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ORIGINAL ARTICLE

A new species of the genus *Crocidura* from China based on molecular and morphological data (Eulipotyphla: Soricidae)

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Abstract A new species of white-toothed shrew, *Crocidura anhuiensis* Zhang, Zhang & Li, **sp. nov.** is described from Mount Huang, China. Genetic sequence (mtDNA Cyt *b* gene) and morphological (external and skull) data are used to distinguish this newly discovered species. The phylogenetic analysis shows that the materials of this work are monophyletic and allied to *C. attenuata* by the uncorrected genetic distance 4.9–5.1%, which suggests a species-level divergence. Morphologically, the materials are different from *C. attenuata* by presenting a greater proportion of tail-to-body ratio and the presence of an obvious tooth root in the mandible. Based on those data, the unnamed species is described as a new species which is currently known only from the Wild Monkey Valley, Mount Huang, Anhui Province, China.

Key words White-toothed shrew, Anhui, phylogenetics, morphology.

1 Introduction

The white-toothed shrews genus, *Crocidura* (Eulipotyphla: Soricidae: Crocidurinae) is one of the most widely distributed genera in the world. It is continuing recognized up to now and contains about 198 species (Wolsan & Hutterer, 1998; Hutterer, 2005; Mittermeier & Wilson, 2018). The genus was well researched in Asia, especially in Southeast Asia, more than a dozen species were reported, such as *C. kegoensis*, *C. gathornei*, *C. ninoyi*, *C. zaitsevi*, *C. sokolovi*, *C. hikmiya* and *C. sapaensis* in recent years (Lunde & Musser, 2004; Jenkins *et al*., 2007, 2009; Meegaskumbura *et al*., 2007; Esselstyn & Goodman, 2010; Jenkins *et al.*, 2013).

In China, new or records of shrews were continuously reported (Liu *et al*., 2010; He *et al*., 2012, 2018; Liu *et al*., 2016, 2017; Chen *et al*., 2017; Zhang *et al*., 2018). However, most of them were focus on red-toothed shrews (Soricinae), such as *Sorex tundrensis*, *S. roboratus* and *S. minutissimus* (Liu *et al*., 2010; Liu *et al*., 2016, 2017), *Chodsigoa caovansunga* and *C. hypsibia* (He *et al*., 2012; Zhang *et al*., 2018), *Chodsigoa hoffmanni* (Chen *et al*., 2017) and *Pantherina griselda* (He *et al.*, 2018). For the white-toothed shrews, the taxonomy was poorly done and only few works were present (Jiang & Hoffman, 2001; Cheng *et al*., 2017). The systematic relationships among Chinese white-toothed shrews are still confusing. In China, at least 15 specific or subspecific names of *Crocidura* were reported, but most of them were downgraded or synonymized (Allen, 1923, 1938; Jenkins, 1976, Hoffmann, 1987, 1996; Corbet & Hill, 1992; Hutterer, 1993; Jiang & Hoffmann, 2001). So far, about 12 species of *Crocidura* are reported in China (Duan *et al.*, 2011; Jiang *et al*., 2016; Liu & Wu, 2018).

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The present paper is to describe an unnamed species of *Crocidura*, collected from Mount Huang, and revise the systematics of the genus *Crocidura* in the Anhui Province. The genetic and morphological characters of the new species is also analyzed to determine its status.

2 Materials and methods

2.1 Sampling

The pitfall buckets method was used to collect shrews in this study (Goodman & Ingle, 1993). The sampling area contains a part of a tea plantations and its surrounding areas (elev. 500–600 m), lies at the foot of Mount Huang, in southeast Huangshan City, Anhui Province, China (Fig. 1). Plastic bucket traps (12 cm × 15 cm × 28 cm) were buried in the ground as pitfall traps, and checked twice per day (7:00–8:00, 17:00–18:00). Because of the terrain, thirty traps were randomly set in the sampling area rather than straight line fence methods. The sampling area ranges of five square kilometers, in areas of tea plantations, sand land, streams, and vegetable fields.

The sampling individuals were gendered, weighed, measured, and photographed, then taken partly muscle tissues preserved in 100% ethanol for molecular analyses. Fur and skull preparations were deposited at the Biological Museum of Anhui University under registration numbers: AhuHST1501, AhuHST1502, AhuHST103, AhuHST1701, AhuHST1702 and AhuHST1701.

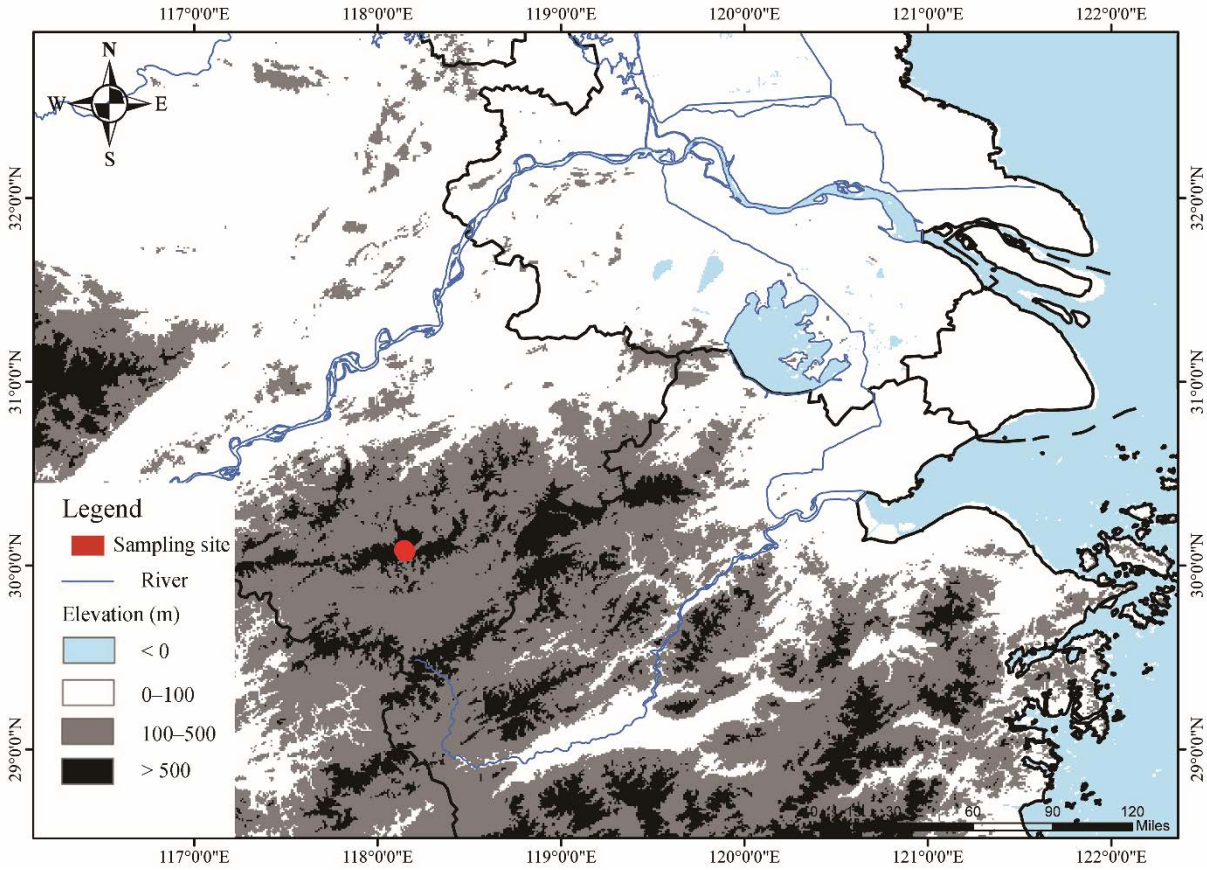

Figure 1. Map of East China indicating the collection localities of Mount Huangshan. Grey shading represents elevations of 100–500 m; black shading represents elevations of > 500 m.

2.2 DNA extraction, PCR amplifcation and sequencing

Genomic DNA was extracted from samples using a standard proteinase K/phenol-chloroform protocol (Sambrook *et al.*, 1989). An EasyPure PCR Purification Kit (TransGene) was used to purify each DNA extraction. The specific primers

for shrews (L–14724-hk3/H–15915-hk3) were used to amplify the mtDNA Cytochrome *b* (Cyt *b*) gene (He *et al.*, 2010). PCR reaction was performed in a 50 μL system containing 20–50 ng of template DNA, 10 μL 2×Easy*Taq* PCR SuperMix polymerase (TransGen Biotech, containing 1.25 U Ex *Taq*, 0.4 mM dNTP, 4 mM Mg^{2+}), and 0.5 μM of each primer. Thermal cycling for the Cyt *b* fragment was as follows: 35 cycles of denaturation at 95°C for 30 s, annealing at 55°C for 30 s, and extension at 72°C for 1 min, with a final extension of 72°C for 5 min. The PCR products were purified using an EasyPure PCR Purifcation Kit (TransGene), and sequenced directly using the primers used in PCRs and the BigDye Terminator v3.0 Ready Reaction Cycle Sequencing Kit (Applied Biosystems) following the manufacturer's instructions on an ABI Prism 3730 automated sequencer. PCR amplification and sequencing were performed on all six samples.

2.3 Phylogenetic analyses

In this study, DNA sequences were obtained, connected, aligned, and corrected by SeqMan (Swindell & Plasterer, 1997). Eighteen sequences were used for genetic analysis, including 12 *Crocidura* species from NCBI and 6 new sequences from this study (Table 1). All sequences were aligned using MUSCLE (Edgar, 2004) with default parameters and checked manually with MEGA 5.0 (Tamura *et al.*, 2011). Lengths of the fragments were trimmed and newly obtained sequences were deposited in GenBank (Table 1). Bayesian inference (BI) analyses implemented in the program MRBAYES v3.1.2 (Ronquist & Huelsenbeck, 2003) were used to estimate evolutionary relationships among taxa. The Asian house shrew (*Suncus murinus*) and the Etruscan shrew (*Suncus etruscus*) were used as outgroups as they are related to *Crocidura* shrews (Ohdachi *et al*., 2006).

Table 1. Samples used for molecular phylogenetic analysis in this study.

Species	NO of GenBank	Reference	Field number	Collection area
Crocidura attenuata	GU358515	Esselstyn *et al*., 2009	AMCC101492	China
	AB175082	Ohdachi *et al*., 2004	AMNH101492	Vietnam
Crocidura fuliginosa	GU981271	He *et al*., 2010	19701	China
	AB175079	Ohdachi *et al*., 2004	AMNH101526	Vietnam
Crocidura horsfieldii	EU122213	Meegaskumbura *et al*., 2007	WHT6869	Sri Lanka
	AB175078	Ohdachi *et al*., 2004	HA6214	Thailand
Crocidura lasiura	AB077072	Ohdachi *et al*., 2004	SO2Kmisc59	Russia
	MK410312	Arai *et al*., 2019	SH38Red4	South Korea
Crocidura leucodon	EF417545	Dubey *et al*., unpublished	2003.217	Unknown
	MH602272	Mahmoudi *et al*., 2018	ZMFUM4610	Unknown
Crocidura rapax	AB175086	Ohdachi *et al*., unpublished	SO-03/3/15-3	China (Taiwan)
	AB057420	Ohdachi *et al*., 2001	SO-2000/12/21-1	China (Taiwan)
Crocidura shantungensis	AB077278	Ohdachi *et al*., 2004	SO2Kmisc63	Russia
	AB077080	Ohdachi *et al*., 2004	SO2Kmisc60	Russia
Crocidura sibirica	AB077087	Ohdachi *et al*., 2004	SO2000/7/28-3	China
	EU742583	Bannikova *et al*., 2008	f.c. Teletzkoe 19	Russia
Crocidura tanakae	HM587032	Bannikova *et al*., 2011	ZISP:99028	Laos
	KX946006	Chen & Liu, 2016	EMEI	China
Crocidura wuchihensis	FJ814043	Esselstyn *et al*., 2009	ROM116129	Unknown
	AB175085	Ohdachi *et al*., 2004	AMNH101508	Vietnam
Crocidura indochinensis	HM587024	Bannikova *et al*., 2011	ZISP:97670	Vietnam
	HM587023	Bannikova *et al*., 2011	ZISP:97669	Vietnam
Crocidura anhuiensis Zhang, Zhang & Li, **sp. nov.**	MK546383	This study	AhuHST1501	China
	MK546384	This study	AhuHST1502	China
	MK546385	This study	AhuHST1503	China
	MK546386	This study	AhuHST1701	China
	MK546387	This study	AhuHST1702	China
	MK546388	This study	AhuHST1703	China
Suncus murinus	JF784171	Guo *et al*., 2011	LongwanSm512	China
Suncus etruscus	JN556043	Meegaskumbura *et al*., 2011	Unknown	India

2.4 Morphological analyses

External and skull data were measured up to 0.1 mm by a vernier caliper. The weights were measured up to 0.1 g by an electronic scale. The following external and skull measurements were taken (Meegaskumbura *et al*., 2007; Jenkins *et al*., 2009):

BB—breadth of braincase;
BL—basal length;
BMM—breadth of premolar upper jaw;
BPM—breadth of premolar bony palate;
BR1—breadth of rostrum at narrowest point;
BR2—breadth of rostrum at broadest point;
BSL—basilar length;
BW—body weight;
CIL—condylo-incisive length;
DD—depth of dentary;
EH—ear height;
FFL—length of forefoot;
GL—greatest length of skull;
HB—height of braincase;
HBL—length of head and body;
HL—length of head;
HFL—length of hindfoot;
I-Un3—incisor-3rd unicuspid length;
LAL—length of lower arm;
LDI—length of dentary, including incisors;
LDT1—length of dentary teeth, excluding incisors;
LDT2—length of dentary teeth, including incisors;
LIOB—least interorbital breadth;
LR—length of rostrum;
MH—mandible height;
ML—mandible length;
PAL—palatilar length;
PL—palatal length;
PPL—post-palatal length;
PW1—breadth of palate between the buccal margins of second molars;
PW2—breadth of palate between the lingual margins of last molars;
TBL—length of tibia;
TL—length of tail;
UTRL—upper toothrow length.

2.5 Principal components analysis

IBM SPSS Statistics 21 was used for statistical analysis. Principal Components Analysis (PCA) of external and skull variables was respectively carried out to evaluate whether the *Crocidura* sp. and *C. attenuata* occupy different niches.

3 Results

In total, six individuals of white-toothed shrews were collected by the pitfall trap.

3.1 Molecular phylogenetic analyses

The BI phylogenetic trees were constructed based on Cyt *b* sequences (1140 bp). The results by BI displayed strong node support values (Fig. 2). The six individuals, temporary named as *Crocidura* sp., combined into a monophyletic clade,

Table 2. The pairwise uncorrected *p*-distance (%) of the Cyt *b* sequences used in this study.

Species/individual	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
AhuHST1501																			
AhuHST1502	0.002																		
AhuHST1503	0.002	0.000																	
AhuHST1701	0.005	0.005	0.005																
AhuHST1702	0.001	0.001	0.001	0.004															
AhuHST1703	0.001	0.001	0.001	0.004	0.000														
C. attenuata	0.050	0.050	0.050	0.051	0.049	0.049													
C. fuliginosa	0.138	0.138	0.138	0.137	0.137	0.137	0.140												
C. horsfieldii	0.160	0.160	0.160	0.158	0.158	0.158	0.165	0.155											
C. lasiura	0.106	0.106	0.106	0.105	0.105	0.105	0.117	0.141	0.150										
C. leucodon	0.178	0.178	0.178	0.179	0.177	0.177	0.191	0.173	0.187	0.179									
C. rapax	0.117	0.117	0.117	0.118	0.116	0.116	0.126	0.143	0.154	0.040	0.184								
C. shantungensis	0.178	0.178	0.178	0.176	0.176	0.176	0.176	0.167	0.181	0.164	0.168	0.158							
C. sibirica	0.170	0.170	0.170	0.166	0.169	0.169	0.168	0.169	0.194	0.180	0.194	0.169	0.093						
C. tanakae	0.127	0.128	0.128	0.126	0.126	0.126	0.150	0.135	0.150	0.122	0.175	0.123	0.182	0.154					
C. wuchihensis	0.134	0.135	0.135	0.133	0.133	0.133	0.142	0.149	0.147	0.147	0.191	0.138	0.172	0.172	0.137				
C. indochinensis	0.127	0.127	0.127	0.129	0.126	0.126	0.128	0.135	0.161	0.130	0.195	0.125	0.176	0.168	0.134	0.083			
Suncus murinus	0.218	0.218	0.218	0.216	0.217	0.217	0.233	0.214	0.201	0.204	0.202	0.210	0.210	0.227	0.212	0.228	0.218		
S. etruscus	0.243	0.243	0.243	0.241	0.242	0.242	0.249	0.219	0.221	0.251	0.221	0.239	0.204	0.232	0.240	0.207	0.206	0.182	

as the sister species of *C. attenuata* with high node support values.

The percent pairwise uncorrected distances between *Crocidura* sp. and *C. attenuata* ranged from 4.9% to 5.1% (Table 2). It indicates that *Crocidura* sp. is a quite different species allied to *C. attenuata* as a 2–11% divergence of Cytochrome *b* may indicate the species-level divergence among mammal groups (Bradley & Baker, 2001).

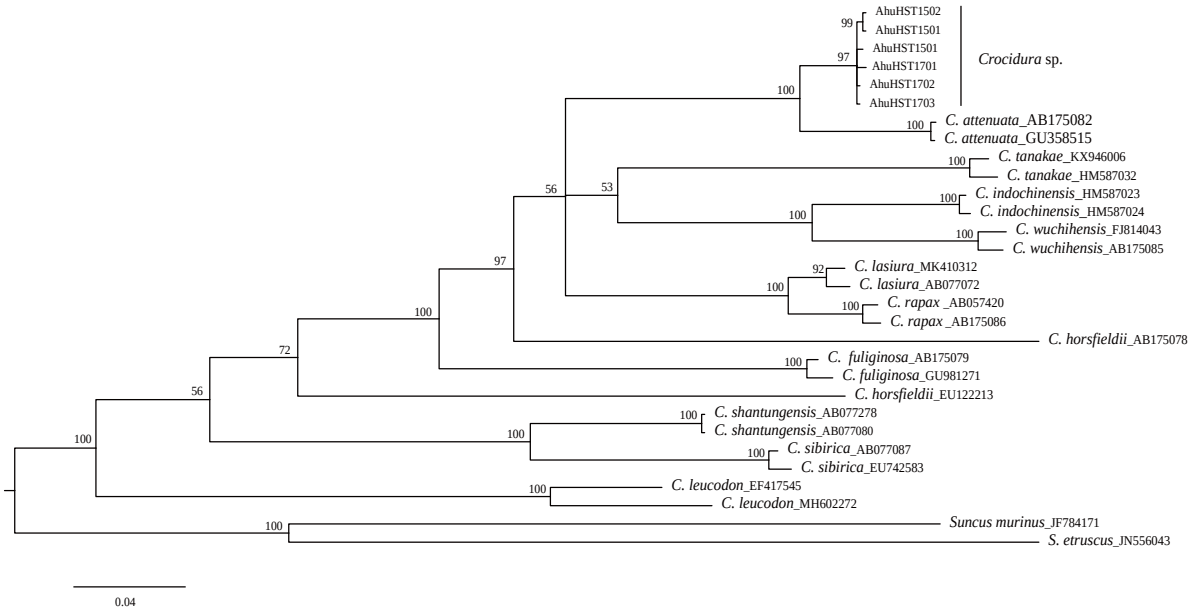

Figure 2. The Bayesian consensus tree resulting from analysis of mitochondrial DNA Cyt *b* gene for Chinese *Crocidura* species. Numbers near the nodes are Bayesian posterior probabilities.

3.2 Principal component analysis

The *Crocidura* sp. is sympatric distributed with *C. attenuata* and it is also allied to the latter based on the Cyt *b* phylogenetic analysis (Fig. 2). Therefore, the *Crocidura* sp. and *C. attenuata* are compared.

According to the PCA for external morphological data, two principal components were extracted from the correlation matrix, which explained 74.7% of the variation in the data. PC1 accounts for 61.18% of the variation and is positively correlated with all variables (loading > 0.562), reflecting a size effect. PC2 represents 13.52% of the variation and is dominated by HL and HBL (loading > 0.282) (Table 3). *Crocidura attenuata* occurs along the most negative region of PC1 in accordance with the short head length and hind foot length, while *Crocidura* sp. occurs along the most positive region of PC1 in accordance with its greater ear height (Fig. 3A). Therefore, we choose EH and HF for the X and the Y-axis, respectively, and draw a new scatter plot in which the two species clearly clustered into different regions (Fig. 3B).

Table 3. Factor loadings of the two principal components (PC) axes of external variables*.

Variables	FAC1	FAC2
HL	0.781	0.282
HBL	0.562	0.759
TL	0.802	-0.029
FF	0.727	-0.501
HF	0.731	-0.401
LAL	0.872	-0.003
TBL	0.853	0.1
EH	0.881	-0.054
Eigenvalue	4.894	1.082
Explained variance (%)	61.18	13.52

*Factor loadings of the first two PC axes based on eight external variables of *Crocidura* sp. and *C. attenuata*.

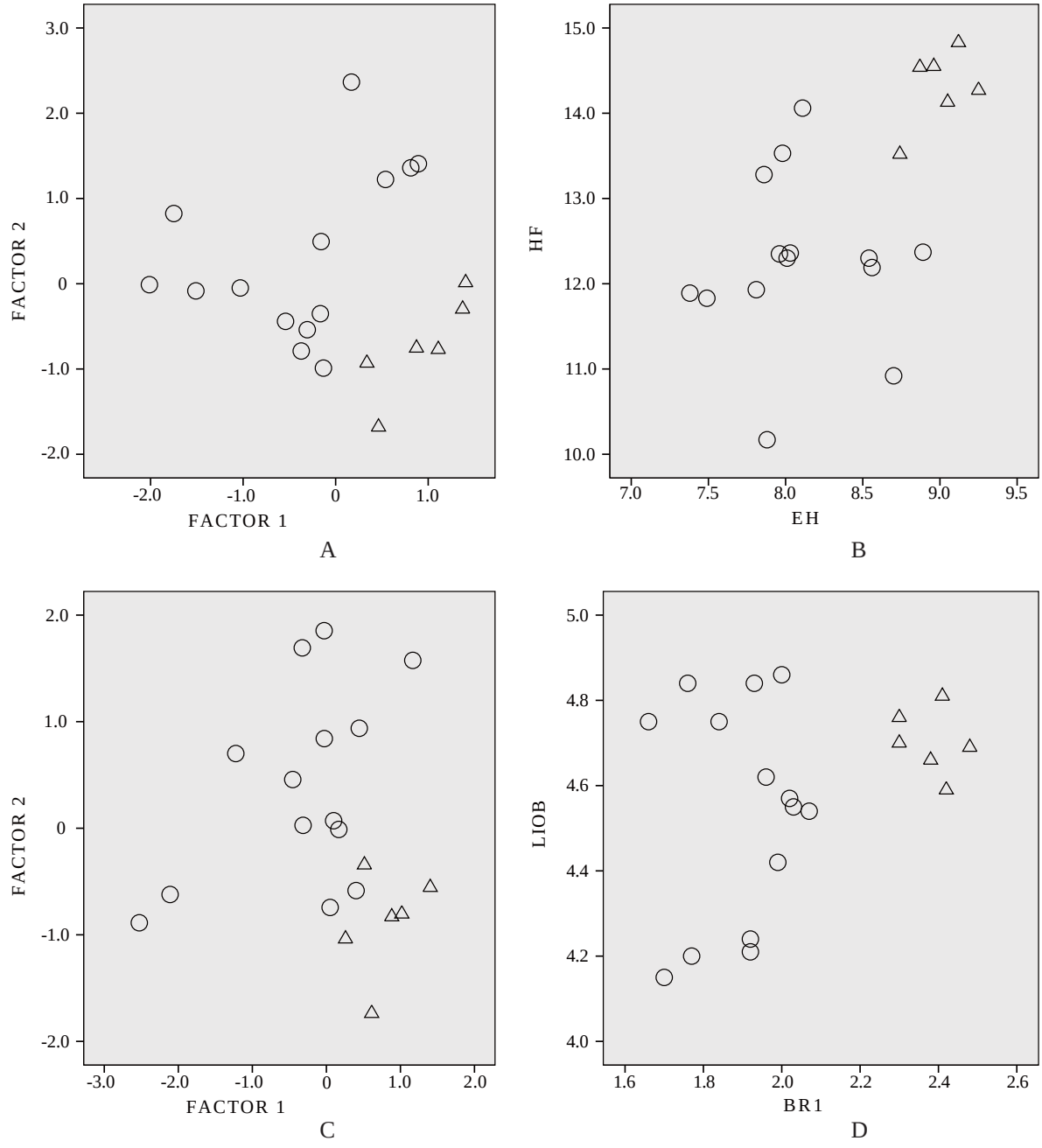

Figure 3. Bivariate, and multivariate analyses among species of *Crocidura* sp. (triangle) and *C. attenuata* (circle). A. Plot of the first 2 principal components from a PCA of 8 external body measurements. B. Bivariate plots of external variables among 2 species. C. Plot of the first 2 principal components from a PCA of 12 skull measurements. D. Bivariate plots of skull variables among 2 species.

PCA was also employed in the analysis of 12 skull variables. Results show that *Crocidura* sp. and *C. attenuata* differed primarily on PC1, which explained 68.5% of the variation. PC2 explained 10.326% of the total variance and had high positive loadings for LDT1 and LDT2 and IUN3 (loading > 0.279) (Table 4). PC1 was primarily a size axis, with high positive loadings for linear measurements reflecting skull dimensions, upper tooth row length, mandible length, length of dentary teeth (excluding incisors), and condyloincisive length (loading > 0.934). The two species overlapped substantially on PC1, indicating little variation in overall size (Fig. 3C). Similarly, when LIOB and BR1 were used as X and Y axes, the two species could be clearly distinguished in the scatter plot (Fig. 3D).

The above analyses indicate that *Crocidura* sp. and *C. attenuata* occupy different regions of morphospace for both skull and external features and are morphologically diagnosable. Combined with a phylogenetic analysis, the *Crocidura* sp. is recognized as a quite different species, and described as a new species here.

Table 4. Factor loadings of the two principal components (PC) axes of skull variables*.

Variables	FAC1	FAC2
UTRL	0.937	0.091
ML	0.934	0.034
LDI	0.961	-0.172
LDT1	0.636	0.605
LDT2	0.791	0.279
DD	0.871	0.088
CIL	0.939	-0.122
PL	0.92	-0.215
LR	0.878	-0.276
LIOB	0.768	0.085
BR1	0.594	-0.649
IUN3	0.561	0.429
Eigenvalue	8.22	1.239
Explained variance (%)	68.502	10.326

*Factor loadings of the first two PC axes based on 12 skull variables from *Crocidura* sp. and *C. attenuata*.

3.3 Systematics

***Crocidura anhuiensis* Zhang, Zhang & Li, sp. nov.**

Diagnosis. The new species is a medium-sized *Crocidura*. The general colour of the body, including the tail, is gray-brown. The venter is slightly lighter colored than the dorsum. There are not long and dark guard hairs present among the gray hairs on either dorsal or ventral side of body (Fig. 4). Dorsal surfaces of hands and feet are semi-naked, appearing pinkish brown, with sparse brown hairs on the digits. In general, the total length of this species is 60.9–78.1 mm, the tail length 48.3–59.2 mm, the ear height 8.7–9.3 mm, and the weight 10.5–13.5 g (Table 5).

The skull is slightly flimsy, lambdoid crest clearly visible, the sagittal crest is obvious and protruding. The teeth are white, the upper incisor is vertical and downwardly pointing, the lower incisor teeth protruding to the front. Eight teeth, including three unicuspid teeth in the upper row; six teeth, including an incisor in the mandible in the lower jaw. The condyloincisive length is 20.8–22.4 mm, braincase height 5.5–5.5 mm, and braincase width 9.1–9.9 mm. The length of dentary, including incisors, is 13.9–14.1 mm, while the depth of the dentary is 5.6–6.4 mm (Table 5).

Description. It has small eyes, round ears, and the bear extends behind the ear. The dorsal pelage is gray-brown and slightly darker; while the venter is slightly paler than the dorsum. The tail color is similar to that of the pelage. The slender tail's length is only 76% of the head length, and semi-nude, with sparse bristled hairs on the proximal half, having small short hairs, basally attenuated, with long and protruding hair at the end of the tail. The skin is semi-nude on the back of the palm and sole, showing pink skin, with sparse short brown hairs around the ankle. The soles of the feet are moderately pigmented, with small fleshy protuberances, ring-shaped in the palmar.

Skull with a long and moderately narrow rostrum, narrow maxillary region, and relatively broad interorbital region. The suture between the occipital and parietal bones is depressed and obviously anterior to the lambdoidal crest, giving the impression of a prominent lambdoidal crest. The posterlingual border of the teeth is not so rounded; the posterior border of the teeth is deeply concave. The posterobuccal crest of the paracone of M^2 forming a smooth W-shaped loph in unworn dentition. External and skull measurements (mm) of the holotype (AhuHST1702) (Fig. 5): GL 19.8, BL 17.7, BSL 17.0, CIL 21.2, PL 8.6, PAL 7.8, PPL 8.7, LR 8.9, BB 9.5, LIOB 4.6, PW1 6.6, PW2 2.5, BR1 2.4, BR2 6.9, BPM 1.2, BMM 1.4, HB 5.2, I-UN3 4.5, UTRL 10.1, ML 11.3, LDI 14.8, LDT1 6.6, LDT2 7.8, DD 6.3, MH 5.4.

Holotype. Specimen AhuHST1702, an adult female, from the Monkey Valley, Mount Huang Scenic Area, Anhui Province, China (30°05′04.36″N, 118°08′40.04″E; elev. 562 m), June 2017, coll. H. Zhang, C.C. Wang and L. Zhou.

Paratypes. Four females, AhuHST1501, AhuHST1502, AhuHST1503 (30°04′35.47″N, 118°09′05.43″E; elev. 508 m), and AhuHST1703 (30°05′04.57″N, 118°08′36.12″E; elev. 567 m), Monkey Valley, Mount Huang Scenic Area, Anhui province, China, April 2015 and May 2017, coll. L.F. Qian, H. Zhang, C.C. Wang and L. Zhou. One male, AhuHST1701, Monkey Valley, Mount Huang Scenic Area, Anhui province, China (30°05′04.36″N, 118°08′40.04″E; elev. 562 m), May 2017, coll. H. Zhang, C.C. Wang and L. Zhou.

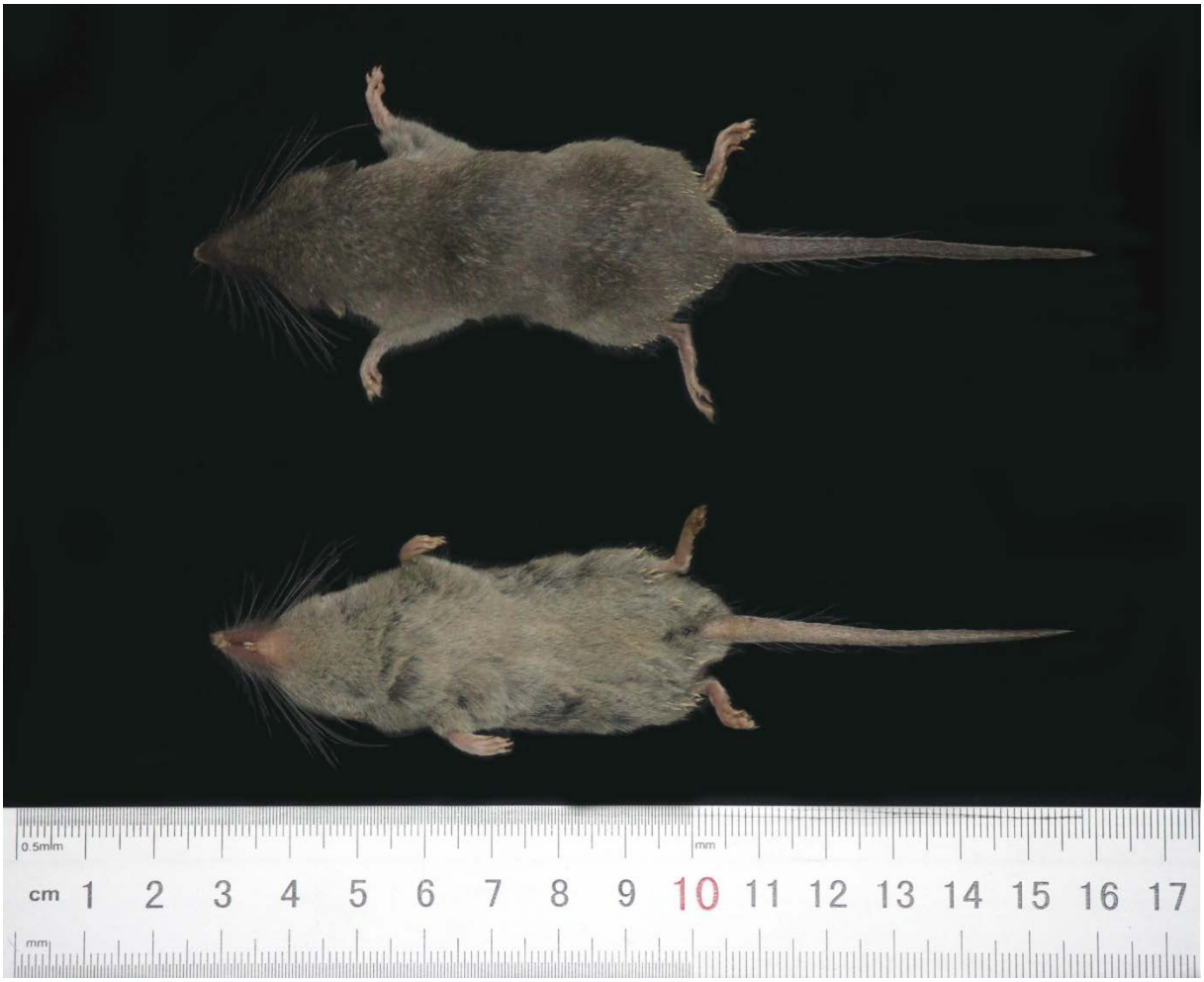

Figure 4. External morphology of *Crocidura anhuiensis* Zhang, Zhang & Li, **sp. nov.** (AhuHST1702), dorsal and ventral view.

Distribution. Currently, the new species is only known from two tea plantations in the wild Monkey Valley, Mount Huang, Anhui Province, China.

Etymology. The specific name is referring to its type locality, Anhui Province, China.

Common names. We suggest “Anhui white-toothed shrew” as an English common name of the new species, and “安徽麝鼩” as a Chinese common name.

Comparisons. The new species shares similarities in hair color and head and body size to *C. attenuata*, but is distinguished by having a longer tail length and ear height; the ratio of TL to HBL of *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.** is 76.4%, greater than that of *C. attenuata* (68.1%) (Table 3). The skull of *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.** has a similar size as in *C. attenuata* (Table 5) but the most obvious difference is the length of the rostrum and the breadth of the rostrum at the narrowest point; the BR1 of *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.** (2.3–2.5 mm) is significantly longer than that of *C. attenuata* (1.7–2.1 mm). In addition, the incisors of the new species are curved in ventral, but straight in *C. attenuata* (Figs 6–7). More significantly, the naked tooth roots in the mandible are visible in *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.**, and the convex portion of the molar forms a larger angle (Figs 6–7).

The new species also have obvious morphological differences with other species of *Crocidura* (Smith & Xie, 2010). It is different from *C. wuchihensis* by the ratio of TL to HBL is 67% (Shaw *et al.*, 1966), rather than 76.4% in the new species. Another species, *C. shantungensis* is the smallest white-toothed shrew in Eurasia, similar in size to *C. wuchihensis*: the tail is very short, less than 70% HBL, and broad at base, tapering to tip, while the new species has a larger body and an especially longer tail.

Compared to *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.**, *C. fuliginosa* is a very large and long-tailed shrew, with the TL usually more than 80%, but less than 90% of HBL. Its dorsal pelage is smoky brown to dark grayish black, the tail dark brown in upside and slightly paler in downside. As a contrast, *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.** is smaller and has the pelage lighter than those of *C. fuliginosa*. Moreover, *Crocidura lasiura* is also a larger shrew, with a thick tail and nearly

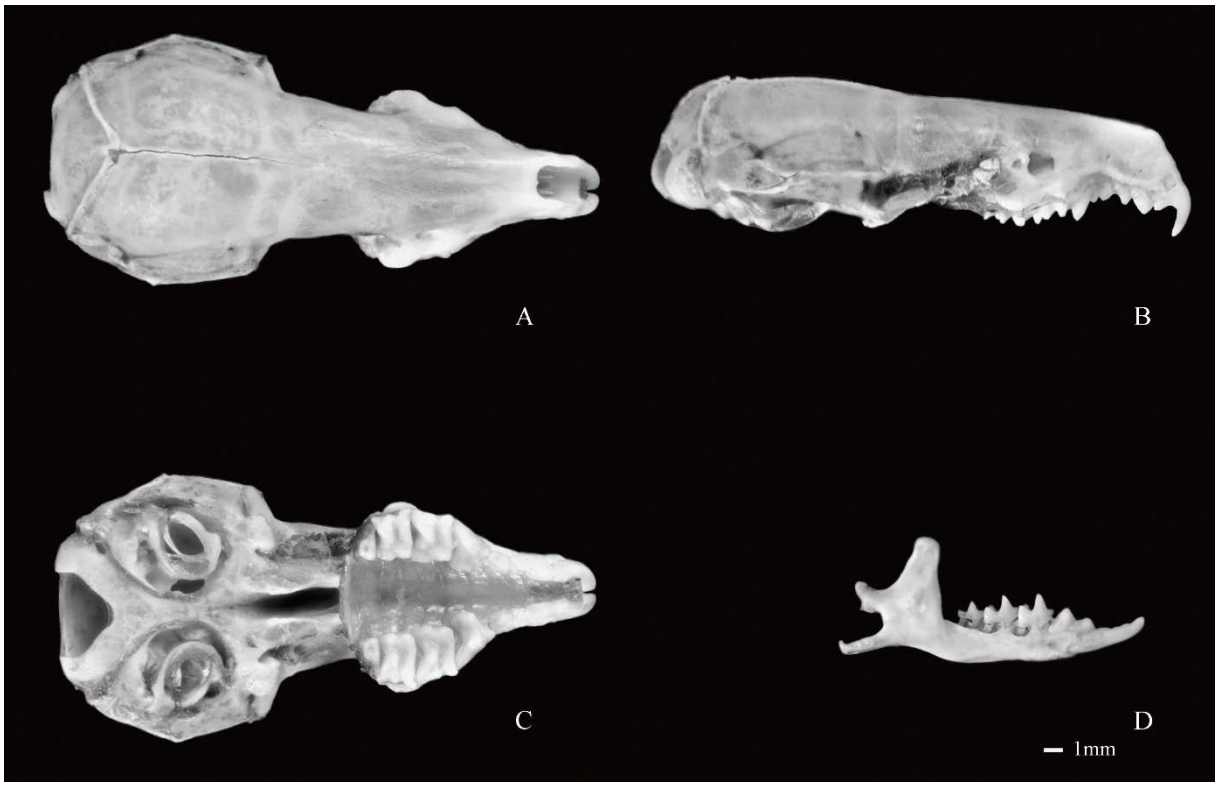

Figure 5. Images of the crania and mandible of *Crocidura anhuiensis* Zhang, Zhang & Li, **sp. nov.** (AhuHST1702). A. Crania, dorsal view. B. Crania, laterial view. C. Crania, ventral view. D. mandible.

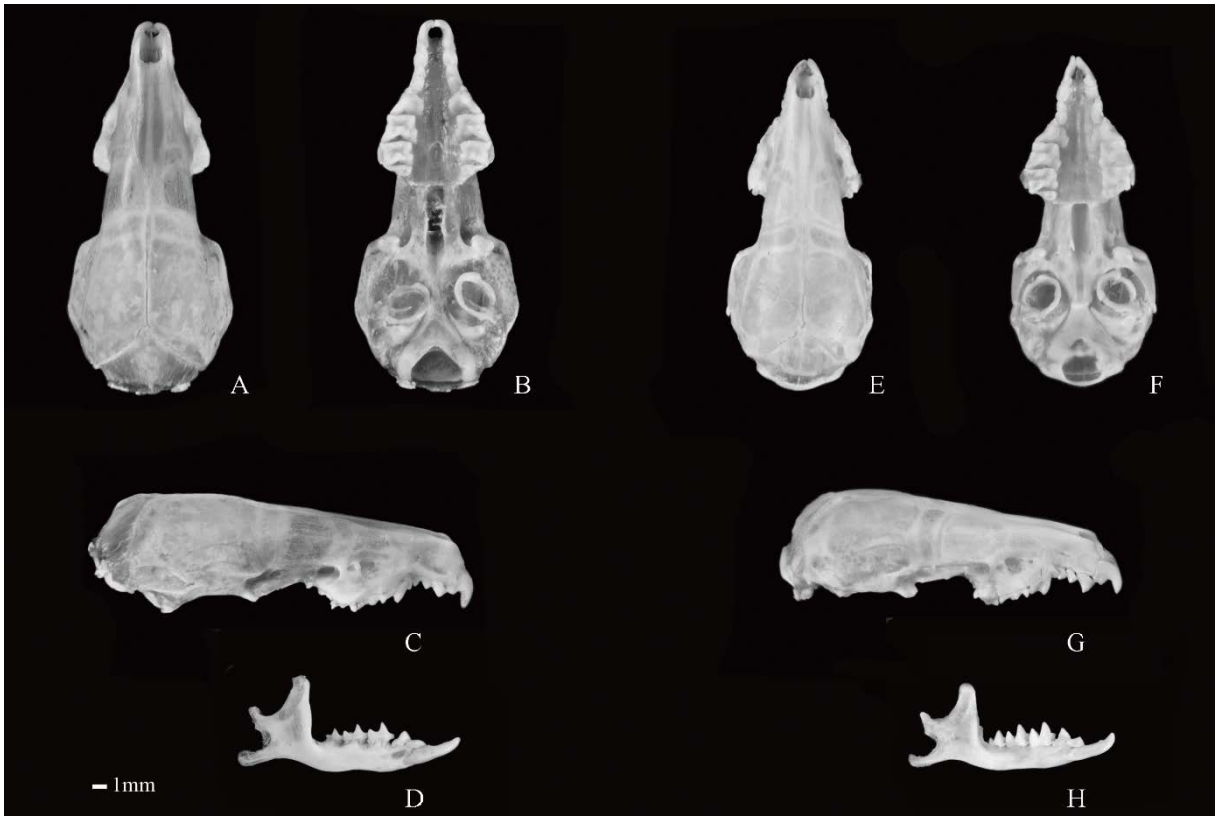

Figure 6. Images of crania and mandibles of *Crocidura anhuiensis* Zhang, Zhang & Li, **sp. nov.** (AhuHST1703) and *C. attenuata* (AhuHS12). A–C. *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.**, crania, dorsal, ventral and laterial views. D. *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.**, mandible. E–G. *C. attenuata*, crania, dorsal, ventral and laterial views. H. *C. attenuata*, mandible.

mono-colored. Its ratio of the TL to HBL is about 45%, rather than 76.4% in the new species.

Additionally, *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.** also has a smaller head length (vs. *C. fuliginosa* and *C. pullata*), smaller mandibular length (vs. *C. fuliginosa*), longer tail (vs. *C. pullata*, *C. vorax*, *C. rapax* and *C. horsfieldii*), longer forefeet (vs. *C. vorax*, *C. rapax* and *C. horsfieldii*), and longer breadth and height of braincase (vs. *C. pullata*, *C. vorax*, *C. rapax* and *C. horsfieldii*) (Jiang & Hoffman, 2001; Table 6).

Table 5. External and skull measurements for *C. anhuiensis* Zhang, Zhang & Li, sp. nov. and *C. attenuata*.

	C. anhuiensis Zhang, Zhang & Li, **sp. nov.** (*n* = 6)		*C. attenuata* (*n* = 14)	
	Range	Mean (± SD)	Range	Mean (± SD)
BW(g)	10.5–13.5	11.6 ± 1.3	4.4–14.0	8.1 ± 2.9
HL (mm)	26.9–28.7	27.8 ± 0.8	22.7–30.2	26.8 ± 2.2
HBL (mm)	60.9–78.1	69.5 ± 7.1	50.5–83.5	67.0 ± 8.6
TL (mm)	48.3–59.2	53.1 ± 4.3	24.4–59.2	45.6 ± 7.2
FF (mm)	9.2–9.9	9.6 ± 0.3	7.0–9.9	8.8 ± 0.9
HF (mm)	13.5–14.8	14.3 ± 0.5	10.2–14.1	12.3 ± 1.0
LAL (mm)	10.7–12.1	11.4 ± 0.6	8.3–12.1	10.2 ± 1.1
TBL (mm)	17.1–18.4	17.7 ± 0.5	14.0–18.4	16.5 ± 1.4
EH (mm)	8.7–9.3	9.0 ± 0.2	7.4–8.9	8.1 ± 0.4
GL (mm)	19.7–21.0	20.3 ± 0.6	16.6–21.4	18.7 ± 1.3
BL (mm)	17.0–18.0	17.6 ± 0.5	14.6–18.6	16.6 ± 1.0
BSL (mm)	16.5–17.5	17.0 ± 0.4	14.0–17.4	15.9 ± 1.1
CIL (mm)	20.8–22.4	21.7 ± 0.7	17.9–22.6	20.0 ± 1.3
PL (mm)	8.3–9.3	8.8 ± 0.4	6.8–8.8	8.0 ± 0.6
PAL (mm)	7.4–8.4	7.9 ± 0.4	6.4–8.2	7.4 ± 0.5
PPL (mm)	8.7–9.9	9.2 ± 0.5	7.7–9.9	8.8 ± 0.7
LR (mm)	8.1–9.8	8.8 ± 0.6	6.2–8.1	7.4 ± 0.7
BB (mm)	9.1–9.9	9.6 ± 0.3	8.2–9.8	9.0 ± 0.5
LIOB (mm)	4.6–4.8	4.7 ± 0.1	4.2–4.9	4.5 ± 0.3
PW1 (mm)	6.3–7.1	6.7 ± 0.3	5.5–6.7	6.3 ± 0.4
PW2 (mm)	2.4–3.0	2.6 ± 0.2	1.6–2.9	2.3 ± 0.3
BR1 (mm)	2.3–2.5	2.4 ± 0.1	1.7–2.1	1.9 ± 0.1
BR2 (mm)	6.7–7.2	6.8 ± 0.3	5.7–6.9	6.5 ± 0.4
BPM (mm)	1.1–1.6	1.3 ± 0.2	1.0–1.8	1.4 ± 0.2
BMM (mm)	1.4–1.7	1.5 ± 0.1	1.2–1.8	1.5 ± 0.2
HB (mm)	5.0–5.5	5.2 ± 0.2	4.4–5.6	5.1 ± 0.3
I–UN3 (mm)	4.5–4.8	4.6 ± 0.1	3.4–5.3	4.3 ± 0.6
UTRL (mm)	9.1–10.1	9.6 ± 0.4	7.8–9.9	9.0 ± 0.6
ML (mm)	10.2–11.6	10.8 ± 0.6	7.7–12.0	10.1 ± 1.1
LDI (mm)	13.9–14.1	14.5 ± 0.4	11.0–14.3	13.2 ± 1.0
LDT1 (mm)	5.1–6.6	6.1 ± 0.6	4.2–7.1	6.0 ± 0.8
LDT2 (mm)	7.8–8.9	8.4 ± 0.4	6.5–8.8	8.2 ± 0.7
DD (mm)	5.6–6.4	6.0 ± 0.3	5.0–6.3	5.8 ± 0.4
MH (mm)	4.8–5.5	5.2 ± 0.3	4.2–5.5	4.9 ± 0.4

4 Discussion

According to the first report by Ellerman & Morrison-Scott (1951), only four white-toothed shrews (*Crocidura*) species were listed from China. In the second half of the century, the species numbers increased gradually, and ten species were

Table 6. Means (± SD) and ranges of external and skull measurements (mm) of South Chinese *Crocidura*.

Variablea	*C. anhuiensis* Zhang, Zhang & Li, **sp. nov.** (*n* = 6)	C. *shantungensis* (*n* = 16)*	C. *fuliginosa* (*n* = 73)*	C. *pullata* (*n* = 20)*	C. *vorax* (*n* = 12)*	C. *rapax* (*n* = 10)*	C. *horsfieldii* (*n* = 13)*
HB	69.50 ± 7.08 60.88–78.10	58.7 ± 3.57 51.0–64.0	86.3 ± 6.7 72.0–100.0	83.2 ± 4.00 73.0–89.0	67.3 ± 9.77 54.0–90	64.1 ± 4.51 56.0–70.0	61.1 ± 6.18 49.0–71.0
TL	53.10 ± 4.33 48.34–59.24	36.0 ± 4.63 28.0–45.0	74.1 ± 5.4 62.0–89.0	44.2 ± 4.38 39.0–53.0	46.7 ± 3.34 41.0–51.0	42.4 ± 2.80 38.0–47.0	40.8 ± 5.97 30.0–48.0
HF	14.31 ± 0.46 13.52–14.83	11.2 ± 0.79 10.0–12.5	16.5 ± 1.1 15.0–19.0	15.06 ± 0.66 14.0–16.0	12.3 ± 0.78 11.0–14.0	11.9 ± 0.60 11.0–13.0	11.0 ± 1.04 10.0–13.0
CIL	21.66 ± 0.72 20.81–22.38	16.63 ± 0.28 16.16–17.22	23.26 ± 0.64 22.04–25.00	20.26 ± 0.46 19.45–21.21	19.09 ± 0.77 17.74–20.11	18.14 ± 0.27 17.45–18.33	17.18 ± 0.40 16.14–17.82
IOB	4.70 ± 0.08 4.59–4.81	3.79 ± 0.16 3.48–4.09	5.18 ± 0.24 4.64–5.71	4.76 ± 0.13 4.51–5.03	4.02 ± 0.20 3.70–4.36	4.06 ± 0.13 3.78–4.21	4.06 ± 0.16 3.81–4.40
BB	9.61 ± 0.26 9.12–9.85	7.49 ± 0.17 7.14–7.77	10.33 ± 0.35 9.40–11.19	9.27 ± 0.20 8.92–9.63	8.40 ± 0.48 7.57–9.06	8.32 ± 0.35 7.64–8.78	8.17 ± 0.25 7.69–8.61
BH	5.24 ± 0.20 4.97–5.51	3.94 ± 0.20 3.67–4.35	5.47 ± 0.22 4.42–5.95	4.63 ± 0.18 4.37–4.99	4.75 ± 0.22 4.37–5.03	4.51 ± 0.19 4.12–4.73	4.39 ± 0.21 3.88–4.75
RL	8.80 ± 0.60 8.12–9.76	5.34 ± 0.17 5.06–5.67	8.33 ± 0.34 7.61–9.14	7.01 ± 0.21 6.62–7.43	6.30 ± 0.49 5.59–7.08	6.20 ± 0.30 5.75–6.58	5.77 ± 0.26 5.09–6.13
PPL	9.23 ± 0.45 8.66–9.86	7.57 ± 0.33 7.12–8.37	10.44 ± 0.36 9.30–11.18	9.03 ± 0.25 8.51–9.57	8.88 ± 0.39 8.37–9.56	8.55 ± 0.34 7.88–9.03	8.04 ± 0.18 7.77–8.40
ML	10.81 ± 0.57 10.21–11.58	8.63 ± 0.27 8.00–9.24	12.61 ± 0.41 11.74–13.45	10.59 ± 0.26 10.12–11.09	9.60 ± 0.37 8.77–10.12	9.58 ± 0.39 8.70–10.13	9.18 ± 0.26 8.78–9.85

*Data from Jiang & Hoffman (2001).

recorded in the book, *A Complete Checklist of Mammal Species and Subspecies in China and a Taxonomic and Geographic Reference* (Wang, 2003). In the latest list of Chinese vertebrates (Jiang *et al*., 2016; Liu & Wu, 2018), a total of 12 species of *Crocidura* were recorded. Of these, two species (*C. attenuata* and *C. shantungensis*) were reported distributing in Anhui Province (Wang, 1990, 2003; Jiang *et al*., 2016; Liu & Wu, 2018), and *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.** is the third species of white-toothed shrew for Anhui Province.

In addition, the new species is also adjacent in locality with *C. grisensens*, which was firstly reported in Fujian. The latter species has been controversial. It was once considered to be a synonym of *C. fuliginosa*, but then transferred to *C. attenuata* by Jiang & Hoffman (2001) by rechecking it typical materials. In morphology, the holotype of *C. grisescens* has its tail length about 58% of HB (Zhuge, 1993), while 76.4% in the new species.

Three individuals, AhuHST1501, AhuHST1502 and AhuHST1503, were captured in an undisturbed mountainous area and mossy forests (508 m in elevation, Fig. 8A). The forests near a stream, dominated in bamboo and moss on the ground. Two individuals, AhuHST1701 and AhuHST1702, were collected in a tea plantation which is an artificial habitat, mainly

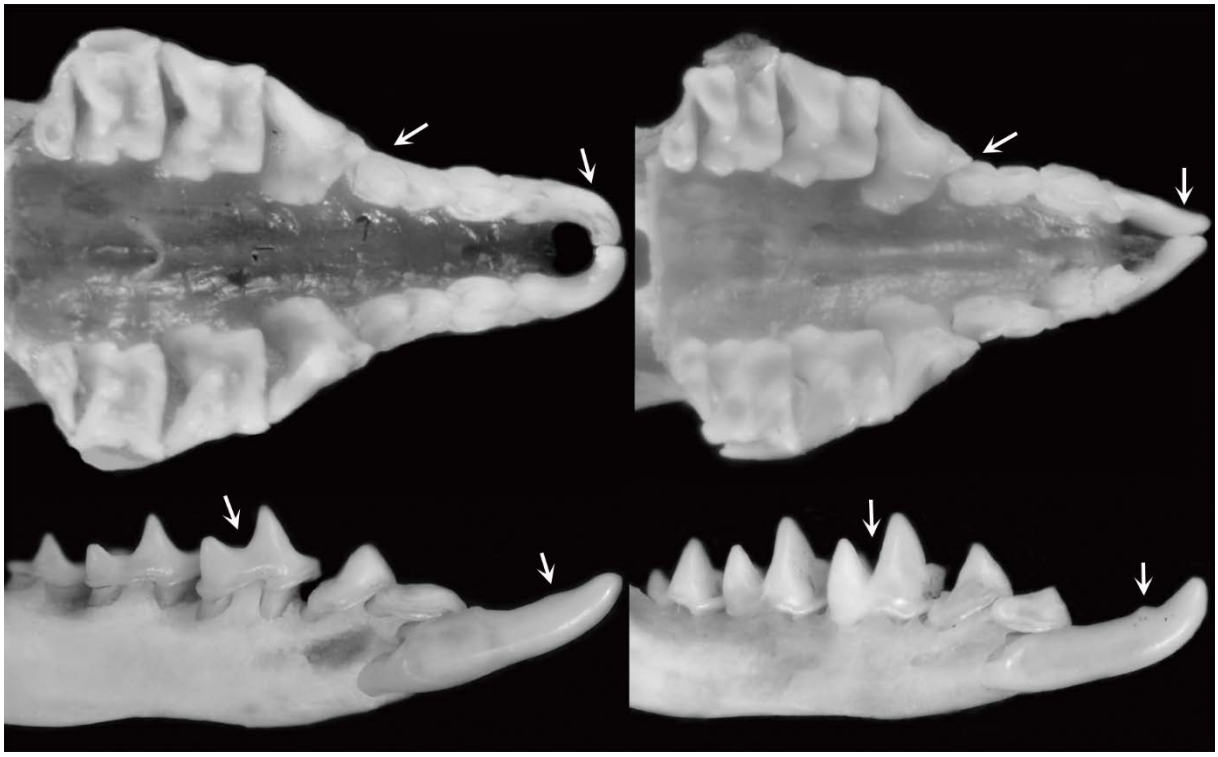

Figure 7. Comparison of local tooth characteristics between *Crocidura anhuiensis* Zhang, Zhang & Li, **sp. nov.** (AhuHST1702) and *C. attenuata* (AhuHS12).

Figure 8. Typical habitat of *Crocidura anhuiensis* Zhang, Zhang & Li, **sp. nov.** in wild monkey valley, Mount Huangshan, Anhui Province, China. A. Mossy forest. B. Tea plantation.

consisting of tea trees, rocky soil, intermittent plant cover and without humus blanketing (562 m in elevation, Fig. 8B). Another individual AhuHST1703, was collected in a local vegetable garden cultivating vegetables (567 m in elevation), which is near the locality of AhuHST1701 and AhuHST1702.

However, whether the *C. anhuiensis* Zhang, Zhang & Li, **sp. nov.** is living in the range of 500–600 m elevation is not sure, a larger range of elevation for a suitable habitat is possible. A more detailed survey of shrews in Mount Huang should be done future to understand the species diversity and evaluate its conservation status.

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References

Allen, G.M. 1923. New Chinese insectivores. *American Museum Novitates*, 100: 1–11.

Allen, G.M. 1938. *The mammals of China and Mongolia. In*: Granger, W. (ed.). Natural History of Central Asia, vol. 11. Central Asiatic Expeditions of the American Museum of Natural History, New York. 600 pp.

Bradley, R.D., Baker, R.J. 2001. A test of the genetic species concept: cytochrome-b sequences and mammals. *Journal of Mammalogy*, 82(4): 960–973. doi: 10.1644/1545-1542(2001)082<0960:ATOTGS>2.0.CO;2.

Chen, Z.Z., He, K., Huang, C., Wan, T., Lin, L.K., Liu, S.Y., Jiang, X.L. 2017. Integrative systematic analyses of the genus *Chodsigoa* (Mammalia: Eulipotyphla: Soricidae), with descriptions of new species. *Zoological Journal of the Linnean Society*, 180(3): 694–713. doi: 10.1093/zoolinnean/zlw017.

Cheng, F., Wan, T., Chen, Z.Z., Koju, N.P., He, K., Jiang, X.L. 2017. First records of Taiwanese Gray Shrew (*Crocidura tanakae*) in Yunnan Province, China. *Chinese Journal of Zoology*, 98(3): 731–743. doi: 10.13859/j.cjz.201705016.

Corbet, G.B., Hill, J.E. 1992. *The Mammals of the Indomalayan Region: A Systematic Review*. Oxford University Press, New York. viii + 488 pp., 45 figs.

Duan, H.S., Yang, Z.Q., Liu, Y.R. 2011. List revision of insectivorous in China and its distribution. *Journal of Huazhong Normal University (Nat. Sci.)*, 45(3): 466–471.

Edgar, R.C. 2004. Muscle: a multiple sequence alignment method with reduced time and space complexity. *BMC Bioinformatics*, 5(1): 113. doi: 10.1186/1471-2105-5-113.

Ellerman, J.R.S., Morrison-Scott, T.C.S. 1951. *Checklist of Palaearctic and Indian Mammals 1758 to 1946*. British Museum (Natural History), London. 810pp.

Esselstyn, J.A., Goodman, S.M. 2010. New species of shrew (Soricidae: *Crocidura*) from Sibuyan Island, Philippines. *Journal of Mammalogy*, 91(6): 1467–1472. doi: 10.1644/10-MAMM-A-002.1.

Goodman, S.M., Ingle, N.R. 1993. Sibuyan Island in the Philippines—threatened and in need of conservation. *Oryx*, 27(3): 174–180.

He, K., Deng, K., Jiang, X.L. 2012. First record of Van sung's shrew (*Chodsigoa caovansunga*) in China. *Zoological Research*, 33(5): 542–544. doi: 10.3724/SP.J.1141.2012.05542.

He, K., Li, Y.J., Brandley, M.C., Lin, L.K., Wang, Y.X., Zhang, Y.P., Jiang, X.L. 2010. A multi-locus phylogeny of Nectogalini shrews and influences of the paleoclimate on speciation and evolution. *Molecular Phylogenetics and Evolution*, 56(2): 734–746. doi: 10.1016/j.ympev.2010.03.039.

He, K., Chen, X., Chen, P., He, S.W., Cheng, F., Jiang, X.L., Campbell, K.L. 2018. A new genus of Asiatic short-tailed shrew (Soricidae, Eulipotyphla) based on molecular and morphological comparisons. *Zoological Research*, 39(5): 321–334. doi; 10.24272/j.issn.2095-8137.2018.058.

Hoffmann, R.S. 1987. A review of the systematics and distribution of Chinese red-toothed shrews (Mammalia: Soricinae). *Acta Theriologica Sinica*, 7: 100–139.

Hoffmann, R.S. 1996. Noteworthy shrews and voles from the Xizang-Qinghai Plateau. *In*: Genoways, H.H., Baker, R.J. (eds), *Contributions in Mammalogy: a Memorial Volume Honoring Dr. J. Knox Jones, Jr*. The Museum, Texas Tech University, Lubbock. pp. 155–168.

Hutterer, R. 1993. Order Insectivora. *In*: Wilson, D.E., Reeder, D.M. (eds), *Mammal Species of the World (2nd Edition)*. Smithsonian Institution Press, Washington, D.C. pp. 69–130.

Hutterer, R. 2005. Order Soricomorpha. *In*: Wilson, D.E, Reeder, D.A. (eds), *Mammal Species of the World: A Taxonomic and Geographic Reference (Third Edition)*. Johns Hopkins University Press, Baltimore. pp. 220–311.

Jenkins, P.D. 1976. Variation in Eurasian shrews of the genus *Crocidura* (Insectivora: Soricidae). *Bulletin of the British Museum of Natural History*, 30: 271–309.

Jenkins, P.D., Abramov, A.V., Rozhnov, V.V., Makarova, O.V. 2007. Description of two new species of white-toothed shrews belonging to the genus *Crocidura* (Soricomorpha: Soricidae) from Ngoc Linh Mountain, Vietnam. *Zootaxa*, 1589: 57–68.

Jenkins, P.D., Lunde, D.P., Moncrieff, C.B. 2009. Chapter 10. Descriptions of new species of *Crocidura* (Soricomorpha: Soricidae) from mainland Southeast Asia, with synopses of previously described species and remarks on biogeography. *Bulletin of the American Museum of Natural History*, 331(1): 356–406. doi: 10.1206/582-10.1.

Jenkins, P.D., Abramov, A.V., Bannikova, A.A., Rozhnov, V.V. 2013. Bones and genes: resolution problems in three Vietnamese species of *Crocidura* (Mammalia, Soricomorpha, Soricidae) and the description of an additional new species. *ZooKeys*, 313: 61–79. doi: 10.3897/zookeys.313.4823

Jiang, X.L., Hoffmann, R.S. 2001. A revision of the white-toothed shrews (*Crocidura*) of southern China. *Journal of Mammalogy*, 82(4): 1059–1079. doi: 10.1644/1545-1542(2001)082<1059:AROTWT>2.0.CO;2.

Jiang, Z., Jiang, J., Wang, Y., Zhang, E., Zhang, Y., Li, L., Xie, F., Cai, B., Cao, L., Zheng, G. 2016. Red list of China's vertebrates. *Biodiversity Science*, 24(5): 500–551. doi: 10.17520/biods.2016076.

Liu, S.Y., Wu, Y. 2018. *Hand Book of The Mammals of China*. The Straits Publishing & Distributing Group, Fuzhou. pp. 32–37.

Liu, Y., Wang, H., Liu, S.Y. 2010. First confirmation of the distribution of tundra shrew (*Sorex tundrensis*) in China. *Acta Theriologica Sinica*, 30(4): 439–443.

Liu, Z., Yang, X., Xie, R., Liu, H., Jin, Z., Zhang, X. 2016. First confirmation of the distribution of flat-skulled shrew (*Sorex roboratus*) in China. *Acta Theriologica Sinica*, 36(4): 459–463. doi: 10. 16829 /j. slxb. 201604011.

Liu, Z., Zhang, J.S., Sun, Y.X., Yang, X., Jin, Z.M. 2017. New locations of *Sorex minutissimus* was found in northeast China. *Chinese Journal of Zoology*, 52(3): 514–520. doi: 10.13859/j.cjz.201703018.

Lunde, D.P., Musser, G.G. 2004. Description of a new species of *Crocidura* (Soricomorpha : Soricidae, Crocidurinae) from Ke Go Nature Reserve, Vietnam. *Mammal Study*, 29(1): 27–36. doi: 10.3106/mammalstudy.29.27.

Meegaskumbura, S., Meegaskumbura, M., Pethiyagoda, R., Manamendra-Arachchi, K. 2007. *Crocidura hikmiya*, a new shrew (Mammalia: Soricomorpha: Soricidae) from Sri Lanka. *Zootaxa*, 1665(1): 19–30.

Mittermeier, R.A., Wilson, D.E. 2018. *Handbook of the Mammals of the World, Volume 8: Insectivores, Sloths, and Colugos*. Lynx edicions, Barcelona. 710 pp.

Ohdachi, S.D., Hasegawa, M., Iwasa, M.A., Vogel, P., Oshida, T., Lin, L.K., Abe, H. 2006. Molecular phylogenetics of soricid shrews (Mammalia) based on mitochondrial cytochrome *b* gene sequences: with special reference to the Soricinae. *Journal of Zoology*, 270(1): 177–191. doi: 10.1111/j.1469-7998.2006.00125.x.

Ronquist, F., Huelsenbeck, J.P. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics*, 19(12): 1572–1574.

Sambrook, J., Fritsch, E.F., Maniatis, T. 1989. *Molecular Cloning: A Laboratory Manual (2nd Edition)*. Cold Spring Harbor Laboratory Press, Cold Springs Harbor. 1659 pp.

Shaw, T.H., Wang, S., Lu, C.K., Chang, L.K. 1966. A survey of the Mammals of Hainan Island, China. *Acta Zootaxonomica Sinica*, 3(3): 260–276.

Smith, A.T., Xie, Y. 2010. *A Guide to the Mammals of China*. Princeton University Press, Princeton, New Jersey. pp. 298–302.

Swindell, S.R., Plasterer, T.N. 1997. Seqman. Contig assembly. *Methods in Molecular Biology*, 70: 75–89.

Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M., Kumar, S. 2011. MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular Biology and Evolution*, 28(10): 2731–2739. doi: 10.1093/molbev/msr121.

Wang, Q.S. 1990. *The Mammal Fauna of Anhui*. Anhui Publishing House of Science and Technology, Heifei. 315pp.

Wang, Y.X. 2003. *A Complete Checklist of Mammal Species and Subspecies in China and a Taxonomic and Geographic Reference*. China Forestry Publishing House. Beijing. 394 pp.

Wolsan, M., Hutterer, R. 1998. Appendix: List of the living species of shrews. *In*: Wojcik, J.M., Wolsan, M. (eds.), *Evolution of Shrews*. Mammal Research Institute, Polish Academy of Sciences, Bialowieza. pp. 425–448.

Zhang, H., Qian, L.F., Zhou, L., Wang, C.C., Yang, L., Tan, K., Zhan, H.S., Zhao, K., Zhang, B.W. 2018. Discovery of de Winton′s shrew (*Chodsigoa hypsibia*) in Dabie Mountains, Anhui Province. *Chinese Journal of Zoology*, 53(1): 40–45. doi: 10.13859/j.cjz. 201801005.

Zhuge, Y. 1993. *Crocidura* (Insectivora: Soricidae). *In*: Zhuge, Y., Gu, H.Q. (eds.), *Fauna of Zhejiang: Mammalia*. Zhejiang Science and Technology Publishing House, Hangzhou. pp. 19–23.