A New Species of the Genus *Scincella* Mittleman, 1950 (Squamata: Scincidae) from Sichuan Province, Southwest China, with a Diagnostic Key of *Scincella* Species in China

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Abstract The genus *Scincella* Mittleman, 1950 of the family Scincidae currently includes 38 species. To date, however, taxonomic assessment remains challenging. Here, phylogenetic analyses based on DNA sequences of four mitochondrial genes supported a putative new species from Sichuan Province, Southwest China, as an independent lineage. Uncorrected genetic distance of 16S rRNA between the new species and closest congener was 8%, and the population was morphologically distinguishable from all other known congeners. We herein describe the *Scincella* population as a new species based on both phylogeny and comparative morphology. The new species can be distinguished from its congeners by a combination of the following morphological characters: (1) body slender, medium-sized, snout-vent length 35.0–62.1 mm; (2) infralabials seven, rarely eight; (3) supraciliaries 5–7; (4) tympanum deeply sunk without lobules; (5) midbody scale-row counts 27–30; (6) dorsal scales smooth and enlarged, paravertebral scale-row counts 60–75, ventral scale-row counts 46–59, gulars 25–30; (7) upper edge of lateral longitudinal stripes relatively straight with six rows of dorsal scales in middle; (8) number of enlarged, undivided lamellae beneath finger IV 9–11, number of enlarged, undivided lamellae beneath toe IV 13–16; (9) ventral side of tail densely ornamented with dark brown or black spots; and (10) grayish-brown discontinuous regular dorsal stripes 5–7, distinct black dorsolateral stripes, starting from posterior corner of eye and continuing to lateral side of tail. A diagnostic key to all *Scincella* members from China is also provided. The new species is currently only known from Wenchuan and Lixian counties, Sichuan Province, China, and brings the number of *Scincella* species in China to 12. This study emphasizes the incompleteness of knowledge on herpetodiversity in China.

1. Introduction

The family Scincidae is one of the most diverse groups of lizards globally, currently containing 164 genera and 1 743 species (Uetz *et al.*, 2022). The smooth skink genus *Scincella* Mittleman in Scincidae contains 38 species, with fragmented distribution across the North American continent (five species) to Japan, Korean Peninsula, China, and Southeast Asia (Ouboter, 1986; Uetz *et al.*, 2022). These terrestrial skinks are commonly found in forests among weeds near streams and in hillside fragments, as well as hot-dry valleys in the Hengduan Mountains. Species within the genus are characterized by their small size, elongated body, short limbs, relatively long tail, smooth subcycloid scales (most species), small oblong head with transparent disc in a movable lower eyelid, absence of supranasals, pentadactyl hindlimbs, one row of basal subdigital lamellae (most species),

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median preanals overlapping lateral ones, four or more scales bordering the parietals between the upper secondary temporals, and lower secondary temporal overlapping the upper one (Greer and Shea, 2003; Lim, 1998; Nguyen *et al.*, 2010a; Nguyen *et al.*, 2010b; Nguyen *et al.*, 2010c).

The phylogenetic relationships between *Scincella* and many other Southeast Asian lygosomine skinks remain unresolved due to their many morphological similarities (e.g., Nguyen *et al.*, 2010a, 2010b). Based on examination of museum specimens, Ouboter (1986) undertook a major revision of *Scincella*, resulting in many synonymies. Morphological similarity and taxonomic uncertainty have hindered progress in the systematics of smooth skinks, with only a few species described in the past two decades, including five taxa discovered from Vietnam (Darevsky *et al.*, 2004; Nguyen *et al.*, 2019, 2020; Nguyen *et al.*, 2010a, 2010c), one from Cambodia (Neang *et al.*, 2018), one from Mexico (García-Vázquez *et al.*, 2010), and one from Japan (Koizumi *et al.*, 2022). In China, the genus is currently represented by 11 species, including *S. barbouri* (Stejneger, 1925), *S. doriae* (Boulenger, 1887), *S. formosensis* (Van Denburgh, 1912), *S. monticola* (Schmidt, 1925), *S. huanrenensis* Zhao and Huang, 1982, *S. modesta* (Günther, 1864), *S. potanini* (Günther, 1896), *S. przewalskii* (Bedriaga, 1912), *S. reevesii* (Gray, 1838), *S. schmidti* (Barbour, 1927), and *S. tsinlingensis* (Hu, 1966). Although Wang and Zhao (1986) reviewed *Scincella* in China, generic diversity remains understudied.

From 2004 to 2020, a total of 14 *Scincella* specimens were collected from Wenchuan and Lixian counties in Sichuan Province, China (Figure 1). These specimens most closely resembled *S. potanini*, *S. monticola*, and *S. tsinlingensis*, but differed from the latter three species and all other known *Scincella* members. Phylogenetic analyses based on mitochondrial DNA and morphological comparisons suggested that the *Scincella* specimens from Wenchuan and Lixian counties in Sichuan Province were distinct, which we herein describe as a new species.

2. Materials and Methods

2.1. Sampling A total of 50 specimens were examined in this study. All newly collected specimens were fixed in 10% buffered formalin and later transferred to 75% ethanol for preservation. Liver and muscle tissues used for molecular analysis were preserved in 95% alcohol at −20℃. All specimens were deposited in the Herpetological Museum, Chengdu Institute of Biology (CIB), Chinese Academy of Sciences, Chengdu City, Sichuan Province, China.

2.2. DNA extraction, polymerase chain reaction (PCR), and sequencing Genomic DNA was extracted from liver and muscle tissues using a DNA extraction kit (Sangon Biotech, Shanghai, China). Partial fragments of mitochondrial non-coding regions (i.e., mitochondrial 16S rRNA (16S), 12S rRNA (12S), cytochrome b (Cyt *b*), and cytochrome oxidase I (COI) were amplified using the primers listed in Table 1. A 25-μl reaction was set for bi-directional PCR, containing 12.5 μl of Thermo Scientific DreamTaq PCR Master Mix, 9.5 μl of molecular grade
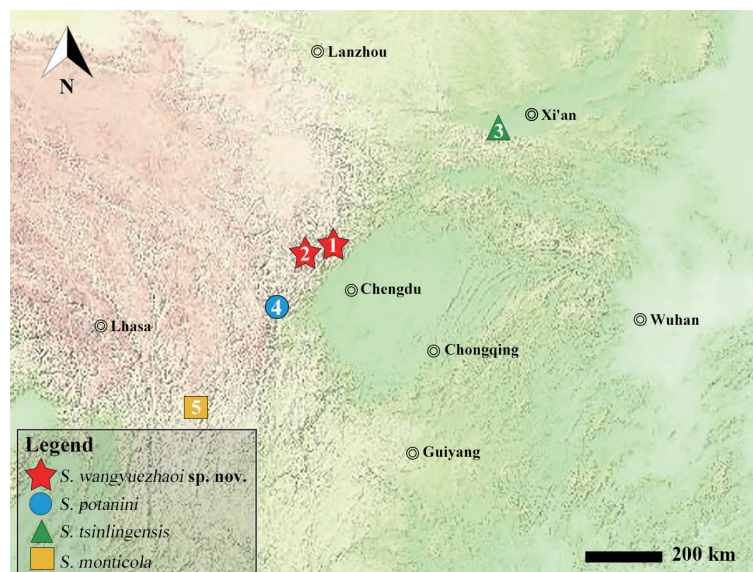

Figure 1 Sampling localities and distribution of the *Scincella wangyuezhaoi* **sp. nov.**, *S. potanini*, *S. monticola*, and *S. tsinlingensis* in China. 1. Wenchuan County, Sichuan Province; 2. Lixian County, Sichuan Province; 3. Zhouzhi County, Shaanxi Province; 4. Kangding County, Sichuan Province; 5. Shangri-La County, Yunnan Province.

water, 1 μl of each 10 μM primer, and 1 μl of template DNA, carried out using an Applied Biosystems ProFlex PCR System. Thermocycling profiles for amplification were as follows: initial denaturation step at 95°C for 5 min, 36 cycles of denaturation at 95°C for 40 s, annealing for 40 s (see Table 1 for annealing temperatures), extension at 72°C for 1 min, and final extension at 72°C for 10 min, with maintenance at 10°C. The PCR products were sequenced on an ABI Prism 3 730 automated DNA sequencer by Chengdu TSINGKE Biological Technology Co. Ltd. (Chengdu, China). All newly generated sequences were deposited in GenBank (Table 2). Homologous DNA sequences of voucher specimens of related species were downloaded from GenBank and included in phylogenetic analysis.

2.3. Phylogenetic analyses For molecular analysis, *Sphenomorphus cryptotis* Darevsky, Orlov, and Cuc, 2004 was selected as an outgroup to root the tree based on Pyron *et al.* (2013) (Table 2). Four mitochondrial genes from 11 muscle and liver samples were newly sequenced in this study, and 58 sequences were downloaded from GenBank, representing 42 individuals and 20 *Scincella* species (including our putative new species). Details on these materials are shown in Table 2.

Initial nucleotide sequences were manually verified using SeqMan (Skwor, 2012), then combined with data from GenBank. Sequences were aligned in MEGA X (Kumar *et al.*, 2018) using ClustalW (Thompson *et al.*, 1997) with default settings. The sequences were concatenated using PhyloSuite v.1.2.2 (Zhang *et al.*, 2020). For optimal partitioning strategies and evolutionary substitution models, the aligned data were analyzed using PartitionFinder v.2.1.1 (Lanfear *et al.*, 2012), implementing a greedy search algorithm under Akaike Information Criterion (AIC). Phylogenetic trees were constructed using both maximum-likelihood (ML) and Bayesian inference (BI) approaches. Analysis suggested that the best partition scheme was 12S/16S/COI/Cyt *b* fragments. The GTR + I + G model was selected as the best model for 12S rRNA, 16S rRNA, COI, and Cyt *b*. ML analysis was performed using RAxML v.8.2.10 (Stamatakis, 2014) with the above selected model and 1000 bootstrap pseudoreplicates. BI

analysis was implemented in MrBayes v.3.2.6 (Ronquist and Huelsenbeck, 2003) and run for 600 million generations, with sampling every 100 generations. Once the standard deviation of split frequencies reached < 0.01, analysis was not continued. In total, 25% of generated trees were discarded as burn-in. Tree nodes were considered well supported at a Bayesian posterior probability (BPP) ≥ 0.95 and ML ultrafast bootstrap support (BS) ≥ 95 space (Felsenstein, 2004; Hillis and Bull, 1993). Trees were visualized using FigTree v.1.4.3 (Rambaut, 2012). Uncorrected *p*-distances for 16S were calculated using default parameters in MEGA X (Kumar *et al.*, 2018).

2.4. Morphological analysis Morphometric data were taken from 46 well-preserved specimens (voucher information is provided in Table 2). Measurements were recorded to the nearest 0.1 mm with digital calipers by Ru-Wan Jia following Zhao *et al.* (1999), Wang and Zhao (1986), Nguyen *et al.* (2010c), Neang *et al.* (2018), and Nguyen *et al.* (2019). A total of 44 morphological characteristics were measured, including: **SVL** = snout-vent length (distance from tip of snout to posterior edge of vent); **TaL** = tail length (distance from posterior margin of vent to tip of tail); **TaW** = tail width (widest section of tail posterior to hemipenial bulge); **TaD** = tail depth (ventral to dorsal surface of tail); **AGD** = axilla-groin distance (distance between posterior edge of forelimb insertion and anterior edge of hindlimb insertion); **MBW** = midbody width (measured from lateral surface to opposing lateral edge at midpoint of axilla-groin region); **MBD** = midbody depth (measured from ventral surface to dorsal surface at midpoint of axilla-groin region); **HL** = head length (distance from the tip of the snout to the articulation of jaw); **HW** = maximum head width (greatest width between the left and right articulations of jaw); **HD** = head depth (measured from ventral to dorsal surface of head at jaw articulations); **ED** = eye diameter (maximum horizontal diameter of eye); **PDD** = palpebral disc diameter (maximum horizontal diameter of palpebral disc); **TD** = tympanum diameter (ear opening diameter, maximum diameter of ear); **END** = eye-narial distance (from anterior margin of eye to posterior margin of nare); **SNL** = snout length (distance from the tip of the snout to

Table 1 Details of primers used for PCR amplification and sequencing.

DNA marker	Primer name	Primer sequence (5′–3′)	Annealing temperature	Reference
12S	L1091-F	AAACTGGGATTAGATACCCCACTAT	55.0°C	Kocher *et al.*, 1989
	H1478-R	GAGGGTGACGGGCGGTGTGT		
16S	16SL-F	TGTTTACCAAAAACATAGCCTTTAGC	49.0°C	Linkem *et al.*, 2011
	16SL-R	TAGATAGAAACCGACCTGGATT		
Cyt *b*	L14724-F	GACTTGAAAAACCACCGTTG	50.0°C	Xiao *et al.*, 2001
	Ei700r-R	GGGGTGAAAGGGGATTTT(AG)TC		
COI	RepCOI-F	TNTTMTCAACNAACCACAAAGA	48.5°C	Nagy *et al.*, 2012
	RepCOI-R	ACTTCTGGRTGKCCAAARAATCA		

Table 2 Localities, voucher information, and GenBank accession numbers for all samples used in this study. CBC = Centre for Biodiversity Conservation; CIB = Herpetological Museum, Chengdu Institute of Biology, Chinese Academy of Sciences; DCC = David Cannatella field number; DL = Dr. Li Ding's personal catalogue numbers; ITBCZ = Institute of Tropical Biology Collection of Zoology; KU = University of Kansas Biodiversity Institute; KUZ = Zoological Collection, Kyoto University Museum; XM = Dr. Xiao-Mao Zeng's personal catalogue numbers; ZFMK = Zoologisches Forschungsmuseum Alexander Koenig; ZMMU = Zoological Museum of Moscow University.

Species	Locality	Voucher ID	16S	12S	COI	Cyt *b*
Scincella wangyuezhaoi **sp. nov.**	China: Sichuan, Wenchuan	CIB 87246	OP941172	OP942191	OQ402205	-
Scincella wangyuezhaoi **sp. nov.**	China: Sichuan, Lixian	CIB 119518	OP941173	OP942193	-	-
Scincella wangyuezhaoi **sp. nov.**	China: Sichuan, Lixian	CIB 119510	OP941174	OP942192	OQ402206	-
Scincella monticola	China: Yunnan, Shangri-La	DL-YNJC2020824	OP955962	OP955952	-	-
Scincella potanini	China: Sichuan, Kangding	DL-KD202109071	OP935937	OP942203	OP942210	OQ448540
Scincella potanini	China: Sichuan, Kangding	DL-KD202109072	OP935987	OP942208	OP942209	-
Scincella potanini	China: Sichuan, Kangding	DL-KD2018070302	OP935989	OP942204	OP942211	OQ448542
Scincella potanini	China: Sichuan, Kangding	XM6920	OP935998	OP942205	OP942212	OQ448543
Scincella huanrenensis	Korea: Gangwon-do, Pyeongchang-gun	-	NC030779	NC030779	NC030779	NC030779
Scincella huanrenensis	Korea: Gangwon-do, Pyeongchang-gun	G390SH	KU507306	KU507306	KU507306	KU507306
Scincella vandenburghi	Korea: Yeongwol-gun	-	NC030776	NC030776	NC030776	NC030776
Scincella vandenburghi	Korea: Yeongwol-gun	G389SV	KU646826	KU646826	KU646826	KU646826
Scincella modesta	China: Hubei, Yichang	CIB 119023	OP942189	OP942202	OP942213	OQ448538
Scincella modesta	China: Hubei, Yichang	CIB 119024	-	OP942207	OP942214	OQ448539
Scincella modesta	China: Jiangsu, Nanjing	NB2017030715	MN702771	MN702771	MN702771	MN702771
Scincella modesta	China: Jiangsu, Nanjing	No. 0216	NC048521	NC048521	NC048521	NC048521
Scincella reevesii	China: Guangdong, Zhaoqing	NC054206	NC054206	NC054206	NC054206	-
Scincella reevesii	China: Guangdong, Zhaoqing	-	MN832615	MN832615	MN832615	-
Scincella lateralis	-	KU 289460	JF498077	JF497948	-	-
Scincella lateralis	USA: Texas	DCC 2842	HM852503	HM852476	-	-
Scincella cherriei	-	-	JF498076	JF497947	-	-
Scincella assatus	-	KU 289795	JF498074	JF497946	-	-
Scincella assatus	-	KU 291286	JF498075	-	-	-
Scincella gemmingeri	-	-	AY308294	-	-	-
Scincella rufocaudata	Vietnam: Ha Tinh	ZFMK 76239	HM773217	-	-	-
Scincella rufocaudata	Vietnam: Ha Tinh	ZFMK 76238	HM773216	-	-	-
Scincella rupicola	Thailand	KUZ 40458	AB057403	AB057388	-	-
Scincella nigrofasciata	Vietnam: Ba Ria-Vung Tau, Dinh Mountain	ITBCZ 6344	-	-	MK990605	-
Scincella nigrofasciata	Cambodia: Mondulkiri, Keo Seima W.S.	CBC 02546	-	-	MH119614	-

Continued Table 2

Species	Locality	Voucher ID	16S	12S	COI	Cyt *b*
Scincella badenensis	Vietnam: Tay Ninh, Ba Den Mountain	ITBCZ 5966	-	-	MK990602	-
Scincella badenensis	Vietnam: Tay Ninh, Ba Den Mountain	ITBCZ 5993	-	-	MK990603	-
Scincella melanosticta	Vietnam: Gia Lai, Kon Chu Rang N.R.	ZMMU NAP-06376	-	-	MH119622	-
Scincella melanosticta	Vietnam: Gia Lai, Kon Chu Rang N.R.	ZMMU NAP-05519	-	-	MH119621	-
Scincella doriae	Vietnam: Lam Dong, Bidoup - Nui Ba N.P.	ZMMU R-13268-01062	-	-	MH119617	-
Scincella doriae	Vietnam: Lam Dong, Bidoup - Nui Ba N.P.	ZMMU R-13268-00412	-	-	MH119616	-
Scincella baraensis	Vietnam: Binh Phuoc	ITBCZ 6534	-	-	MT742256	-
Scincella baraensis	Vietnam: Binh Phuoc	ITBCZ 6536	-	-	MT742258	-
Scincella formosensis	China: Taiwan	KUZ R37516	-	-	-	AB818818
Scincella formosensis	China: Taiwan	KUZ R46902	-	-	-	AB818831
Scincella boettgeri	Southern-Ryukyu Islands	KUZ R68007	-	-	-	AB818798
Scincella boettgeri	Southern-Ryukyu Islands	KUZ R68006	-	-	-	AB818797
Sphenomorphus cryptotis	China: Guangxi, Shangsi	CIB 119027	OP942190	OP942206	OP942215	OQ448544

the anterior corner of eye); **IND** = internasal distance (minimum distance between the inner margins of the external nares); **IOD** = interorbital distance (minimum distance between the inner edges of the upper eyelids); **FLL** = forelimb length (measured from forelimb insertion to tip of finger IV or longest digit); **HLL** = hind-limb length (measured from hind-limb insertion to tip of toe IV or longest digit); **T4L** = toe IV length (measured from the most basal part to tip of toe IV); **F4L** = finger IV length (measured from the most basal part to tip of finger IV); **MBSR** = midbody scale-row count (number of longitudinal scale rows measured around widest point of midbody); **DBR** = dorsal scale rows between dorsolateral stripes (number of dorsal scale rows at midbody between dark dorsolateral stripes, following Inger *et al.* (1990)); **NU** = enlarged, differentiated nuchal count (X pairs or absence); **PVSR** = paravertebral scale-row count (number of scale rows counted between parietals and the just posterior margin of hindlimbs); **VSR** = ventral scale-row count (number of scale rows counted between gulars and precloacals); **L** = loreal count (left/right); **AGSR** = axilla-groin scale-row count (number of scale rows counted between posterior edge of forelimb insertion and anterior edge of hind-limb insertion); **SL** = supralabial count (left/right); **IfL** = infralabial count (left/right); **SC** = superciliary count (left/right); **SO** = supraocular count (left/right); **TEM** = enlarged temporal count (left/right); **FTSR** = scale-row on the dorsal surface of the finger and toe (single or paired); **F4S** = number of enlarged, undivided lamellae beneath finger IV (left/right); **T4S** = number of enlarged, undivided lamellae beneath toe IV (left/right); **MT** = maxillary teeth count (left only); **LT** = lower teeth count (left only); **PF** = prefrontals in contact with each other (Yes: in contact/No: not in contact/absence); **FP** = frontoparietals in contact with each other (Yes: in contact/No: not in contact/absence); **P** = parietals in contact with each other (Yes: in contact/No: not in contact/absence); **chin-shields** = paired large scales behind mental or postmentals); **gulars** = many minor scales in the center of the ventral head (number of scale rows counted between the first scale behind the chin-shields and the middle of the forelimb); **limbs adpressed** = toes overlap/in contact/not in contact with fingers when limbs adpressed. Values of paired characters were recorded in left to right order. Nomenclature for head shields followed Smith (1935).

Morphological data used for comparisons were taken from previously published literature: i.e., Taylor (1963); Darevsky and Nguyen (1983); Ouboter (1986); Wang and Zhao (1986); Darevsky and Orlov (1997); Zhao *et al.* (1999); Gonzalez *et al.* (2005); Stuart and Emmett (2006); Stuart *et al.* (2006); Nguyen *et al.* (2010a); Nguyen *et al.* (2010c); Pham *et al.* (2015); Neang *et al.* (2018); and Nguyen *et al.* (2019). Some morphological data that have not been used prior to the study, such as PDD, F4L, VSR, gulars, AGSR, and F4S, are provided (Table 3). To reduce the impact of

allometry, a size-corrected value of the ratio of each character to SVL was calculated for morphometric analyses. We conducted principal component analysis of size-corrected variables and simple bivariate scatterplots using our morphometric data with Origin 2021 (OriginLab, Northampton, USA) to test the morphological separation between taxa and assess major loading components SVL, HL/SVL, HW/SVL, AGD/SVL, FLL/SVL, HLL/SVL, F4L/SVL, T4L/SVL, MBSR, DBR, PVSR, VSR, gulars, and AGSR were the major loading components recovered. These contributing characters were plotted using multivariate analysis. Differences were tested by comparing the new species to *S. potanini* and *S. monticola*. Statistical analysis was carried out with a normalized dataset using Z scores.

3. Results

3.1. Phylogenetic analyses and genetic divergence
The ML and BI phylogenetic trees were constructed based on four mitochondrial genes (12S, 385 bp; 16S, 480 bp; Cyt *b*, 611 bp; COI, 556 bp) from 21 species, with a total length of 2 032 bp. Both the ML and BI analyses resulted in a largely identical topology (Figure 2).

Overall, four major matrilines were resolved. The skinks from Southwest China were nested within the genus *Scincella* and were distinct from their congeners, which formed a highly isolated and monophyletic clade with unresolved internal relationships. The new taxon was sister clade to ((*S. vandenburghi* + *S. modesta*) + (*S. boettgeri* + *S. formosensis*)), with relatively low node support (BPP = 29; BS = 0.51; Figure 2).

The uncorrected inter- and intraspecific *p*-distances are shown in Table 4. The *Scincella* specimens from Wenchuan and Lixian, Sichuan, showed low genetic distance, with intraspecific genetic divergences ranging from 0.0%–1.0%, but differed substantially from other congeners, with interspecific genetic divergences ranging from 8.0% (vs. *S. monticola* and *S. vandenburghi*) to 11.0% (vs. *S. reevesii* and *S. rupicola*) (Table 4). The 16S rRNA genetic distance between the putative new species and closely related *S. monticola* and *S. vandenburghi* was 8%, greater than the distance that typically represents species differentiation in lizards (> 3%) (Vences *et al.*, 2005).

3.2. Morphological analyses
The putative new species was most similar to *S. potanini* and *S. monticola*. However, based on morphological comparisons (Table 5), the new species differed significantly from *S. potanini, S. monticola*, and all other species, especially in the MBSR, DBR, gulars, and T4S characters. The new species was also distinguished based on PCA (Figure 3), with the PC1 and PC2 eigenvectors accounting for 42.6% and 16.2% of the variance, respectively (58.8% cumulatively). As illustrated in the PC1 and PC2 scatter plots, samples of each species were clustered together. The new species did not

overlap with any other species, while *S. potanini* and *S. monticola* clustered together and could not be separated.

Our analysis demonstrated that the new species from Wenchuan and Lixian was distinct from all other described *Scincella* species based on both morphological characters and phylogenetic analysis. Thus, we describe the population from Wenchuan and Lixian, Sichuan, as a new species herein.

3.3. Taxonomic account
Scincella wangyuezhaoi sp. nov. Jia, Ren, Jiang, & Li (Figures 4–6, 7A)

Chresonymy *Scincella potanini* — Shi and Zhao 1980: 135 (in part); Zhao 2003: 115 (in part).

Holotype CIB 87244 (field no. ZL0013) (Figures 5–6), adult female, collected from Shapai Village, Caopo Town, Wenchuan County, Sichuan Province, China; coordinates 31°18.845′ N, 103°19.364′ E; elevation 1 900 m a.s.l., by Cheng Li on 30 May 2004.

Paratypes Six individuals were collected from the same locality as the holotype: CIB 87247 and CIB 87250, adult males, and CIB 87245, CIB 87246, CIB 87248, and CIB 87249, adult females; coordinates 31°18.845′ N, 103°19.364′ E; elevation 1 900 m a.s.l.; collected on 30–31 May 2004 by Cheng Li. Seven specimens were collected from Shuluogou, Lixian County, Sichuan Province, China; CIB 119509, CIB 119512, CIB 119515, and CIB 119518, adult males, CIB 119516 and CIB 119519, adult females, and CIB 119510, juvenile; coordinates 31°23.356′ N, 103°49.154′ E; elevation 2 818 m a.s.l.; collected on 30 May 2020 by Xiao-Mao Zeng, Jun Ping, Jin-Long Liu, Xing-Zhong Wang, and Ze-Zhong Li.

The holotype and 13 paratypes are preserved in the Herpetological Museum, Chengdu Institute of Biology (CIB), Chinese Academy of Sciences, Chengdu, Sichuan, China.

Etymology This species epithet "*wangyuezhaoi*" is named after Professor Yue-Zhao Wang in recognition of his research on Chinese amphibians and reptiles and his continuous support of young herpetologists in China. We propose "Wenchuan's Ground Skink" as the common English name and "wèn chuān huá xī (汶川滑蜥)" as the Chinese name.

Diagnosis *Scincella wangyuezhaoi* **sp. nov.** is assigned to the genus *Scincella* Mittleman, 1950 based on molecular phylogenetic analyses and the following morphological characteristics: (1) body slender, snout short and blunt; (2) prefrontals and frontoparietals normal but not healed; (3) eyelids developed, lower eyelids with transparent eyelid window, no postnasal; (4) first enlarged nuchals obliquely connected to parietals; (5) one pair of enlarged cloacal scales; and (6) scales with limbs, toes five, 4th toe dorsal surface rows two (Wang and Zhao, 1986; Zhao *et al.*, 1999).

Scincella wangyuezhaoi **sp. nov.** can be distinguished from all other congeners by the following combination of morphological

Table 3 Morphometric and meristic characters of *Scincella wangyuezhaoi* **sp. nov.** All units are in mm. "*" = tail incomplete. Abbreviations of morphological characters are provided in Materials and Methods section.

Specimen number	Holotype	Paratypes													Min−Max
	CIB87244	CIB87245	CIB87246	CIB87247	CIB87248	CIB87249	CIB87250	CIB 119510	CIB 119512	CIB 119515	CIB 119516	CIB 119518	CIB 119519	CIB 119509	
Sex	Female	Female	Female	Male	Female	Female	Male	juvenile	Male	Female	Female	Male	Male	Male	
SVL	61.0	37.7	58.7	48.2	51.9	52.3	50.4	30.1	55.5	62.1	57.9	41.6	37.3	35.0	30.1−61.0
TaL	71.7	37.5	27.6+	25.2	65.4	68.0+	33.3	–	81.6	51.3+	–	51.9	–	–	
Primary tail	Yes	Yes	*	Yes	Yes	*	Yes	*	Yes	*	*	Yes	*	*	
TaW/SVL	0.09	0.13	0.09	0.10	0.08	0.10	0.09	0.09	0.09	0.09	0.09	0.09	0.11	0.08	0.08−0.13
TaD/SVL	0.09	0.11	0.08	0.09	0.08	0.11	0.08	0.06	0.08	0.09	0.09	0.09	0.09	0.11	0.06−0.11
HL/SVL	0.16	0.25	0.17	0.18	0.15	0.16	0.14	0.21	0.16	0.16	0.16	0.18	0.19	0.19	0.14−0.25
HW/SVL	0.14	0.21	0.14	0.15	0.14	0.14	0.14	0.13	0.10	0.12	0.12	0.13	0.13	0.13	0.10−0.21
HD/SVL	0.11	0.15	0.10	0.12	0.10	0.10	0.10	0.09	0.09	0.09	0.09	0.11	0.12	0.12	0.09−0.15
ED/SVL	0.04	0.06	0.04	0.03	0.04	0.04	0.05	0.03	0.04	0.03	0.04	0.05	0.06	0.06	0.03−0.06
PDD/SVL	0.02	0.04	0.02	0.03	0.02	0.02	0.02	0.02	0.02	0.01	0.02	0.02	0.02	0.02	0.01−0.04
TD/SVL	0.03	0.03	0.02	0.03	0.03	0.03	0.03	0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02−0.03
PDD/TD	1.74	0.92	1.22	1.10	1.48	1.53	1.38	1.08	0.87	1.40	1.49	1.00	1.14	0.95	0.87−1.74
END/SVL	0.05	0.08	0.05	0.05	0.05	0.06	0.06	0.05	0.04	0.04	0.05	0.05	0.05	0.05	0.04−0.08
SNL/SVL	0.07	0.12	0.07	0.07	0.08	0.08	0.09	0.07	0.06	0.06	0.07	0.07	0.08	0.07	0.06−0.12
IND/SVL	0.05	0.07	0.05	0.05	0.04	0.04	0.05	0.04	0.04	0.04	0.04	0.04	0.05	0.04	0.04−0.07
IOD/SVL	0.08	0.11	0.10	0.08	0.08	0.08	0.07	0.08	0.07	0.06	0.07	0.09	0.11	0.10	0.06−0.11
MBW/SVL	0.20	0.29	0.16	0.16	0.17	0.16	0.18	0.14	0.16	0.18	0.15	0.14	0.15	0.15	0.14−0.29
MBD/SVL	0.17	0.20	0.13	0.12	0.15	0.14	0.12	0.09	0.09	0.12	0.12	0.11	0.13	0.12	0.09−0.20
AGD/SVL	0.57	0.92	0.61	0.58	0.60	0.61	0.56	0.50	0.62	0.63	0.60	0.58	0.57	0.55	0.50−0.92
FLL/SVL	0.20	0.27	0.20	0.24	0.20	0.19	0.22	0.21	0.23	0.21	0.20	0.22	0.23	0.23	0.20−0.27
HLL/SVL	0.28	0.43	0.24	0.29	0.27	0.29	0.28	0.36	0.31	0.28	0.26	0.34	0.25	0.29	0.24−0.43
F4L/SVL	0.06	0.10	0.06	0.06	0.06	0.06	0.06	0.06	0.07	0.06	0.06	0.06	0.06	0.06	0.06−0.10
T4L/SVL	0.10	0.17	0.10	0.12	0.10	0.12	0.11	0.09	0.11	0.11	0.11	0.12	0.06	0.11	0.06−0.17
NU left/right	3/3	3/3	3/3	3/3	4/4	2/3	3/4	2/2	3/2	4/3	2/2	3/3	3/2	2/2	2−3/2−4
SL left/right	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7	7/7
IfL left/right	7/6	7/7	7/6	6/7	7/7	6/6	7/7	7/7	6/7	7/7	6/6	7/7	7/7	7/7	6−7/6−7
SC left/right	7/7	6/6	5/5	7/7	7/7	7/7	7/6	6/6	6/6	6/6	6/6	6/6	6/6	6/6	5−7/5−7
SO left/right	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4
TEM left/right	2/2	2/2	1+2/1+2	2+3/2+3	2+2/1+2	2+3/2+3	2/2	1+2/1+2	1+2/1+2	1+2/1+2	2+2/2+2	1+2/1+2	2+2/2+2	1+2/1+2	
L left/right	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2	2/2
Chin-shields	3	3	3	3	3	3	3	3	3	3	3	3	3	3	3
Postnasals	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Continued Table 3

Character	Holotype	Paratypes												Min–Max
Postmental	1	1	1	1	1	1	1	1	1	1	1	1	1	1
Enlarged cloacal scales (pair)	1	1	1	1	1	1	1	1	1	1	1	1	1	1
MBSR	28	30	29	30	27	27	27	28	28	28	28	28	28	27–30
DBR	6	6	6	6	6	6	6	6	6	6	6	6	6	6
PVSR	66	65	60	70	66	66	70	74	74	72	70	75	68	60–75
VSR	49	51	47	56	51	46	50	54	59	54	59	56	52	46–59
Gulars	25	26	26	30	26	28	26	25	25	25	25	25	25	25–30
AGSR	60	76	54	77	68	53	58	78	76	72	70	70	66	53–78
FTSR	2	2	2	2	2	2	2	2	2	2	2	2	2	2
F4S left/right	10/10	9/9	14/13	10/10	9/9	10/10	11/11	11/11	11/10	11/11	10/10	10/10	10/10	9–11/9–11
T4S left/right	–/14	–/15	14/13	–/14	14/14	14/8+	15/15	15/15	15/13	15/16	14/15	–/13	15/15	14–15/13–16
MT	20	26	18	20	19	16	14	18	22	22	15	18	18	14–26
LT	22	20	20	18	19	21	12	16	20	22	19	16	16	16–22
PF	Yes	Yes	Yes	Yes	Yes	Yes	Yes	No	Yes	Yes	No	No	No	
FP	Yes	Yes	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	
P	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	
Limbs adpressed	No	No	in contact	No	No	No	No	No	No	No	No	No	No	

characters: (1) body slender, medium-sized, snout-vent length 35.0–62.1 mm; (2) infralabials seven, rarely eight; (3) supraciliaries 5–7; (4) tympanum deeply sunk without lobules; (5) midbody scale-row counts 27–30; (6) dorsal scales smooth and enlarged, paravertebral scale-row counts 60–75, ventral scale-row counts 46–59, gulars 25–30; (7) upper edge of lateral longitudinal stripes relatively straight with six rows of dorsal scales in middle; (8) number of enlarged, undivided lamellae beneath finger IV 9–11, number of enlarged, undivided lamellae beneath toe IV 13–16; (9) ventral side of tail densely ornamented with dark brown or black spots; and (10) grayish-brown discontinuous regular dorsal stripes 5–7, distinct black dorsolateral stripes, starting from posterior corner of eye and continuing to lateral side of tail.

Description of holotype CIB 87244 (Figures 5–6): adult female, SVL 61.0 mm; snout short, obtuse; lower eyelid with undivided transparent disc; tympanum deeply sunk with prominent oblique edge; tail primary; head elongated, HL 9.7 mm (HL/SVL 0.16), longer than wide, HW 8.8 mm (HW/HL 0.90), slightly depressed, HD 6.4 mm (HD/HL 0.66); neck rather slender, slightly distinct from head; toes five, 4th toe dorsal surface rows two.

Head Snout rounded in profile and dorsal view, SNL 4.4 mm, more than twice as long as TD (1.8 mm); ear vertically oval, TD 1.8 mm; ED 2.5 mm; PDD 1.1 mm, proportion of palpebral disc and ear opening snout broad 0.58; END 3.1 mm; IND 2.9 mm, IOD 5.1 mm; snout broad, visible from above, in contact with 1st SL laterally, nasals and frontonasal posteriorly; MT 20, LT 16; supranasals absent; frontonasal broad, subtrapezoidal in shape, anterior side forming almost straight suture (0.6 mm) with rostral, posterior width 1.7 mm, as wide as rostral, slightly more than twice as wide as length (0.8 mm), in contact with nasals and 1st loreal laterally, posterior margin slightly touching prefrontals; prefrontals in slight contact, laterally bordered by two loreals, frontal posteriorly; frontal elongated, rhombus-shaped, posterior part much longer than anterior; frontal in contact with 1st and 2nd supraoculars laterally, frontoparietals posteriorly, anterior corner of rostral end slightly separating posterior portions of prefrontals medially, posterior corner of frontal slightly overlapping medial suture between frontoparietals; two frontoparietals in contact with each other, each diamond-shaped, together forming butterfly shape, in contact with 2nd, 3rd, and 4th supraoculars laterally, interparietal and parietals posteriorly; interparietal relatively small, rhombus-shaped, with posterior portion slightly longer than anterior, in contact with parietals posteriorly, anterior corner of interparietal acute, slightly intruding into median suture between frontoparietals; parietals large, in contact with each other posteriorly, narrowly contacting 4th supraocular and posterior supraciliary scale, in broad contact with upper secondary temporal laterally and enlarged nuchal scales
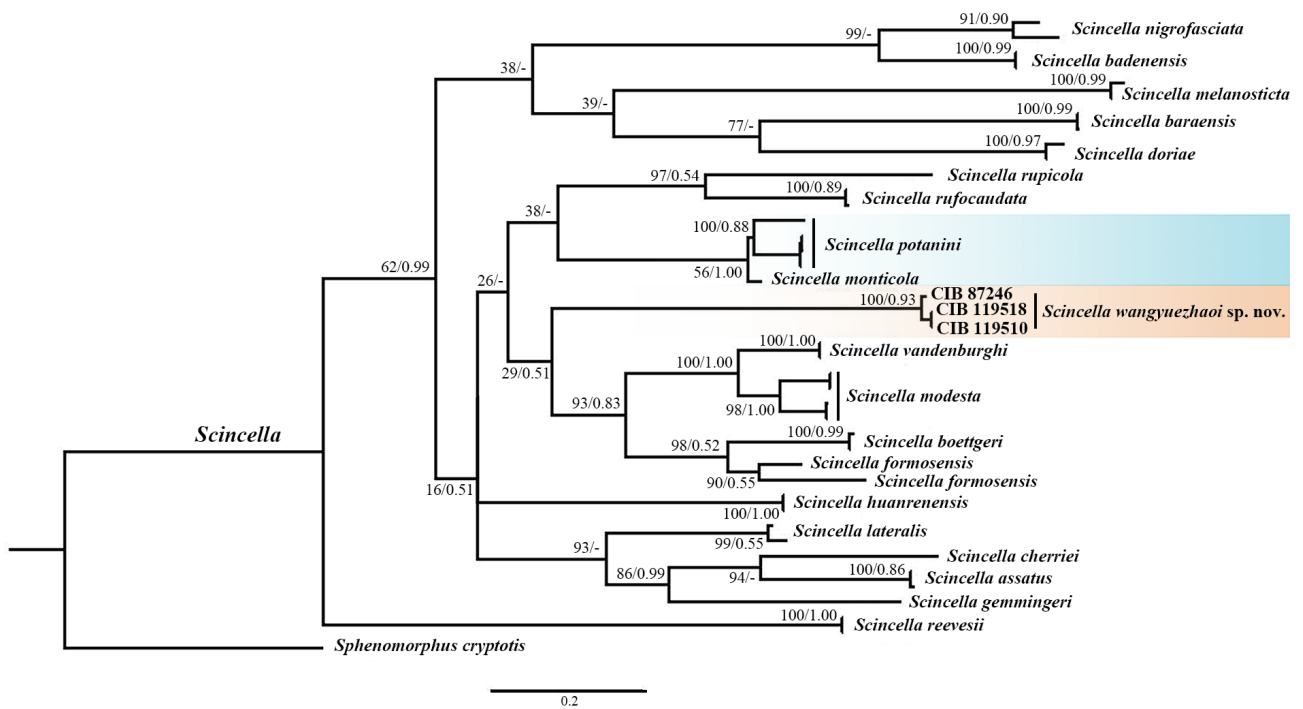
Table 5 Comparison of diagnostic morphometrics of *Scincella wangyuezhaoi* **sp. nov.** and three morphologically similar congeners from Southwest China.

Selected characters	*Scincella wangyuezhaoi* **sp. nov.** N = 14	*S. potanini* N = 14	*S. monticola* N = 4	*S. tsinlingensis* N = 10
SVL	35.0–62.1	26.6–57.9	36.3–52.9	44.0–57.4
TaW/SVL	0.08–0.13	0.07–0.11	0.07–0.10	0.08–0.11
TaD/SVL	0.06–0.11	0.07–0.10	0.08–0.10	0.09–0.10
HL/SVL	0.16–0.25	0.12–0.20	0.16–0.17	0.14–0.18
HW/SVL	0.10–0.21	0.09–0.16	0.13	0.11–0.13
HD/SVL	0.09–0.15	0.08–0.12	0.10–0.11	0.09–0.12
ED/SVL	0.03–0.06	0.03–0.05	0.04–0.05	0.04–0.05
PDD/SVL	0.01–0.04	0.01–0.03	0.02	0.02
TD/SVL	0.02	0.01–0.03	0.01–0.02	0.02
END/SVL	0.04–0.08	0.03–0.05	0.04–0.05	0.03–0.05
SNL/SVL	0.06–0.12	0.05–0.08	0.06–0.07	0.05–0.07
IND/SVL	0.04–0.07	0.03–0.05	0.04–0.05	0.03–0.04
IOD/SVL	0.06–0.11	0.06–0.10	0.07–0.08	0.07–0.09
MBW/SVL	0.14–0.29	0.09–0.20	0.11–0.16	0.13–0.19
MBD/SVL	0.09–0.20	0.09–0.13	0.10–0.16	0.12–0.15
AGD/SVL	0.50–0.92	0.52–0.72	0.56–0.65	0.58–0.70
FLL/SVL	0.20–0.27	0.11–0.25	0.13–0.19	0.18–0.22
HLL/SVL	0.24–0.43	0.17–0.31	0.20–0.22	0.24–0.30
F4L/SVL	0.06–0.10	0.03–0.06	0.03–0.05	0.05–0.07
T4L/SVL	0.06–0.17	0.05–0.10	0.05–0.07	0.09–0.11
NU left	2–4	3	3–4	2–4
SL left	7	7–8	7	7
IfL left	6–7	6–7	6–7	7–8
SC left	5–7	6–7	6–7	6–7
SO left	4	4	4	4
TEM left	1+2–2+3	1+2–2+2	1+2–2+2	1+2–2+3
Chin-shields (pair)	3	3	3	3
MBSR	27–30	24–27	23–24	26–28
DBR	6	4	4	4
PVSR	60–75	62–80	69–73	70–90
VSR	46–59	45–64	45–52	57–72
Gulars	25–30	23–25	22–24	23–28
AGSR	53–78	61–82	65–74	72–90
FTSR	2	2	2	2
F4S left	9–11	7–10	8–10	9–10
T4S left	14–15	10–13	10–12	13–16
MT left	14–26	9–20	14–20	18–26
LT left	16–22	10–18	12–19	16–22
PF	Yes/No	Yes/No	Yes	Yes/No
FP	Yes	Yes	Yes	Yes
P	Yes/No	Yes	Yes	Yes
Limbs adpressed	No/in contact	No	No	No

above by small palpebral scales; supralabials seven, 1st smallest, 5th located ventral to window of eye, 6th largest; infralabials seven (left) and six (right), 1st smallest, 5th largest, rectangular or pentagonal; primary temporals two, lower larger, sub-rhomboid, ventrally in contact with 5th and 6th SL, posteriorly in contact with lower secondary temporal, upper primary temporal sub-rhomboid, posteriorly in contact with both secondary temporals; secondary temporals two, lower smaller,
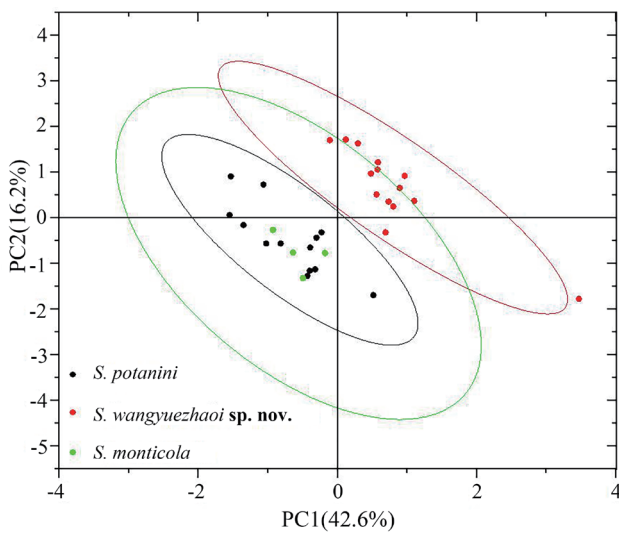
Figure 3 Scatter plot of PC1 and PC2 of principal component analysis based on the morphometric measurements, distinguishing the targeted new species and its closely related species. Red, black, and green plots represent *Scincella wangyuezhaoi* **sp. nov.**, *S. potanini*, and *S. monticola*, respectively.

Figure 4 Paratype of *Scincella wangyuezhaoi* **sp. nov.** (CIB 119518) in life. Photograph by Jinlong LIU, courtesy of Xiaomao ZENG.

broadly touching upper, in contact with 7th SL ventrally, upper secondary temporal about twice as large as lower, in contact with parietals dorsally and nuchal scales posteriorly; nuchal scales three, bordering posterior edge of parietals, relatively enlarged in comparison with adjacent posterior scales. Mental rounded, in contact with 1st IfL laterally, postmental posteriorly; postmental large, in contact with 1st and 2nd IfL laterally, 1st chinshield posteriorly; chinshield pairs three, 1st pair in broad contact medially with each other, contacting 2nd–3rd IfL laterally, 2nd pair separated by sub-triangular gular scale, contacting 3rd–4th IfL laterally, 3rd pair separated medially by three gular scales,

in contact with 5th–6th IfL laterally, three gular scales posteriorly; gulars 28.

Body, limbs, and tail Body relatively stout, SVL 61.0 mm; axilla groin relatively long, AGD 34.9 mm (AGD/SVL 0.57); MBW 12.4 mm (MBW/SVL 0.20), MBD 10.6 mm (MBD/SVL 0.17); primary tail relatively long, TaL 71.7 mm, TaL/SVL 1.17; tail width approximately equal to tail height: TaW 5.8 mm (TaW/SVL 0.09), TaD 5.2 mm (TaD/SVL 0.09); forelimbs short, FLL 12.2 mm (FLL/SVL 0.20); hindlimbs longer than forelimbs, HLL 17.2 mm (HLL/SVL 0.28).

Body scales smooth, cycloid, imbricate; dorsal scales significantly larger than ventral scales, slightly larger than those on lateral body and gular scales; scales on anterior flanks between tympanic region and posterior margin of axilla smaller than adjacent dorsal scales; MBSR 30; PVSR 63; VSR 43; AGSR 60; enlarged preanal scale pairs one, median scales overlapping outer scales; dorsal scale rows, longitudinal scale rows on dorsum between dorsolateral stripes 6+2(1/2); limbs pentadactyl, toes not in contact with fingers when limbs adpressed; digits slender, F4L 3.6 mm, T4L 6.4 mm; F4S 9 (left), F4S 10 (right), T4S 15 (left), T4S 14 (right).

Coloration in life In life, the female holotype CIB 87244 had the same color as male paratype CIB 119518 (Figure 4). Dorsal surface of head, dorsum, and base of tail dark bronze-brown, side of head between tip of snout and forelimb insertion light brown; dorsal surface of remaining tail reddish-brown. Dark broken irregular dorsal stripes anteriorly and on tail and posteriorly on body, formed by series of dark dots or elongated black spots, including wider dark paravertebral stripe; anterior part of dorsum with dorsal stripes formed by series of dots, posterior part of dorsum with dark dot-formed regular dorsal stripes reaching base of tail, continuing with dark stripes on dorsal surface of tail, extending about one-third of tail length; light laterodorsal stripes from behind eye, through temporals, along dorsolateral scale row to lateral sides of tail, and fading at one-third of tail length; large distinct irregular black longitudinal dorsolateral stripe on each side of body, covering two to three scale rows, starting as narrow stripe covering about one scale row, running from posterior corner of eye through upper temporals, above tympanum, expanding wider to two scale rows above axilla, running below light dorsolateral stripe, along upper flanks through upper angle of groin to lateral surface of tail, becoming indistinct at posterior lateral tail; body flanks ventrally with black longitudinal streaks on bluish-brown background; ventrolateral surfaces from below level of eye to axillary region with longitudinal whitish-grey streaks and dark marking on reddish-brown background; lateral surfaces of tail reddish-brown; dorsal surfaces of limbs with irregular dark blotches on dark brown background. Ventral surfaces of head, gular region, body, and limbs
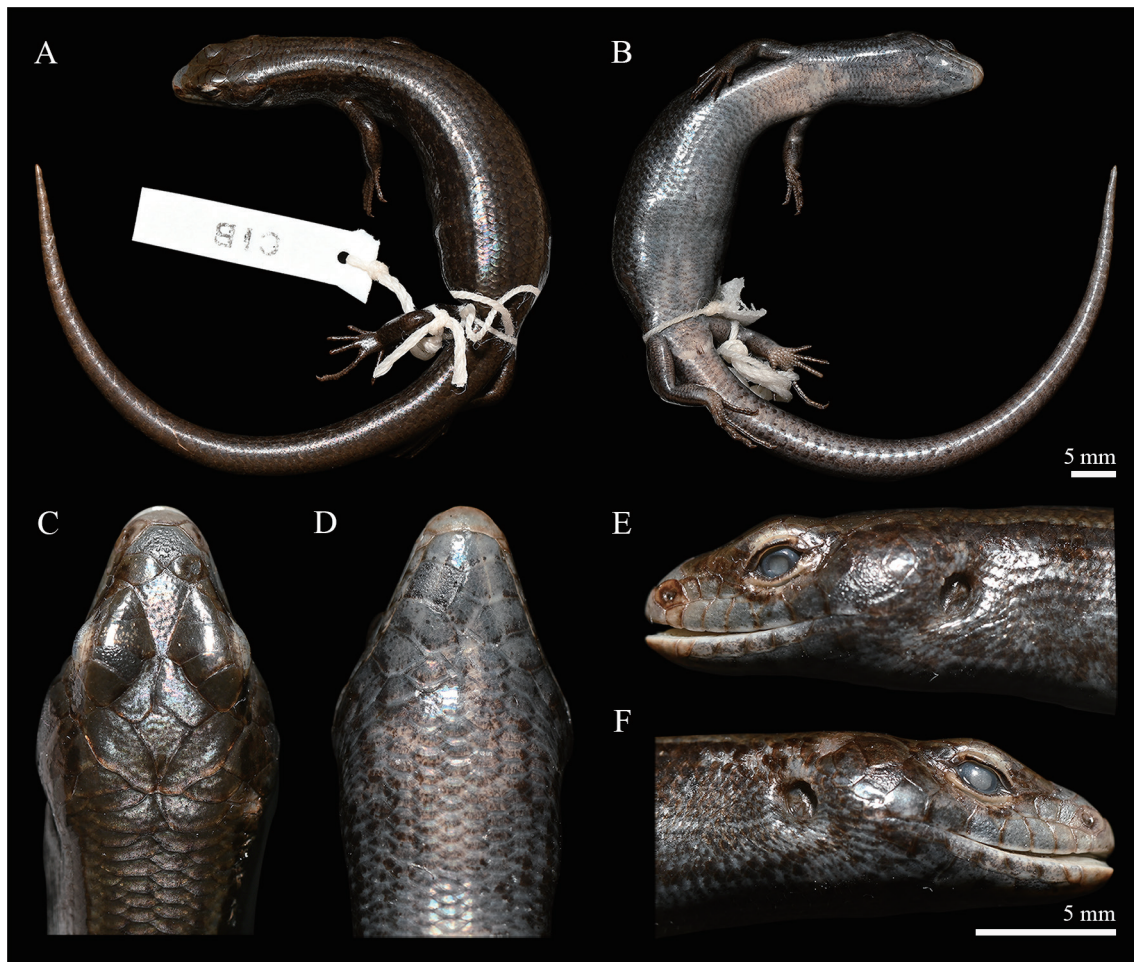
Figure 5 Holotype of *Scincella wangyuezhaoi* **sp. nov.** (CIB 87244) in preservative. A: Dorsal view of body; B: Ventral view of body; C: Dorsal side of head view; D: Ventral side of head view; E: Left side of head view; F: Right side of head view. Scale bar: 5 mm. Photographs by Zongyuan GAO.

uniformly whitish-grey; ventral surface of tail uniform pinkish-cream. Palmar surfaces of hands and thenar surfaces of feet dark grey. Iris light-grey.

Coloration in preservative In preservative, dorsal surfaces of holotype dark grayish-brown; upper margin of lateral longitudinal striation relatively straight. Ventral head with faint irregular dark spots, pineal ocellus present as single white dot on posterior part of interparietal; two wide dorsolateral black stripes distinctly present; lateral sides of tail with small dark spots; dark brown or black spots densely distributed on ventral tail; throat and ventral surface of body and limbs grayish-cream; ventral surface of tail lighter cream; palmar surfaces of hands, fingers, and toes brown (Figures 5–6).

Variation Paratypes (Table 3) resemble holotypes in most morphometric and meristic characters and coloration, with the following character variations: (1) MBSR: 27–30; (2) PVSR and VSR: 60–75 and 46–59, respectively; (3) gulars: 25–30; (4) AGSR: 53–78; (5) posterior temporals: three posterior temporals in CIB 87247 and CIB 87249; (6) nuchals: four nuchal scales on left in CIB 87248 and CIB 119519; two nuchal scales on left in CIB 87249, CIB 119509, CIB 119510, and CIB 119516; (7) infralabials: six scales in CIB 87247, CIB 87249, CIB 119516, and CIB 119518; (8) superciliary counts: five superciliaries in CIB 87246; seven superciliaries in CIB 87244, CIB 87247, CIB 87248, and CIB 87250; (9) F4S and T4S: 9–11 and 13–16, respectively; (10) MT and LT: 14–26 and 16–22, respectively; (11) prefrontals: prefrontals not in contact in CIB 119509, CIB 119512, CIB 119515, and CIB 119518; (12) parietals: parietals not in contact in CIB 87247; (13) limbs adpressed: toes in contact with fingers when limbs adpressed in CIB 87247; and (14) color pattern: denser black dots on head and dorsal in CIB 119509, CIB 119510, CIB 119512, CIB 119515, CIB 119516, CIB 119518, and CIB 119519. Moreover, TaW/SVL, AGD/SVL, MBW/SVL, MBD/SVL, HL/SVL, HW/SVL, HD/SVL, PDD/SVL, END/SVL, SNL/SVL, IND/SVL, FLL/
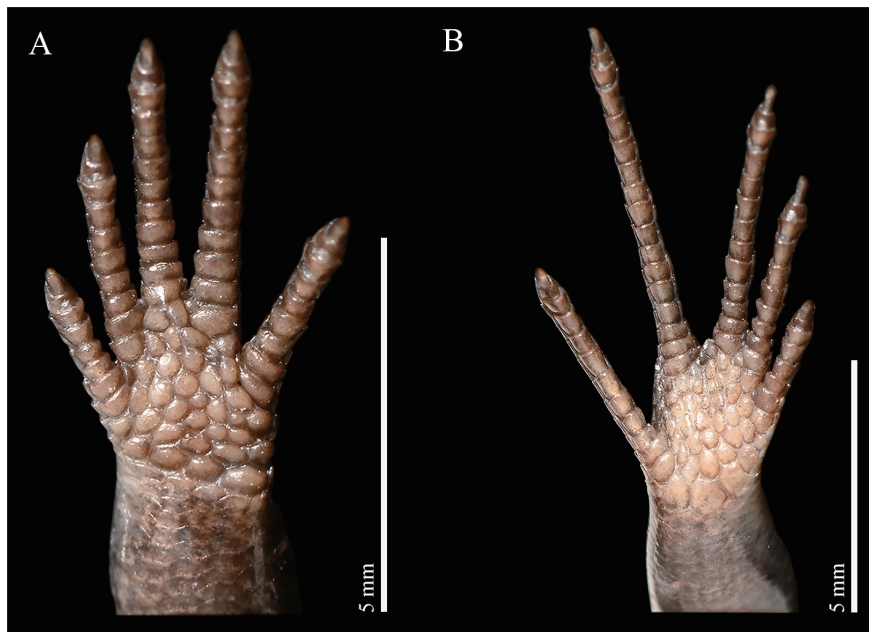
Figure 6 Holotype of *Scincella wangyuezhaoi* **sp. nov.** (CIB 87244) in preservative. A: Ventral side of hand view; B: Ventral side of foot view. Scale bar: 5 mm. Photographs by Zongyuan GAO.
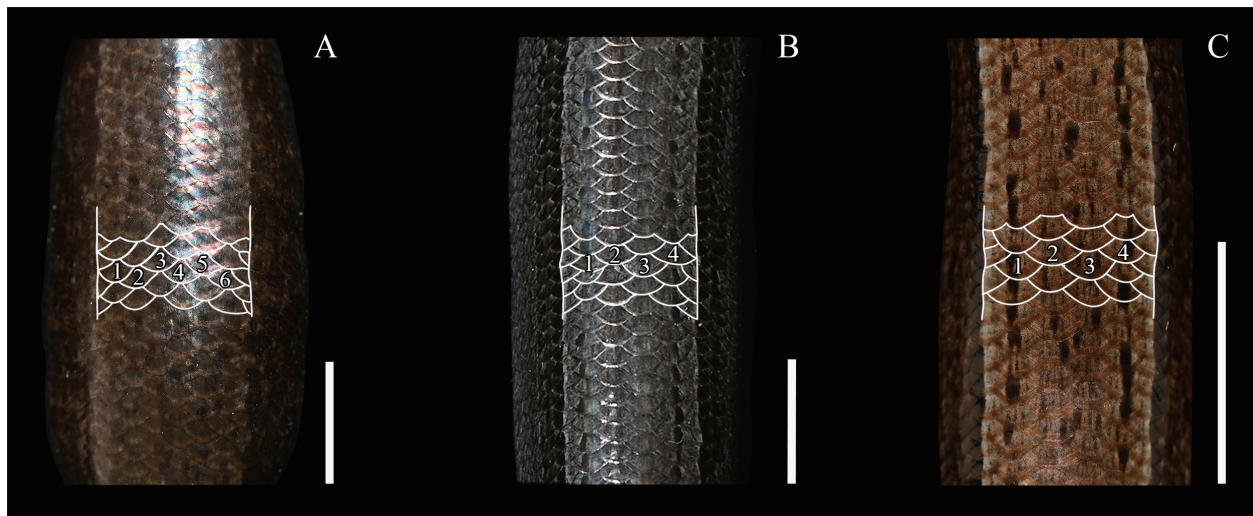

Figure 7 Comparison of DBR of *Scincella wangyuezhaoi* **sp. nov.**, *S. potanini* and *S. monticola*. A: *S. wangyuezhaoi* **sp. nov.**; B: *S. potanini*; C: *S. monticola*. Photographs by Zongyuan GAO.

SVL, HLL/SVL, T4L/SVL, and F4L/SVL are higher in CIB 87245 compared to other specimens. Other minor variations are shown in Table 3.

Distribution and natural history The new species is currently only known from Shapai Village, Caopo Town, Wenchuan County, Sichuan Province, and Shuluogou, Lixian County, Sichuan Province, China (Figure 1).

All specimens were collected in rocky areas with decaying leaf litter at elevations of 1 900–3 100 m a.s.l. in both dry and wet seasons. The new species was mostly active during the day, observed on rocky walls or leaf litter surface in caves and between rocks. Sympatric lizards included *Diploderma zhaoermii* (Gao and Hou, 2002). The diet and reproductive biology of the new species remain unknown. However, four well-developed offsprings were found in a pregnant female, suggesting that the new species may be ovoviviparous, similar to *S. tsinlingensis*,

S. huanrenensis, and *S. reevesii*, but different from *S. potanini*, *S. monticola*, *S. modesta*, and *S. formosensis*.

Ecology Wenchuan and Lixian Counties are located in Hengduan Mountain Region (HMR) of Sichuan Province. The most typical geomorphological feature of HMR is a series of north-south mountains and deep valleys arranged in parallel with each other. The terrain fluctuates greatly, with the highest altitude drop of 6 000 meters (Chen and Ai, 1983). The type series of *S. wangyuezhaoi* **sp. nov.** was collected in the shores of ditches and small ponds in HMR. These shores were covered by low (height usually less than 30 cm) halophilic vegetation (Figure 8).

Comparisons The morphological characters distinguishing the new species from its Asian congeners are as follows: from *S. apraefrontalis* by more MBSR (27–30 vs. 18), more supralabials and infralabials (7 vs. 6 and 6–7 vs. 5, respectively), more T4S (14–15 vs. 8–9), and prefrontals present (vs. absent) (Nguyen *et al.*, 2010c); from *S. badenensis* by greater number of TD/SVL (0.02 vs. 0.03), fewer MBSR (27–30 vs. 32–36), more nuchal pairs (2–4 vs. 0–1), fewer superciliaries (5–7 vs. 8–9), fewer T4S (14–15 vs. 18–20), and toes not in contact with fingers when limbs adpressed (vs. overlapping or separated) (Nguyen *et al.*, 2019); from *S. baraensis* by fewer DBR (6 vs. 8), fewer VSR (46–59 vs. 64–66), fewer superciliaries (5–7 vs. 8), fewer F4S and T4S (9–11 vs. 12–13 and 14–15 vs. 18–20, respectively), weak auricular lobules absent (vs. present), and enlarged dorsal scales (vs. small) (Nguyen *et al.*, 2020); from *S. boettgeri* by fewer T4S (14–15 vs. 15–16) (Ouboter, 1986); from *S. capitanea* by fewer MBSR (27–30 vs. 30–32), fewer T4S (14–15 vs. 15–17), and neck narrower than head (vs. neck wider than head) (Ouboter 1986); from *S. darevskii* by shorter SVL (30.1–62.1 mm vs. 88.6 mm), fewer supraoculars (4 vs. 5), weak auricular lobules absent (vs. present), and enlarged dorsal scales (vs. small) (Nguyen *et al.*, 2010c); from *S. devorator* by fewer T4S (14–15 vs. 19) and prefrontals always in contact (vs. not in contact) (Darevsky *et al.*, 2004; Nguyen *et al.*, 2011); from *S. dunan* by upper margin of lateral longitudinal striation relatively straight (vs. wavy) and little (vs. large) dark irregular spots densely scattered under the dorsolateral stripes (Koizumi *et al.*, 2022); from *S. melanosticta* by fewer MBSR (27–30 vs. 30–32), fewer T4S (14–15 vs. 16–22), fewer superciliaries (5–7 vs. 8–9), and toes not in contact with fingers when limbs adpressed (vs. overlapping) (Bourret and Bour, 2009; Neang *et al.*, 2018; Smith, 1935; Taylor, 1963); from *S. nigrofasciata* by greater number of TD/SVL (0.02 vs. 0.03), fewer MBSR (27–30 vs. 32–33), fewer DBR (6 vs. 8), fewer T4S (14–15 vs. 15–17), and toes not in contact with fingers when limbs addressed (vs. overlapping or separated) (Neang *et al.*, 2018); from *S. ochracea* by more supralabials (7 vs. 5) and auricular lobules absent (vs. present) (Bourret and Bour, 2009; Neang *et al.*, 2018; Pham *et al.*, 2015); from *S. punctatolineata* Boulenger by more MBSR (27–30 vs. 24–26), more T4S (14–15 vs. 12–14), and nuchals present (vs.

Figure 8 Habitat of *Scincella wangyuezhaoi* **sp. nov.** at the type locality. Photograph by Jinlong LIU, courtesy of Xiaomao ZENG.

absent) (Smith 1935); from *S. rara* by more MBSR (27–30 vs. 24) and single row of lamellae beneath toes and fingers II–IV (vs. double) (Darevsky and Orlov, 1997); from *S. rufocaudata* by fewer MBSR (27–30 vs. 30–34), fewer DBR (6 vs. 10), fewer T4S (14–15 vs. 16–22), fewer superciliaries (5–7 vs. 8), and toes not in contact with fingers when limbs adpressed (vs. overlapping) (Darevsky and Nguyen, 1983; Neang *et al.*, 2018); from *S. rupicola* by fewer MBSR (27–30 vs. 33–36), fewer DBR (6 vs. 8), fewer T4S (14–15 vs. 18–21), fewer superciliaries (5–7 vs. 7–9), and toes not in contact with fingers when limbs adpressed (vs. overlapping) (Smith 1935; Taylor 1963; Neang *et al.*, 2018); from *S. vandenburghi* by more T4S (14–15 vs. 12) (Schmidt, 1927); and from *S. victoriana* by more MBSR (27–30 vs. 26), and smooth scales on dorsum and tail (vs. keeled) (Ouboter 1986).

Among Chinese species, *Scincella wangyuezhaoi* **sp. nov.** differs morphologically from *S. potanini* by more MBSR (27–30 vs. 24–27), more DBR (6 vs. 4), more gulars (25–30 vs. 23–25), more T4S (14–15 vs. 10–13), and greater F4L/SVL (0.06–0.10 vs. 0.03–0.06); from *S. monticola* by more MBSR (27–30 vs. 23–25), more DBR (6 vs. 4), more gulars (25–30 vs. 22–24), more T4S (14–15 vs. 10–12), and greater FLL/SVL (0.20–0.27 vs. 0.13–0.19), HLL/SVL (0.24–0.43 vs. 0.20–0.22), and F4L/SVL (0.06–0.10 vs. 0.03–0.05); from *S. tsinlingensis* by more DBR (6 vs. 4) and greater IND/SVL (0.04–0.07 vs. 0.03–0.04). Other morphological characteristics distinguishing the new species from *S. potanini*, *S. monticola*, and *S. tsinlingensis* are summarized in Table 5. For the remaining congeners in China, *Scincella wangyuezhaoi* **sp. nov.** differs from *S. modesta* by upper margin of lateral longitudinal striation relatively straight (vs. wavy) (Wang and Zhao, 1986); from *S. formosensis* Günther by upper margin of lateral longitudinal striation relatively straight (vs. wavy) (Wang and Zhao, 1986); from *S. huanrenensis* by fewer DBR (6 vs. 8) and prefrontals always in contact (vs. not in contact) (Chen *et al.*,

2001; Zhao and Huang, 1982); from *S. barbouri* by fewer T4S (14–15 vs. 15–17) and fewer nuchals (2–4 vs. 4–5) (Ouboter, 1986; Stejneger, 1925); from *S. przewalskii* by more supralabials (7 vs. 6), more supraoculars (4 vs. 3), more superciliaries (5–7 vs. 4–5), and fewer T4S (14–15 vs. 17) (Wang and Zhao, 1986); from *S. reevesii* by postnasals absent (vs. one postnasal pair present), greater FLL/SVL (0.20–0.27 vs. 0.16–0.19), fewer MBSR (27–30 vs. 32), fewer DBR (6 vs. 8), more VSR (46–59 vs. 44–45), more gulars (25–30 vs. 23–25), fewer T4S (14–15 vs. 16–17), and upper margin of lateral longitudinal striation relatively straight (vs. wavy); from *S. schmidti* by more MBSR (27–30 vs. 26), more DBR (6 vs. 4), and more lamellae beneath toe IV (14–15 vs. 11) (Barbour, 1927); from *S. doriae* by fewer MBSR (27–30 vs. 34–37), fewer DBR (6 vs. 10), fewer T4S (14–15 vs. 15–18), toes not in contact with fingers when limbs adpressed (vs. overlapping), and upper margin of lateral longitudinal striation relatively straight (vs. wavy) (Boulenger, 1887; Bourret and Bour, 2009; Smith, 1935; Taylor, 1963).

4. Discussion

DBR is a conservative trait for identifying *Scincella* species Previous studies have found that the number of dorsal scale rows at the midbody between the dark dorsolateral stripes (DBR) is a relatively conservative trait with important taxonomic implications for *Scincella* (Neang *et al.*, 2018; Nguyen *et al.*, 2019; 2020; Wang and Zhao, 1986). The DBR is conserved in different populations of certain species, but distinguishable from other species groups. Here, although *Scincella wangyuezhaoi* **sp. nov.** was phylogenetically close to *S. potanini* and *S. monticola*, DBR comparisons among these species indicated clear morphological differences (Figure 7). As taxonomy and identification remain relatively elusive among *Scincella* species, the use of DBR could facilitate fast identification during field surveys. Therefore, our results agree with those of Wang and Zhao (1986), suggesting that *Scincella* could be divided into four groups based on DBR: i.e., DBR 4: *S. potanini*, *S. monticola*, *S. tsinlingensis*, *S. huanrenensis*, and *S. schmidti*; DBR 6: *Scincella wangyuezhaoi* **sp. nov.**, *S. barbouri*, *S. darevskii*, *S. doriae*, *S. formosensis*, *S. modesta*, *S. ochracea*, and *S. przewalskii*; DBR 8: *S. baraensis*, *S. nigrofasciata*, *S. rupicola*, and *S. reevesii*; DBR 10: *S. badenensis*, *S. melanosticta*, and *S. rufocaudata*.

Diversity and identification of *Scincella* species in China The description of *Scincella wangyuezhaoi* **sp. nov.** increases the current number of *Scincella* species to 39, with 12 recorded from China (Uetz *et al.*, 2022; Zhao *et al.*, 1999; this study), including *Scincella wangyuezhaoi* **sp. nov.**, *S. potanini*, *S. tsinlingensis*, *S. modesta*, *S. huanrenensis*, *S. reevesii*, *S. barbouri*, *S. doriae*, *S. formosensis*, *S. przewalskii*, and *S. schmidti*. The discovery of a new *Scincella* species indicates that reptile fauna in China

remains insufficiently studied and future field surveys are needed to more accurately assess herpetodiversity. Our study further highlights the importance of taxonomic research and biodiversity assessment for conservation. To facilitate future taxonomic work, we provide a key to the species of *Scincella* in China based on Wang and Zhao (1986).

Diagnostic key to *Scincella* species in China

1A Supraoculars 3..***S. przewalskii***
1B Supraoculars 4...**2**
2A Postnasal pairs 1..***S. reevesii***
2B Postnasals absent..**3**
3A Upper margin of lateral longitudinal striation relatively straight...**4**
3B Upper margin of lateral longitudinal striation wavy................**8**
4A DBR 6..................................***Scincella wangyuezhaoi* sp. nov.**
4B DBR 4...**5**
5A T4S 10–13...**6**
5B T4S 13–16...**7**
6A MBSR 23–24...***S. monticola***
6B MBSR 24–27...***S. potanini***
7A Infralabials 6...***S. huanrenensis***
7B Infralabials 7–8...***S. tsinlingensis***
8A DBR 4...***S. schmidti***
8B DBR 6...**9**
9A Toes and fingers overlap when limbs adpressed...........***S. doriae***
9B Toes separated or in contact with fingers when limbs adpressed..**10**
10A PVSR 70..***S. barbouri***
10B PVSR 53–69..**11**
11A MBSR 26–28, rarely 30.....................................***S. formosensis***
11B MBSR 28–30...***S. modesta***

Distribution of *Scincella* in HMR on eastern edge of Tibetan Plateau Despite its ecological and biogeographical importance, the biodiversity of HMR remains poorly understood. Five *Scincella* species have been recognized in HMR, including *Scincella wangyuezhaoi* **sp. nov.**, *S. potanini*, *S. monticola*, *S. tsinlingensis*, and *S. doriae* (Günther, 1896; Schmidt, 1925; Hu and Zhao, 1966; Boulenger, 1887; this study). Based on recent findings, we speculate that the true biodiversity of HMR be seriously underestimated, and future herpetofaunal surveys and taxonomic revisions are needed for *Scincella* species in the region. For example, species of *Diploderma* (Lacertilia: Agamidae) in HMR have been widely misidentified as *Diploderma flaviceps*, while they were suggested to be different species out of hot-dry valley of Dadu River (Gao and Hou, 2002; Manthey *et al.*, 2012; Wang *et al.*, 2019a; Wang *et al.*, 2019b). The distribution pattern of *Scincella* is similar to that of *Diploderma*, and they are difficult to distinguish morphologically due to a lack of previous research. Therefore, further studies should focus on the cryptic diversity and taxonomic revision of *Scincella* species in HMR.

For instance, all *Scincella* populations distributed in the Tianquan, Yuexi, Meigu, Yanbian, and Ganzi counties of Sichuan are currently identified as *S. potanini*, but no taxonomic study has been conducted for this widely distributed species (Wang and Zhao, 1986; Zhao *et al.*, 1999). Furthermore, the systematic relationship between *S. potanini* and *S. monticola* is questionable, with no molecular data available for either *S. potanini* or *S. monticola* prior to this study. Based on topotypic materials, our results indicated that *S. monticola* was phylogenetically closest to *S. potanini* and could not be distinguished from the latter species. Specifically, the *p*-distance between *S. potanini* and *S. monticola* was only 3.0% and the two species could not be separated by PCA. Thus, further studies are required to clarify the taxonomy of *Scincella* species in HMR.

References

Barbour T. 1927. A new lizard from China. Copeia, 165: 95–95

Boulenger G. A. 1887. An account of the Scincoid lizards collected from Burma for the Genoa Civic Museum by Messrs. GB Comotto and L. Fea. Ann Mus Civ Stor Nat Genova, Serie 2, 4: 618–624

Bourret R., Bour R. 2009. Les lezards de l'Indochine. Edition Chimaira, Frankfurt am Main. 624 pp (In French)

Chen B. W., Ai C. X. 1983. Discussion on indosinian cycle in the Hengduanshan Region (Transect Mountain). Acta Geosci Sinica, 5(3): 25–40 (In Chinese)

Chen S. L., Hikida T., Han S. H., Shim J. H., Oh H. S., Ota H. 2001. Taxonomic status of the Korean populations of the genus *Scincella* (Squamata: Scincidae). J Herpetol, 35(1): 122–129

Darevsky I., Nguyen V. 1983. New and little known lizard species from Vietnam. Zool Zhurnal, 62(12): 1827–1837

Darevsky I. S., Orlov N. L. 1997. A new genus and species of scincid lizards from Vietnam: the first Asiatic skink with double rows of basal subdigital pads. J Herpetol, 31(3): 323–326

Darevsky I. S., Orlov N. L., Ho T. C. 2004. Two new lygosomine skinks of the genus *Sphenomorphus* Fitzinger, 1843 (Sauria, Scincidae) from northern Vietnam. Russ J Herpetol, 11(2): 111–120

Felsenstein J. 2004. Inferring phylogenies. Sinauer associates Sunderland, MA. 580 pp

Gao Z., Hou M. 2002. Description of a new *Japalura* species from western Sichuan Province, China. Sichuan J Zool, 21(1): 3–5

García Vázquez U. O., Canseco Márquez L., de Oca A. N. M. 2010. A new species of *Scincella* (Squamata: Scincidae) from the Cuatro Ciénegas Basin, Coahuila, Mexico. Copeia, 2010(3): 373–381

Gonzalez M., Lwin K., Vindum J. 2005. New records for *Scincella* Victoriana (Shreve, 1940) from the Chin Hills, Myanmar. Proc California Acad Sci, 56(26): 391–392

Gray J. E. 1838. XXXIV.—Catalogue of the slender-tongued Saurians, with descriptions of many new genera and species. Ann Mag Nat Hist, 2(10): 287–293

Greer A. E., Shea G. 2003. Secondary temporal scale overlap pattern: a character of possible broad systematics importance in sphenomorphine skinks. J Herpetol, 37(3): 545–549

Günther A. 1864. The Reptiles of British India. London (Taylor and Francis): xxvii + 452 pp

Günther A. 1896. Report on the collections of reptiles, batrachians and fishes made by Messrs. Potanin and Berezowski in the Chinese provinces Kansu and Sze-chuen. Ann Mus Zool Acad Sci St Petersbourg, 1: 199–219

Hillis D. M., Bull J. J. 1993. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. Systematic Biol, 42(2): 182–192

Hu S. C., Djao E. M., Liu C. C. 1966. A herpetological survey of the Tsinling and Ta-Pa Shan region. Acta Zool Sinica, 18(1): 57–89 (In Chinese)

Inger R. F., Zhao E., Shaffer H., Wu G. 1990. Report on a collection of amphibians and reptiles from Sichuan, China. Fieldiana Zool, 58: 1–24

Kocher T. D., Thomas W. K., Meyer A., Edwards S. V., Pääbo S., Villablanca F. X., Wilson A. C. 1989. Dynamics of mitochondrial DNA evolution in animals: amplification and sequencing with conserved primers. Proc Natl Acad Sci, 86(16): 6196–6200

Koizumi Y., Ota H., Hikida T. 2022. A new species of the genus *Scincella* (Squamata: Scincidae) from Yonagunijima Island, Southern Ryukyus, Japan. Zootaxa, 5128(1): 61–83

Kumar S., Stecher G., Li M., Knyaz C., Tamura K. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. Mol Biol Evol, 35(12): 1547–1549

Lanfear R., Calcott B., Ho S. Y., Guindon S. 2012. PartitionFinder: combined selection of partitioning schemes and substitution models for phylogenetic analyses. Mol Biol Evol, 29(6): 1695–1701

Lim L. J. 1998. The Taxonomy of West Malaysian and Singapore Scincidae (Reptilia: Suria). Master Thesis, National University of Singapore

Linkem C. W., Diesmos A. C., Brown R. M. 2011. Molecular systematics of the Philippine forest skinks (Squamata: Scincidae: *Sphenomorphus*): testing morphological hypotheses of interspecific relationships. Zool J Linn Soc, 163(4): 1217–1243

Manthey U., Denzer W., Hou M., Wang X. 2012. Discovered in historical collections: Two new *Japalura* species (Squamata: Sauria: Agamidae) from Yulong Snow Mountains, Lijiang Prefecture, Yunnan, PR China. Zootaxa, 3200(1): 27–48

Nagy Z. T., Sonet G., Glaw F., Vences M. 2012. First large-scale DNA barcoding assessment of reptiles in the biodiversity hotspot of Madagascar, based on newly designed COI primers. PLoS One, 7(3): e34506

Neang T., Chan S., Poyarkov N. A., Jr. 2018. A new species of smooth skink (Squamata: Scincidae: *Scincella*) from Cambodia. Zool Res, 39(3): 220–240

Nguyen S. N., Nguyen V. D. H., Nguyen L. T., Murphy R. W. 2019. A new skink of the genus *Scincella* Mittleman, 1950 (Squamata: Scincidae) from Ba Den Mountain, Tay Ninh Province, southern Vietnam. Zootaxa, 4648(2): 273–286

Nguyen S. N., Nguyen V. D. H., Nguyen L. T., Murphy R. W. 2020. A new

skink of the genus *Scincella* Mittleman, 1950 (Squamata: Scincidae) from southern Vietnam. Zootaxa, 4868(3): 423–434

Nguyen T. Q., Ananjeva N. B., Orlov N. L., Rybaltovsky E., Böhme W. 2010a. A new species of the genus *Scincella* Mittlemann, 1950 (Squamata: Scincidae) from Vietnam. Russ J Herpetol, 17(4): 269–274

Nguyen T. Q., Nguyen T. T., Orlov N. L. 2010b. New record of the Mountain ground skink *Scincella monticola* (Schmidt, 1925) (Squamata: Scincidae) from Cao Bang Province, Vietnam. Herpetol Notes, 3(1): 201–203

Nguyen T. Q., Nguyen V. S., Böhme W., Ziegler T. 2010c. A new species of *Scincella* (Squamata: Scincidae) from Vietnam. Folia Zool, 59(2): 115–121

Nguyen T. Q., Schmitz A., Nguyen T. T., Orlov N. L., BoHme W., Ziegler T. 2011. Review of the genus *Sphenomorphus* Fitzinger, 1843 (Squamata: Sauria: Scincidae) in Vietnam, with description of a new species from Northern Vietnam and Southern China and the first record of *Sphenomorphus mimicus* Taylor, 1962 from Vietnam. J Herpetol, 45(2): 145–154

Ouboter P. E. 1986. A revision of the genus *Scincella* (Reptilia: Sauria: Scincidae) of Asia, with some notes on its evolution. Zool Verh, 229(1): 1–66

Pham A. V., Le D. T., Nguyen S. L., Ziegler T., Nguyen T. Q. 2015. New provincial records of skinks (Squamata: Scincidae) from northwestern Vietnam. Biodivers Data J, 3: e4284

Pyron R. A., Burbrink F. T., Wiens J. J. 2013. A phylogeny and revised classification of Squamata, including 4 161 species of lizards and snakes. BMC Evol Biol, 13(1): 1–54

Rambaut A. 2012. FigTree v.1.4.3. Available at http://tree.bio.ed.ac.uk/software/fifigtree/

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

Schmidt K. P. 1925. New reptiles and a new salamander from China. Amer Mus Nat Hist, 157: 1–5

Schmidt K. P. 1927. Notes on Chinese reptiles. Bull Amer Mus Nat Hist, 54: 467–551

Shi B. N., Zhao E. M. 1980. The Fauna of Sichuan Resources. Vol. 1. Chengdu: Sichuan People's Press, 135 pp (In Chinese)

Skwor T. 2012. The use of DNASTAR Lasergene Educational Software with Molecular Techniques to Support Bacterial Identification. Proc Adv Biol Lab Educ, 33: 327–334

Smith M. A. 1935. The Fauna of British India, Including Ceylon and Burma. Reptilia and Amphibia. Vol. II. Sauria. Taylor and Francis, London. xiii + 440 pp + 1 pl

Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics, 30(9): 1312–1313

Stejneger L. 1925. Description of a new scincid lizard and a new burrowing frog from China. J Wash Acad Sci, 15(7): 150–152

Stuart B. L., Emmett D. A. 2006. A collection of amphibians and reptiles from the Cardamom Mountains, southwestern Cambodia. Fieldiana Zool, 2006(109): 1–27

Stuart B. L., Sok K., Neang T. 2006. A collection of amphibians and reptiles from hilly eastern Cambodia. Raffles B Zool, 54(1): 129–155

Taylor E. H. 1963. The lizards of Thailand. Univ Kansas Sci Bull, 44(14): 687–1077

Thompson J. C. 1912. On reptiles new to the Island Arcs of Asia. Herpetol Notices, 3: 1–5

Thompson J. D, Gibson T. J, Plewniak F., Jeanmougin F., Higgins D. G. 1997. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res, 25(24): 4876–4882

Uetz P, Freed P, Hošek J. 2022. The reptile database. http://www.reptile-database.org

Vences M., Thomas M., Bonett R. M., Vieites D. R. 2005. Deciphering amphibian diversity through DNA barcoding: chances and challenges. Philos T R Soc B, 360(1462): 1859–1868

Wang K., Che J., Lin S., Deepak V., Aniruddha D. R., Jiang K., Jin J., Chen H., Siler C. D. 2019a. Multilocus phylogeny and revised classification for mountain dragons of the genus *Japalura* (Reptilia: Agamidae: Draconinae) from Asia. Zool J Linn Soc, 185(1): 246–267

Wang K., Jiang K., Ren J., Zou D., Wu J., Che J., Siler C. D. 2019b. A new species of Dwarf *Japalura sensu lato* (Reptilia: Squamata: Agamidae) from the upper Mekong River in Eastern Tibet, China, with notes on morphological variation, distribution, and conservation of two congeners along the same river. Zootaxa, 4544(4): 505–522

Wang Y. Z., Zhao E. M. 1986. Studies on Chinese species of *Scincella* (Scincidae, Sauria). Acta Herpetol Sinica, 5(4): 267–277 (In Chinese)

Xiao W., Zhang Y., Liu H. 2001. Molecular systematics of Xenocyprinae (Teleostei: Cyprinidae): taxonomy, biogeography, and coevolution of a special group restricted in East Asia. Mol Phylogenet Evol, 18(2): 163–173

Zhang D., Gao F., Jakovlić I., Zou H., Zhang J., Li W. X., Wang G. T. 2020. PhyloSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Mol Ecol Resour, 20(1): 348–355

Zhao E., Huang K. 1982. A survey of amphibians and reptiles in Liaoning Province. Acta Herpetol Sinica, 1(1): 11–12

Zhao E., Zhao K., Zhou K. 1999 Fauna Sinica. Reptilia. Vol. 2. Squamata. Lacertilia. Beijing: Science Press, 312–336 pp (In Chinese)

Zhao E. M. 2003. Colored Atlas of Reptiles of Sichuan. Beijing, China Forestry Press, 83–84 (In Chinese)

Appendix

Specimens examined (*n* = 32)

Scincella monticola (*n* = 4): China: Yunnan, Weixi: CIB 6969, CIB 6970, CIB 6971, and China: Yunnan, Shangri-La: DL-YNJC2020824.

Scincella potanini (*n* = 14): China: Sichuan, Kangding: CIB 85805, CIB 85806, CIB 85807, CIB 72253–60, DL-KD202109071, DL-KD202109072, DL-KD2018070302.

Scincella reevesii (*n* = 4): China: Guangdong, Guangzhou: CIB 7215, CIB7216, CIB 7219, and China: Guangxi: CIB 7218.

Scincella tsinlingensis (*n* = 10): China: Shannxi, Zhouzhi: CIB 7226, CIB 7240, CIB 7246, CIB 7249, CIB 7251, CIB 7252, CIB 7253, CIB 7258, CIB 7259, CIB 7261.