrap with 500 replications while gaps/missing data were treated using pairwise deletion.

Results

Phylogenetic analyses. The phylogenetic trees constructed using ML and BI methods were identical in topology, based on the concatenated cyt*b*, RAG1, and RAG2 fragments. We present only the ML tree (Fig. 1). Results of phylogenetic analyses showed that *Uropsilus* is a highly supported monophyletic group, including the two newly collected specimens from Mt. Fansipan (MLBS = 100% and PP = 1.0). The monophyly of the two Fansipan specimens was strongly supported by both methods (MLBS=100% and PP=1.0). The uncorrected *p*-distances (%, min-max) for cyt*b* between *Uropsilus* species are shown in Table 1. The Fansipan population differed from other populations in that the uncorrected *p*-distances were in the range from 3.22% (vs. *Uropsilus* sp. 6 from Mt. Wuliang and the western slope of Mt. Ailao, Yunnan, China) to 20.7% (vs. *U. investigator*). The Fansipan population formed monophyletic clusters with *Uropsilus* sp. 6 (3.22–3.94%), followed by *U. atronates* (8.63–10.18%).

Bradly & Baker (2001) and Baker & Bradly (2006) hypothesized that the 2–10% genetic variation of cyt*b* between mammalian populations could be indicative of valid species, and genetic distances greater than 10% could indeed indicate the presence of distinct species. Among the eight recognized species of *Uropsilus*, the uncorrelated *p*-distances were in the range of 7.65% (*U. andersoni* vs. *U. aequodonenia*) to 20.37% (*U. atronates* vs. *U. investigator*). This study revealed that the Fansipan population is genetically distinct with an uncorrelated *p*-distance in the range of 8.63% (vs. *U. atronates*) to 20.70% (vs. *U. investigator*) from the currently recognized eight species (Table 1); and these values are greater than the intraspecific uncorrelated *p*-distance of the eight species. Furthermore, the Fansipan specimens showed differences in morphological characteristics from the other eight *Uropsilus* species (Thomas 1912; Allen 1923; Hoffmann 1984; Kryštufek & Motokawa 2018; Hu *et al*. 2021). Therefore, we describe a new shrew mole species of the genus *Uropsilus*, based on specimens collected from Vietnam for the first time.

Species description

Uropsilus fansipanensis sp. nov.

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Holotype. IEBR-M-8101 (field number Motokawa 837), an adult male, from Mount Fansipan, Hoang Lien National Park, close to the 2900-m camping station (22°18.804 N and 103°45.92 E), Lao Cai Province, Vietnam collected by Masaharu Motokawa on May 1, 2022, deposited in the Department of Vertebrate Zoology, Institute of Ecology and Biological Resources (IEBR), Vietnam Academy of Science and Technology, Hanoi. Skull was extracted. The body was preserved in 70% ethanol as a wet specimen.

Paratype. IEBR-M-8102 (field number Motokawa 914), an adult male, from Mt. Fansipan, Hoang Lien National Park, along the Tram Ton–Fansipan peak trail (22°18.783 N and 103°45.92 E), Lao Cai Province, Vietnam, collected by Shinya Okabe on May 5, 2022, deposited in the IEBR. Skull was extracted. The body was preserved in 70% ethanol as a wet specimen.

TABLE 1. Uncorrected *p*-distance matrix showing percentage pairwise genetic divergences (%, min-max) for the cyt*b* gene between *Uropsilus* species/population in this study.

	Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	*U. fansipanensis* **sp. nov.**	0.08														
2	*Uropsilus* sp. 6	3.22–3.94	0.0–1.45													
3	*U. atronates*	8.63–10.18	7.99–10.43	0.0–7.9												
4	*U. gracilis*	9.05–9.51	8.42–9.85	8.43–10.28	0.0–1.35											
5	*Uropsilus* sp. 5	9.51–9.86	8.75–9.68	9.18–10.71	8.41–8.9	0.0–0.39										
6	*U. soricipes*	8.77–9.72	8.77–10.31	9.47–11.14	7.83–9.47	3.14–4.1	0.0–3.29									
7	*U. dabieshanensis*	11.08–11.45	11.18–11.83	11.17–13.89	9.73–10.43	9.82–10.33	10.22–11.51	0.0–0.39								
8	*Uropsilus* sp. 4	8.29–8.44	8.02–8.46	8.62–10.58	7.22–7.81	8.8–9.41	8.34–9.8	12.08–12.53	0.0–0.47							
9	*Uropsilus* sp. 3	11.14–11.29	10.25–10.67	9.76–11.23	10.54–11.25	10.19–10.59	10.29–10.66	11.81–12.02	9.01–9.21	0.0–0.0						
10	*Uropsilus* sp. 2	14.37–14.73	13.75–14.76	15.15–16.28	13.96–14.5	14.51–14.94	14.01–15.25	13.68–14.13	13.91–14.45	14.66–14.98	0.0–0.31					
11	*U. nivatus*	13.99–14.69	13.64–15.16	12.74–15.56	11.46–12.58	13.55–14.48	13.0–14.47	14.88–15.52	11.57–12.67	13.07–13.74	13.81–14.7	0.0–2.36				
12	*U. andersoni*	14.95–15.55	15.21–15.87	14.57–16.15	14.19–14.86	14.54–14.98	14.19–15.28	15.11–15.87	13.65–14.74	15.03–15.37	13.72–14.29	9.81–10.68	0.39–0.79			
13	*U. aequodonenia*	15.45–16.03	15.41–16.49	14.67–16.43	13.81–14.66	13.46–14.08	12.72–14.7	15.97–16.44	14.09–14.75	15.38–15.73	14.61–15.28	9.61–11.07	7.65–8.28	0.08–0.39		
14	*Uropsilus* sp. 1	18.85–20.26	19.15–20.59	17.28–19.0	16.42–18.31	16.52–17.3	16.81–18.38	16.74–18.11	17.85–19.0	17.99–18.98	17.47–18.61	16.84–18.34	17.78–18.94	17.3–18.23	0.0–2.44	
15	*U. investigator*	20.23–20.7	18.97–20.35	17.22–20.37	17.85–18.96	16.93–17.49	16.86–18.03	17.09–18.01	17.57–19.18	17.28–18.16	17.78–18.98	17.53–19.14	18.22–19.38	18.43–19.73	9.67–10.29	0.0–4.72

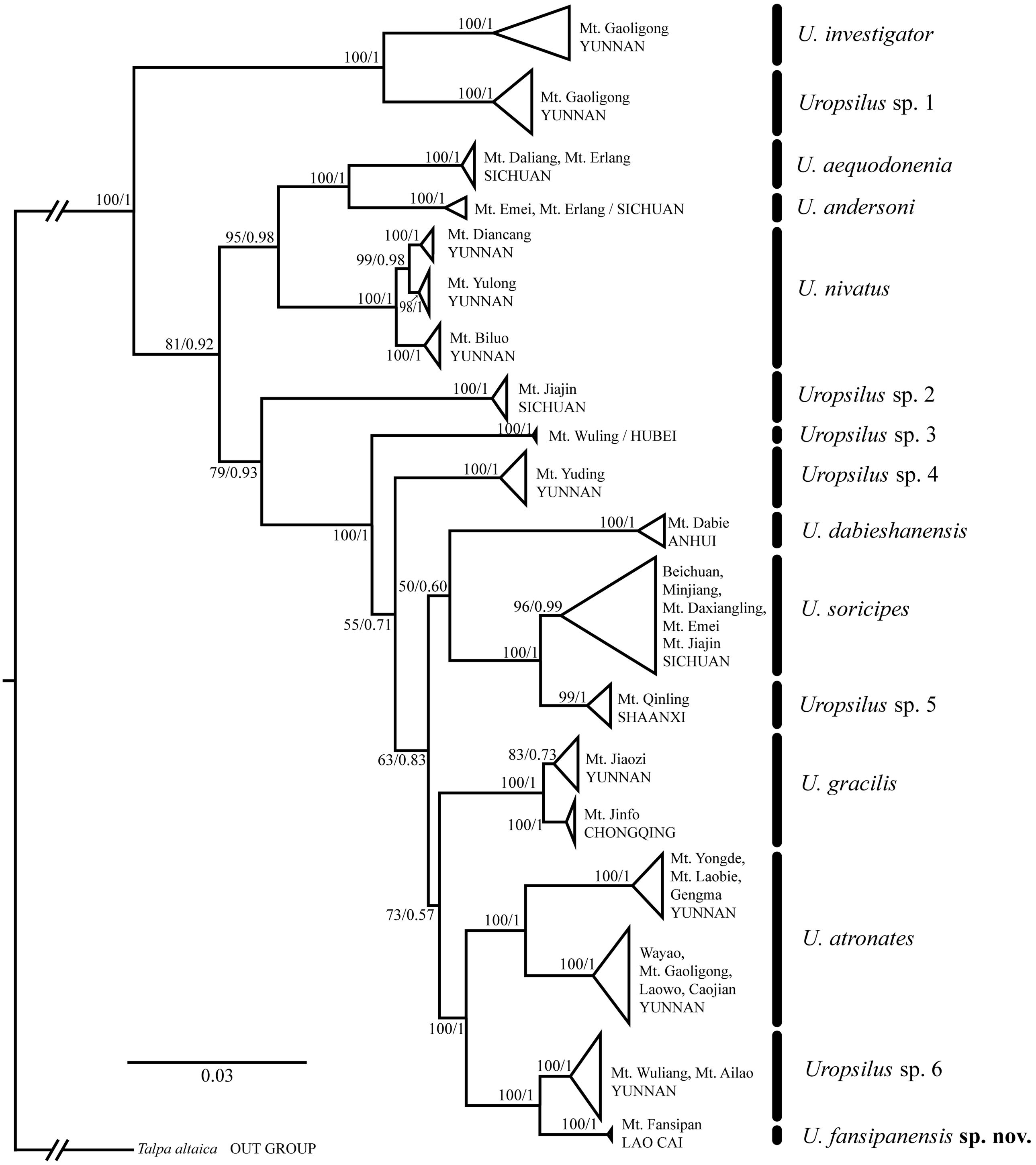

FIGURE 1. Maximum likelihood (ML) tree based on cyt*b*, RAG1, and RAG2 concatenated sequences for shrew mole species of genus *Uropsilus*. Maximum likelihood bootstrap support (MLBS) and Bayesian posterior probabilities (PP) are shown at each node (MLBS/PP).

Diagnosis. Medium-sized shrew mole. Body bicolor, dorsum lightly reddish-brown and venter dark gray, but the separation between the dorsum and venter is not obvious. The tip of the fur on the back reddish-brown, and the rest is gray. The tail uniformly dark gray, long, slender, and covered with small scales arranged in rings; gradually darken from base to tip. Short bristle hairs sparsely covering the tail from the base to the tip, and longer at the tip of the tail. The mastoid process developed sideways and pointed out. The interorbital region broad and parallel. The zygomatic arch stouter. The foramen magnum very large. The lacrimal foramen well developed and much larger than the infraorbital foramen. The orbital process oriented upwards anteroposteriorly. Dental formula I 2/1, C 1/1, P 4/4, M 3/3 = 38 including teeth of I1, I2, C1, P1, P2, P3, P4, M1, M2, M3 / i2, c1, p1, p2, p3, p4, m1, m2, m3 in the dentition. The buccal view of the upper fourth premolar (P4) triangular shape. The lower third premolar (p3) large in size. The lower first and third premolars (p1 and p3, respectively) approximately the same size. The lower canine (c1) larger than p1.

Description of holotype. Adult male, medium-sized shrew mole with a total length of 140.0 mm and a body mass of 8.0 g (Fig. 2). The reddish-brown dorsal pelage distinct from the dark gray ventral pelage. The tail dark gray, its length (62.5 mm) slightly more than 80% of the head-body length (77.5 mm). Nose elongated with nostrils facing outwards; snout bicolored, upper part dark gray and lower part yellowish. The pinna protrudes (E 8.51 mm) covered by sparse gray hair. Limbs covered with scales down to the toes with long, sharp, and opaque claws; forefoot short but fat (FF1 = 8.66 mm, FF2 = 9.66 mm); hindfoot long and slender (HF1 = 13.41 mm, HF2 = 15.16 mm), and the four limbs have the same color as the tail, with small black speckled scales. The small eyes, barely noticeable under the fur.

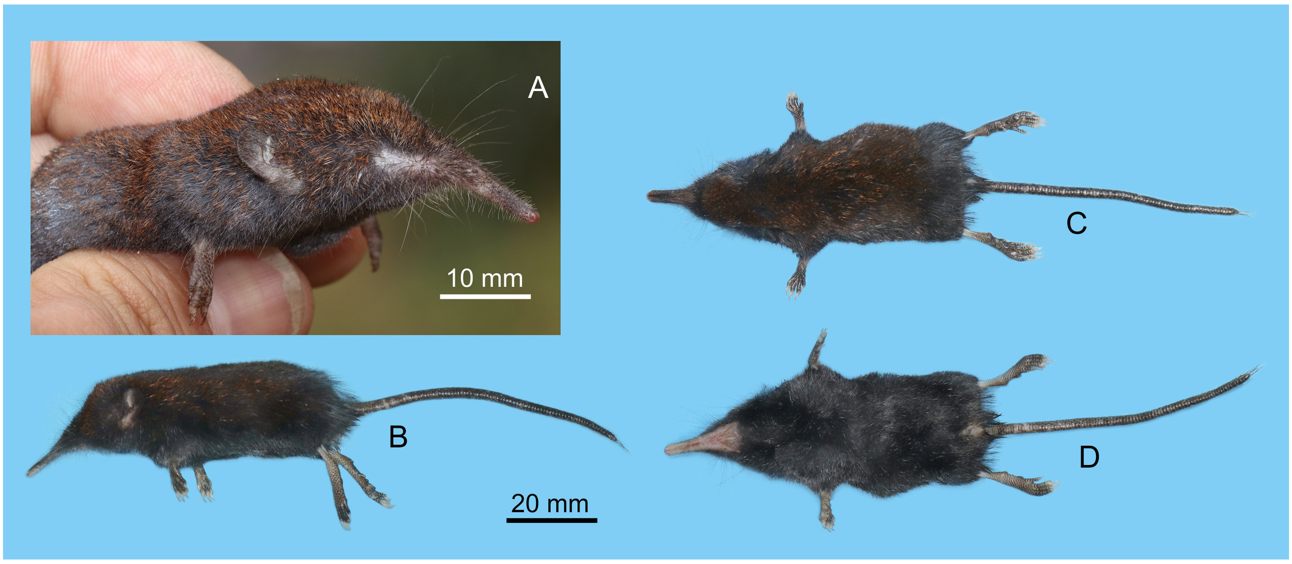

FIGURE 2. Lateral view of the body (A), lateral view (B), dorsal view (C), and ventral view (D) of the holotype (IEBR-M-8101) of *Uropsilus fansipanensis* sp. nov.

The skull (Fig. 3) long, and pyriform shaped with a short rostrum and a rounded braincase; palate relatively broad and possessing a sudden edge at the posterior end; pterygoid region deeply set; temporal ridges recognizable and converge in an X-shape; squamosal arm of the zygomatic arch sturdy; orbit locating at the midpoint of the skull; squamous processes sharp; bullae incomplete; pterygoid processes pointed saw-shaped; lacrimal foramen well developed and much larger than the infraorbital foramen; orbital process oriented upwards anteroposteriorly (Fig. 4). The mandible long and slender; coronoid process sharp and rear-facing crest; masseteric fossa arachnoid. Dental formula I 2/1, C 1/1, P 4/4, M 3/3 = 38 including teeth of I1, I2, C1, P1, P2, P3, P4, M1, M2, M3 / i2, c1, p1, p2, p3, p4, m1, m2, m3 in the dentition (Fig. 3). The upper first incisor (I1) taller than the second incisor (I2); both I1 and I2 lingually concave; the upper canine (C1) slightly larger than the upper first premolar (P1); the upper third premolar (P3) small and the smallest tooth in the upper tooth row. The remaining upper premolars are shown from larger size to smaller size in the following order: upper fourth premolar (P4), upper second premolar (P2), and P1. The upper first molar (M1) larger than the upper second molar (M2); length and width of M1 are almost equal, and the same was observed in M2. The lower first incisor absent; the lower first and third premolars (p1 and p3, respectively) approximately the same size; the lower canine (c1) larger than p1; the lower second molar (m2) possesses a large concavity on its lingual side and protoconids from m2 is the highest cusp in the lower toothrow.

Variation. The discoloration of the scales at the base of the tail showed substantial variation between the holotype and the paratype; the latter is strongly discolored. This is probably because the paratype is older than the holotype.

Etymology. The specific epithet "*fansipanensis*" refers to the type locality of the new species, Mt. Fansipan. We suggest "Fansipan shrew mole" and "Chuột chũi vòi phan-xi-pan" for the common names in English and Vietnamese, respectively.

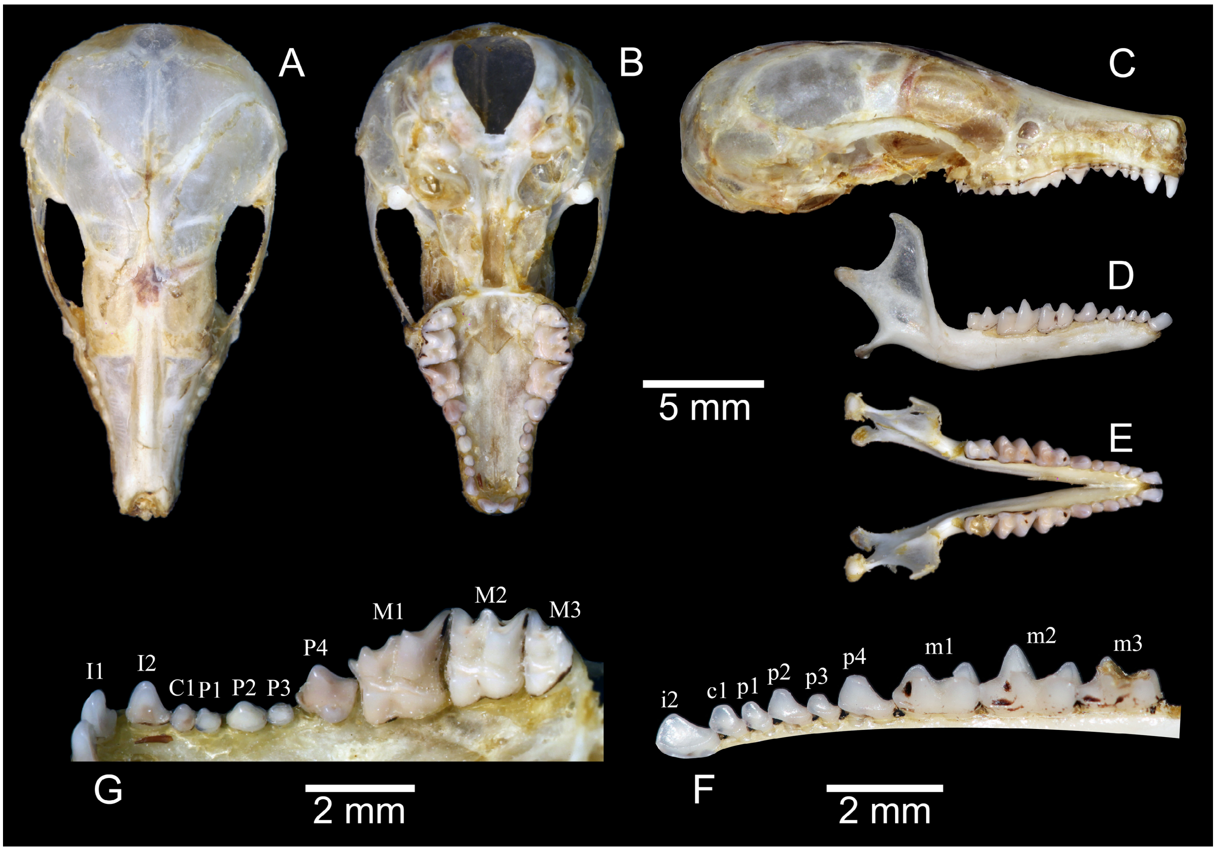

FIGURE 3. Dorsal view (A), ventral view (B), lateral view (C) of cranium, lateral view (D), dorsal view (E) of mandible, lower toothrow (right side, lingual view, F), and upper toothrow (right side, lingual view, G) of holotype (IEBR-M-8101) of *Uropsilus fansipanensis* **sp. nov.**.

Ecological notes. *U. fansipanensis* was found in a dwarf mountain forest on Mt. Fansipan, at an elevation of approximately 2800–2900 m. The surrounding habitat was grassy with shrubs on a thick and moist humus layer close to a small bamboo forest and a travel trail. During the field survey in May, which corresponds to the end of spring in northern Vietnam, the daily temperature fluctuates from 1 to 20°C, and sometimes rain occurs (Fig. 5A).

Distribution. *U. fansipanensis* is presently known only from the type locality in Mt. Fansipan, Hoang Lien National Park, Lao Cai Province, northwestern Vietnam (Figs. 5B, 6).

Comparisons (measurements are in mm)**.** All members of *Uropsilus* have a primary coloration of brown dorsal and gray ventral fur, while they differ in terms of their tail color. *U. fansipanensis*, *U. soricipes*, *U. gracilis*, *U. andersoni*, and *U. atronates* have a uniformly colored tail. On the other hand, *U. investigator*, *U. nivatus*, *U. aequodonenia*, and *U. dabieshanensis* have a bicolor tail, with the upper part being darker than the underside (Table 2; Liu *et al*. 2013; Wan 2015; Hu *et al*. 2021).

U. fansipanensis overlaps basic external morphological measurements with most of the other species of *Uropsilus* (Table 3). Nevertheless, it has a longer tail (T: 61.0–62.5) and hindfoot (HF: 13.41–13.57) than *U. dabieshanensis* (T: 52.4–54.1, HF: 12.8–12.9), and a shorter tail than *U. aequodonenia* (T: 67–73).

U. fansipanensis shows overlap in most cranial measurements (Table 4) with *U. soricipes*, *U. nivatus,* and *U. atronates*, except a slightly larger anterior labial margin of the second upper molars than *U. nivatus* and *U. atronates* (M2-M2: 6.36–6.40 *vs.* 6.15–6.35 *vs.* 5.95–6.3). Nevertheless, it can be distinguished in several cranial measurements from the other five *Uropsilus* species as detailed below. *U. fansipanensis* has smaller upper toothrow length (UTRL: 9.03–9.07 *vs.* 9.1–10.7), palatal length (MPL: 9.62–9.75 *vs.* 9.68–11.2), lower toothrow length (MTRL: 8.30–8.31 *vs.* 8.43–9.09), mandible length (LM: 13.52–13.77 *vs.* 14.01–15.00), and braincase height (BH: 6.90–6.91 *vs.* 7.18–7.6) than *U. gracilis*.

U. fansipanensis has a slightly wider snout (GBSn: 7.39–7.62 *vs.* 7.13–7.35) and longer mandible length (LM: 13.52–13.77 *vs.* 11.95–13.42) than *U. investigator*, while it has a shorter upper toothrow length (UTRL: 9.03–9.07 *vs.* 9.10–9.80).

TABLE 2. Comparison of morphological diagnostic characters among the nine *Uropsilus* species. Symbols showing: +, presence; ¬, absence; >, larger; <, smaller; =, similar size.

Species	Tail color	Lacrimal foramen vs infraorbital foramen	Orbital process	Number of teeth	P3	i3	p3	c1
U. fansipanensis **sp. nov.**	uniform	larger	upwards	38	+	¬	= p1	> p1
U. soricipes	uniform	similar	downwards	34	¬	¬	¬	> p1
U. gracilis	uniform	similar	downwards	38	+	¬	< p1	= p1
U. investigator	bicolored	smaller	downwards	38	+	¬	< p1	> p1
U. andersoni	uniform	similar	downwards	38	+	+	¬	> p1
U. aequodonenia	bicolored	smaller	downwards	36	¬	+	¬	> p1
U. nivatus	bicolored	smaller	downwards	38	+	¬	< p1	> p1
U. atronates	uniform	smaller	downwards	38	+	¬	< p1	= p1
U. dabieshanensis	bicolored	smaller	downwards	38	+	¬	< p1	> p1

TABLE 3. External measurements of nine *Uropsilus* species in mm. The number of specimens studied is indicated within parentheses.

Species	Source (n)	TL	T	HB	E	HF1 (HF2)	Wt
U. fansipanensis **sp. nov.**	This study (holotype, IEBR-M-8101)	140.0	62.5	77.5	8.51	13.41 (15.16)	8.0
	This study (paratype, IEBR-M-8102)	135.0	61.0	74.0	8.82	13.57 (14.88)	8.0
U. soricipes	Hoffmann 1984 (17)		50–69	66–80		14–17*	
U. gracilis	Thomas 1912		55	66	9	13.5	
	Jiang & Hoffmann 2013		57–73	65–81	7–10	– (14–17)	
	Liu *et al*. 2013		67.94±0.91	70.61±0.16		14.34±0.04	
	Hoffmann 1984 (13)		67–78	69–84		15–18*	
U. investigator	Hoffmann 1984 (10)		54–75	67–83		13–16*	
U. andersoni	Thomas 1912 (holotype)		67	70		15.5	
	Hoffmann 1984 (16)		59–72	65–83		14–17.5*	7.4–11.2
U. aequodonenia	Liu *et al*. 2013 (holotype)		70	72	8	14	11
	Kryštufek & Motokawa 2018		67–73	72–82		14–16*	11
U. nivatus	Allen 1923 (1)		60	68		– (15)	
	Hoffmann 1984 (9)		56–62	65–77		14–15*	
	Kryštufek & Motokawa 2018		57.5–65	68–74	5.5–9	12–14.5*	5.9–7.5
U. atronates	Allen 1923 (holotype)		57	67	10	– (14)	
	Hoffmann 1984 (13–14, Yunnan)		57–65(14)	65–70 (13)		14–15.5*(14)	
	Hoffmann 1984 (?, Burma)		61–73	67–81		15–17*	
U. dabieshanensis	Hu *et al*. 2021 (4)	118.6–136.4	52.4–54.1		8.1–8.9	12.8–12.9	6.2–8.9

* The original source did not distinguish between HF1 and HF2.

TABLE 4. Cranial measurements of nine *Uropsilus* species in mm. The number of specimens studied is indicated within parentheses.

Species	Source (n)	PL	BL	MPL	GNB	ZB	GBSn	LBO	BH	UTRL	M2-M2	LM	MTRL
U. fansipanensis sp. nov.	This study (holotype, IEBR-M-8101)	20.40	16.62	9.62	10.96	10.49	7.39	5.51	6.90	9.03	6.40	13.52	8.30
	This study (paratype IEBR-M-8102)	20.69	16.98	9.75	11.07	10.67	7.62	5.80	6.91	9.07	6.36	13.77	8.31
U. soricipes	This study (BMNH 1911.9.8.12)	21.69	17.42	10.39	11.38	11.10		5.49	6.49	9.87	6.94	14.13	9.08
	Hoffmann 1984 (15–19)	20.0–21.5(15)		9.25– 10.5(19)	10.75–11.85(15)	9.85–11.5(15)		5.15–5.55(14)		8.65–9.75(19)	6.15–6.85(14)		
	Hu *et al*. 2021 (9)	20.36–21.45	16.88–17.81		10.60–11.43	10.10–10.43	7.45–7.69	5.36–5.58	6.58–7.12		6.25–6.69	12.18–14.30	8.15–8.65
U. gracilis	This study (type, BMNH 1911.9.8.13)	20.51	16.36	9.27	10.25	9.57		4.94	7.68	8.94	6.01	13.92	8.82
	Thomas 1912 (type, BMNH 1911.9.8.13)	20.5	16.5	–	10	10		5		9.1			
	Hoffmann 1984 (13)	21.95–22.9		10.55–11.2	11.8–12.35	10.2–12.05		5.85–6.3		10.2–10.7			
	Hu *et al*. 2021 (4)	20.58–21.78	16.08–17.34	9.68–10.26	10.93–11.55	10.12–10.30	6.70–7.64	5.25–5.50	7.18–7.61		6.19–6.27	14.01–15.00	8.43–9.09
U. investigator	This study (type, BMNH 1922.9.1.16)	20.97		9.46	11.11	10.27			6.67	9.21	6.47	13.68	8.48
	Hoffmann 1984 (1–10)	20.0 – 22.35(8)		9.5–10.25(10)	10.9–11.45(8)	10.15–10.6(5)		5.9(1)		9.10–9.8(10)	6.7(1)		
	Hu *et al*. 2021 (4)	20.51–21.56	16.47–17.23	9.48–10.03	10.44–11.42	9.70–10.66	7.13–7.35	5.12–5.36	6.48–7.08		5.58–6.21	11.95–13.42	8.21–9.06
U. andersoni	This study (BMNH 1911.2.1.30, 31)	21.35–21.78	17.09–17.55	10.00–10.24	11.15–11.35	10.01–10.31		5.32–5.58	6.93–7.15	9.71–9.99	6.61–6.83	14.03–14.55	9.02–9.19
	Thomas 1912 (type, BMNH 1911.2.1.25)	21.7	17.5		11.3	11.6		5.5		9.7			
	Hoffmann 1984 (6–14)	20.65–22.1(10)		9.55–10.15(14)	11.05–11.6(6)	10.2–11.4(6)		5.2–5.7(6)		9.25–9.95(14)	6.35–6.7(6)		
	Hu *et al*. 2021 (3)	20.79–22.28	16.37–17.50	9.84–10.06	11.06–11.46	10.81–11.17	7.66–7.79	5.34–5.54	6.65–7.51		5.93–6.48	12.22–14.64	8.49–9.07
U. aequodonenia	Liu *et al*. 2013 (Holotype)	21.25	16.70	9.80	11.30	10.75	7.60		7.50	9.10	6.50	13.30	
	Hu *et al*. 2021 (3)	20.75–22.03	17.19 – 17.86	9.93–10.31	11.12–11.72	10.64–11.18	7.42–8.02	5.54–5.68	6.60–7.51		6.21–6.69	14.30–14.51	8.30–9.22

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TABLE 4. (continued)

Species	Source (n)	PL	BL	MPL	GNB	ZB	GBSn	LBO	BH	UTRL	M2-M2	LM	MTRL
U. nivatus	Allen 1923 (1)	20	16	9.7		10				9			8.2
	Hoffmann 1984 (3–7)	19.8–20.8(7)		9.1–10.2(7)	10.75–11.5(7)	9.9–11.2(6)		5.05–5.95(7)		8.75–9.65(7)	6.15–6.35(3)		
U. atronates	Allen 1923 (1)	20.5	16.4	9.2		10.2				8.8			8.0
	Hoffmann 1984 (4–12, Yunnan)	19.9–21.0(12)		8.95–9.75(11)	10.35–11.55(11)	10.2–10.8(?)		5.3–5.95(11)		8.45–9.25(11)	5.95–6.3(4)		
	Hoffmann 1984 (?, Burma)	20.7–22.1		9.75–10.8	11.25–12.05	10.5–11.45		5.9–6.2		9.35–10.3			
U. dabieshanensis	Hu *et al*. 2021 (4)	21.11–21.76	17.59–17.98	10.08–10.32	10.93–11.52	10.40–11.02	7.94–8.78	5.27–5.91	6.57–6.84		6.85–7.04	14.47–15.09	8.40–8.79

U. fansipanensis has a shorter profile length (PL: 20.4–20.69 *vs.* 20.65–22.28), shorter upper (UTRL: 9.03–9.07 *vs.* 9.25–9.95) and lower (MTRL: 8.30–8.31 *vs.* 8.49–9.07) toothrow length than *U. andersoni*.

U. fansipanensis has a shorter profile length (PL: 20.4–20.69 *vs.* 20.75–22.03), basal length (BL: 16.62–16.98 *vs.* 16.70–17.86), and palatal length (MPL: 9.62–9.75 *vs.* 9.80–10.31) than *U. aequodonenia*.

U. fansipanensis has a shorter profile length (PL: 20.4–20.69 *vs.* 21.11–21.76), shorter basal length (BL: 16.62–16.98 *vs.* 17.59–17.98), shorter palatal length (MPL: 9.62–9.75 *vs.* 10.08–10.32), shorter mandible length (LM: 13.52–13.77 *vs.* 14.47–15.09), shorter lower toothrow length (MTRL: 8.30–8.31 *vs.* 8.40–8.79), a narrower snout (GBSn: 7.39–7.62 *vs.*7.94–8.78), narrower greatest width across the upper second molars (M2-M2: 6.36–6.40 *vs.* 6.85–7.04), and higher braincase height (BH: 6.90–6.91 *vs.* 6.57–6.84) than *U. dabieshanensis*.

Moreover, *U. fansipanensis* is distinguishable from all other *Uropsilus* species by the orientation of its orbital process (Fig. 4; Table 2). Specifically, the orbital process in *U. fansipanensis* is oriented upwards posteriorly, whereas in the other eight species, it is oriented downwards (Fig. 4). Lacrimal foramen and infraorbital foramen are separated by the orbital process, and the development of lacrimal foramen is an important morphological character distinguishing the genus *Uropsilus* from other genera of the family Talpidae (Hutchison 1968; Motokawa 2004). *U. fansipanensis* has a well-developed lacrimal foramen much larger than the infraorbital foramen, whereas the other eight species have lacrimal foramen smaller or similar in size to the infraorbital foramen (Fig. 4).

U. fansipanensis has 38 teeth in total, similar to *U. gracilis*, *U. investigator, U. nivatus, U. atronates,* and *U. dabieshanensis* in lacking i3, while different from *U. soricipes* (34 teeth, it lacks P3, i3, and p3), *U. aequodonenia* (36 teeth, it lacks P3 and p3), and *U. andersoni* (38 teeth, it lacks p3) (Table 2; see Thomas 1912). *U. fansipanensis* is characterized by the size of p3, which is well-developed and approximately equal to the lower first premolar (p1). In contrast, p3 is smaller than p1 in *U. gracilis*, *U. investigator*, *U. nivatus*, *U. atronates*, and *U. dabieshanensis* (Table 2). Additionally, *U. fansipanensis* is distinguished from *U. gracilis* and *U. atronates* by having c1 larger than p1, while these characteristics are shared with the remaining six species (Table 2; Allen 1923).

Discussion

This study provides the first record of shrew moles in Vietnam, which demonstrates a close relationship and large sharing fauna between northern Vietnam and southern China. This result expands the confirmed distribution of the genus *Uropsilus* from southern China to northern Vietnam. Such distributional pattern is also shared by several vertebrate species. For example, *Typhlomys chapensis*, *Episoriculus umbrinus*, *Euroscaptor orlovi* (Mammalia), and *Diploderma chapaense* (Reptile) are distributed both in northern Vietnam and southern China (Abramov *et al.* 2017; Cheng *et al*. 2017; Kryštufek & Motokawa 2018; Wang *et al.* 2018).

The two specimens from Vietnam represent the new species *U. fansipanensis* that clearly diverged genetically from the currently recognized eight species of the genus *Uropsilus*. In addition, *U. fansipanensis* is characterized by unique morphological characteristics of upwards orientation of orbital process and well-developed lacrimal foramen, which is larger than the infraorbital foramen. These characters have been considered important taxonomic characters in the family Talpidae (Hutchison 1968; Motokawa 2004).

U. fansipanensis was discovered farthest south at an elevation of nearly 2900 m, in a temperate climate zone on the highest mountain in the Hoang Lien Son Range, which is considered the southeasternmost extension of the Himalayan mountains. In addition, Hu *et al.* (2021) reported the easternmost record of *Uropsilus* with the description of *Uropsilus dabieshanensis* in the high mountains above 1000 m and at high latitudes in eastern China. The remaining seven species of this genus are distributed in high mountain areas across central and southern China, ranging from 1500 to 4500 m (Kryštufek & Motokawa 2018). This distribution pattern provides evidence of the adaptation of *Uropsilus* to low average temperatures in alpine areas.

Our study, in combination with Wan *et al*. (2013, 2018) and Hu *et al*. (2021), indicated that the shrew mole genus *Uropsilus* entertains both high cryptic diversity and largely cryptic diversification. The recently discovered species tend to occupy narrowly distributed regions with wet and cold climatic conditions or isolated alpine areas, especially in the southeasternmost and easternmost ends of mountain ranges where *U. fansipanensis* and *U. dabieshanensis*, respectively, are found. The shrew mole genus *Uropsilus* currently consists of nine species in addition to six possible undescribed taxa (Wan *et al*. 2013, 2018; Hu *et al*. 2021). *U. fansipanensis* has a relatively small genetic distance of 3.22–3.94% from *Uropsilus* sp. 6, a lineage distributed in Yunnan province, southeastern China. This genetic distance might suggest that *Uropsilus* sp. 6 might be conspecific with *U. fansipanensis,* but further research based on morphological comparison is needed to confirm the taxonomic status of *Uropsilus* sp. 6.

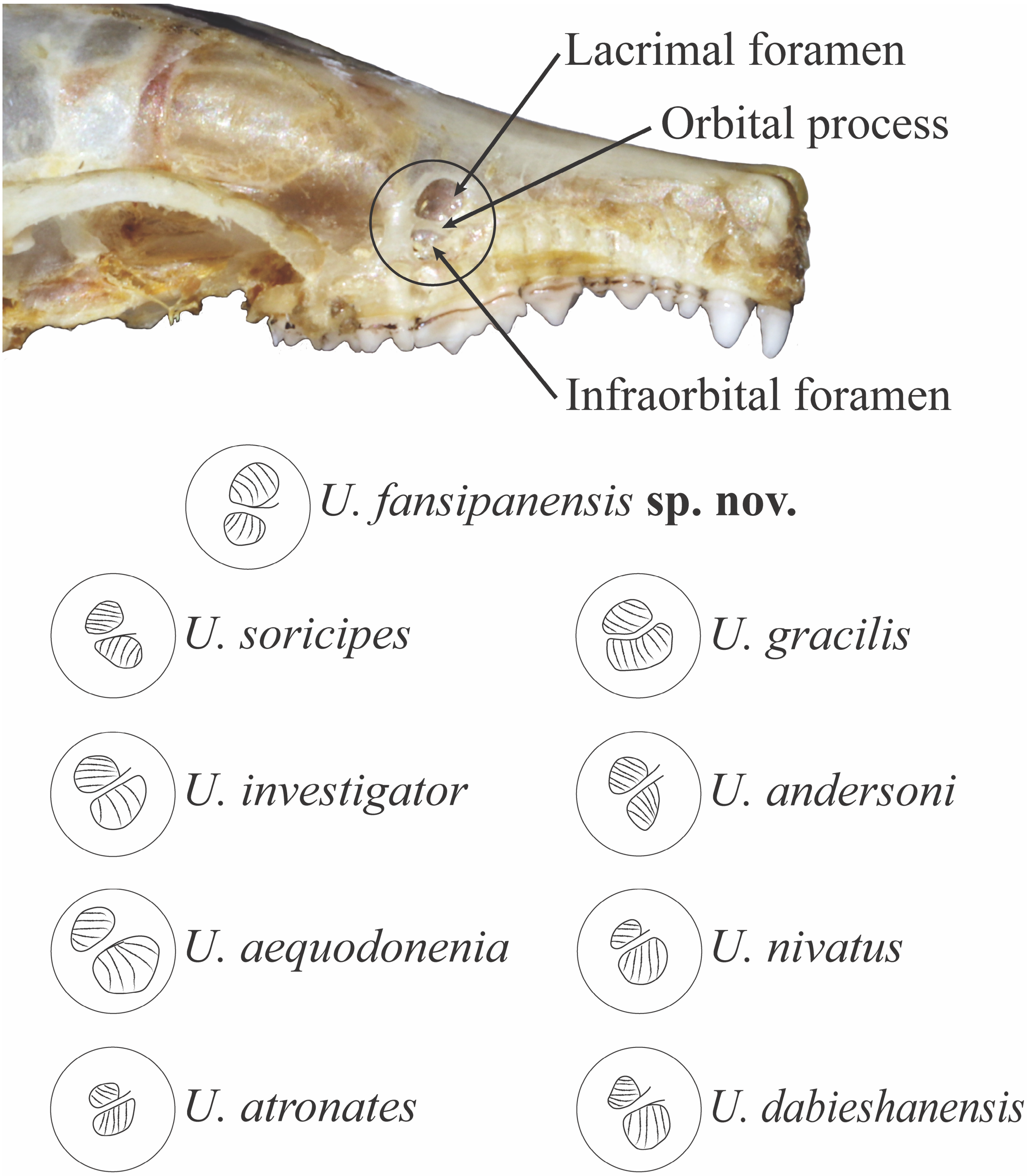

FIGURE 4. Illustrations of orbital process, lacrimal foramen, and infraorbital foremen of *Uropsilus fansipanensis* **sp. nov.** (IEBR-M-8101), *U. soricipes* (BMNH 1911.9.8.12), *U. gracilis* (BMNH 1911.9.8.13), *U. investigator* (BMNH 1922.9.1.16), *U. andersoni* (BMNH 1911.2.1.30), *U. aequodonenia* (Liu *et al*. 2013), *U. nivatus* & *U. atronates* (Wan 2015), and *U. dabieshanensis* (Hu *et al*. 2021).

The complex mountain topography can cause geographic isolation in high-altitude areas, which is known as the sky island theory (He & Jiang 2014; Bui *et al*. 2020b). Wan *et al*. (2018) suggested that the speciation of *Uropsilus* might be related to strong geographical isolation and ecological gradients provided by topographical diversity. Therefore, we believe that the speciation of *U. fansipanensis* is linked to its geographical isolation and the climate around the highest peak in northwestern Vietnam.

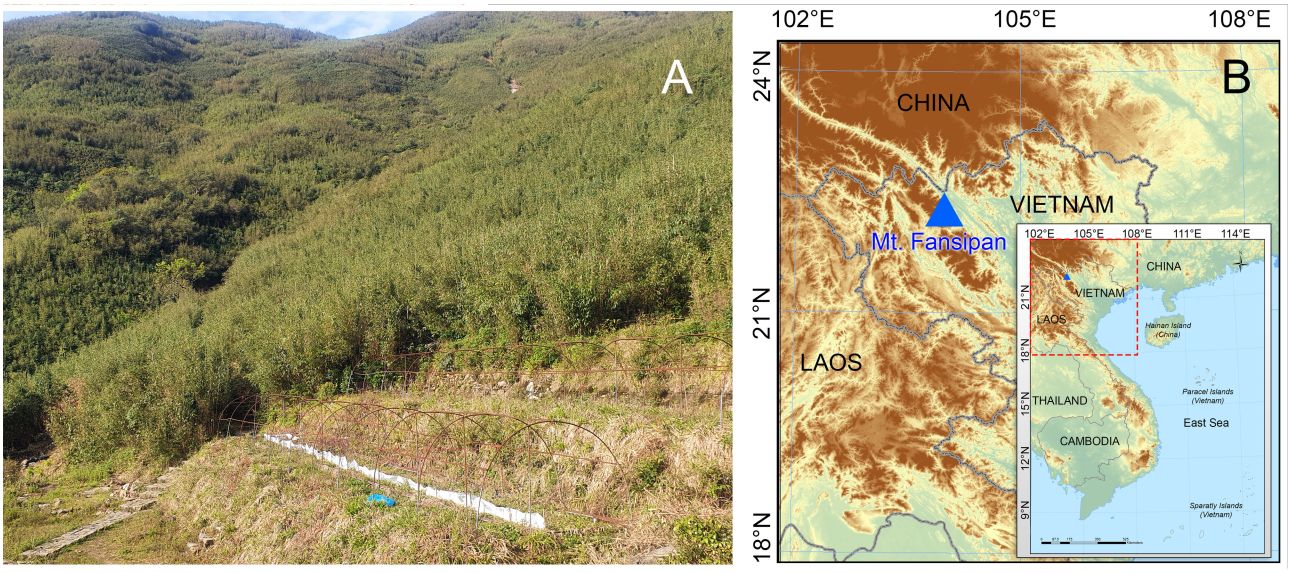

FIGURE 5. Habitat (A) and map showing the type locality (B) of *Uropsilus fansipanensis* **sp. nov.** in Mt. Fansipan, Hoang Lien National Park, Lao Cai province, northwestern Vietnam.

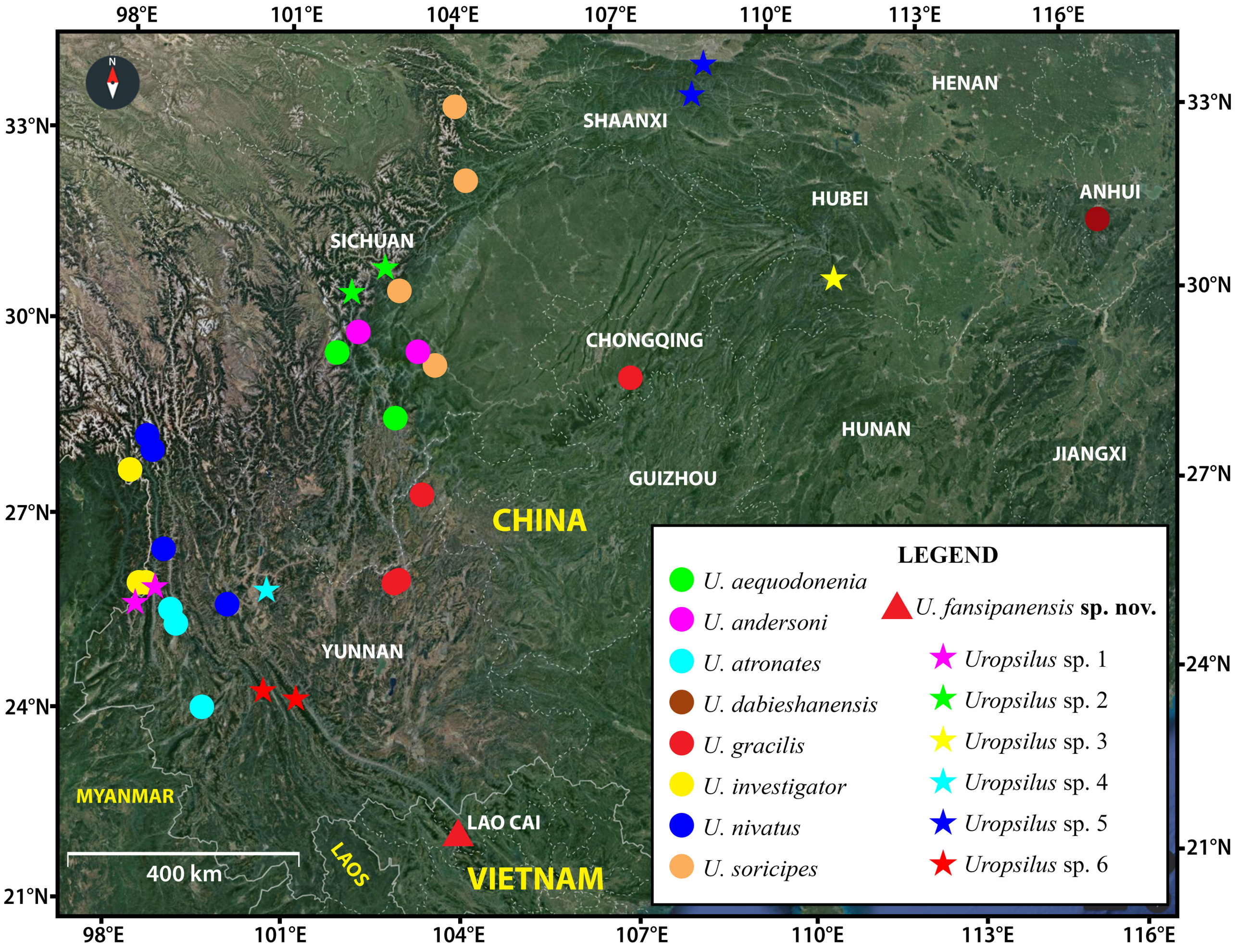

FIGURE 6. Distribution map of *Uropsilus* in China (re-illustrated from Hu *et al*. 2021) and Vietnam. Base map is from Google Earth.

Information on cryptic species plays a crucial role in the accurate assessment of biodiversity and conservation (Bickford *et al*. 2007; Beheregaray & Caccone 2007; Leys *et al*. 2016; Fišer *et al*. 2018). Shrew moles of the genus *Uropsilus* are a prime example of cryptic species in mountainous regions which involves several isolated alpine areas with altitudes of more than 2000 m. On the basis of our finding of the new species and the new distribution of the genus *Uropsilus*, it is implied the existence of further cryptic biodiversity in northern Vietnam. It is desirable to conduct further study for taxonomy and biodiversity assessment for future conservation there.

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APPENDIX 1. List of accession numbers of GenBank sequences

Species	Specimen voucher	Location		GenBank Accession Number			Reference
		Area	Province	cyt*b*	RAG1	RAG2	
U. fansipanensis **sp. nov.**	IEBR-M-8101	Mt. Fansipan	Lao Cai	OQ509373	OQ509371	OQ512024	This study
	IEBR-M-8102	Mt. Fansipan	Lao Cai	OQ509374	OQ509372	OQ512025	This study
U. soricipes	SAF-09700	Mt. Jiajin	Sichuan	MH209649	MH210208	MH210330	Wan *et al.*, 2018
	KIZ-028553	Mt. Emei	Sichuan	KF778191	KF778317	KF778350	Wan *et al.*, 2013
	KIZ-028554	Mt. Emei	Sichuan	KF778192	KF778318	KF778351	Wan *et al.*, 2013
	KIZ-028555	Mt. Emei	Sichuan	KF778194	KF778320	KF778373	Wan *et al.*, 2013
	KIZ-028556	Mt. Emei	Sichuan	KF778193	KF778319	KF778374	Wan *et al.*, 2013
	KIZ-0905019	Beichuan	Sichuan	MH209650	MH210209	MH210331	Wan *et al.*, 2018
	KIZ-0905021	Beichuan	Sichuan	MH209651	MH210210	MH210332	Wan *et al.*, 2018
	KIZ-0905059	Beichuan	Sichuan	MH209652	MH210211	MH210333	Wan *et al.*, 2018
	KIZ-0905060	Beichuan	Sichuan	MH209653	MH210212	MH210334	Wan *et al.*, 2018
	KIZ-0905083	Beichuan	Sichuan	MH209654	MH210213	MH210335	Wan *et al.*, 2018
	KIZ-0905409	Mt. Daxiangling	Sichuan	MH209734	MH210284	MH210409	Wan *et al.*, 2018
	SAF-092069	Minjiang	Sichuan	MH209719	MH210269	MH210394	Wan *et al.*, 2018
U. gracilis	KIZ-028544	Mt. Jinfo	Chongqing	KF778208	KF778312	KF778368	Wan *et al.*, 2013
	KIZ-028545	Mt. Jinfo	Chongqing	KF778209	KF778311	KF778369	Wan *et al.*, 2013
	KIZ-028546	Mt. Jinfo	Chongqing	KF778206	KF778313	KF778371	Wan *et al.*, 2013
	KIZ-028547	Mt. Jinfo	Chongqing	KF778207	KF778310	KF778370	Wan *et al.*, 2013
	KIZ-028548	Mt. Jinfo	Chongqing	KF778205	KF778309	KF778372	Wan *et al.*, 2013
	KIZ-0810137	Mt. Jiaozishan	Yunnan	MH209658	MH210217	MH210339	Wan *et al.*, 2018
	KIZ-0810159	Mt. Jiaozishan	Yunnan	MH209659	MH210218	MH210340	Wan *et al.*, 2018
	KIZ-0810160	Mt. Jiaozishan	Yunnan	MH209660	MH210219	MH210341	Wan *et al.*, 2018
	KIZ-0810191	Mt. Jiaozishan	Yunnan	MH209661	MH210220	MH210342	Wan *et al.*, 2018
	KIZ-0810488	Mt. Jiaozishan	Yunnan	MH209662	MH210221	MH210343	Wan *et al.*, 2018
	KIZ-0811175	Mt. Jiaozishan	Yunnan	MH209664	MH210223	MH210345	Wan *et al.*, 2018
U. investigator	KIZ-028527	Mt. Gaoligong	Yunnan	KF778154	KF778269	KF778364	Wan *et al.*, 2013
	KIZ-028530	Mt. Gaoligong	Yunnan	KF778155	KF778270	KF778366	Wan *et al.*, 2013
	KIZ-201211136	Mt. Gaoligong	Yunnan	MH209680	MH210236	MH210359	Wan *et al.*, 2018
	KIZ-201211149	Mt. Gaoligong	Yunnan	MH209685	MH210241	MH210364	Wan *et al.*, 2018
	KIZ-201211160	Mt. Gaoligong	Yunnan	MH209686	MH210242	MH210365	Wan *et al.*, 2018
	KIZ-201211169	Mt. Gaoligong	Yunnan	MH209687	MH210243	MH210366	Wan *et al.*, 2018
U. andersoni	SAF-06948	Mt. Erlang	Sichuan	MH209738	MH210288	MH210413	Wan *et al.*, 2018
	KIZ-Z201405738	Mt. Emei	Sichuan	MH209675	MH210232	MH210354	Wan *et al.*, 2018
	KIZ-Z201405739	Mt. Emei	Sichuan	MH209676	MH210233	MH210355	Wan *et al.*, 2018
U. aequodonenia	KIZ-0906042	Mt. Daliangshan	Sichuan	MH209766	MH210315	MH210424	Wan *et al.*, 2018
	KIZ-0906074	Mt. Daliangshan	Sichuan	MH209767	MH210316	MH210425	Wan *et al.*, 2018
	KIZ-0906075	Mt. Daliangshan	Sichuan	MH209768	MH210317	MH210426	Wan *et al.*, 2018
	SAF-04010	Mt. Erlang	Sichuan	MH209699	MH210254	MH210379	Wan *et al.*, 2018
	SAF-07940	Mt. Erlang	Sichuan	MH209698	MH210253	MH210378	Wan *et al.*, 2018

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Species	**Specimen voucher**	**Location**		**GenBank Accession Number**			**Reference**
		Area	**Province**	**cyt*b***	**RAG1**	**RAG2**	
U. nivatus	KIZ-022469	Mt. Biluo	Yunnan	KF778166	KF778292	KF778359	Wan *et al.*, 2013
	KIZ-022473	Mt. Biluo	Yunnan	KF778168	KF778291	KF778356	Wan *et al.*, 2013
	KIZ-022974	Mt. Biluo	Yunnan	KF778170	KF778293	KF778360	Wan *et al.*, 2013
	KIZ-022975	Mt. Biluo	Yunnan	KF778167	KF778294	KF778361	Wan *et al.*, 2013
	KIZ-022976	Mt. Biluo	Yunnan	KF778169	KF778284	KF778362	Wan *et al.*, 2013
	KIZ-016768	Mt. Yulong	Yunnan	KF778174	KF778282	KF778347	Wan *et al.*, 2013
	KIZ-016769	Mt. Yulong	Yunnan	KF778171	KF778287	KF778344	Wan *et al.*, 2013
	KIZ-016770	Mt. Yulong	Yunnan	KF778173	KF778289	KF778346	Wan *et al.*, 2013
	KIZ-016783	Mt. Yulong	Yunnan	KF778172	KF778288	KF778345	Wan *et al.*, 2013
	KIZ-016797	Mt. Yulong	Yunnan	KF778175	KF778290	KF778348	Wan *et al.*, 2013
	KIZ-022467	Mt. Diancang	Yunnan	KF778176	KF778285	KF778352	Wan *et al.*, 2013
	KIZ-022468	Mt. Diancang	Yunnan	KF778178	KF778295	KF778353	Wan *et al.*, 2013
	KIZ-022470	Mt. Diancang	Yunnan	KF778177	KF778283	KF778357	Wan *et al.*, 2013
	KIZ-022471	Mt. Diancang	Yunnan	KF778179	KF778286	KF778358	Wan *et al.*, 2013
U. atronates	KIZ-H2004	Wayao	Yunnan	MH209712	MH210262	MH210387	Wan *et al.*, 2018
	KIZ-H2040	Wayao	Yunnan	MH209713	MH210263	MH210388	Wan *et al.*, 2018
	KIZ-H2054	Wayao	Yunnan	MH209714	MH210264	MH210389	Wan *et al.*, 2018
	KIZ-H2056	Wayao	Yunnan	MH209715	MH210265	MH210390	Wan *et al.*, 2018
	KIZ-H2078	Wayao	Yunnan	MH209718	MH210268	MH210393	Wan *et al.*, 2018
	KIZ-2012121120	Laowo	Yunnan	MH209711	MH210261	MH210386	Wan *et al.*, 2018
	KIZ-H2413	Laowo	Yunnan	MH209708	MH210258	MH210383	Wan *et al.*, 2018
	KIZ-201211251	Mt. Gaoligong	Yunnan	MH209688	MH210244	MH210367	Wan *et al.*, 2018
	KIZ-0904339	Caojian	Yunnan	MH209655	MH210214	MH210336	Wan *et al.*, 2018
	KIZ-0904402	Caojian	Yunnan	MH209657	MH210216	MH210338	Wan *et al.*, 2018
	KIZ-028532	Mt. Yongde	Yunnan	KF778184	KF778304	KF778333	Wan *et al.*, 2013
	KIZ-028533	Mt. Yongde	Yunnan	KF778183	KF778308	KF778334	Wan *et al.*, 2013
	KIZ-028534	Mt. Yongde	Yunnan	KF778185	KF778302	KF778337	Wan *et al.*, 2013
	KIZ-028535	Mt. Yongde	Yunnan	KF778186	KF778305	KF778338	Wan *et al.*, 2013
	KIZ-028536	Gengma	Yunnan	KF778181	KF778267	KF778335	Wan *et al.*, 2013
	KIZ-028537	Gengma	Yunnan	KF778182	KF778268	KF778336	Wan *et al.*, 2013
	KIZ-0212334	Mt. Laobieshan	Yunnan	MH209478	MH210298	MH210423	Wan *et al.*, 2018
U. dabieshanensis	AE1612YLP017	Mt. Dabie	Anhui	MT199125	MT211605	MT211608	Hu *et al.*, 2021
	AE1807FZL007	Mt. Dabie	Anhui	MT199126	MT211606	MT211609	Hu *et al.*, 2021
	AE1907FZL001	Mt. Dabie	Anhui	MT199127	MT211607	MT211610	Hu *et al.*, 2021
	AE2005YLP001	Mt. Dabie	Anhui	MT710697	MT710698	MT710699	Hu *et al.*, 2021

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Species	Specimen voucher	Location		GenBank Accession Number			Reference
		Area	Province	cyt*b*	RAG1	RAG2	
Uropsilus sp. 1	KIZ-TC1304166	Mt. Gaoligong	Yunnan	MH209736	MH210286	MH210411	Wan *et al.*, 2018
	KIZ-TC1304268	Mt. Gaoligong	Yunnan	MH209737	MH210287	MH210412	Wan *et al.*, 2018
	KIZ-020527	Mt. Gaoligong	Yunnan	KF778159	KF778274	KF778367	Wan *et al.*, 2013
	KIZ-020539	Mt. Gaoligong	Yunnan	KF778160	KF778275	KF778331	Wan *et al.*, 2013
	KIZ-028526	Mt. Gaoligong	Yunnan	KF778156	KF778271	KF778363	Wan *et al.*, 2013
	KIZ-028528	Mt. Gaoligong	Yunnan	KF778158	KF778272	KF778365	Wan *et al.*, 2013
	KIZ-028529	Mt. Gaoligong	Yunnan	KF778157	KF778273	KF778330	Wan *et al.*, 2013
Uropsilus sp. 2	KIZ-028549	Mt. Jiajin	Sichuan	KF778161	KF778280	KF778376	Wan *et al.*, 2013
	KIZ-028550	Mt. Jiajin	Sichuan	KF778162	KF778277	KF778375	Wan *et al.*, 2013
	KIZ-028551	Mt. Jiajin	Sichuan	KF778165	KF778279	KF778329	Wan *et al.*, 2013
	KIZ-028552	Mt. Jiajin	Sichuan	KF778163	KF778281	KF778377	Wan *et al.*, 2013
	KIZ-028557	Mt. Jiajin	Sichuan	KF778164	KF778278	KF778328	Wan *et al.*, 2013
Uropsilus sp. 3	SAF-06040	Mt. Wushan	Hubei	MH209692	MH210247	MH210371	Wan *et al.*, 2018
	SAF-06042	Mt. Wushan	Hubei	MH209693	MH210248	MH210372	Wan *et al.*, 2018
Uropsilus sp. 4	KIZ-BC1110001	Mt. Wuding	Yunnan	MH209643	MH210202	MH210324	Wan *et al.*, 2018
	KIZ-BC1110002	Mt. Wuding	Yunnan	MH209648	MH210207	MH210329	Wan *et al.*, 2018
	KIZ-BC1110012	Mt. Wuding	Yunnan	MH209644	MH210203	MH210325	Wan *et al.*, 2018
	KIZ-BC1110129	Mt. Wuding	Yunnan	MH209645	MH210204	MH210326	Wan *et al.*, 2018
	KIZ-BC1110180	Mt. Wuding	Yunnan	MH209646	MH210205	MH210327	Wan *et al.*, 2018
	KIZ-BC1110202	Mt. Wuding	Yunnan	MH209647	MH210206	MH210328	Wan *et al.*, 2018
Uropsilus sp. 5	KIZ-016096	Mt. Qinling	Shannxi	KF778195	KF778266	KF778339	Wan *et al.*, 2013
	KIZ-016099	Mt. Qinling	Shannxi	KF778198	KF778315	KF778343	Wan *et al.*, 2013
	KIZ-016101	Mt. Qinling	Shannxi	KF778199	KF778276	KF778340	Wan *et al.*, 2013
	KIZ-016109	Mt. Qinling	Shannxi	KF778196	KF778314	KF778341	Wan *et al.*, 2013
	KIZ-016219	Mt. Qinling	Shannxi	KF778197	KF778296	KF778342	Wan *et al.*, 2013
Uropsilus sp. 6	KIZ-019509	Mt. Wuliang	Yunnan	KF778187	KF778301	KF778324	Wan *et al.*, 2013
	KIZ-019515	Mt. Wuliang	Yunnan	KF778189	KF778316	KF778322	Wan *et al.*, 2013
	KIZ-019517	Mt. Wuliang	Yunnan	KF778188	KF778307	KF778323	Wan *et al.*, 2013
	KIZ-028538	Mt. Wuliang	Yunnan	KF778190	KF778306	KF778354	Wan *et al.*, 2013
	KIZ-AL1303012	Mt. Ailao	Yunnan	MH209638	MH210197	MH210319	Wan *et al.*, 2018
	KIZ-AL1305058	Mt. Ailao	Yunnan	MH209639	MH210198	MH210320	Wan *et al.*, 2018
	KIZ-AL1305099	Mt. Ailao	Yunnan	MH209640	MH210199	MH210321	Wan *et al.*, 2018
	KIZ-AL1305152	Mt. Ailao	Yunnan	MH209641	MH210200	MH210322	Wan *et al.*, 2018
	KIZ-AL1305230	Mt. Ailao	Yunnan	MH209642	MH210201	MH210323	Wan *et al.*, 2018