



A new species of the genus *Takydromus* (Squamata: Lacertidae) from Tianjingshan Forestry Station, northern Guangdong, China

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Abstract

Many early descriptions of species of the genus *Takydromus* were based on limited diagnostic characteristics. This has caused considerable challenges in accurate species identification, meaning that a number of cryptic species have been erroneously identified as known species, resulting in substantially underestimated species diversity. We have integrated evidence from morphology and DNA sequence data to describe a new species of the Asian Grass Lizard, *Takydromus albomaculosus* **sp. nov.**, based on two specimens from Tianjingshan Forestry Station, Ruyuan County, Guangdong Province, China. The new species can be distinguished from other known *Takydromus* species by distinctive morphological differences and significant genetic divergence in the mitochondrial COI gene. Morphologically, the new species differs from the known 22 congeners in the following combination of characters: relatively large body size, SVL 70.9 mm in female, 65.5 mm in male; presence of three or four pairs of femoral pores and four pairs of chin-shields; supraoculars three, rarely four, the posterior loreal either in contact with the anteriormost supraocular or not; the presence of supraciliary granules; the presence of six rows of ventral scales, strongly keeled in the male, and smooth but with the outermost row keeled in the female; the presence of enlarged and keeled lateral scales in a row above the ventrals, but shorter than the ventrals; subdigital lamellae 23–24 under the fourth finger and 29–30 under the fourth toe; dorsal surface brown, ventral surface green, flank dark brown or brown black with several prominent white round spots; the presence of a pair of white longitudinal dorsolateral stripes and a pair of white longitudinal ventrolateral stripes. *Takydromus albomaculosus* sp. nov. represents the twenty-third species of this genus, of which six species occur in northern Guangdong, where the biodiversity level of *Takydromus* is the second highest in the world, just below that of Taiwan.

Key words: China, Lacertidae, *Takydromus*, morphology, mtDNA, new species, taxonomy

Introduction

The Asian Grass Lizard genus *Takydromus* Daudin, 1802 is distributed in the East Asian islands (Ryukyu Archipelago, Japan, Taiwan) and over a broad range from the Russian far east, extending southward across the Chinese mainland, Indochina, northeastern India, Borneo, the Natuna Islands, Sumatra, Bangka and Java. There are 22 currently recognized species (Uetz *et al.* 2017), of which 17 species occur in East Asia, including *Takydromus kuehnei* Van Denburgh, 1909, *T. amurensis* Peters, 1881, *T. wolteri* Fischer, 1885, *T. sexlineatus* Daudin, 1802, *T. septentrionalis* Günther, 1864, *T. sylvaticus* (Pope 1928), and *T. intermedius* Stejneger, 1924, all of which occur in the Chinese mainland; the latter three are recognized as endemic to the Chinese mainland (Zhao *et al.* 1999; Cai *et al.* 2011). Another 10 species only occur in the Ryukyu Archipelago, Japan and Taiwan, and are endemic to these islands (Lue & Lin 2008), namely *T. dorsalis* Stejneger, 1904, *T. formosanus* Boulenger, 1894, *T. hsuehshanensis* Lin & Cheng, 1981, *T. sauteri* Van Denburgh, 1909, *T. smaragdinus* Boulenger, 1887, *T. stejnegeri* Van Denburgh, 1912, *T. tachydromoides* (Schlegel, 1838), *T. toyamai* Takeda & Ota, 1996, *T. lueyanus* Lue & Lin, 2008, and *T.*

viridipunctatus Lue & Lin, 2008. Of the remaining five species of the genus *Takydromus*, *T. hani* Chou, Truong & Pauwels, 2001, and *T. madaensis* Bobrov, 2013 are only found in Vietnam (Chou *et al.* 2001; Bobrov 2013), while *T. haughtonianus* Jerdon, 1870, *T. khasiensis* Boulenger, 1917, and *T. sikkimensis* Günther, 1888 have only been reported in northern India (Arnold 1997; Bhupathy *et al.* 2009).

Previous studies have reported *T. kuehnei*, *T. sexlineatus*, *T. septentrionalis*, *T. sylvaticus*, and *T. intermedius* in northern Guangdong Province, southern China (Fellowes *et al.* 2003; Li *et al.* 2011; Yang *et al.* 2010). In addition, Vogt (1914) described *Tachydromus chinensis* based on a single male specimen from this area; however, Arnold (1997) suggested that this specimen was actually a member of the species *T. kuehnei*. During herpetological surveys in Tianjingshan Forestry Station (24.45°–24.95°N, 112.5°–114.07°E; Fig. 1), the northern Guangdong Province, we collected two lacertid specimens significantly different from the above five recognized species, which belonged to the genus *Takydromus* on basis of the following external morphological characters: lateral teeth tricuspid; temporal scales usually keeled; at least some ventral body scales keeled; 0–5 femoral pores on each side (Arnold 2007). Close examination of its external morphology and molecular analyses revealed that it is different from all the known congeners, as we describe in detail below.

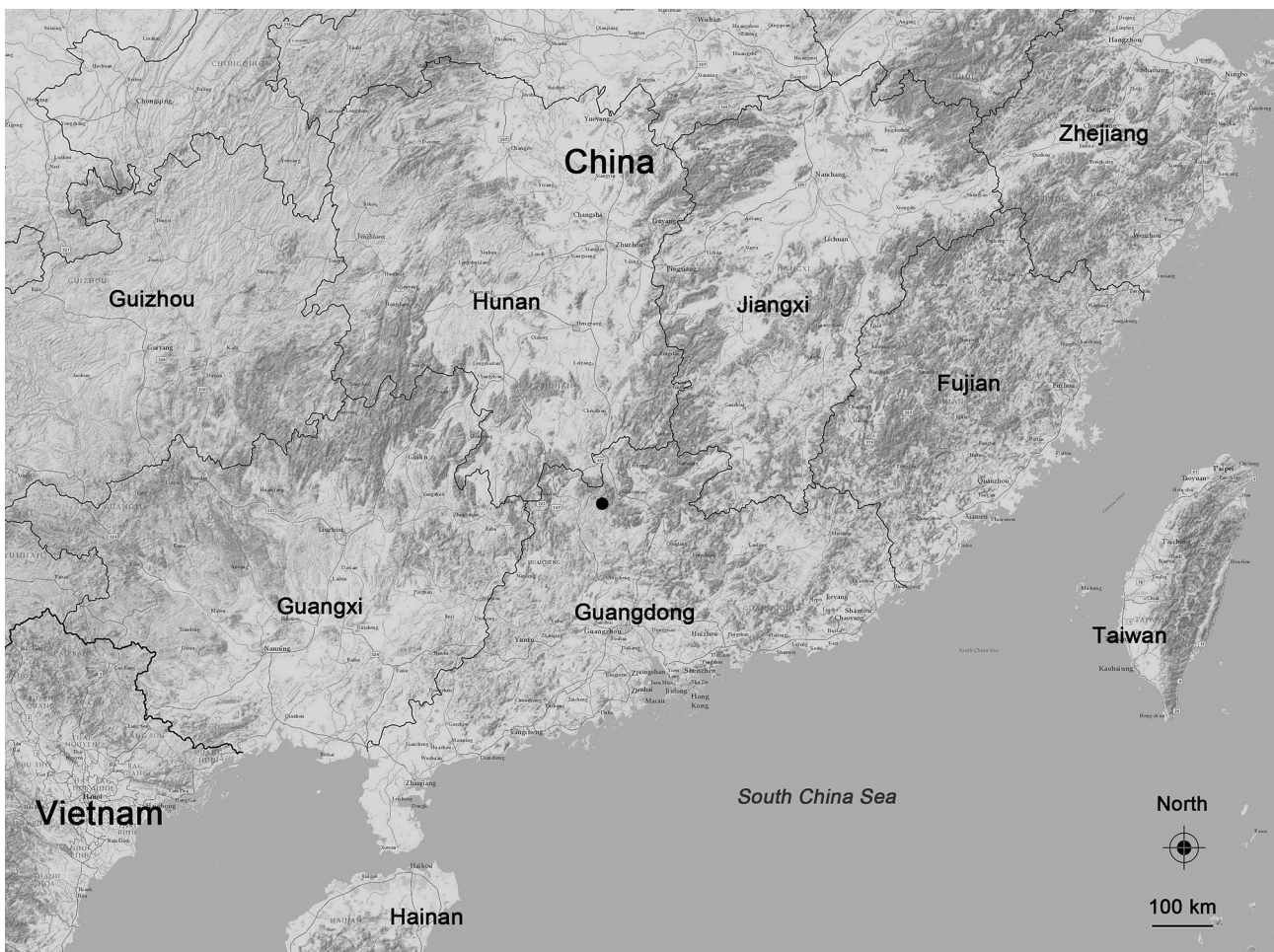


FIGURE 1. Map of southern and eastern China showing the collection locality (black round dot) of specimens of *Takydromus albomaculosus* sp. nov.: Tianjingshan Forestry Station, Ruyuan County, Guangdong Province, China.

Materials and methods

Molecular data. For molecular analyses, we selected a total of 44 samples from the unnamed *Takydromus* taxon from northern Guangdong, China and 15 recognized species of the genus *Takydromus* from the East Asian area; of which 13 samples of five known species are provided in this study, included five samples of *T. intermedius*, two of *T. kuehnei*, one of *T. septentrionalis*, four of *T. sexlineatus*, one of *T. sylvaticus*; other 30 samples of 15 known

Takydromus species obtained from GenBank, included one of *T. intermedius*, two of *T. kuehnei*, three of *T. septentrionalis*, three of *T. sexlineatus*, one of *T. sylvaticus*, three of *T. amurensis*, two of *T. dorsalis*, two of *T. sauteri*, two of *T. formosanus*, two of *T. hsuehshanensis*, two of *T. smaragdinus*, two of *T. stejnegeri*, one of *T. tachydromoides*, one of *T. toyamai* and three of *T. wolteri*. *Eremias argus* was used as the out-group. Details of samples sequenced for mitochondrial COI gene and their associated GenBank (NCBI, USA) accession numbers are presented in Table 1.

TABLE 1. Localities, voucher information, and GenBank accession numbers for all specimens used in this study.

ID.	Species	Locality	Voucher No.	COI gene
(1)	<i>Takydromus albomaculosus</i> sp. nov.	China: Tianjingshan Forestry Station, Ruyuan, Guangdong	SYS r001292	MF631870
(2)	<i>Takydromus amurensis</i>	China:	HRB1506080	NC_030209
(3)	<i>Takydromus amurensis</i>	Korea: Seoul		AY248535
(4)	<i>Takydromus amurensis</i>	Korea: Seoul		AY248534
(5)	<i>Takydromus dorsalis</i>	Japan: Ishigaki Island, Ryukyu		AY248537
(6)	<i>Takydromus dorsalis</i>	Japan: Ishigaki Island, Ryukyu		AY248536
(7)	<i>Takydromus formosanus</i>	China: Taiwan		AY248604
(8)	<i>Takydromus formosanus</i>	China: Taiwan		AY248603
(9)	<i>Takydromus hsuehshanensis</i>	China: Taiwan		AY248562
(10)	<i>Takydromus hsuehshanensis</i>	China: Taiwan		AY248560
(11)	<i>Takydromus intermedius</i>	China:		AY248538
(12)	<i>Takydromus intermedius</i>	China: Mt. Emei, Sichuan (type locality)	SYS r001601	MF631858
(13)	<i>Takydromus intermedius</i>	China: Mt. Emei, Sichuan (type locality)	SYS r001602	MF631859
(14)	<i>Takydromus intermedius</i>	China: Maolan Nature Reserve, Libo, Guizhou	SYS r000856	MF631860
(15)	<i>Takydromus intermedius</i>	China: Mt. Badagongshan, Sangzhi, Hunan	SYS r001330	MF631861
(16)	<i>Takydromus intermedius</i>	China: Mt. Badagongshan, Sangzhi, Hunan	SYS r001331	MF631862
(17)	<i>Takydromus kuehnei</i>	China: Taipei, Taiwan		AY248540
(18)	<i>Takydromus kuehnei</i>	China: Taipei, Taiwan		AY248539
(19)	<i>Takydromus kuehnei</i>	China: Jiulianshan Nature Reserve, Longnan, Jiangxi	SYS r001268	MF631863
(20)	<i>Takydromus kuehnei</i>	China: Heishiding Nature Reserve, Fengkai, Guangdong	SYS r001338	MF631864
(21)	<i>Takydromus sauteri</i>	China: Lanyu, Taiwan		AY248543
(22)	<i>Takydromus sauteri</i>	China: Pingdong, Taiwan		AY248541
(23)	<i>Takydromus septentrionalis</i>	China: Fujian		AY248544
(24)	<i>Takydromus septentrionalis</i>	China: Fujian		AY248545
(25)	<i>Takydromus septentrionalis</i>	China:		JX196703
(26)	<i>Takydromus septentrionalis</i>	China: Makeng Village, Jingning, Zhejiang	SYS r000912	MF631865
(27)	<i>Takydromus sexlineatus</i>	China: Guangxi		NC_022703
(28)	<i>Takydromus sexlineatus</i>	China: Hong Kong		AY248546
(29)	<i>Takydromus sexlineatus</i>	China: Hong Kong		AY248547
(30)	<i>Takydromus sexlineatus</i>	China: Heishiding Nature Reserve, Fengkai, Guangdong	SYS r001335	MF631866
(31)	<i>Takydromus sexlineatus</i>	China: Heishiding Nature Reserve, Fengkai, Guangdong	SYS r001336	MF631867

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TABLE 1. (Continued)

ID.	Species	Locality	Voucher No.	COI gene
(32)	<i>Takydromus sexlineatus</i>	China: Heishiding Nature Reserve, Fengkai, Guangdong	SYS r001337	MF631868
(33)	<i>Takydromus sexlineatus</i>	China: Heishiding Nature Reserve, Fengkai, Guangdong	SYS r001522	MF631869
(34)	<i>Takydromus smaragdinus</i>	Japan: Okinawa Island, Ryukyu,		AY248551
(35)	<i>Takydromus smaragdinus</i>	Japan: Okinawa Island, Ryukyu,		AY248549
(36)	<i>Takydromus stejnegeri</i>	China: Pingdong, Taiwan		AY248553
(37)	<i>Takydromus stejnegeri</i>	China: Taipei, Taiwan		AY248552
(38)	<i>Takydromus sylvaticus</i>	China: Xiuning, Anhui		JX290083
(39)	<i>Takydromus sylvaticus</i>	China: Longhu Forestry Station, Shaowu, Fujian	SYS r001276	MF631871
(40)	<i>Takydromus tachydromoides</i>	Japan: Yakushima		AY248554
(41)	<i>Takydromus toyamai</i>	Japan: Miyako Island, the Ryukyus		AY248556
(42)	<i>Takydromus wolteri</i>	/		NC_018777
(43)	<i>Takydromus wolteri</i>	/		JX181764
(44)	<i>Takydromus wolteri</i>	China:		AY248557
(45)	<i>Eremias argus</i>	China: Inner Mongolia Autonomous Region	UOG:ROM37510	HQ733938

DNA was extracted from liver tissue using a standard phenol-chloroform extraction protocol (Sambrook *et al.* 1989). The fragment of mitochondrial COI gene was PCR amplified and sequenced using the primers COI-L (5'-GCTGGTACYGGCTGAACTGTCTACCC-3') and COI-H (5'-CARTGNACRAATCCRCCCATRATTGC-3') (Tseng *et al.* 2015). PCR amplifications were performed in a 25 μ L reaction volume with the following cycling conditions: an initial denaturing step at 94°C for 7 min; 40 cycles of denaturing at 94°C for 40 s, annealing at 46°C for 30 s and extending at 72°C for 1 min, and a final extending step of 72°C for 8 min. PCR products were purified with spin columns. The purified products were sequenced with both forward and reverse primers using a BigDye Terminator Cycle Sequencing Kit (ThermoFisher Scientific, Waltham, MA) according to the manufacturer's guidelines. The products were sequenced on an ABI Prism 3730 automated DNA sequencer (Shanghai Majorbio Bio-pharm Technology Co., Ltd).

Sequence alignment was first conducted using Clustal X 2.0 (Thompson *et al.* 1997) with default parameters, then checked and manually revised. The data were tested in jmodeltest v2.1.2 with Akaike and Bayesian information criteria, resulting the best-fitting nucleotide substitution models are GTR + I + G. Phylogenetic relationships were reconstructed using maximum likelihood (ML) implemented in RaxmlGUI 1.3 (Silvestro & Michalak 2012), and Bayesian inference (BI) using MrBayes 3.12 (Ronquist & Huelsenbeck 2003). For ML analysis, we used the rapid-bootstrapping algorithm (1000 replicates) with the thorough ML search option. Bootstrap values less than 70 were collapsed. For BI analysis, two independent runs with four Markov Chain Monte Carlo simulations were performed for ten million iterations and sampled every 1000th iteration. The first 25% of samples were discarded as burn-in. Convergence of the Markov Chain Monte Carlo simulations was assessed using Tracer v.1.4 (<http://tree.bio.ed.ac.uk/software/tracer/>). We also calculated pairwise sequence divergence based on uncorrected *p*-distance implemented in MEGA 6 (Tamura *et al.* 2013).

Morphological data. We examined a total of 51 specimens of seven known *Takydromus* species and the undescribed *Takydromus* species from the Chinese mainland, included 32 adult and 19 juvenile specimens. Measurements of all 32 adult specimens were taken with a digital caliper to the nearest 0.1 mm. Abbreviations of measurements followed the convention of Lue & Lin (2008), including: SVL, snout-vent length, from tip of snout to anterior margin of vent; TaL, tail length; HL, head length, from tip of snout to anterior margin of ear opening; HW, head width, measured at the broadest point; HH, head height, measured at the highest point; SKL, skull length, from tip of snout to posterior margin of occipital; SEL, snout-eye length, from tip of snout to anterior margin of eye; SAL, snout-arm length, from tip of snout to anterior margin of forelimb; ALL, arm-leg length, from middle of the forelimb to middle of hindlimb; TFL, tibia-fibula length; RUL, radius-ulna length; LTL, length of fourth toe on hindlimb, excluding claw; HLL, hindlimb length. Moreover, we examined 19 external morphological

characters for all 51 specimens (Table 4). Modified abbreviations of these characters followed Arnold (1997) and Lue & Lin (2008), and are explained as follows: CS, chin-shields; FP, femoral pores; SPL, supralabials; IFL, infralabials; SPO, supraocular; SPC, supraciliary; SPT, supratemporals; ADSR, anterior dorsal scale rows, distinctly enlarged and keeled scales on anterior dorsum, counted transversely at position of forelimbs; PDSR, posterior dorsal scale rows, counted transversely at the position of hind limbs; LDSN, dorsal scale numbers, counted longitudinally from posterior margin of occipital to posterior margin of hind limbs; MDSR, transverse dorsal scale rows at mid-body; VR, ventral scale rows, counted transversely at mid-body; VN, ventral scale numbers, counted longitudinally from the posterior margin of collars to the anterior margin of preanal scales; TSRF, enlarged and keeled scale rows above ventrals on flank; SSRF, small flat and granular scales in a transverse row on flank at mid-body; MBSR, scales in a transverse row at mid-body, including ventrals; CSR, caudal scale rows, counted around the tail in the position of the 11th to 13th subcaudal scales; SDLF-IV, subdigital lamellae under fourth finger, and fourth toe (SDLT-IV).

We obtained comparative morphological data from the literature for *T. hani* (Chou *et al.* 2001), *T. viridipunctatus* and *T. lueyanus* (Lue & Lin 2008), *T. sikkimensis* (Bhupathy *et al.* 2009), *T. madaensis* (Bobrov 2013), and *T. sylvaticus* (Pope 1928, 1929; Yang & Wang, 2010), *T. smaragdinus* and *T. toyamai* (Takeda & Ota 1996); *T. kuehnei* (van Denburgh 1909; Arnold, 1997; Norval *et al.* 2012), *T. intermedius* (Stejneger 1924), *T. amurensis*, *T. dorsalis*, *T. formosanus*, *T. hsuehshanensis*, *T. sauteri*, *T. stejnegeri*, *T. tachydromoides* (Takeda & Ota 1996; Lue & Lin 2008), *T. sexlineatus*, *T. wolteri*, *T. septentrionalis*, and *T. khasiensis* (Arnold 1997; Zhao *et al.* 1999). All examined specimens are listed in Appendix I. Measurements (in mm) and body proportions of the seven known species and a new species described in this study of the genus *Takydromus* from the Chinese mainland are provided in Appendix II.

All studied specimens and materials were deposited in the Museum of Biology, Sun Yat-sen University (SYS), Guangzhou, and the Chengdu Institute of Biology (CIB), the Chinese Academy of Sciences, Chengdu, China.

Results

The Maximum likelihood (ML) and Bayesian inference (BI) phylogenetic trees are constructed based on partial DNA sequences of the mitochondrial COI gene with a total length of 707-bp from 15 known *Takydromus* species from East Asia and the new species of *Takydromus* from northern Guangdong, China described in detail below (Fig. 2). The two analyses resulted in essentially identical topologies with poor basal node support values. *Takydromus kuehnei*, *T. sexlineatus*, *T. smaragdinus*, *T. tachydromoides*, *T. sauteri* and *T. amurensis* formed uncertain clustering relationships due to the low support value; but all other species grouped into two clades with moderately strong node support values, named Clade A and Clade B, respectively. Clade A contains *T. dorsalis*, *T. sylvaticus*, *T. intermedius* and the population of *Takydromus* from Tianjingshan Forestry Station in northern Guangdong. Clade B is composed of *T. formosanus*, *T. hsuehshanensis*, *T. stejnegeri*, *T. wolteri*, *T. septentrionalis* and *T. toyamai*, which is essentially consistent with the results of Tseng (2015) (Fig. 2). *Takydromus viridipunctatus* and *T. lueyanus*, which are not included in our study, are nested in Clade B in the molecular phylogenetic trees of Tseng (2015). In both ML and BI trees, all samples of the same species clusters into one group with strong node support values, the largest uncorrected *p*-distances being 6.4% among four samples of *T. kuehnei* (Table 2). In clade A, the population from the northern Guangdong is strongly supported as a sister taxon to the clade formed by *T. dorsalis*, *T. sylvaticus* and *T. intermedius*. Further, the lowest uncorrected *p*-distance among the population from the northern Guangdong and the 15 known species is 13.3%. The value is significantly higher than those observed between known species; for example, *p*-distances of 7.5–7.9% between *T. formosanus* and *T. wolteri*, 8.5–9.0% between *T. stejnegeri* and *T. toyamai*, 12.1–12.3% between *T. dorsalis* and *T. sylvaticus*. These results indicate that the population from the northern Guangdong is a separately evolving lineage, representing a distinct species. Morphologically, this species from northern Guangdong can be distinguished from all known *Takydromus* species by a combination of morphological characters, including large body size, distinctive white round spots on the flanks, usually supraoculars three, four pairs of chin-shields, three or four pairs of femoral pores, relatively long hindlimbs in the male, and increased subdigital lamellae in the fourth finger and fourth toe.

Based on molecular and morphological evidences, we hereby describe the specimens collected from Tianjingshan Forestry Station, northern Guangdong of China as a new species.

TABLE 2. Uncorrected *p*-distances (in %) among the *Tachydromus* species studied, based on the mitochondrial COI gene

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1. <i>T. amurensis</i>	0.3–0.9															
2. <i>T. dorsalis</i>	19.0–20.2	0.7														
3. <i>T. formosanus</i>	18.4–19.4	19.0–19.2	1.3													
4. <i>T. hsuhshehanensis</i>	18.2–18.3	20.5–20.9	10.4–11.9	0.7												
5. <i>T. intermedius</i>	17.8–20.5	12.8–15.6	15.8–18.3	17.5–20.0	0.1–2.2											
6. <i>T. kuehnei</i>	20.5–21.6	20.6–22.1	18.5–19.1	18.6–20.5	19.8–22.3	0.1–6.4										
7. <i>T. sauteri</i>	16.1–17.5	19.9–20.8	16.3–17.2	17.0–17.6	16.9–19.9	18.3–21.6	5.6									
8. <i>T. septentrionalis</i>	17.6–19.0	18.5–19.9	11.4–13.1	10.6–11.8	17.9–20.6	18.8–21.9	14.5–16.0	0.4–1.3								
9. <i>T. sexlineatus</i>	21.6–22.6	19.9–20.5	18.2–19.0	17.4–17.6	17.5–19.9	21.0–22.1	16.2–19.0	17.4–19.0	0.4–1.1							
10. <i>T. smaragdinus</i>	18.7–19.8	18.0–18.6	18.7–20.2	18.1–18.6	17.9–21.2	19.1–21.4	16.3–17.7	17.3–18.7	20.4–21.0	0.9						
11. <i>T. albomaculosus</i> sp. nov.	20.0–20.2	13.3–13.7	16.7–17.5	18.3–18.5	13.4–15.7	18.9–20.3	17.9–18.5	17.1–18.3	17.5–17.7	16.2						
12. <i>T. stejnegeri</i>	18.2–19.5	20.8–21.2	12.7–13.4	11.7–12.4	19.0–21.8	19.8–22.1	16.5–16.8	7.4–8.4	19.4–20.0	18.1–19.2	19.9–20.8	1.7				
13. <i>T. sylvaticus</i>	21.1–21.4	12.1–12.3	17.9	19.1–19.5	13.4–15.8	19.2–19.9	17.5–18.3	18.5–19.5	19.3–19.7	19.1–20.0	16.8	17.5–18.7	0			
14. <i>T. tachydromoides</i>	20.6–21.4	17.4–17.6	19.3–19.9	20.5–20.7	18.1–20.5	19.5–20.7	19.5–20.3	20.4–21.7	21.0–21.2	19.0–19.8	20.5	19.9–20.2	16.9			
15. <i>T. toyamai</i>	17.3–17.5	19.8–20.3	13.0–13.5	11.9–12.1	17.7–19.9	19.7–20.8	16.9–17.1	8.5–9.5	19.1–19.5	18.1–18.5	20.3	8.5–9.0	20.4	20.3		
16. <i>T. wolteri</i>	18.4–18.6	18.5–19.0	7.5–7.9	10.2–11.6	17.3–20.3	18.6–20.3	17.1–17.7	11.6–13.2	17.5–17.9	17.5–19.2	16.9	12.4–13.4	19.1–19.5	20.4–21.1	12.9–13.3	1.7
17. <i>Eremias_argus</i>	22.1–22.3	23.5–24.4	22.4–23.2	18.9	21.1–23.7	20.8–22.1	20.7–22.0	22.6–23.7	20.1–20.3	21.4	22.4	21.9–22.4	23.9	23.6	23.7	22.2–23.5

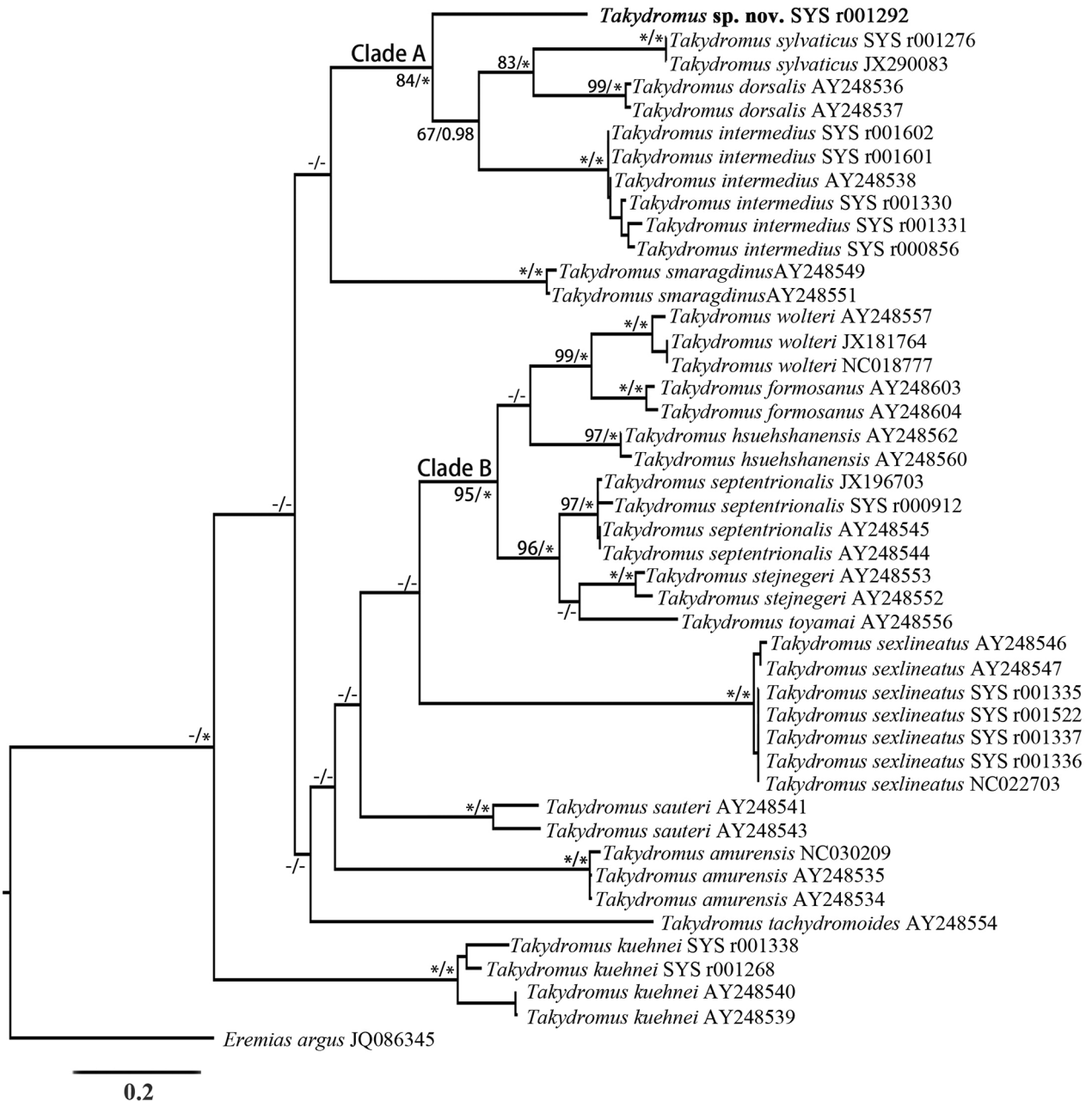


FIGURE 2. Maximum-likelihood phylogram of the genus *Takydromus* from partial DNA sequences of the mitochondrial COI gene. Number at the node is bootstrap support / posterior probability (BS/PP). "*" means BS is 100 or PP is 1.00, "-" means BS less than 70 or PP less than 0.90.

Systematics

Takydromus albomaculosus sp. nov.

Fig. 3, Fig. 4: A

Holotype. SYS r001624, adult male, from the Tianjingshan Forestry Station (24.69°N, 113.03°E; 699 m a.s.l., datum = WGS84; see Fig. 1), Ruyuan County, Guangdong Province, China, collected on 1 May 2009 by Shi-Ping Gong.

Paratype. SYS r001292, adult female, from the Zhongdong Village (24.69° N, 112.98°E; 618 m a.s.l., datum = WGS84), Ruyuan County, Guangdong Province, China, collected on 31 July 2015 by Ying-Yong Wang.

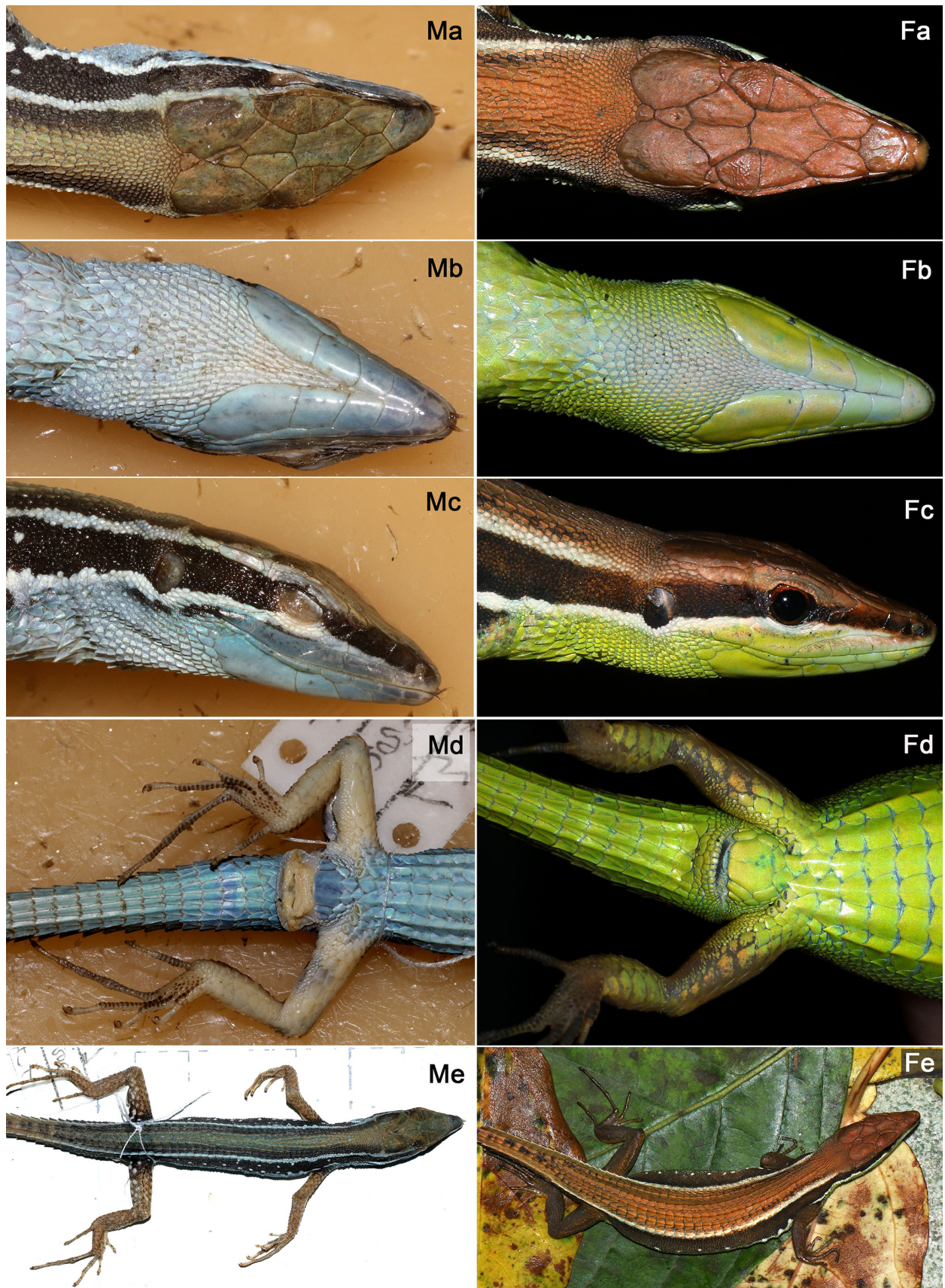


FIGURE 3. Showing the main morphological features of *Takydromus albomaculosus* sp. nov.: M: male holotype SYS r001624; F: female paratype SYS r001296. a: dorsal view of head and nape; b: ventral view of head and neck; c: lateral view of head and neck; d: showing ventral scales on posterior belly and hindlimbs, femoral pores, preanal scales and subcaudals; e: dorsal head and body.

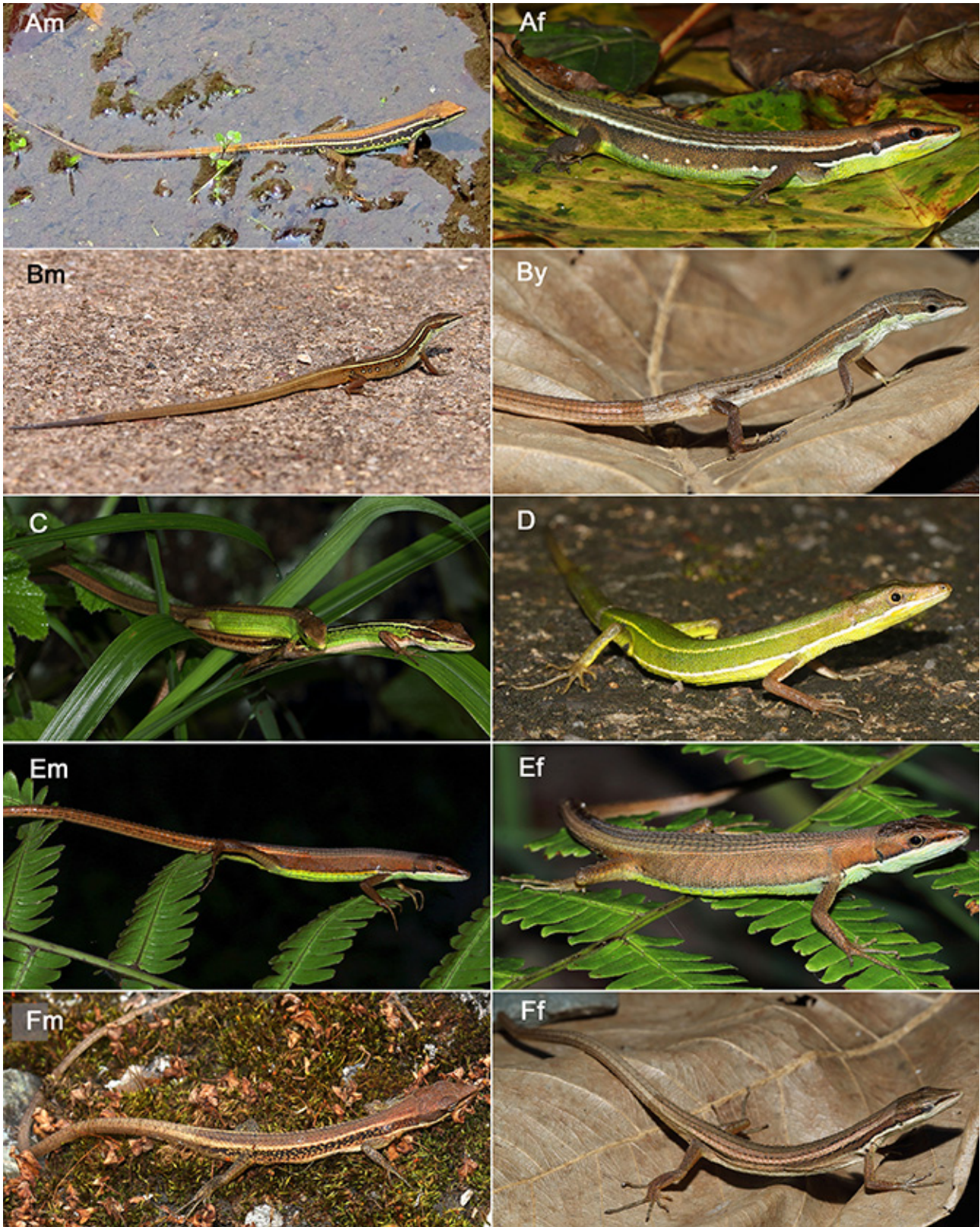


FIGURE 4. The general aspects (in life) of six species occurring on the Chinese mainland. **A:** *Takydromus albomaculosus* sp. nov., **Am:** adult male holotype SYS r001624; **Af:** adult female paratype SYS r001292; **B:** *T. sexlineatus*, **Bm:** adult male SYS r000127; **By:** subadult female SYS r001335; **C:** *T. septentrionalis*, upper: adult female; lower: adult male; **D:** *T. sylvaticus*, adult male topotype SYS001276; **E:** *T. intermedius*, **Em:** adult male topotype SYS r001601; **Ef:** adult female topotype SYS r001602; **F:** *T. kuehnei*, **Fm:** adult male specimen SYS r001268; **Ff:** adult female specimen SYS r001338.

Etymology. The specific name “*albomaculosus*” refers to the “white round spots” on the flanks of body, which are the diagnostic features of this new species. We propose the standard English name “white spotted East Asian Grass Lizard”, and the Chinese name “Tianjingshan Cao Xi”.

Diagnosis. *Takydromus albomaculosus* sp. nov. differs from other species of the genus *Takydromus* by a combination of the following characteristics: (1) body size large, SVL 70.9 mm in female, 65.5 mm in male; (2) hindlimb relatively long in male, HLL 55% of SVL, 1.11 times as long as ALL; (3) subdigital lamellae 23–24 under the fourth finger, 29–30 under fourth toe; (4) chin-shields four on each side; (5) femoral pores, three or four on each side; (6) supraoculars three, rarely four, the posterior loreal either in contact with the anteriormost supraocular or not; (7) supraciliary granules present; (8) presence of six ventral scale rows, strongly keeled in male, smooth but outermost row keeled in female; (9) enlarged and keeled lateral scales in a row above ventrals, but shorter than ventrals; (10) presence of a pair of white longitudinal dorsolateral stripes and a pair of white longitudinal ventrolateral stripes; (11) dorsal surface brown, ventral surface green, flank dark brown or brown black with several particular white round spots.

Description of Holotype. An adult male; body size slightly large, SVL 65.5 mm; trunk of body relatively short, ALL 32.4 mm, 49% of SVL; head slightly long, HL 16.1 mm, HW 9.2 mm, HH 7.8 mm, HL 25% of SVL; skull almost equal to the head length, SKL 16.2 mm; snout moderately long, SEL 6.9 mm, 43% of HL; rostral large, pentagonal, in contact with left and right first supralabials posteriorly and supranasals dorsolaterally; nostril surrounded by a supranasal, a postnasal and first supralabial on each side; supranasal single on each side, large, in contact with each other dorso-medially, separating rostral from frontonasal, and in contact with anterior loreal posteriorly; postnasal one, in contact with supranasal dorsally, with anterior loreal posteriorly, with first supralabial ventrally; supralabials six on each side, the fifth one largest, under the eye; loreals two on each side, anterior one smaller than posterior one; posterior loreal in contact with anteriormost supraocular and anteriormost supraciliary scale posteriorly; supraoculars three on each side, the posteriormost one much smaller than others; supraciliaries four on each side, second one longest, posterior three separated from supraoculars by supraciliary granules; frontonasal large, smooth, separated from frontal by a pair of prefrontals; prefrontals two, weakly keeled, in contact with each other medially, with frontal and anteriormost supraocular posteriorly, with loreals laterally, respectively; a single frontal hexagonal, weakly keeled, in contact with anterior two supraoculars laterally, with frontoparietals and parietals posteriorly; frontoparietals two, pentagonal, in contact with each other medially, with parietal and interparietal posteriorly, respectively; interparietal diamond, surrounded by two frontoparietals and two parietals; parietal pit visible; parietals two, large, weakly keeled, slightly in contact with each other medially; a single occipital between two parietals; temporal scales granular, slightly keeled; supratemporals three on each side, keeled, anteriormost one largest, longer than total length of posterior two; mental large, semielliptical; infralabials six on each side; four pairs of chin-shields, anterior two pairs in contact with each other medially, posterior two pairs separated from each other by longitypical gular scales; following gular scales gradually increasing in size, keeled, and imbricated; enlarged, strongly keeled median gular scales extending anteriorly to the line joined posterior edges of ears; collars clear, composed of scales in 12 rows pointed backwards, and forming a free serration; enlarged, imbricated dorsal scales on body with strong keel oriented posteriorly that form continuous ridges, extending anteriorly beyond forelimbs on to the nape, in six rows in position of forelimbs, six rows in position of hindlimbs; seven rows at mid-body, including a much smaller and discontinuous central row; longitudinal dorsal scales (LDSN) 53; ventrals in six rows, imbricate, strongly keeled and pointed posteriorly; longitudinal ventral scales (VN) 23; lateral body scales in 15 (left) and 14 (right) rows in the mid-body region, including a row of scales adjoining the ventrals, enlarged and keeled, shorter than ventrals; five rows of scales on lower flanks reduced, flattened, keeled; eight (left) and seven (right) rows of small granular scales on upper flanks; a discontinuous row of scales adjoining outermost dorsal scale row reduced, flattened, keeled; a total of 42 scales in a transverse row in mid-body region; a single preanal entire, enlarged, surrounded by continuous series of moderate sized scales anteriorly and laterally; four femoral pores on each side.

Forelimbs moderately long, RUL 8.3 mm, 13% of SVL; scales on anterior and dorsal surfaces of upper arm enlarged, keeled, rhomboid, imbricate, in seven rows; scales on rear of upper arm smooth, in two rows; scales on ventral surface of upper arm granular, homogeneous in size; one row of markedly enlarged smooth scales running on anterior surface of forearm; scales on ventral surfaces of forearm smooth, flatted, in four rows; scales on dorsal surface of forearm keeled, heterogeneous in size, extending to wrist; dorsal scales on hand smooth; scales on palm granular; dorsal scales on fingers in a row, smooth; subdigital lamellae under fingers I–V respectively (left/right)

10/9, 13/13, 19/19, 24/24, 13/13, most of subdigital lamellae entire; relative lengths of appressed fingers $I < V < II < III < IV$; hindlimbs slender and long, fourth toe beyond the collar when hindlimb adpressed along the side of the body; HLL 35.9 mm, 55% of SVL, 111% of ALL; TFL 9.5 mm, 15% of SVL; LTL 11.8 mm, 18% of SVL; three rows of large smooth scales running beneath thigh with traces of a fourth; two rows of enlarged keeled scales and two rows of small keeled scales on dorsal surface of thigh; granular scales homogeneous in size on rear of thigh; internal tibial scale rows two, one formed by enlarged and smooth scales, another formed by weakly keeled scales; dorsal tibial scale flat, keeled, heterogeneous in size, extending to dorsal surface of foot; scales on sole of the foot granular; dorsal scales on toes in a row, smooth; subdigital lamellae under toes I–V respectively (left/right) 12/13, 15/15, 21/21, 29/30, 17/16; basal three subdigital lamellae of toe IV divided, most of remaining ones entire; relative lengths of appressed toes $I < II < V < III < IV$.

Tail regenerated, TaL 121.2 mm, with strongly keeled scales in 16 rows at base (fifth subcaudal scale), in 12 rows in position of the 13th to 15th subcaudal scales; paired vertebral series of large scales on tail extending on to hind body.

Color in life. Dorsal surface of head, body and tail bright brown, dorsal limbs grey brown; labial series and ventral surface of head, body, limbs and tail green; lateral surfaces of head, body and anterior tail brown black, dorsally extending to the outer half of the third dorsal scale row on body; a pair of longitudinal white dorsolateral stripes beginning at the supraciliary position, running along the supratemporals and outermost dorsal scale rows, posteriorly extending to the anterior part of the tail; a pair of longitudinal white ventrolateral stripes, separating the brown-black region from green region, beginning at the posterior edges of the postnasals, through the lower parts of the loreals, subocular position, lower parts of the temporal region, lower edges of ear openings, upper parts of upper arm insertions, extending to anterior parts of ventrolateral flanks; several white round spots present on flanks and lateral surfaces of basal tail.

Color in preservative. In 75% ethanol, labial series and ventral surface pale blue, dorsal surface brown, slightly tinged with blue; lateral surfaces of head and body black; white round spots and two pairs of longitudinal stripes more distinct.

Variation. Measurements, scalation and body proportions of the paratype are given in Tables 3 and 4.

The new species exhibits noticeable sexual dimorphism. All ventrals show strong longitudinal keels, with enlarged keeled median gular scales extending anteriorly to the line joining the posterior edges of ears in the male holotype; whereas in the adult female paratype SYS r001292, the intermediate four rows smooth, with only the outermost row keeled, enlarged keeled median gular scales not extending anteriorly to the level of the ears. In the female paratype, the trunk of the body relatively elongated, ALL 57% of SVL (49% in the male holotype), rather more longitudinal ventral scales, VN 26 (23 in holotype); hindlimbs relatively short, HLL 47% of SVL, fourth toe reaches the anterior belly when hindlimb adpressed along the side of the body, whereas in the holotype, HLL is 55% of SVL, with the fourth toe beyond the collar. In addition, the paratype also shows the following variations (Fig. 3: B, Fig. 4: Af): prefrontals three; supraoculars four on left side, the first one very small, granular, in contact with posterior loreal, whereas on the right side, there supraoculars, the anteriormost one not in contact with the posterior loreal; two parietals completely divided by interparietal and occipital; lateral surfaces of head, body and anterior tail dark brown; white dorsolateral longitudinal stripes beginning from anterior neck.

Distribution, ecological notes and behavior. *Takydromus albomaculosus* sp. nov. is currently only found in the Tianjingshan Forestry Station, located on the southern slope of the Nanling Mountains, Ruyuan County, Guangdong Province, southern China (Fig. 1). They are montane dwellers, living near water and roads: the holotype SYS r001624 was found in the drain at the roadside at 17:00 in early summer; paratype SYS r001292 was found sleeping on a drooping leaf of false reed (*Neyraudia reynaudiana*) at height of 1.6 m from the ground around 22:00 on a midsummer night, surrounded by rice fields, about 5 m away from the road.

Comparisons. In this study we only compare the new species with the other 21 recognized species, excluding *T. haughtonianus*, which is currently an uncertain species and poorly known (Arnold 1997; Jordan 1870).

Takydromus albomaculosus sp. nov. can be distinguished from the recognized 21 congeners by the following characteristics: (1) the presence of several particular white round spots on the flanks vs. flanks with white ocellus bordered by black edges in *T. sexlineatus* (Fig. 4: Bm, Bf), same white spots absent in the remaining 20 species; (2) the presence of a pair of distinct longitudinal dorsolateral stripes white in adult male and female vs. absent or dorsolateral stripes blurred, pale brown only present in old individuals in *T. amurensis*, *T. wolteri*, *T. intermedius* (Fig. 4: Em, Ef), *T. kuehnei* (Fig. 4: Fm, Ff), *T. sikkimensis*, *T. dorsalis*, *T. smaragdinus*, *T. sauteri*, *T. toyamai*, *T.*

formosanus, *T. hsuehshanensis*, *T. tachydromoides* and *T. hani*; yellowish, only present in adult males in *T. septentrionalis* (Fig. 4: C); yellowish white, only present in old individuals in *T. sylvaticus* (Fig. 4: D); white in mature males, pale brown in females *T. lueyanus* and *T. viridipunctatus*; (3) three supraoculars, rarely four, the posterior loreal in contact with the anteriormost supraocular or not vs. always having four supraoculars on each side, the posterior loreal in contact with the anteriormost supraocular in *T. amurensis*, *T. wolteri*, *T. septentrionalis*, *T. sylvaticus*, *T. intermedius*, *T. kuehnei*, *T. dorsalis*, *T. smaragdinus*, *T. sauteri*, *T. stejnegeri*, *T. toyamai*, *T. formosanus*, *T. hsuehshanensis*, *T. tachydromoides*, *T. lueyanus*, *T. viridipunctatus* and *T. hani*; usually four, occasionally three in *T. septentrionalis*; (4) the presence of 3–4 pairs of femoral pores vs. only one pair in *T. septentrionalis*, *T. wolteri*, *T. khasiensis*, *T. smaragdinus*, *T. sauteri*, *T. stejnegeri*, *T. toyamai*, 1–2 pairs in *T. sexlineatus*, 2 pairs in *T. formosanus*, *T. hsuehshanensis*, *T. tachydromoides*, *T. lueyanus*, *T. viridipunctatus*; 6–8 pairs in *T. hani*; (5) the presence of 6 ventral scale rows vs. 8 ventral scale rows in *T. septentrionalis*, *T. wolteri*, *T. amurensis*, *T. sexlineatus*, *T. khasiensis*, *T. formosanus*, *T. hsuehshanensis*, *T. tachydromoides*, *T. stejnegeri*, *T. toyamai*, and *T. hani*; 12 rows in *T. sikkimensis*; (6) the presence of four pairs of chin-shields vs. 3 pairs in *T. septentrionalis*, *T. sexlineatus*, *T. khasiensis*, *T. sikkimensis*, *T. formosanus*, *T. smaragdinus*, *T. toyamai*, *T. hsuehshanensis*, *T. lueyanus*, and *T. viridipunctatus*; (7) dorsal surface of head and body brown vs. green in *T. dorsalis*, *T. sauteri*, *T. smaragdinus*, *T. toyamai*, *T. sylvaticus* and *T. hani*. In addition, *T. albomaculosus* **sp. nov.** differs from *T. madaensis*, described in Vietnam, by having two loreals on each side (vs. three), subdigital lamellae under toe IV 29–30 (vs. 17), ventral surface pale blue in 75% ethanol (vs. ventral surface of head and body grey, subcaudals light color).

TABLE 3. Measurements (in mm) and body proportions of *Takydromus albomaculosus* **sp. nov.** from northern Guangdong, China. See Materials and methods section for abbreviations.

	Holotype SYS r001624 (male)	Paratype SYS r001292 (female)
SVL	65.5	70.9
TaL	121.2	189.1
HL	16.1	16.7
HW	9.2	9.5
HH	7.8	8.1
SKL	16.2	16.7
SEL	6.9	8.7
ALL	32.4	40.2
SAL	25.5	27.0
RUL	8.3	7.5
HLL	35.9	33.5
TFL	9.5	8.9
LTL	11.8	11.9
TaL/SVL	1.85	2.67
HL/SVL	0.25	0.24
HL/HW	1.75	1.76
SKL/HL	1.01	1.00
SEL/HL	0.43	0.52
ALL/SVL	0.49	0.57
SAL/SVL	0.39	0.38
RUL/SVL	0.13	0.11
HLL/SVL	0.55	0.47
TFL/SVL	0.15	0.13
LTL/SVL	0.18	0.17
HLL/ALL	1.11	0.83

TABLE 4. Selected scale counts of the eight species of the genus *Takydromus* from the Chinese mainland. See Material and methods for abbreviations.

	<i>albomacul osus</i> sp. nov. n=2	<i>amurensis</i> n=2	<i>wolteri</i> n=1	<i>septentrionalis</i> n=25	<i>sexlineatus</i> n=5	<i>intermedius</i> n=8	<i>kuehnei</i> n=5	<i>sylvaticus</i> n=3
CS	4	4	4	3	3	4–5	4 (rarely 3*)	4
FP	3–4	4	1	1	1	2–3	3–5	3
SPL	6–7	5–7	7	5–8	5–6	6–7	6–7	5–7
IFL	6–7	6–7	6–7	5–6	4–5	5–7	5–6	5–7
SPO	3, (rarely 4 [#])	4	4	4, (rarely 3 [#])	3	4	4	4
SPC	4–6	4	4	3–5	3	4–5	4	4–5
SPT	3	2–3	3	1–4	2–3	2–5	3–4	2–4
ADSR	6	7–8	9	6–8	6	6–8	5–7	#
PDSR	6	6–7	7	4–6	4	6	6	9–10
MDSR	7	7–8	8	5–6	4	7–8	6–7	11–14
LDSN	52–53	46	56	37–46	34–35	36–46	42–47	67–81
MBSR	42–43	33–38	36	34–42	28–33	40–44	39–44	45–47
SSRF	13–14	5–9	10	7–11	6–8	12–15	13–16	13
VR	6	8	8	8	8	6	6	6
VN	23–26	27	30	25–29	26–27	21–24	27–29	26–29
ESRF	1	1–3	3	2–3	2–3	1	0–1	0
CSR	12	16–18	16	12–14	14	12	12–13	12
SDLF-IV	23–24	18–19	17	18–22	13–16	20–21	18–20	21–22
SDLT-IV	29–30	24–25	22–23	23–28	19	26–27	23–24	27–28

*: Three chin-shields only present on left side of SYS r001338

#: Four supraoculars only present on right side of SYS r001292

#: Three supraoculars only present on one side in three of 25 specimens

Takydromus albomaculosus **sp. nov.** further differs from seven known species occurring on the Chinese mainland in the following characteristics: **(1)** body size relatively large, SVL 65.5 mm and 70.5 mm for two specimens *vs.* small, SVL not exceeding 60 mm in *T. sylvaticus*, *T. intermedius* and *T. kuehnei*; **(2)** longitudinal ventral scale number 23–26 *vs.* 26–29 in *T. sylvaticus*, 21–24 in *T. intermedius*, 27–29 in *T. kuehnei*; **(3)** longitudinal dorsal body scales (LDSN) 52–53 *vs.* 34–35 in *T. sexlineatus*, 37–46 in *T. septentrionalis*, 46 in two specimens of *T. amurensis*, 36–46 in *T. intermedius*, 42–47 in *T. kuehnei* 67–81 in *T. sylvaticus*; **(4)** scales in a transverse row at mid-body (MBSR) 42–43 *vs.* 34–42 in *T. septentrionalis*, 33–38 in *T. amurensis*, 45–47 in *T. sylvaticus*; **(5)** relatively more subdigital lamellae, SDLF-IV 23–24, SDLT-IV 29–30 *vs.* SDLF-IV 20–21, SDLT-IV 26–27 in *T. intermedius*, SDLF-IV 18–20, SDLT-IV 23–24 in *T. kuehnei*, SDLF-IV 18–19, SDLT-IV 24–25 in *T. amurensis*, SDLF-IV 18–19, SDLT-IV 24–25 in *T. wolteri*; **(6)** ventral surface green *vs.* pale grey, or pale brown in males, pale green in females in *T. septentrionalis*, white, slightly stained pale green in *T. sexlineatus*, pale beige to white in *T. kuehnei*, grey white in *T. amurensis*, white in *T. wolteri*. In addition, *T. albomaculosus* **sp. nov.** differs from *T. septentrionalis* (in parenthesis) in having lateral surfaces brown black or dark brown (*vs.* green in adult individuals), most of the subdigital lamellae entire (*vs.* almost all divided). *Takydromus albomaculosus* **sp. nov.** differs from *T. sexlineatus* in the presence of supraciliary granules between supraoculars and supraciliaries (*vs.* absent). *Takydromus albomaculosus* **sp. nov.** differs from *T. sylvaticus* in the presence of one row of enlarged and keeled scales above the ventrals (*vs.* absent); and longitudinal ventrolateral stripes extended posteriorly to the anterior flanks (*vs.* to groins of thighs). *Takydromus albomaculosus* **sp. nov.** differs from *T. kuehnei* in having a single postnasal (*vs.* two). *Takydromus albomaculosus* **sp. nov.** differs from *T. amurensis* in having relatively long

hindlimbs in the male, HLL 55% of SVL (*vs.* 43%), fourth toe beyond the collar when hindlimb adpressed along the side of the body in male (*vs.* reaching the anterior belly), trunk of body relatively short in male, ALL 49% of SVL (*vs.* 59%), ventrals strongly keeled in male (*vs.* intermediate four rows smooth, outer two rows weakly keeled), temporal scales granular, slightly keeled (*vs.* flat, smooth). *Takydromus albomaculosus* **sp. nov.** differs from *T. wolteri* in having relatively long hindlimbs in the male, HLL 55% of SVL (*vs.* 43%), fourth toe beyond the collar when hindlimb adpressed along the side of the body in male (*vs.* reaching the anterior belly), temporal scales slightly keeled (*vs.* smooth), most of the subdigital lamellae entire (*vs.* almost all divided).

Discussion

The description of *Takydromus albomaculosus* **sp. nov.** brings the total number of species of this genus to 23, of which six occur in northern Guangdong, China, where the biodiversity level of *Takydromus* is the second highest in the world, just below that of Taiwan (Lue & Lin 2008). As noted, the new species is sympatrically distributed with *T. septentrionalis* and *T. kuehnei* in Tianjingshan Forestry Station (see Appendix I).

The major challenge confronting biodiversity conservation is that the vast majority of the world's species remain undiscovered (Grismer *et al.* 2013). In the genus *Takydromus*, most of the recognized species were described between the 19th Century and the early 20th Century, using only a few morphological features. In some cases, the limited diagnostic characteristics resulted in considerable challenges for accurate species identification, and meant that a number of cryptic species have been erroneously identified as known species, leading to substantially underestimated species diversity. For example, *T. haughtonianus* currently is only known from a single type specimen described by Jordan (1870) and is still an uncertain species because the scale features all occur as minority conditions in *T. sexlineatus* (Arnold 1997). *Takydromus viridipunctatus* and *T. luyeanus* were misidentified as *T. formosanus* in previous decades (Lue & Lin 2008). In our phylogenetic trees (Fig. 2), two populations of *T. kuehnei* from Jiulianshan Nature Reserve, Jiangxi (SYS r001268) and from Heishiding Nature Reserve, Guangdong (SYS r001338) are sister taxa to *T. kuehnei* from Taiwan (AY248539, AY248530) with moderate divergence (uncorrected *p*-distances are 4.8% and 6.4%, respectively). Morphologically, the geographical populations of *T. kuehnei* from the Chinese mainland and Taiwan are quite variable in the following characteristics: ventrals moderately keeled in males, weakly keeled in females, but outermost rows always strongly keeled, and all ventrals point posteriorly in Chinese mainland animals, whereas they are smooth throughout in Taiwanese animals (Lue & Lin 2008); usually there are 12 caudal scale rows in the position of the 11th to 13th as opposed to 14 in the Taiwan population (Lue & Lin 2008). In Chinese mainland animals (Fig. 4: F), supraciliary granules are only present between the posterior two supraoculars and the supraciliary scales. The color distribution is: ventral surface light yellow, slightly tinged green on the throat, dark flanks with dense light yellow spots, dorsolateral stripes pale brown in adult male animals, ventral surface white, dorsum and flanks without stripes and spots in females. In addition, *Tachydromus chinensis* from northern Guangdong as described by Vogt (1914) was considered a synonym of *T. kuehnei* by Arnold (1997), but we consider that it is more similar to *T. intermedius* reported in the same area (Li *et al.* 2011). In the original description by Vogt (1914), the single male specimen in alcohol had a pale green ventral surface and a bright ventrolateral streak from the nostril, extending along the lower eyelid to the groin; the same color features are also exhibited in male *T. intermedius* (Fig. 4 Ef), but not exhibited in the Chinese mainland *T. kuehnei* (Fig. 4 Fm, Ff). Therefore, a re-evaluation of early species delineation and an accurate assessment of species diversity using integrative evidence from morphology, DNA sequence data, and behavior based on extensive surveys and sampling is necessary (Will *et al.* 2005; Padial *et al.* 2010).

Acknowledgments

We thank J. Zhao, J. Wang, Z.T. Lyu and Z.Y. Liu for their help with the fieldwork, and Z.C. Zeng and G.L. Chen for the lab work. This work was partially supported by the specimen platform of China, teaching specimen sub-platform (<http://mnh.scu.edu.cn/>) to Y.Y. Wang, the National Natural Science Foundation of China (No.31471966), the Funds for Environment Construction & Capacity Building of GDAS' Research Platform (2016GDASPT-0107), and GDAS Special Project of Science and Technology Development (2017GDASCX-0107).

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APPENDIX I. List of specimens examined.

- Takydromus amurensis* (n=2): China: Heilongjiang Province: SYS r001635; Suifenhe City: SYS r001647.
- Takydromus wolteri* (n=1): China: Heilongjiang Province: SYS r001636.
- Takydromus septentrionalis* (n=25): China: Jiangxi Province: Mt. Sanqing: SYS r000179; Wuyuan County: Mt. Dazhang: SYS r000644, 653–655; Guixi City: Yangjifeng Nature Reserve: SYS r000115, 0133, 0135, 0147; Yanshan County: Wuyishan Nature Reserve: SYS r000642; Guangfeng County: Tongboshan Nature Reserve: SYS r000656, 0471, 0472, 0741, 0742, 0772; Jinggangshan City: Mt. Jinggang: SYS r000282, 1307; Zhejiang Province: Jingning County, Dongkeng: SYS r000912; Fujian Province: Wuyishan City: Sangang Village: SYS r000667, 0676, 0678; Guangdong Province: Ruyuan County: Tianjingshan Forestry Station: SYS r000929, 0930; unknown locality: SYS r000168.
- Takydromus sexlineatus* (n=5): China: Guangdong Province: Fengkai County: Heishiding Nature Reserve: SYS r001335, 1336, 1337, 1552; Guangxi Zhuang Autonomous Region: Shangs County: Shiwandashan Forest Park: SYS r000127.
- Takydromus intermedius* (n=8): China: Sichuan Province: Mt. Emei: SYS r001601, 1602, CIB 3745 and 3750; Guizhou Province: Libo County: Maolan Nature Reserve: SYS r000856; Hunan Province: Sangzhi County: Badagongshan Nature Reserve: SYS r001330, 1331; Guangxi Zhuang Autonomous Region: Hechi City: Jiuwanshan Nature Reserve: SYS r001553.
- Takydromus sylvaticus* (n=3): China: Jiangxi Province: Guixi City: Yangjingfeng Nature Reserve: SYS r000159, 0184; Fujian Province: Shaowu City: Longhu Forestry Station: SYS r001276.
- Takydromus kuehnei* (n=5): China: Jiangxi Province: Longnan County: Jiulianshan Nature Reserve: SYS r001268; Guangdong Province: Fengkai County: Heishiding Nature Reserve: SYS r000119, 0132, 1338; Renhua County: Huangshakeng Village: SYS r000206.

APPENDIX II. Measurements (in mm) and proportions of body of the eight species of the genus *Takydromus* from China mainland. See Material and methods for abbreviations.

	<i>T. albomaculosus</i> sp. nov.			<i>T. septentrionalis</i>			<i>T. amurensis</i>			<i>T. walteri</i>			<i>T. sexlineatus</i>			<i>T. intermedius</i>			<i>T. kuehnei</i>			<i>T. sylvaticus</i>		
	Male 001624	Female 001292		Males n=9	Females n=6	Male 001635	Female 001636	Males n=2	Female 001335	Male 001601	Females n=3	Male n=2	Female 001338	Males n=2	Female 001338	Males n=2	Female 00184							
SVL	65.5	70.9		52.8-73.5 (64.0±7.3)	51.8-74.7 (64.0±7.9)	61.3	58.4	50.8-56.0 (53.4)	43.6	45.9-56.0 (50.1±5.2)	48.6-54.2 (51.4)	54.9	36.8-56.0 (46.4)				38.9							
TaL	121.2	189.1		171.8-245.4 (211.0±24.0)	105.5-230.0 (175.5±51.3)	#	106.8	163.1 (n=1)	96.9	123.1-149.2 (136.2)	149.8-166.2 (158.0)	#	124.5 (n=1)				124.9							
HL	16.1	16.7		12.6-16.5 (14.8±1.4)	11.9-15.5 (13.9±1.4)	13.8	10.6	10.7-10.9 (10.8)	11.0	11.4-12.2 (11.7±0.4)	12.1-13.0 (12.6)	12.3	9.4-13.6 (11.5)				9.5							
HW	9.2	9.5		7.4-11.2 (9.4±1.3)	6.8-9.9 (8.4±1.4)	8.8	7.1	6.0-6.5 (6.3)	6.1	6.8-7.1 (6.9±0.2)	6.6-7.7 (7.2)	6.7	4.8-7.3 (6.1)				5.2							
HH	7.8	8.1		6.1-10.1 (8.3±1.3)	6.0-8.8 (7.3±1.0)	7.0	5.8	5.3-5.5 (5.4)	5.2	5.2-5.6 (5.4±0.2)	5.4-5.8 (5.6)	4.9	3.9-6.1 (5.0)				3.6							
SKL	16.2	16.7		12.7-16.8 (15.0±1.5)	12.0-16.0 (14.3±1.6)	13.7	11.4	10.8-11.6 (11.2)	11.4	12.0-12.5 (12.2±0.3)	12.5-13.2 (12.9)	12.9	9.7-13.7 (11.7)				10.0							
SEL	6.9	8.7		5.4-6.9 (6.4±0.5)	5.2-7.0 (6.3±0.7)	6.2	4.8	4.6-4.9 (4.8)	5.1	5.3-5.9 (5.5±0.3)	5.4-6.0 (5.7)	6.0	4.6-7.0 (5.8)				4.1							
ALL	32.4	40.2		29.5-42.8 (35.5±4.4)	29.7-44.7 (36.6±5.1)	35.9	34.3	28.7-32.8 (30.8)	24.0	24.3-30.6 (27.1±3.2)	25.5-28.5 (27.0)	32.0	18.2-32.0 (25.1)				19.4							
SAL	25.5	27.0		19.4-26.7 (24.1±2.4)	20.5-26.4 (23.2±2.3)	20.7	18.2	17.1-19.9 (18.5)	17.0	18.7-20.5 (19.9±1.0)	19.0-20.8 (19.9)	19.8	14.4-20.1 (17.3)				15.2							
RUL	8.3	7.5		6.0-9.5 (8.1±1.0)	6.1-8.8 (7.9±1.0)	7.1	5.8	6.2-6.8 (6.5)	6.9	5.6-6.7 (6.3±0.6)	6.6-7.0 (6.8)	6.3	5.0-7.1 (6.31)				5.4							
HLL	35.9	33.5		27.2-37.0 (33.0±3.7)	24.8-35.5 (30.9±3.6)	26.4	22.0	20.5-22.5 (21.5)	23.8	24.5-27.1 (25.8±1.3)	27.8-29.4 (28.6)	27.1	19.2-28.5 (23.9)				19.3							
TFL	9.5	8.9		6.6-10.2 (9.0±1.1)	6.8-10.0 (8.9±1.2)	7.4	6.5	6.5-7.2 (6.9)	7.4	7.3-7.6 (7.4±0.2)	7.4-7.7 (7.6)	7.0	5.1-7.7 (6.4)				5.6							
LTL	11.8	11.9		9.0-12.3 (11.0±1.0)	9.6-12.3 (10.9±0.9)	9.2	8.2	7.3	8.5	9.1-9.5 (9.3±0.2)	9.8-10.7 (10.3)	10.2	7.2-9.0 (8.1)				7.3							
TaL/SVL	1.85	2.67		2.69-3.51 (3.23±0.26)	2.04-3.37 (2.81±0.63)	#	1.83	2.91 (n=1)	2.22	2.54-3.25 (2.90)	3.07-3.08 (3.08)	#	3.38 (n=1)				3.21							
HL/SVL	0.25	0.24		0.22-0.24 (0.23±0.01)	0.21-0.23 (0.22±0.01)	0.23	0.18	0.19-0.21 (0.20)	0.25	0.22-0.25 (0.24±0.02)	0.24-0.25 (0.25)	0.22	0.24-0.26 (0.25)				0.24							

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APPENDIX II. (Continued)

	<i>T. albomaculosus</i> sp. nov.		<i>T. septentrionalis</i>		<i>T. amurensis</i>		<i>T. wolteri</i>		<i>T. sextineatus</i>		<i>T. intermedius</i>		<i>T. kuehnei</i>		<i>T. sylvaticus</i>	
	Male	Female	Males	Females	Male	Female	Males	Female	Males	Female	Males	Females	Male	Female	Males	Female
	001624	001292	n=9	n=6	001635	001636	n=2	001335	001601	n=3	n=2	001338	n=2	001338	n=2	000184
HL/HW	1.75	1.76	1.45-1.70 (1.58 ± 0.10)	1.51-1.75 (1.62 ± 0.10)	1.57	1.49	1.68-1.78 (1.73)	1.73	1.80	1.68-1.72 (1.70 ± 0.02)	1.69-1.83 (1.76)	1.84	1.86-1.96 (1.91)	1.84	1.86-1.96 (1.91)	1.83
SKL/HL	1.01	1.00	0.99-1.04 (1.01 ± 0.02)	1.01-1.06 (1.03 ± 0.02)	0.99	1.08	1.01-1.06 (1.04)	1.06	1.04	1.02-1.05 (1.04 ± 0.02)	1.02-1.03 (1.02)	1.05	1.01-1.03 (1.02)	1.05	1.01-1.03 (1.02)	1.05
SEL/HL	0.43	0.52	0.41-0.45 (0.43 ± 0.01)	0.44-0.47 (0.45 ± 0.01)	0.45	0.45	0.43-0.45 (0.44)	0.40	0.46	0.46-0.48 (0.47 ± 0.01)	0.45-0.46 (0.46)	0.49	0.49-0.51 (0.50)	0.49	0.49-0.51 (0.50)	0.43
ALL/SVL	0.49	0.57	0.52-0.59 (0.55 ± 0.03)	0.54-0.60 (0.57 ± 0.02)	0.59	0.59	0.56-0.59 (0.58)	0.54	0.55	0.53-0.55 (0.54 ± 0.01)	0.52-0.53 (0.53)	0.58	0.49-0.57 (0.53)	0.58	0.49-0.57 (0.53)	0.50
SAL/SVL	0.39	0.38	0.36-0.40 (0.38 ± 0.01)	0.32-0.40 (0.36 ± 0.03)	0.34	0.31	0.34-0.36 (0.35)	0.36	0.39	0.37-0.42 (0.40 ± 0.03)	0.38-0.39 (0.39)	0.36	0.36-0.39 (0.38)	0.36	0.36-0.39 (0.38)	0.39
RUL/SVL	0.13	0.11	0.11-0.14 (0.13 ± 0.01)	0.11-0.13 (0.12 ± 0.01)	0.12	0.10	0.12	0.12	0.16	0.12-0.14 (0.14 ± 0.01)	0.13-0.14 (0.14)	0.11	0.13-0.14 (0.13)	0.11	0.13-0.14 (0.13)	0.14
HLL/SVL	0.55	0.47	0.48-0.55 (0.52 ± 0.02)	0.43-0.52 (0.49 ± 0.03)	0.43	0.38	0.40	0.47	0.55	0.48-0.53 (0.51 ± 0.03)	0.54-0.57 (0.56)	0.49	0.51-0.52 (0.52)	0.49	0.51-0.52 (0.52)	0.50
TFL/SVL	0.15	0.13	0.13-0.15 (0.14 ± 0.01)	0.13-0.15 (0.14 ± 0.01)	0.12	0.11	0.13	0.13	0.17	0.14-0.16 (0.15 ± 0.01)	0.14-0.16 (0.15)	0.13	0.14	0.13	0.14	0.14
LTL/SVL	0.18	0.17	0.16-0.19 (0.17 ± 0.01)	0.15-0.19 (0.17 ± 0.01)	0.15	0.14	0.13-0.14 (0.14)	0.16	0.19	0.16-0.20 (0.19 ± 0.02)	0.20	0.19	0.16-0.20 (0.18)	0.19	0.16-0.20 (0.18)	0.19
HLL/ALL	1.11	0.83	0.86-0.99 (0.93 ± 0.04)	0.71-0.94 (0.85 ± 0.08)	0.74	0.64	0.69-0.71 (0.70)	0.87	0.99	0.89-1.01 (0.96 ± 0.06)	1.03-1.09 (1.06)	0.85	0.89-1.05 (0.97)	0.85	0.89-1.05 (0.97)	0.99