# A new species of shrew moles, genus Uropsilus Milne-Edwards, 1871 (Mammalia, Eulipotyphla, Talpidae), from the Wuyi Mountains, Jiangxi Province, eastern China 

Xueyang Ren ${ }^{1 \oplus}$, Yifan Xu${ }^{\top}$, Yixian $\mathrm{Li}^{2}$, Hongfeng $\mathrm{Yao}^{1 \oplus}$, Yi Fang ${ }^{3}$, Laxman Khanal ${ }^{4 \oplus}$, Lin Cheng ${ }^{3}$, Wei Zeng ${ }^{5}$, Xuelong Jiang ${ }^{2 \oplus}$, Zhongzheng Chen ${ }^{1,2 \oplus}$<br>1 Collaborative Innovation Center of Recovery and Reconstruction of Degraded Ecosystem in Wanjiang Basin Co-founded by Anhui Province and Ministry of Education, School of Ecology and Environment, Anhui Normal University, Wuhu 241002, China<br>2 State Key Laboratory of Genetic Resources and Evolution \& Yunnan Key Laboratory of Biodiversity and Ecological Security of Gaoligong Mountain, Kunming Institute of Zoology, Chinese Academy of Sciences, Kunming, Yunnan 650204, China<br>3 Jiangxi Wuyi Mountain National Nature Reserve, Shangrao 334000, China<br>4 Central Department of Zoology, Institute of Science and Technology, Tribhuvan University, Kathmandu 44618, Nepal<br>5 Southwest Survey and Planning Institute of National Forestry and Grassland Administration, Kunming 650216, China<br>Corresponding authors: Xuelong Jiang (jiangxl@mail.kiz.ac.cn); Zhongzheng Chen (zhongzheng112@126.com)

Academic editor: Nedko Nedyalkov
Received: 25 August 2023
Accepted: 12 November 2023
Published: 7 December 2023

ZooBank: https://zoobank. org/566E6FFE-05B9-4962-8CFD5F88D68704E3

Citation: Ren X, Xu Y, Li Y, Yao H, Fang Y, Khanal L, Cheng L, Zeng W, Jiang X, Chen Z (2023) A new species of shrew moles, genus Uropsilus Milne-Edwards, 1871 (Mammalia, Eulipotyphla, Talpidae), from the Wuyi Mountains, Jiangxi Province, eastern China. ZooKeys 1186: 25-46. https://doi.org/10.3897/ zookeys.1186.111592

Copyright: © Xueyang Ren et al.
This is an open access article distributed under terms of the Creative Commons Attribution License (Attribution 4.0 International CC BY 4.0).


#### Abstract

Asian shrew moles, genus Uropsilus, are the most primitive members of family Talpidae. They are distributed mainly in southwestern China and adjacent Bhutan, Myanmar, and Vietnam. In June 2022, we collected five specimens of Uropsilus from Mount Huanggang, Jiangxi Province, eastern China, which is the highest peak of the Wuyi Mountains. We sequenced two mitochondrial (CYT B and 12S rRNA) and three nuclear (PLCB4, RAG1, and RAG2) genes to estimate the phylogenetic relationship of the five shrew moles. We also compared their morphology with recognized species within the genus. Our results show that these specimens collected from Mount Huanggang differ from all named species in Uropsilus. We formally describe the species here as Uropsilus huanggangensis sp. nov. Morphologically, the new species is distinguishable from the other Uropsilus species by the combination of dark chocolate-brown pelage, long snout, enlarged first upper incisor, similarly sized lacrimal and infraorbital foramens, and the curved and sick-le-like coronoid process. The genetic distances of the cytochrome b (CYT B) gene between $U$. huanggangensis and other recognized Uropsilus species ranged between 9.3\% and $16.4 \%$. The new species is geographically distant from other species in the genus and is the easternmost record of the Uropsilus. The divergence time of $U$. huanggangensis was estimated to be the late Pliocene ( $1.92 \mathrm{Ma}, 95 \% \mathrm{Cl}=0.88-2.99$ ).


Key words: Mount Huanggang, small mammals, taxonomy, Uropsilinae

## Introduction

The shrew moles of the genus Uropsilus Milne-Edwards, 1871 are the sole living genus in the subfamily Uropsilinae in Talpidae (Mckenna et al. 1997; Hutterer 2005). These insectivores primarily inhabit the mountains of southwestern China, as well as adjacent areas in Bhutan and northeastern Myanmar, where they inhabit montane forests at 1,400-3,600 m elevation (IUCN 2015; Hoffmann
and Lunde 2008). Although the fossil record is sparse, the age of the associated fossils and the timing of the molecular evolution of mammals suggest that the subfamily Uropsilinae would have flourished and spread widely across Eurasia before the Late Miocene (Meredith et al. 2011). In contrast to other moles that have developed adaptive features such as broad front claws and reduced external ears, shrew moles exhibit shrew-like characteristics, including slender front claws, exposed external ears, and long tails almost equal in length to their bodies. All these morphological characteristics suggest that they have retained the terrestrial habits of primitive moles (Allen 1938). Phylogenetic relationships constructed using morphological methods (Motokawa 2004; Sánchez-Villagra et al. 2006) and molecular phylogenetic methods (Douady and Douzery 2003; Shinohara et al. 2003) consistently support that Uropsilus forms the basal branch in the phylogenetic tree of the family Talpidae.

The genus Uropsilus was first described by Milne-Edwards (1871) based on the specimens from Muping (= Baoxing) in Sichuan, China. The type species of the Uropsilus is $U$. soricipes Milne-Edwards, 1871, which has a dental formula of: I $2 / 1, C 1 / 1$, P 3/3, M 3/3 = 34. Thomas (1912) described two new species belonging to two new genera: Rhynchonax andersoni Thomas, 1911 from Mount Omisan (= Mount Emei), Sichuan, with the dental formula: I 2/2, C 1/1, P 4/3, M 3/3 = 38; and Nasillus gracilis Thomas, 1911 from Chin-fu-san (= Jinfo shan), Chongqing, with the dental formula: I 2/1, C 1/1, P 4/4, M 3/3 = 38. Later, Thomas (1922) described $N$. investigator Thomas, 1922, based on larger specimens collected in the Kia-kiang-Salween of Yunnan compared to $N$. gracilis. Additionally, Allen (1923) described two new subspecies of $R$. andersoni: $R$. andersoni atronates Allen, 1923 from Salween drainage, Yunnan; and R. andersoni nivatus Allen, 1923 from Lijiang, Yunnan, China. However, the classification of the shrew moles into three genera had been widely disputed. Osgood (1937) considered two genera (Uropsilus Milne-Edwards, 1871 and Nasillus Thomas, 1911) in the Uropsilinae and merged the genus Rhynchonax Thomas, 1911 into the genus Uropsilus. Ellerman and Morrison-Scott (1951) assigned all genera to Uropsilus and placed the named species in five subspecies of U. soricipes: U. s. soricipes, U. s. gracilis, U. s. andersoni (including atronates), U. s. investigator and U. s. nivatus. The proposition of one genus is recognized by most scholars (Cranbrook 1960-1961; Corbet and Hill 1980; Honacki et al. 1982; Hutterer 2005). Hoffmann (1984) conducted a systematic study of this group and recognized three species: $U$. soricipes, $U$. gracilis, and $U$. andersoni under the single genus Uropsilus. However, Wang and Yang (1989) believed that investigator and gracilis were distributed in the same domain, and there was no intermediate transition type, so the $U$. s. investigator should be an independent species. Since then, the view that there are four species of Uropsilus has been widely accepted (Hoffmann and Lunde 2008).

Recently, Liu et al. (2013) described U. aequodonenia Liu et al., 2013 from Puge County, Sichuan, China, which has a dental formula of I $2 / 2, \mathrm{C} 1 / 1, \mathrm{P} 3 / 3$, and M $3 / 3=36$. Wan et al. (2013) suggested that $U$. nivatus and $U$. atronates are valid species based on molecular data. Furthermore, they identified seven recognized species and five putative species. Wan (2015) described six new species, but these designations were not recognized because they did not follow the International Code of Zoological Nomenclature (ICZN 2012). Wan et al. (2018) generated gene trees using additional specimens, which phylogenetic analyses revealed that species of Uropsilus could be sorted into three distinct lineages. One lineage
includes $U$. investigator from western Yunnan and acts as the basal position of the genus; the second lineage includes $U$. aequodonenia, $U$. andersoni, and $U$. nivatus from Northern Yunnan and western Sichuan; and the third contains $U$. soricipes, U. gracilis, U. atronates. Additionally, Hu et al. (2021b) used multivariate analyses as well as phylogenetic analyses to describe a new species, U. dabieshanensis Hu et al., 2021, from the Dabie Mountains, Anhui Province, eastern China. The phylogenetic results indicate that the lineage of Uropsilus has two matrilines. More recently, Bui et al. (2023) described a new species, U. fansipanensis, from the northwestern Vietnam. Thus, nine taxa are currently recognized as full species under the genus Uropsilus: U. aequodonenia, U. andersoni, U. gracilis, U. investigator, U. soricipes, U. atronates, U. nivatus, U. dabieshanensis, and U. fansipanensis. Of all known species, $U$. dabieshanensis is the only one found in eastern China and is considered to have the easternmost distribution of the genus.

During a biodiversity study in June 2022, five shrew mole specimens were collected from the Wuyi Mountains, Jiangxi Province, eastern China (Fig. 1). Our molecular analysis reveals that the five specimens are genetically distinct from all recognized Uropsilus species and potentially represents a new species. In this study, we integrate genetic and morphometric approaches to elucidate the taxonomy and phylogeny of these specimens.

## Materials and methods

## Sampling

In June 2022, five Uropsilus specimens were collected on Mount Huanggang in Wuyishan National Nature Reserve, Yanshan, Jiangxi Province, eastern China (Fig. 1). Specimens were collected using Sherman and pitfall (plastic buckets


Figure 1. Sampling localities of specimens used in the phylogenetic analysis.

15 cm in diameter and 28 cm in depth) traps. All specimens were euthanized, and muscle or liver tissue was extracted from each and preserved in pure alcohol for subsequent molecular studies. All specimens and tissues were deposited at the Biological Museum of Anhui Normal University (AHNU). Animals were handled in compliance with the animal care and use guidelines of the American Society of Mammologists (Sikes et al. 2016), following the guidelines and regulations approved by the internal review board of AHNU (approval no. AHNU-ET2021002), and with the permissions of local government authorities.

## Phylogenetic analyses

Genomic DNA of the five specimens of Uropsilus from Mount Huanggang was extracted from the liver and muscle tissues using a DNA extraction kit (Tiangen DNeasy Blood and Tissue Kit, Beijing, China). Two mitochondrial genes (cytochrome b [CYT B], 12S rRNA [12S]) and three nuclear genes (phospholipase C beta 4 [PLCB4], recombination activating protein 1 [RAG1], and recombination activating protein 2 [RAG2]) were amplified using the primer pairs outlined in Suppl. material 1. The PCR products were purified and sequenced in both directions using the BigDye Terminator Cycle Kit v. 3.1 (Invitrogen, Waltham, MA, USA) on an ABI 3730xI sequencer (Applied Biosystems, Waltham, MA, USA). The obtained sequences were assembled using SeqMan (DNASTAR, Lasergene v. 7). Corresponding sequences of 38 specimens of nine recognized species and six unrecognized species of Uropsilus were downloaded from the GenBank (Suppl. material 2). We downloaded sequences of Talpa altaica and Sorex araneus as out-group taxa following Wan et al (2018). All sequences were then aligned in MEGA v. 11 (Tamura et al. 2021).

The uncorrected $p$-distance of the CYT B gene between species was calculated in MEGA v. 11 (Tamura et al. 2021). We used maximum likelihood (ML) and Bayesian inference (BI) methods to conduct phylogenetic analyses of mitochon-drial-nuclear genes (mtDNA + nDNA, 4090 bp) concatenated datasets in PhyloSuite (Zhang et al. 2020). The best-fit partitioning scheme and evolutionary models were selected using PartitionFinder v. 2.0 with the greedy algorithm under the Bayesian information criterion (BIC) (Suppl. material 3) (Lanfear et al. 2012).

## Molecular dating

We used BEAST v. 2.6.6 (Bouckaert et al. 2019) to estimate divergence times based on the Birth-Death model as the tree prior and relaxed lognormal as the clock model prior. Evolutionary models or partition schemes were estimated based on the Bayesian Information Criterion (BIC) in PartitionFinder v. 2.0 (Lanfear et al. 2012). Two fossil calibrations were used following the guide of Wan et al. (2018): (1) the first division of Uropsilus at 6.18 Ma ( $95 \%$ HPD: 4.27-8.65 Ma), with a lognormal distribution prior (mean: 6.20, SD: 0.215 , offset: 0.02 ), so the median age was at 6.08 Ma and the $95 \% \mathrm{Cl}$ was $4.27-8.65 \mathrm{Ma}$; (2) the earliest known $U$. soricipes from the Early Pleistocene $2.0-2.4 \mathrm{Ma}$, with an exponential distribution prior (offset $=2.0, \mathrm{M}=0.67$ [2.0×0.333]), so the median age was 2.46 Ma and the $95 \% \mathrm{Cl}$ was $2.03-4.01 \mathrm{Ma}$. Each analysis was run for 100 million generations, sampling every 10000 generations. The first $10 \%$ of the samples were discarded as burn-in. Convergence was assessed using Tracer v. 1.7 (Rambaut et al. 2018).

## Morphological measurements and analyses

We examined and measured the specimens of Uropsilus in the Kunming Institute of Zoology (KIZ), Chinese Academy of Sciences, and AHNU. A total of 83 specimens were examined and they were assigned to $U$. aequodonenia $(n=2)$, $U$. andersoni $(n=6)$, U. atronates $(n=25), U$. dabieshanensis $(n=6), U$. gracilis ( $n=16$ ), U. investigator $(n=11)$, U. nivatus $(n=7)$, U. soricipes $(n=5)$, and Uropsilus sp. nov. $(n=5)$ (Appendix 1).

The body weight (Wt) and four external measurements, including head and body length (HBL), tail length (TL), hindfoot length (HF), and ear length (EL), were taken from specimen labels or field notes. Twenty-one craniodental measurements were taken with digital calipers to the nearest 0.01 mm , following Yang et al. $(2005,2007)$. All the craniodental measurements were taken by a single observer. The following measurements were taken:

| PL | Profile length; |
| :--- | :--- |
| HB | Height of braincase; |
| GNB | Greatest neurocranium breadth Cranial breadth; |
| BS | Basion-Staphylion; |
| GBSn | Greatest breadth of snout; |
| BBP ${ }^{1}-\mathbf{P}^{2}$ | Maxillary sides $P^{1}-P^{2}$ Interdental external width; |
| MPL | Palatal length; |
| APB | Anterior palatal breadth; |
| LUTR | Length of upper tooth row; |
| PPB | Posterior palatal breadth; |
| P $^{4}-\mathbf{M}^{3}$ | Distance from the upper fourth premolar to the upper third molar; |
| Id-Gol | From infradentale to gonion laterale; |
| M $^{1}-\mathbf{M}^{3}$ | Upper molar row length; |
| HVR | Oral height of the vertical ramus; |
| GBUM | Great breadth of upper molars; |
| Coh-M | From the highest point of the Condyle process to the upper third molar; |
| ML | Mandible length; |
| GBLM | Greatest breadth of lower molars; |
| Id-Coh | From infradentale to the hight point of the condyle process; |
| LBO | least breadth between orbits; |
| LBTR | Length of below tooth row. |

We compared morphology of the new species with other species of Uropsilus. Comparative morphological characters of these other species were obtained from Thomas (1912, 1922), Allen et al. (1923), Hu et al. (2021b), and Bui et al. (2023), and we followed these authors' terminologies in our morphological description of the new species. Meanwhile, to better distinguish between the different species, we compared the ratio of GNB to PL, as well as the ratio of TL to HBL.

Overall similarities of skulls were assessed first through principal component analyses (PCA) based on the $21 \log _{10}$-transformed craniodental variables. Groups of individuals sharing a comparable morphology were then discriminated through discriminant analysis (DA). To make the results more concise, we limited the PCA and DA analyses to the six taxa with the same dental for-
mula, including: $U$. atronates, $U$. dabieshanensis, $U$. gracilis, $U$. investigator, $U$. nivatus, and the new species. The PCA and DA were conducted in SPSS v. 22.0 (SPSS Inc., USA). Furthermore, independent sample $t$-tests were conducted to test the variances of measurements highly correlated with PC1 and PC2 (i.e. LUTR, LBTR, GBSn, and GBUM; loading >0.8) between the new species and the other species.

## Results

## Phylogenetic analyses

We obtained 4090-bp-long sequences for each voucher specimen, including 2002-bp mitochondrial [CYT B (1140 bp) and $12 S$ (862 bp)] and 2088-bp nuclear [PLCB4 (330 bp), RAG1 (1008 bp), and RAG2 (750 bp)] sequences. All the new sequences were deposited in the GenBank [OQ730193-OQ730207, OQ725651-OQ725655, OR161365-OR161369, Suppl. material 2]. The uncorrected $p$-distance of CYT B reveals a high genetic divergence between the new species and all other nominal Uropsilus species, ranging from 9.3\% (with U. gracilis) to $16.4 \%$ (with U. investigator) (Table 1).

The ML and BI trees recovered similar topologies (Fig. 2). In all phylogenetic trees, sequences of the new species from Mount Huanggang formed a monophyletic clade with high support (SH-aLRT = 100, Utboot = 100, and PP = 1.00). The new species has a sister relationship with the clade that is comprised of $U$. atronates, Uropsilus sp. $6, U$. fansipanensis, and U. gracilis; this clade is strongly supported in the BI tree ( $\mathrm{PP}=1.0$ ), but this relationship only has moderate support in the ML tree ( $\mathrm{SH}-\mathrm{aLRT}=89.6$, Utboot $=76$ ). BEAST divergence analyses show that the divergence of the new species from the others was estimated to be at the early Pleistocene (1.92 Ma, 95\% CI $=0.88-2.99$ ) (Fig. 3).

## Morphological analyses

All external and skull measurements are given in Table 2. The PCA, which was based on 21 craniodental measurements, produced two axes with eigenvalues exceeding 2.0 , which explained $57.24 \%$ and $10.53 \%$ of the variance ( $67.77 \%$ total) (Table 3). The first principal component (PC1) is positively correlated with LUTR and LBTR (loading $>0.80$ ), indicating it mainly represents tooth row length. The second principal component (PC2) has high positive loadings on GBSn and GBUM (loading > 0.85). The independent-sample $t$-tests further show significant differences of at least two of the four measurements (i.e. LUTR, LBTR, GBSn, and GBUM) between the new species and $U$. atronates, $U$. dabieshanensis, $U$. gracilis, $U$. investigator, $U$. nivatus ( $p<0.05$; Suppl. material 4). A plot of PC1 and PC2 (Fig. 4) shows Uropsilus sp., U. investigator, and $U$. dabieshanensis occupy the positive region of PC1, indicating that these three species have longer tooth rows than $U$. atronates, $U$. nivatus, and U. gracilis. The new species plots on the near-origin area of PC2, while $U$. investigator occupies the negative regions and $U$. dabieshanensis occupies the positive region, suggesting that the snout and upper molars of the new species are relatively narrower than $U$. dabieshanensis but broader than those in $U$. investigator. The DA shows that $98.60 \%$ of the species are


Figure 2. Molecular phylogenetic tree of Uropsilus based on mitochondrial-nuclear concatenated data and analyzed using maximum likelihood and Bayesian inference analyses. Numbers above branches refer to Bayesian posterior probabilities (PP). Numbers below branches indicate SH-like approximate likelihood ratio test supports (SH-aLRT)/ultrafast bootstrap supports (UFBoot). Scale bars represent substitutions per site.


Figure 3. Divergence times estimated using BEAST based on mitochondrial-nuclear concatenated data. Node numbers refer to divergence time in million years ( Ma ) and Bayesian posterior probabilities (PP).
correctly classified based on the 21 craniodental measurements, with only one specimen labeled as $U$. investigator misclassified as $U$. nivatus. The first two canonical axes (CAN 1-2) explains $63.30 \%$ and $19.40 \%$ of the total variation, respectively (Table 3). In CAN 1 and CAN 2 plots (Fig. 4), specimens of the new species are separate from the others and remain close to $U$. nivatus and $U$. investigator.

|  | Species | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 1 | U. huanggangensis sp. nov. |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 2 | U. gracilis | 0.093 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | U. soricipes | 0.094 | 0.084 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 4 | U. fansipanensis | 0.094 | 0.092 | 0.091 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 5 | $U$ U atronates | 0.100 | 0.097 | 0.095 | 0.095 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | U. dabieshanensis | 0.104 | 0.097 | 0.105 | 0.108 | 0.125 |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | U. nivatus | 0.133 | 0.113 | 0.126 | 0.130 | 0.133 | 0.139 |  |  |  |  |  |  |  |  |  |  |  |
| 8 | U. aequodonenia | 0.138 | 0.130 | 0.122 | 0.143 | 0.142 | 0.147 | 0.103 |  |  |  |  |  |  |  |  |  |  |
| 9 | U. andersoni | 0.139 | 0.134 | 0.132 | 0.138 | 0.144 | 0.141 | 0.099 | 0.079 |  |  |  |  |  |  |  |  |  |
| 10 | U. investigator | 0.164 | 0.164 | 0.155 | 0.180 | 0.175 | 0.158 | 0.163 | 0.167 | 0.165 |  |  |  |  |  |  |  |  |
| 11 | U. sp. 1 | 0.161 | 0.157 | 0.154 | 0.172 | 0.160 | 0.155 | 0.157 | 0.156 | 0.162 | 0.097 |  |  |  |  |  |  |  |
| 12 | U. sp. 2 | 0.134 | 0.130 | 0.135 | 0.133 | 0.145 | 0.128 | 0.133 | 0.137 | 0.129 | 0.160 | 0.158 |  |  |  |  |  |  |
| 13 | U. sp. 3 | 0.100 | 0.108 | 0.104 | 0.108 | 0.104 | 0.114 | 0.126 | 0.142 | 0.139 | 0.158 | 0.160 | 0.135 |  |  |  |  |  |
| 14 | U. sp. 4 | 0.091 | 0.077 | 0.088 | 0.083 | 0.097 | 0.118 | 0.116 | 0.135 | 0.133 | 0.164 | 0.165 | 0.132 | 0.089 |  |  |  |  |
| 15 | U. sp. 5 | 0.097 | 0.086 | 0.039 | 0.094 | 0.101 | 0.097 | 0.127 | 0.128 | 0.135 | 0.154 | 0.150 | 0.135 | 0.101 | 0.090 |  |  |  |
| 16 | U. sp. 6 | 0.094 | 0.091 | 0.091 | 0.038 | 0.093 | 0.110 | 0.132 | 0.144 | 0.141 | 0.172 | 0.172 | 0.130 | 0.100 | 0.082 | 0.090 |  |  |
| 17 | U. sp. 7 | 0.088 | 0.087 | 0.084 | 0.088 | 0.099 | 0.099 | 0.127 | 0.133 | 0.132 | 0.157 | 0.157 | 0.131 | 0.096 | 0.085 | 0.079 | 0.095 |  |
| 18 | U. sp. 8 | 0.139 | 0.120 | 0.133 | 0.137 | 0.136 | 0.138 | 0.121 | 0.122 | 0.127 | 0.169 | 0.156 | 0.087 | 0.139 | 0.137 | 0.137 | 0.139 | 0.130 |

Table 2. External and skull measurements ( mm ) used in morphometric analyses of the genus Uropsilus, including mean values, standard deviations, range, sample size and the ratio of partial measurements.

|  | U. huanggangensis sp. nov. | U. dabieshanensis | U. gracilis | U. atronates | U. investigator | U. nivatus | U. aequodonenia | U. andersoni | U. soricipes | U. fansipanensis |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| W | $8.80 \pm 0.38$ | $9.28 \pm 1.25$ | $8.84 \pm 0.95$ | $6.93 \pm 0.92$ | $7.25 \pm 0.88$ | $8.00 \pm 1.38$ | 8 | $9.04 \pm 0.57$ | $9.52 \pm 1.34$ | 8.0; 8.0 |
|  | 8.17-9.19; 5 | 7.63-10.52; 6 | 7.30-10.20; 14 | 5.50-8.80; 15 | 5.90-8.40; 10 | 6.40-10.90; 7 |  | 8.20-9.80; 5 | 7.20-11.70; 10 |  |
| HBL | $72.40 \pm 1.34$ | $72.67 \pm 1.89$ | $69.86 \pm 4.15$ | $65.27 \pm 2.76$ | $71.65 \pm 4.30$ | $69.71 \pm 2.14$ | 75 | $74.33 \pm 3.01$ | $73.36 \pm 2.69$ | 77.5; 74.00 |
|  | 71.00-74.00; 5 | 69.50-75.00; 6 | 63.00-77.00; 14 | 61.00-69.00; 15 | 66.00-79.00; 10 | 67.00-73.00; 7 |  | 70.00-79.00; 6 | 70.00-79.00; 11 |  |
| TL | $62.60 \pm 3.21$ | $55.50 \pm 3.35$ | $63.57 \pm 6.11$ | $59.73 \pm 4.45$ | $65.40 \pm 4.30$ | $68.86 \pm 3.98$ | 70 | $65.17 \pm 10.68$ | $63.18 \pm 8.21$ | 62.50; 61.00 |
|  | 57.00-65.00; 5 | 52.50-61.50; 6 | 53.00-75.00; 14 | 52.00-68.00; 15 | 60.00-71.00; 10 | 61.00-73.00; 7 |  | 46.00-73.00; 6 | 46.00-73.00; 11 |  |
| HF | $13.10 \pm 0.22$ | $11.75 \pm 1.21$ | $12.96 \pm 0.97$ | $12.80 \pm 0.77$ | $13.20 \pm 1.40$ | $14.14 \pm 1.68$ | 14 | $14.75 \pm 0.76$ | $14.05 \pm 0.99$ | 13.41; 13.57 |
|  | 13.00-13.50; 5 | 10.50-13.00; 6 | 10.00-14.00; 14 | 11.00-14.50; 15 | 11.00-15.00; 10 | 11.00-16.00; 7 |  | 14.00-16.00; 6 | 13.00-16.00; 11 |  |
| EL | $9.20 \pm 0.45$ | $8.33 \pm 0.41$ | $9.39 \pm 1.1$ | $8.07 \pm 0.86$ | $7.95 \pm 0.98$ | $9.50 \pm 0.84$ | 11 | $9.67 \pm 0.58$ | $9.38 \pm 0.74$ | 8.51; 8.52 |
|  | 9.00-10.00; 5 | 8.00-9.00; 6 | 7.00-11.00; 14 | 7.00-9.50; 15 | 6.50-9.50; 10 | 8.00-10.00; 6 |  | 9.00-10.00; 3 | 8.00-10.00; 8 |  |
| PL | $21.44 \pm 0.47$ | $21.04 \pm 0.45$ | $20.89 \pm 0.41$ | $20.12 \pm 0.43$ | $21.19 \pm 0.71$ | $20.78 \pm 0.29$ | 21.91 | $22.06 \pm 0.33$ | $21.05 \pm 0.23$ | 20.4; 20.69 |
|  | 21.00-22.18; 5 | 20.32-21.50; 6 | 19.93-21.81; 16 | 18.99-20.79; 25 | 19.97-22.14; 11 | 20.39-21.12; 7 | 21.91; 1 | 21.59-22.34; 3 | 20.63-21.3; 5 |  |
| GNB | $11.10 \pm 0.17$ | $11.52 \pm 0.29$ | $11.27 \pm 0.20$ | $10.91 \pm 0.23$ | $11.10 \pm 0.34$ | $11.31 \pm 0.25$ | $11.90 \pm 0.19$ | $11.66 \pm 0.18$ | $11.36 \pm 0.26$ | 10.96; 11.07 |
|  | 10.95-11.39; 5 | 11.00-11.86; 6 | 10.88-11.63; 16 | 10.62-11.31; 25 | 10.45-11.64; 11 | 10.98-11.66; 7 | 11.71; 12.09; 2 | 11.49-11.91; 3 | 10.94-11.73; 5 |  |
| GBSn | $7.62 \pm 0.11$ | $8.10 \pm 0.34$ | $7.57 \pm 0.18$ | $7.27 \pm 0.21$ | $7.27 \pm 0.28$ | $7.82 \pm 0.24$ | $8.12 \pm 0.02$ | $7.87 \pm 0.21$ | $7.70 \pm 0.14$ | 7.39; 7.62 |
|  | 7.47-7.77; 5 | 7.65-8.51; 6 | 7.23-7.89; 16 | 6.84-7.72; 25 | 6.92-7.81; 11 | 7.51-8.15; 7 | 8.10; 8.14; 2 | 7.69-8.26; 6 | 7.52-7.92; 5 |  |
| MPL | $9.85 \pm 0.29$ | $9.79 \pm 0.18$ | $9.39 \pm 0.17$ | $8.90 \pm 0.24$ | $9.72 \pm 0.38$ | $9.59 \pm 0.22$ | $10.11 \pm 0.13$ | $10.00 \pm 0.15$ | $9.72 \pm 0.08$ | 9.62; 9.75 |
|  | 9.50-10.21; 5 | 9.46-9.96; 6 | 9.18-9.68; 16 | 8.49-9.33; 25 | 9.19-10.25; 11 | 9.31-9.90; 7 | 9.98; 10.24; 2 | 9.75-10.22; 5 | 9.65-9.85; 5 |  |
| LUTR | $9.47 \pm 0.24$ | $9.46 \pm 0.27$ | $9.02 \pm 0.17$ | $8.65 \pm 0.26$ | $9.38 \pm 0.34$ | $9.17 \pm 0.20$ | $9.61 \pm 0.10$ | $9.55 \pm 0.15$ | $9.24 \pm 0.16$ | 9.03; 9.07 |
|  | 9.12-9.76; 5 | 9.03-9.68; 6 | 8.65-9.25; 16 | 8.23-9.32; 25 | 8.96-9.93; 11 | 8.95-9.40; 7 | 9.51; 9.7; 2 | 9.24-9.68; 6 | 9.04-9.49; 5 |  |
| $\mathrm{P}^{4}-\mathrm{M}^{3}$ | $5.51 \pm 0.14$ | $5.65 \pm 0.24$ | $5.33 \pm 0.12$ | $5.13 \pm 0.19$ | $5.36 \pm 0.21$ | $5.37 \pm 0.16$ | $5.78 \pm 0.07$ | $5.75 \pm 0.15$ | $5.58 \pm 0.20$ |  |
|  | 5.35-5.67; 5 | 5.27-6.03; 6 | 5.05-5.55; 16 | 4.79-5.64; 25 | 5.04-5.64; 11 | 5.11-5.55; 7 | 5.73; 5.86; 2 | 5.53-5.98; 6 | 5.26-5.86; 5 |  |
| $\mathbf{M}^{1}-\mathbf{M}^{3}$ | $4.53 \pm 0.10$ | $4.62 \pm 0.21$ | $4.36 \pm 0.13$ | $4.17 \pm 0.15$ | $4.35 \pm 0.17$ | $4.40 \pm 0.13$ | $4.51 \pm 0.10$ | $4.55 \pm 0.2$ | $4.39 \pm 0.18$ |  |
|  | 4.37-4.62; 5 | 4.29-4.93; 6 | 4.11-4.64; 16 | 3.92-4.62; 25 | 4.15-4.72; 11 | 4.22-4.58; 7 | 4.41; 4.61; 2 | 4.26-4.92; 6 | 4.10-4.58; 5 |  |
| GBUM | $1.92 \pm 0.06$ | $2.02 \pm 0.08$ | $1.84 \pm 0.06$ | $1.76 \pm 0.07$ | $1.71 \pm 0.07$ | $1.83 \pm 0.07$ | $1.82 \pm 0.03$ | $1.89 \pm 0.05$ | $1.82 \pm 0.11$ |  |
|  | 1.82-1.97; 5 | 1.91-2.14; 6 | 1.76-1.95; 16 | 1.62-1.88; 25 | 1.63-1.84; 11 | 1.77-1.94; 7 | 1.79; 1.84; 2 | 1.80-1.97; 6 | 1.72-1.95; 5 |  |
| ML | $13.84 \pm 0.26$ | $14.07 \pm 0.22$ | $13.53 \pm 0.27$ | $12.98 \pm 0.36$ | $13.73 \pm 0.54$ | $13.67 \pm 0.18$ | $14.35 \pm 0.08$ | $14.27 \pm 0.28$ | $13.81 \pm 0.2$ | 13.52; 13.77 |
|  | 13.46-14.12; 5 | 13.80-14.41; 6 | 12.96-13.92; 16 | 12.36-13.75; 25 | 12.85-14.34; 11 | 13.41-13.87; 7 | 14.27; 14.42; 2 | 13.94-14.73; 6 | 13.45-14.02; 5 |  |


|  | U. huanggangensis sp. nov. | U. dabieshanensis | U. gracilis | U. atronates | U. investigator | U. nivatus | U. aequodonenia | U. andersoni | U. soricipes | U. fansipanensis |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Id-Coh | $12.40 \pm 0.35$ | $12.32 \pm 0.32$ | $12.55 \pm 0.19$ | $12.04 \pm 0.33$ | $12.42 \pm 0.65$ | $12.21 \pm 0.26$ | $12.87 \pm 0.41$ | $12.82 \pm 0.38$ | $12.44 \pm 0.46$ |  |
|  | 11.99-12.74; 5 | 11.82-12.74; 6 | 12.28-12.94; 16 | 11.44-12.77; 25 | 11.34-13.26; 11 | 11.86-12.60; 7 | 12.46; 13.28; 2 | 12.38-13.41; 6 | 11.8-13.17; 5 |  |
| LBTR | $8.10 \pm 0.12$ | $8.10 \pm 0.21$ | $7.69 \pm 0.21$ | $7.46 \pm 0.23$ | $8.04 \pm 0.37$ | $7.80 \pm 0.19$ | $8.18 \pm 0.06$ | $8.01 \pm 0.12$ | $7.87 \pm 0.22$ |  |
|  | 7.93-8.20; 5 | 7.84-8.42; 6 | 7.17-8.01; 16 | 7.04-7.84; 25 | 7.50-8.54; 11 | 7.57-8.05; 7 | 8.12; 8.24; 2 | 7.84-8.17; 6 | 7.67-8.22; 5 |  |
| LBO | $5.51 \pm 0.12$ | $5.42 \pm 0.26$ | $5.33 \pm 0.12$ | $5.46 \pm 0.18$ | $5.54 \pm 0.16$ | $5.6 \pm 0.14$ | $5.63 \pm 0.07$ | $5.82 \pm 0.11$ | $5.47 \pm 0.14$ | $5.51 ; 5.80$ |
|  | 5.32-5.65; 5 | 5.05-5.77; 6 | 5.12-5.58; 16 | 5.12-5.79; 25 | 5.23-5.86; 11 | 5.31-5.77; 7 | 5.56; 5.70; 2 | 5.64-5.97; 5 | 5.20-5.61; 5 |  |
| HB | $7.06 \pm 0.15$ | $6.84 \pm 0.40$ | $7.15 \pm 0.26$ | $6.70 \pm 0.23$ | $7.16 \pm 0.31$ | $7.03 \pm 0.15$ | 7.13 | $7.37 \pm 0.28$ | $7.38 \pm 0.29$ | 6.90; 6.91 |
|  | 6.92-7.35; 5 | 6.08-7.22; 6 | 6.65-7.65; 16 | 6.24-7.17; 25 | 6.62-7.68; 11 | 6.77-7.17; 7 | 7.13; 1 | 7.08-7.75; 3 | 6.8-7.52; 5 |  |
| BS | $7.57 \pm 0.16$ | $7.48 \pm 0.24$ | $7.36 \pm 0.22$ | $7.27 \pm 0.29$ | $7.34 \pm 0.19$ | $7.32 \pm 0.13$ | 7.57 | $7.57 \pm 0.36$ | $7.50 \pm 0.09$ |  |
|  | 7.33-7.76; 5 | 7.16-7.73; 6 | 6.97-7.96; 16 | 6.68-7.8; 25 | 6.88-7.59; 11 | 7.12-7.54; 7 | 7.57; 1 | 7.07-7.93; 3 | 7.40-7.65; 5 |  |
| BBP ${ }^{1}-\mathrm{P}^{2}$ | $2.96 \pm 0.11$ | $3.08 \pm 0.17$ | $2.82 \pm 0.09$ | $2.68 \pm 0.10$ | $2.77 \pm 0.09$ | $2.80 \pm 0.09$ | $2.99 \pm 0.06$ | $2.96 \pm 0.05$ | $2.93 \pm 0.08$ |  |
|  | 2.77-3.05; 5 | 2.84-3.38; 6 | 2.67-2.94; 16 | 2.41-2.88; 25 | 2.63-2.94; 11 | 2.63-2.88; 7 | 2.93; 3.05; 2 | 2.90-3.03; 6 | 2.80-3.03; 5 |  |
| APB | $2.58 \pm 0.10$ | $2.55 \pm 0.13$ | $2.36 \pm 0.10$ | $2.33 \pm 0.20$ | $2.50 \pm 0.10$ | $2.45 \pm 0.09$ | $2.51 \pm 0.06$ | $2.34 \pm 0.13$ | $2.37 \pm 0.08$ |  |
|  | 2.45-2.72; 5 | 2.35-2.77; 6 | 2.26-2.67; 16 | 2.00-3.03; 25 | 2.31-2.65; 11 | 2.30-2.58; 7 | 2.45; 2.57; 2 | 2.16-2.47; 6 | 2.28-2.48; 5 |  |
| PPB | $3.23 \pm 0.09$ | $3.29 \pm 0.19$ | $3.13 \pm 0.10$ | $3.06 \pm 0.14$ | $3.13 \pm 0.13$ | $3.34 \pm 0.18$ | $3.50 \pm 0.03$ | $3.27 \pm 0.09$ | $3.20 \pm 0.04$ |  |
|  | 3.10-3.32; 5 | 2.93-3.54; 6 | 2.94-3.31; 16 | 2.68-3.35; 25 | 2.91-3.34; 11 | 3.13-3.59; 7 | 3.47; 3.52; 2 | 3.18-3.40; 6 | 3.12-3.24; 5 |  |
| Id-Gol | $12.96 \pm 0.05$ | $13.14 \pm 0.28$ | $12.06 \pm 0.33$ | $11.43 \pm 0.43$ | $12.85 \pm 0.47$ | $12.69 \pm 0.20$ | $13.09 \pm 0.10$ | $13.07 \pm 0.13$ | $12.83 \pm 0.19$ |  |
|  | 12.90-13.03; 5 | 12.66-13.54; 6 | 11.46-12.68; 16 | 10.79-12.38; 25 | 12.18-13.58; 11 | 12.43-12.98; 7 | 12.99; 13.18; 2 | 12.89-13.3; 6 | 12.61-13.18; 5 |  |
| HVR | $6.31 \pm 0.15$ | $6.39 \pm 0.31$ | $6.32 \pm 0.12$ | $6.00 \pm 0.19$ | $6.22 \pm 0.29$ | $6.32 \pm 0.09$ | $6.73 \pm 0.02$ | $6.63 \pm 0.15$ | $6.44 \pm 0.17$ |  |
|  | 6.10-6.57; 5 | 5.91-6.90; 6 | 6.09-6.49; 16 | 5.67-6.49; 25 | 5.77-6.61; 11 | 6.19-6.49; 7 | 6.71; 6.74; 2 | 6.44-6.84; 6 | 6.30-6.75; 5 |  |
| Coh-M ${ }_{3}$ | $5.79 \pm 0.05$ | $5.56 \pm 0.29$ | $5.68 \pm 0.25$ | $5.36 \pm 0.26$ | $5.81 \pm 0.32$ | $5.78 \pm 0.17$ | 6.45 | $6.07 \pm 0.33$ | $5.90 \pm 0.23$ |  |
|  | 5.72-5.87; 5 | 5.18-6.00; 6 | 5.15-6.11; 16 | 4.81-5.98; 25 | 5.25-6.29; 11 | 5.52-6.00; 7 | 6.45; 1 | 5.67-6.55; 6 | 5.57-6.22; 5 |  |
| GBLM | $1.19 \pm 0.05$ | $1.25 \pm 0.06$ | $1.14 \pm 0.04$ | $1.09 \pm 0.05$ | $1.09 \pm 0.04$ | $1.14 \pm 0.05$ | $1.19 \pm 0.03$ | $1.20 \pm 0.05$ | $1.11 \pm 0.06$ |  |
|  | 1.10-1.25; 5 | 1.18-1.33; 6 | 1.07-1.21; 16 | 1.02-1.19; 25 | 1.03-1.16; 11 | 1.08-1.23; 7 | 1.16; 1.22; 2 | 1.13-1.27; 6 | 1.04-1.19; 5 |  |
| TL/HBL | 86.46\% | 76.37\% | 91.00\% | 91.51\% | 91.28\% | 98.78\% | 93.33\% | 87.68\% | 86.12\% | 83.50\% |
| GNB/PL | 51.80\% | 55.74\% | 53.94\% | 54.24\% | 52.40\% | 54.43\% | 53.45\% | 52.87\% | 53.96\% | 53.61\% |

Table 3．Character loadings，eigenvalues，and percent variance explained on the first two components of a principal com－ ponents analysis and the five canonical axes discriminant function analyses of the genus Uropsilus．

| Variables | PCA |  | DA |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | 1 | 2 | 1 | 2 | 3 | 4 | 5 |
| LUTR | 0.832 | 0.313 | 0.243 | －0．079 | 0.275 | －0．457 | －1．450 |
| LBTR | 0.807 | 0.256 | 0.353 | －0．398 | －0．934 | 0.619 | 0.266 |
| PL | 0.781 | 0.283 | 1.259 | －0．271 | －0．119 | －0．180 | 0.735 |
| Id－Gol | 0.770 | 0.276 | 0.952 | －0．544 | 0.215 | －0．133 | －0．329 |
| ML | 0.667 | 0.302 | 0.625 | 1.142 | －0．602 | －0．854 | －0．317 |
| MPL | 0.647 | 0.198 | －0．754 | －0．556 | 0.599 | 1.207 | 0.877 |
| $\mathrm{P}^{4}-\mathrm{M}^{3}$ | 0.625 | 0.549 | －0．374 | 0.322 | －0．680 | －0．106 | －0．944 |
| $\mathrm{M}^{1}-\mathrm{M}^{3}$ | 0.604 | 0.598 | 0.003 | 0.058 | 0.666 | 0.184 | 0.848 |
| APB | 0.592 | 0.228 | －0．092 | －0．052 | －0．302 | 0.220 | 0.267 |
| GBUM | 0.138 | 0.892 | 0.264 | 0.459 | －0．083 | 0.641 | 0.649 |
| GBSn | 0.211 | 0.854 | －0．276 | 0.421 | 0.475 | －1．268 | 0.024 |
| GBLM | 0.288 | 0.741 | －0．079 | －0．062 | 0.249 | 0.249 | 0.341 |
| BBP1－P ${ }^{2}$ | 0.368 | 0.698 | 0.591 | 0.459 | －0．474 | 0.373 | －0．416 |
| PPB | 0.252 | 0.603 | －0．339 | －0．393 | 0.229 | 0.047 | 0.356 |
| Id－Coh | 0.321 | 0.067 | －1．660 | 0.156 | 0.770 | 0.207 | －0．678 |
| HVR | 0.354 | 0.402 | －0．601 | 0.166 | －0．025 | 0.164 | －0．487 |
| Coh－M ${ }_{3}$ | 0.484 | －0．006 | －0．291 | －0．622 | 0.580 | 0.164 | 1.254 |
| GNB | 0.111 | 0.524 | 0.759 | 0.270 | 0.023 | －0．253 | －0．493 |
| HB | 0.293 | 0.112 | 0.047 | －0．434 | 0.608 | －0．251 | －0．004 |
| BS | 0.179 | 0.218 | 0.195 | 0.256 | －0．424 | 0.515 | 0.104 |
| LBO | 0.184 | －0．070 | －0．203 | －0．254 | －0．585 | －0．497 | 0.476 |
| Eigenvalues | 12.020 | 2.211 | 8.426 | 2.829 | 0.973 | 0.563 | 0.263 |
| Percent variance explained（\％） | 57．24\％ | 10．53\％ | 64．70\％ | 21．70\％ | 7．20\％ | 4．30\％ | 2．00\％ |

Both the molecular and morphological analyses indicate that Uropsilus sp． nov．is diagnosable from all other recognized species of the genus Uropsilus． Based on the diagnosis and monophyly－based phylogenetic species concept （Mayden 1997；Gutierrez and Garbino 2018），we recognize it as a new species， which we formally describe below．

## Taxonomic account

## Uropsilus huanggangensis Chen，Jiang \＆Ren，sp．nov．

https：／／zoobank．org／160BAE4A－EBEB－4177－8A50－ADF35E932D4C
Figs 4， 5

Suggested common name．Huanggang shrew mole；Chinese common name：黄岗鼩鼣。

Type materials．Holotype：AHNU 2022013，an adult male collected by Zhong－ zhen Chen in June 2022 from Mount Huanggang，Wuyishan National Park，Ji－ angxi Province，China（ $27^{\circ} 58^{\prime} 53^{\prime \prime} \mathrm{N}, 117^{\circ} 47^{\prime} 2.4^{\prime \prime} \mathrm{E}$ ，altitude 2061 m a．s．I．）．The dried skin and cleaned skull are deposited in ANHU．Paratypes：AHNU 2022014，AHNU 2022053，AHNU 2022054，and AHNU 2022055； 4 adult specimens collected from Mount Huanggang，Wuyishan National Park，Jiangxi Province，China at ele－ vations between 1830 and 2060 m a．s．I．The specimens are deposited in AHNU．

Etymology．The specific name huanggangensis is derived from Mount Huanggang，the type locality of the new species；the Latin adjectival suffix－ensis means＂belonging to＂．

Diagnosis. The dorsal pelage of $U$. huanggangensis is dark chocolate-brown. The snout is the longest of any species in the genus. The first incisor $I^{1}$ is wide and shows an enlargement at the apex of the rostrum, with a visible gap to $\mathrm{I}^{2}$. $C_{1}$ is larger than $P_{1}$, and $P_{1}$ and $P_{3}$ are similar in size. Tail is slim and relatively short, averaging $86 \%$ of head and body length. The tufts at the tail tip are short. The lacrimal foramen and infraorbital foramen are similar in size. The coronoid process is pointed and converges more upward with an incisive tip. The dental formula is $\mathrm{I} 2 / 1, \mathrm{C} 1 / 1, \mathrm{P} 4 / 4, \mathrm{M} 3 / 3=38$.

Description. Uropsilus huanggangensis is a medium-sized species of Uropsilus (HBL = $72 \pm 1 \mathrm{~mm}, \mathrm{PL}=21.44 \pm 0.47 \mathrm{~mm}$; Table 2). The dorsal pelage is dark chocolate-brown, consisting of brown fur with a light grey base; the ventral fur is slightly paler. The snout is very long, at about 12 mm , and is the longest in the genus. The tail is slim and relatively short (TL = $63 \pm 3 \mathrm{~mm}, 57-65$ $\mathrm{mm})$, about $86 \%$ of the combined head and body length. The tail is black above and slightly paler below, with a sparse tuft of short hair at its tip. The hind foot is covered with short black hair; its length is $13-14 \mathrm{~mm}$ and constitutes approximately $18 \%$ of the combined head and body length.

The outlines of the skull are rounded, and there is a complete zygomatic arch. The rostrum is relatively long, the braincase is narrow, and the proportion of GNB and PL is $51.8 \%$, which is the smallest of any species in the genus (GNB/ PL > 52.4\% in other species). The zygomatic arches are stout and only slightly bow outward. The lacrimal foramen and infraorbital foramen are similar in size.

The dental formula is I $2 / 1, \mathrm{C} 1 / 1, \mathrm{P} 4 / 4, \mathrm{M} 3 / 3=38$. $I^{1}$ is large and wide, causing the enlargement at the apex of the rostrum. $I^{1}$ is bigger than $I^{2}$, and there is a visible gap between them. $\mathrm{C}^{1}$ is almost equal to $\mathrm{P}^{1}$, while $\mathrm{P}^{3}$ is smaller. $\mathrm{P}^{2}$ is larger than $\mathrm{P}^{1}$ and $\mathrm{P}^{3}$. The first upper molar $\mathrm{M}^{1}$ and second upper molar $\mathrm{M}^{2}$ are large, and have well-developed, W-shaped lateral cusps. In contrast, the third upper molars $\mathrm{M}^{3}$ are reduced.


Figure 4. Results of A principal component analysis (PCA) B discriminant function analysis (DA) for partial species with the same dental formula within the genus Uropsilus.


Figure 5. Dorsal and ventral views of three Uropsilus species A U. huanggangensis sp. nov. B U. gracilis $\mathbf{C}$ U. dabieshanensis.

The body of the mandible is long and slender. The coronoid process is high, pointed, and curved to the posterior, with an incisive tip pointing straight to the posterior, resembling the outline of a sickle. The angular process is long, rounded, and points downward at roughly $45^{\circ}$. The first lower premolar $\left(P_{1}\right)$ is slightly smaller than the lower canine $C_{1} . P_{1}$ and $P_{3}$ are similar in size. $M_{2}$ is W-shaped and larger than $M_{1}$ and $M_{3} . M_{3}$ is slightly smaller than $M_{1}$ (Fig. 6).

Comparison. Among other Uropsilus species, U. huanggangensis is morphologically most similar to $U$. dabieshanensis and $U$. gracilis. However, the new species can be distinguished from them by many characteristics.

Compared to $U$. dabieshanensis, $U$. huanggangensis has darker fur, a relatively longer and slimmer tail, and a much larger hindfoot and ear, despite that the heads and body lengths of the two species are almost the same (Table 2; Fig. 5). The tail of $U$. huanggangensis ( $T L=63 \pm 3 \mathrm{~mm}$ ) is relatively longer than $U$. dabieshanensis ( $T L=56 \pm 3 \mathrm{~mm}$ ). Most individuals of $U$. huanggangensis (4 of 5 ) have a tail length of more than 63 mm , while most individuals of $U$. dabieshanensis (5 of 6) have a tail length less than 57 mm . The hairs on the tail (bristle hairs) of $U$. huanggangensis are shorter and sparser than those in $U$. dabieshanensis, and the tufts at the tail tip of $U$. dabieshanensis appear much longer. The skull of U. huanggangensis is much slenderer than in U. dabieshanensis (Fig. 6), and the proportion of GNB and PL (CB / GLS $=53.96 \%$ ) in U. dabieshanensis is greater than that in $U$. huanggangensis (GNB / PL = 51.80\%). The coronoid process is pointed and curved to the posterior in $U$. huanggangensis, while the coronoid process of $U$. dabieshanensis is high and straight, with a squared tip.

Compared to $U$. gracilis, the dorsal pelage of $U$. huanggangensis is much darker. The snout of $U$. huanggangensis is longer, and the incisor is larger than that of $U$. gracilis. The tail of $U$. huanggangensis (TL/HBL $=86 \%$ ) is relatively shorter than U. gracilis (TL / HBL $=91 \%$ ) in proportion, and the tufts at the tail tip of $U$. huanggangensis are much shorter than those in $U$. gracilis. In terms of


Figure 6. Dorsal, ventral, and lateral views of the skull and lateral views of the mandible of three Uropsilus species $\mathbf{A} U$. huanggangensis sp. nov. B U. gracilis $\mathbf{C} U$. dabieshanensis.
body size, $U$. huanggangensis is relatively larger than $U$. gracilis for most external and craniomandibular measurements (Table 2). In particular, the range of Id-Gol (U. huanggangensis $12.90-13.03 \mathrm{~mm}$ vs $U$. gracilis $11.46-12.68 \mathrm{~mm}$ ) between the two species does not overlap. The coronoid process of $U$. gracilis is high and squared, similar to that of $U$. dabieshanensis, but differs from that of $U$. huanggangensis.

Compared to $U$. atronates and $U$. nivatus, the dark chocolate-brown dorsal pelage of $U$. huanggangensis differs from the chestnut red of $U$. atronates and the black-gold pellage of $U$. nivatus. Meanwhile, $U$. huanggangensis is larger than both $U$. atronates and $U$. nivatus for most external and craniomandibular measurements (Table 2).

The pelage color of $U$. huanggangensis is dark chocolate-brown, which is much lighter than the black pelage of $U$. investigator. The ears of $U$. huanggangensis are relatively larger ( $\mathrm{EL}=9.20 \pm 0.45 \mathrm{~mm}$, range $9.00-10.00 \mathrm{~mm}$ ) than that of the $U$. investigator ( $E L=7.95 \pm 0.98 \mathrm{~mm}$, range $6.50-9.50 \mathrm{~mm}$ ). The color of $U$. huanggangensis is uniform compared to the bicolored tail of $U$. investigator. Also, the $P_{1}$ of $U$. investigator is larger than $P_{3}$, while $P^{1}$ and $P_{3}$ of $U$. huanggangensis are similar in size.

Compared to the upward orbital process of $U$. fansipanensis, the orbital process of $U$. huanggangensis is downward. The lacrimal foramen of $U$. fansipanensis is larger than infraorbital foramen, while the two are of similar size in U. huanggangensis.

The dental formula of $U$. huanggangensis is $12 / 1, C 1 / 1, P 4 / 4, \mathrm{M} 3 / 3=38$, which can be easily distinguished from $U$. soricipes (dental formula I 2/1, C 1/1,

P 3/3, M 3/3 = 34), U. andersoni (dental formula I $2 / 2, C 1 / 1, P 4 / 3, \mathrm{M} 3 / 3=38$ ), and $U$. aequodonenia (dental formula I 2/2, C $1 / 1, \mathrm{P} 3 / 3, \mathrm{M} 3 / 3=36$ ).

Distribution and ecology. Uropsilus huanggangensis is currently known only from the type locality on Mount Huanggang, Wuyishan National Park, Jiangxi Province, eastern China, where pecimens were collected at elevations between 1830 and 2060 m a.s.l. Coniferous forests and shrub meadows, with abundant rocks on the ground, dominate the habitat in this area.

## Discussion

For a long time, it was believed that the genus Uropsilus was only distributed in the mountains of southwestern China and adjacent Myanmar (Wan et al. 2013; Kryštufek and Motokawa 2018). Hu et al. (2021b) expanded the known distribution of the genus by reporting the presence of $U$. dabieshanensis on Dabie Mountain, Anhui, eastern China, which represents the easternmost distribution of genus. In the present study, through integrating morphological and molecular approaches, we demonstrate that the isolated population on Mount Huanggang is distinct from all nominal species of Uropsilus and recognize it as a new species, $U$. huanggangensis.

In line with previous studies (Wan et al. 2013; Hu et al. 2021b), our phylogenetic analyses reveal that Uropsilus species can be sorted into two distinct lineages. One lineage includes $U$. investigator and $U$. sp. 1, occupying the basal position of the genus, and the other lineage exhibits a widespread distribution throughout China. Although U. huanggangensis consistently forms a monophyletic group with strong support in all phylogenetic trees, it is worth noting that the phylogenetic trees of Uropsilus species display considerable instability, as previously reported in the literature. Additionally, eight putative new species (Uropsilus sp. 1-8) have been identified but not yet officially described; there is a high level of cryptic diversity and extensive cryptic diversification within the genus. Broader sampling, in-depth gene sequencing, and morphological analysis are needed to improve the understanding of the genus.

As the easternmost occurring species of Uropsilus, our discovery of $U$. huanggangensis significantly expands our knowledge of the geographic distribution of the genus and contributes to our understanding of its macroevolution. The divergence of $U$. huanggangensis is estimated in the early Pleistocene $(1.98 \mathrm{Ma}$, $95 \% \mathrm{Cl}=0.88-2.99$ ). Global cooling and drying events during this period (Qiu and Li 2005; Ge et al. 2013), as well as the isolation effects of Wuyi Mountain and Yangtze River, may have been critical in the divergence of $U$. huanggangensis, and Mount Huanggang may have provided a refuge for $U$. huanggangensis during the ice age. Recently, several new small mammal species have been described in eastern China, such as Chodsigoa dabieshanensis Chen et al., 2022, Crocidua dongyangjiangensis Liu et al., 2020, and Typhlomys huangshanensis Hu et al., 2021, indicating that biodiversity in the region is severely underexplored (Hu et al. 2021a; Chen et al. 2022). The description of $U$. huanggangensis in the Wuyi Mountains region highlights the overlooked biodiversity of the mountains of eastern China. It is therefore crucial to conduct further comprehensive investigations and taxonomic studies on small mammals in this region to gain a deeper understanding of the biodiversity of this region.

## Acknowledgements

We thank the two anonymous reviewers and academic editor for constructive comments and suggestions, and thank Shidong Pu and several field guides for help with specimen collection. We also thank the relevant local government staff for their strong support and assistance.

## Additional information

## Conflict of interest

The authors have declared that no competing interests exist.

## Ethical statement

No ethical statement was reported.

## Funding

This research was funded by the National Natural Science Foundation of China (31900318), Anhui Provincial Natural Science Foundation (2008085QC106), the University Synergy Innovation Program of Anhui Povince (GXXT-2020-075), and the Project of Biological Resource Survey in Wuyishan National Park.

## Author contributions

Formal analysis: $Y X, X R$. Funding acquisition: ZC. Investigation: XJ, ZC, XR, YF, HY, LC, WZ. Methodology: ZC. Resources: XJ, YL, LC, ZC, WZ. Software: YX, ZC, XR. Supervision: ZC. Writing - original draft: XR. Writing - review and editing: ZC, YX, LK, XR.

## Author ORCIDs

Xueyang Ren © https://orcid.org/0000-0002-3137-0309
Yifan Xu © https://orcid.org/0000-0002-8433-1768
Hongfeng Yao © https://orcid.org/0009-0007-2493-2135
Laxman Khanal © https://orcid.org/0000-0003-2411-3627
Xuelong Jiang © https://orcid.org/0000-0003-2052-2490
Zhongzheng Chen © https://orcid.org/0000-0003-3821-0145

## Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

## References

Allen GM (1923) New Chinese insectivores. American Museum Novitates 100: 1-11. http://hdl.handle.net/2246/4530
Allen GM (1938) Mammals of China and Mongolia. Part 1. New York, American Museum of Natural History. https://doi.org/10.2307/1374504
Bouckaert R, Vaughan TG, Barido-Sottani J, Duchêne S, Fourment M, Gavryushkina A, Heled J, Jones G, Kühnert D, Maio DN, Matschiner M, Mendes FK, Müller NF, Ogilvie HA, Plessis LD, Popinga A, Rambaut A, Rasmussen D, Siveroni I, Suchard MA, Wu CH, Xie D, Zhang C, Stadler T, Drummond AJ (2019) BEAST 2.5: An advanced soft-
ware platform for Bayesian evolutionary analysis. PLoS Computational Biology 15(4): e1006650. https://doi.org/10.1371/journal.pcbi. 1006650
Bui HT, Okabe S, Le LTH, Nguyen NT, Motokawa M (2023) A new shrew mole species of the genus Uropsilus (Eulipotyphla: Talpidae) from northwestern Vietnam. Zootaxa 5339(1): 59-78. https://doi.org/10.11646/zootaxa.5339.1.3
Chen ZZ, Hu TL, Pei XX, Yang GD, Yong F, Xu Z, Qu WY, Onditi KO, Zhang BW (2022) A new species of Asiatic shrew of the genus Chodsigoa (Soricidae, Eulipotyphla, Mammalia) from the Dabie Mountains, Anhui Province, eastern China. ZooKeys 1083: 129-146. https://doi.org/10.3897/zookeys.1083.78233
Corbet GB, Hill JE (1980) A world list of mammalian species. London and Ithaca, N.Y., British Museum (Natural History) and Cornell University Press. Journal of Mammalogy 62(4): 860-861. https://doi.org/10.2307/1380617

Cranbrook TE, Cranbrook TEo (1960-1961) Notes on the habits and vertical distribution of some insectivores from the Burma-Tibetan Frontier. Proceedings of the Linnean Society of London 173(2): 121-127. https://doi.org/10.1111/j.1095-8312.1962.tb01305.x
Douady CJ, Douzery EJ (2003) Molecular estimation of eulipotyphlan divergence times and the evolution of "Insectivora". Molecular Phylogenetics and Evolution 28(2): 285-296. https://doi.org/10.1016/S1055-7903(03)00119-2
Ellerman JR, Morrison-Scott TCS (1951) Checklist of Palaearctic and Indian mammals 1758 to 1946. London, British Museum (Natural History). Science 115: 431-432. [1952] https://doi.org/10.1126/science.115.2990.431
Ge J, Dai Y, Zhang Z, Zhao D, Li Q, Zhang Y, Yi L, Wu H, Oldfield F, Guo Z (2013) Major changes in East Asian climate in the mid-Pliocene: Triggered by the uplift of the Tibetan Plateau or global cooling? Journal of Asian Earth Sciences 69: 48-5. https://doi. org/10.1016/j.jseaes.2012.10.009
Gutierrez EE, Garbino GST (2018) Species delimitation based on diagnosis and monophyly, and its importance for advancing mammalian taxonomy. Zoological Research 39(5): 301-308. https://doi.org/10.24272/j.issn.2095-8137.2018.037
Hoffmann RS (1984) A review of the shrew-moles (genus Uropsilus) of China and Burma. Journal of the Mammalogical Society of Japan 10: 69-80. https://doi.org/10.11238/ JMAMMSOCJAPAN1952.10.69
Hoffmann RS, Lunde D (2008) Soricomorpha. In: Smith AT, Xie Y (Eds) A Guide to the Mammals of China. Princeton University Press, Princeton, 297-327.
Honacki JH, Kinman KE, Koeppl JW (1982) Mammals species of the world; a taxonomic and geographic reference. Lawrence, Kan: Allen Press and the Association of Systematics Collections. https://doi.org/10.5860/CHOICE.31-0037
Hu TL, Cheng F, Xu Z, Chen ZZ, Yu L, Ban Q, Li CL, Pan T, Zhang BW (2021a) Molecular and morphological evidence for a new species of the genus Typhlomys (Rodentia: Platacanthomyidae). Zoological Research 42(1): 100-107. https://doi.org/10.24272/j. issn.2095-8137.2020.132
Hu TL, Xu Z, Zhang H, Liu YX, Liao R, Yang GD, Sun RL, Shi J, Ban Q, Li CL, Liu SY, Zhang BW (2021b) Description of a new species of the genus Uropsilus (Eulipotyphla: Talpidae: Uropsilinae) from the Dabie Mountains, Anhui, Eastern China. Zoological Research 42(3): 294-299. https://doi.org/10.24272/j.issn.2095-8137.2020.266
Hutterer R (2005) Order Soricomorpha. In: Wilson DE, Reeder DM (Eds) Mammal Species of the World (3 $3^{\text {rd }}$ edn.). The Johns Hopkins University Press, Baltimore, 220-311. http://taxonomicon.taxonomy.nl/Reference.aspx?id=4992
International Commission on Zoological Nomenclature (2012) Amendment of Articles $8,9,10,21$ and 78 of the International Code of Zoological Nomenclature to expand
and refine methods of publication. Bulletin of Zoological Nomenclature 69(3): 161169. https://doi.org/10.21805/bzn.v69i3.a8.161

IUCN (2015) The IUCN Red List of Threatened Species. Version 2015.3. http://www. iucnredlist.org

Kryštufek B, Motokawa M (2018) Family Talpidae (moles, desmans, star-nosed moles and shrew moles). Handbook of the Mammals of the World 8: 552-619.
Lanfear R, Calcott B, Ho SYW, Guindon S (2012) PartitionFinder: Combined Selection of Partitioning Schemes and Substitution Models for Phylogenetic Analyses. Molecular Biology and Evolution 29(6): 1695-1701. https://doi.org/10.1093/molbev/mss020
Liu Y, Liu SY, Sun ZY, Guo P, Fan ZX, Robert WM (2013) A new species of Uropsilus (Talpidae:Uropsilinae) from Sichuan, China. Acta Theriological Sinica 33(2): 113-122.
Liu Y, Chen SD, Liu BQ, Liao R, Liu YX, Liu SY (2020) A new species of the genus Crocidura (Eulipotyphla: Soricidae) from Zhejiang Pvovince, eastern China. Acta Theriological Sinica 40(1): 1-12. https://doi.org/10.16829/j.slxb. 150340
Mayden RL (1997) A hierarchy of species concepts: The denouement in the saga of the species problem. In: Claridge MF, Dawah HA, Wilson MR (Eds) Species: The Units of Diversity. Chapman \& Hall.
Mckenna MC, Bell SK, Simpson GG (1997) Classification of Mammals Above Species Level. Columbia University Press. https://doi.org/10.5860/CHOICE.35-5657
Meredith RW, Janečka JE, Gatesy J, Ryder OA, Fisher CA, Teeling EC, Goodbla A, Eizirik E, Simão TLL, Stadler T, Rabosky DL, Honeycutt RL, Flynn JJ, Ingram CM, Steiner C, Williams TL, Robinson TJ, Burk-Herrick A, Westerman M, Ayoub NA, Springer MS, Murphy WJ (2011) Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification. Science 334(6055): 521-524. https://doi.org/10.1126/ science. 1211028
Milne-Edwards A (1871) Descriptions of new species, in footnotes, In David Journal d'un voyage en Mongolia et en Chine fait en 1866-68. Nouvelles Archives du Muséum d'Histoire Naturelle, Paris Bull 7: 75-100.

Motokawa M (2004) Phylogenetic relationships within the family Talpidae (Mammalia: Insectivora). Journal of Zoology 263(2): 147-157. https://doi.org/10.1017/ S0952836904004972
Osgood WH (1937) Variable dentition in a Chinese insectivore. Zoological Series of Field Museum of Natural History 20: 365-368. https://doi.org/10.5962/bhl.title. 2967
Qiu ZD, Li CK (2005) Evolution of Chinese mammalian faunal regions and elevation of the Qinghai-Xizang (Tibet) Plateau. Science in China. Series D, Earth Sciences 48(8): 1246-1258. https://doi.org/10.1360/03yd0523

Rambaut A, Drummond AJ, Xie D, Baele G, Suchard MA (2018) Posterior summarization in Bayesian phylogenetics using Tracer 1.7. Systematic Biology 67(5): 901-904. https://doi.org/10.1093/sysbio/syy032
Sánchez-Villagra MR, Horovitz I, Motokawa M (2006) A comprehensive morphological analysis of talpid moles (Mammalia) phylogenetic relationships. Cladistics 22(1): 59-88. https://doi.org/10.1111/j.1096-0031.2006.00087.x
Shinohara A, Campbell KL, Suzuki H (2003) Molecular phylogenetic relationships of moles, shrew moles, and desmans from the new and old worlds. Molecular Phylogenetics and Evolution 27(2): 247-258. https://doi.org/10.1016/S1055-7903(02)00416-5
Sikes RS, Animal Care and Use Committee of the American Society of Mammalogists (2016) Guidelines of the American Society of Mammalogists for the use of wild mammals in research and education. Journal of Mammalogy 97: 663-688. https://doi. org/10.1093/ jmammal/gyw078

Tamura K, Stecher G, Kumar S (2021) MEGA11: Molecular Evolutionary Genetics Analysis Version 11. Molecular Biology and Evolution 38(7): 3022-3027. https://doi. org/10.1093/molbev/msab120
Thomas O (1912) The Duke of Bedford's zoological exploration of Eastern Asia.-XV. On mammals from the provinces of Szechwan and Yunnah, western China. Proceedings of the Zoological Society of London, Wiley Online Library 82(1): 127-141. https://doi. org/10.1111/j.1469-7998.1912.tb07008.x
Thomas O (1922) On mammals from the Yunnan Highlands collected by Mr. George Forrest and presented to the British Museum by Col. Stephenson R. Clarke D. S. O. Annals \& Magazine of Natural History 10(58): 391-406. https://doi. org/10.1080/00222932208632789
Wan T (2015) Phylogeny, Phylogeography and Integrative Taxonomy of Asiatic Shrew Moles (Uropsilinae). PhD. Thesis, University of Chinese Academy of Sciences, Beijing, 163 pp. [In Chinese]
Wan T, He K, Jiang XL (2013) Multilocus phylogeny and cryptic diversity in Asian shrewlike moles (Uropsilus, Talpidae): Implications for taxonomy and conservation. BMC Evolutionary Biology 13(1): 1-13. https://doi.org/10.1186/1471-2148-13-232
Wan T, He K, Jin W, Liu SY, Chen ZZ, Zhang B, Murphy RW, Jiang XL (2018) Climate niche conservatism and complex topography illuminate the cryptic diversification of Asian shrew-like moles. Journal of Biogeography 45(10): 2400-2414. https://doi. org/10.1111/jbi. 13401
Wang YX, Yang G (1989) Editor-in-Chief of Yunnan Disease Control Office and Yunnan Health and Anti-epidemic Station: Yunnan Medical Animal Directory. Kunming: Yunnan Science and Technology Press, 202-210. [In Chinese]
Yang QS, Xia L, Ma Y, Feng ZJ, Quan GQ (2005) A guide to the measurement of mammal skull I: Basic measurement. Chinese Journal of Zoology 40(3): 50-56. https://doi. org/10.13859/j.cjz.2005.03.011
Yang QS, Xia L, Feng ZJ, Ma Y, Quan GQ, Wu Y (2007) A guide to the measurement of mammal skull V: Insectivora and Chiroptera. Chinese Journal of Zoology 42(2): 56-62. https://doi.org/10.13859/j.cjz.2007.02.013
Zhang D, Gao FL, Jakovlić I, Zou H, Zhang J, Li WX, Wang GT (2020) PhyloSuite: An integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Molecular Ecology Resources 20(1): 348-355. https://doi.org/10.1111/1755-0998.13096

## Appendix 1

Specimens examined for this study. Abbreviations: KIZ, Kunming Institute of Zoology, Chinese Academy of Sciences; AHNU, Anhui Normal University.

Uropsilus huanggangensis sp. nov. $(n=5)$ : Mount Huanggang, Jiangxi (AHNU 2022013-014, AHNU 2022053-055).
U. aequodonenia ( $n=2$ ): Mount Daliangshan, Yuexi, Sichuan (KIZ 0906075, KIZ SC2110638).
U. andersoni $(n=6)$ : Mount Erlang, Tianquan, Sichuan (KIZ SC2110004, KIZ SC2110014-015, KIZ Z201505738-739, KIZ Z201505755).
U. atronates ( $n=25$ ): Mount Laobieshan, Yongde, Yunnan (KIZ 0212145, KIZ 0212185, KIZ 0212187, KIZ 0212190, KIZ 0212309, KIZ 0212314, KIZ

0212332, KIZ 0212334, KIZ 0212339, KIZ 0212381-382, KIZ 0212413); Caojian, Yunlong, Yunnan (KIZ 0904362, KIZ 0904420-403); Laowo, Lushui, Yunnan (KIZ 2012121120); Wayao, Baoshan, Yunnan (KIZ H2004, KIZ H2007, KIZ H2013-14, KIZ H2040, KIZ H2052, KIZ H2054, KIZ H2073, KIZ H2090).
U. dabieshanensis $(n=6)$ : Dabie Mountain, Anhui (AHNU 202109002, AHNU 202109115, AHNU 202109302, AHNU 202109337, AHNU 202109409, AHNU 202109457).
U. gracilis ( $n=16$ ): Mount Jinfoshan, Nanchuan, Chongqing (KIZ Y204002, KIZ Y204043); Mount Jiaozishan, Dongchuan, Yunnan (KIZ 0810003, KIZ 0810137, KIZ0810159-160, KIZ 0810191-192, KIZ 0810245, KIZ 0810274, KIZ 0810488, LIZ 0810504); Mount Jiaozishan, Luquan, Yunnan (KIZ 0811149, KIZ 0811175-176); Mount Wumeng, Zhaotong, Yunnan (KIZ 201309117).
U. investigator ( $n=11$ ): Mount Gaoligong, Gongshan, Yunnan (KIZ PM1311422, KIZ PM1312467, KIZ PM1312511, KIZ PM1312570, KIZ PM1312600, KIZ 201211136, KIZ 201211160, KIZ 201211575, KIZ GLGS1945).
U. nivatus ( $n=7$ ): Mount Diancang, Dali, Yunnan (KIZ DL1110269); Mount Cangshan, Dali, Yunnan (KIZ H0122); Mount Yunling, Deqin, Yunnan (KIZ DQ1204010, KIZ DQ1204049); Mount Yunling, Weixi, Yunnan (KIZ WX1204157, KIZ WX1204284); Mount Wushan, Changyang, Hubei (KIZ CY2010353).
U. soricipes $(n=5)$ : Beichuan, Sichuan (KIZ 0905021); Shawan, Leshan, Sichuan (KIZ 0905283, KIZ 0905292, KIZ 0905308); Mount Daxiangling, Shimian, Sichuan (KIZ 0905409).

## Supplementary material 1

PCR amplification primer sequences for CYT B, 12S, RAG1, RAG2, and PLCB4

Authors: Xueyang Ren, Yifan Xu, Yixian Li, Hongfeng Yao, Yi Fang, Laxman Khanal, Lin Cheng, Wei Zeng, Xuelong Jiang, Zhongzheng Chen
Data type: xlsx
Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.

## Supplementary material 2

## Samples and sequences used for molecular analyses

Authors: Xueyang Ren, Yifan Xu, Yixian Li, Hongfeng Yao, Yi Fang, Laxman Khanal, Lin Cheng, Wei Zeng, Xuelong Jiang, Zhongzheng Chen
Data type: xlsx
Explanation note: New sequences generated in this study are shown in bold.
Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.

Link: https://doi.org/10.3897/zookeys.1186.111592.suppl2

## Supplementary material 3

## Partitioning schemes and molecular evolution model used in mitochondrial-nuclear concatenated gene tree estimations

Authors: Xueyang Ren, Yifan Xu, Yixian Li, Hongfeng Yao, Yi Fang, Laxman Khanal, Lin Cheng, Wei Zeng, Xuelong Jiang, Zhongzheng Chen
Data type: xlsx
Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.
Link: https://doi.org/10.3897/zookeys.1186.111592.suppl3

## Supplementary material 4

## Independent-sample t-test

Authors: Xueyang Ren, Yifan Xu, Yixian Li, Hongfeng Yao, Yi Fang, Laxman Khanal, Lin Cheng, Wei Zeng, Xuelong Jiang, Zhongzheng Chen

Data type: xlsx
Explanation note: Independent-sample t-test of the variances of measurements highly correlated with PC1 and PC2 between Uropsilus sp. nov. and U. atronates, U. dabieshanensis, U. gracilis, U. investigator, and U. nivatus.
Copyright notice: This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0/). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this Dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.

[^0]
[^0]:    Link: https://doi.org/10.3897/zookeys.1186.111592.suppl4

