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Research Article

A new skink of the genus *Scincella* Mittleman, 1950 (Squamata, Scincidae) from Son La Province, northwestern Vietnam

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Abstract

A new species of the genus *Scincella* Mittleman, 1950 is described from northern Vietnam based on morphological and molecular evidence. *Scincella truongi* **sp. nov.** is characterized by a combination of the following characters: size medium (SVL up to 59.4 mm); primary temporals 2; external ear opening without lobules; loreals two; supralabials seven or eight; infralabials six or seven; nuchals in three pairs; midbody scales in 28 rows; dorsal scales smooth, in six rows across the back; paravertebral scales 60–67, not widened; ventral scales in 60–70 rows; ten smooth lamellae beneath finger IV and 13–15 beneath toe IV; toes not reaching to fingers when limbs adpressed along body; dorsal surface of body and tail bronze brown with few black spots, a dark stripe running from nostril to eye and extending from posterior corner of eye along upper part of flank to the middle of the tail. In the phylogenetic analyses, the new species is recovered as an independent lineage with no clear sister taxon and at least 17.3% genetic divergence from other species in the genus based on a fragment of the mitochondrial COI gene.

Key words: COI, molecular phylogeny, morphology, *Scincella truongi* sp. nov., Sop Cop Nature Reserve, taxonomy

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Introduction

Son La Province is located in northwestern Vietnam and covered with 40% or 439,592 ha of evergreen forest (The People's Committee of Son La Province 2007). However, the biodiversity of this province is poorly studied, in particular reptiles and amphibians. In recent years, ten new species have been described from Son La, namely *Amolops truongi* Pham, Pham, Ngo, Sung, Ziegler & Le, 2023 (Pham et al. 2023b); *Gracixalus truongi* Tran, Pham, Le, Nguyen, Ziegler & Pham, 2023 (Tran et al. 2023); *Tylototriton anguliceps* Le,

Nguyen, Nishikawa, Nguyen, Pham, Matsui, Bernardes & Nguyen, 2015 (Le et al. 2015a); *T. pasmansi* Bernardes, Le, Nguyen, Pham, Pham, Nguyen & Ziegler, 2020 (Bernardes et al. 2020), *Cyrtodactylus sonlaensis* Nguyen, Pham, Ziegler, Ngo & Le, 2017 (Nguyen et al. 2017); *C. taybacensis* Pham, Le, Ngo, Ziegler & Nguyen, 2019 (Pham et al. 2019); *Hemiphyllodactylus vanhoensis* Luu, Hoang, Ha, Grismer, Murdoch, Sitthivong, Phimpasone & Grismer, 2024 (Luu et al. 2024); *Achalinus quangi* Pham, Pham, Le, Ngo, Ong, Ziegler & Nguyen, 2023 (Pham et al. 2023a); *A. timi* Ziegler, Nguyen, Pham, Nguyen, Pham, Van Schingen, Nguyen & Le, 2019 (Ziegler et al. 2019); and *A. vanhoensis* Ha, Ziegler, Sy, Le, Nguyen & Luu, 2022 (Ha et al. 2022), and ten new country records have been added based on findings from Son La to the herpetofauna of Vietnam (Pham et al. 2014, 2016; Le et al. 2015b; Nguyen et al. 2015b).

The genus *Scincella* Mittleman, 1950 currently contains 39 recognized species with a wide distribution in Asia and America (Uetz et al. 2024). It is characterized by having a lower eyelid with an opaque window (Smith 1935; Taylor 1963; Greer 1974; Ouboter 1986; Nguyen et al. 2010b); supranasals absent, hindlimbs pentadactyl, lamellae under the basal digits in one row (Nguyen et al. 2010b), and lower secondary temporal overlapped by an upper scale (Greer and Shea 2003; Nguyen et al. 2011).

In Vietnam, Nguyen et al. (2009) recorded three species of *Scincella*, viz. *S. doriae* (Boulenger), *S. melanosticta* (Boulenger), and *S. reevesii* (Gray). Since then, a total of 15 species of the genus have been documented from the country (Uetz et al. 2024). During the last five years, three new species have been discovered, namely *S. badenensis* Nguyen, Nguyen, Nguyen & Murphy, 2019 from Tay Ninh Province; *S. baraensis* Nguyen, Nguyen, Nguyen & Murphy, 2020 from Binh Phuoc Province; and *S. ouboteri* Pham, Pham, Le, Ngo, Ngo, Ziegler & Nguyen, 2024 from Hoa Binh Province (Nguyen et al. 2019, 2020; Pham et al. 2024).

During our fieldwork in the evergreen forests of Sop Cop Commune, Sop Cop District, Son La Province, northwestern Vietnam, a new population of forest skinks was uncovered in Sop Cop Nature Reserve (Fig. 1). The collected specimens were assigned to the genus *Scincella* based on morphological examination. Further morphological and molecular analyses showed that they are distinctly differentiated from all other existing species. We therefore describe this population of *Scincella* from Son La Province as a new species herein.

Materials and methods

Sampling

A field survey was conducted in April 2013 in Sop Cop Nature Reserve, Son La Province, northwestern Vietnam. Specimens were collected between 8:00 and 16:00. After having been photographed in life, skinks were anesthetized and euthanized in a closed vessel with a piece of cotton wool containing ethyl acetate (Simmons 2002), fixed in 85% ethanol for ten hours, and then later transferred to 75% ethanol for permanent storage. Tissue samples were preserved separately in 70% ethanol before fixation. Voucher specimens were deposited in the collections of the University of Science (**HUS**), Vietnam National University, Hanoi (**VNU**) and the Institute of Ecology and Biological Resources (**IEBR**), Vietnam Academy of Science and Technology, Hanoi, Vietnam.

Figure 1. Map showing the type locality of *Scincella truongi* sp. nov. in Son La Province, Vietnam

Molecular data and phylogenetic analyses

We sequenced two samples of the new population from Son La Province. Additionally, ten ingroup and one outgroup taxa were included in the phylogenetic analysis following Pham et al. (2024) (Table 1). Tissue samples were extracted using DNeasy blood and tissue kit, Qiagen (Hilden, Germany). Extracted DNA from the fresh tissue was amplified by DreamTaq PCR mastermix (Thermo Fisher Scientific, Lithuania). A fragment of the mitochondrial cytochrome c oxidase subunit I (COI) was sequenced using primer pair LCO1490 (5'-GGTCAACAAATCATAAAGATATTGG-3') and HCO2198 (5'--TAAACTTCAGGGTGACCAAAAAATCA-3') (Folmer et al. 1994). The PCR volume consisted of 21 µl (10 µl of mastermix, 5 µl of water, 2 µl of each primer at 10 pmol/µl, and 2 µl of DNA or higher depending on the quantity of DNA in the final extraction solution). PCR condition was 95 °C for 5 min to activate the taq; with 40 cycles at 95 °C for 30 s, 50 °C for 45 s, 72 °C for 60 s; and the final extension at 72 °C for 6 min.

Table 1. Uncorrected ("p") distance matrix showing percentage pairwise genetic divergence (COI) between the new species (highlighted in bold) and closely related species.

	Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1	MG935701 *Sphenomorphus maculata*	–																					
2	MH119607 *Scincella reevesii*	23.08	–																				
3	MH119609 *Scincella reevesii*	23.43	0.46	–																			
4	MH119611 *Scincella rufocaudata*	21.23	8.12	8.42	–																		
5	MH119612 *Scincella rufocaudata*	22.58	8.88	8.88	2.91	–																	
6	MH119613 *Scincella* sp.	19.65	15.47	15.62	13.02	13.17	–																
7	MH119616 *Scincella doriae*	20.18	21.26	21.27	19.22	19.37	17.27	–															
8	MH119617 *Scincella doriae*	20.34	21.10	21.11	19.22	19.37	17.91	0.92	–														
9	MH119619 *Scincella melanosticta*	23.80	18.38	18.38	19.45	18.99	19.60	18.71	18.87	–													
10	MH119621 *Scincella melanosticta*	23.16	18.07	18.07	18.84	18.68	19.60	18.40	18.55	0.92	–												
11	MH119625 *Scincella rupicola*	21.02	20.74	21.06	18.54	19.02	16.61	20.14	20.14	21.50	21.67	–											
12	MH119627 *Scincella rupicola*	22.38	20.73	20.89	19.00	19.48	16.92	19.99	19.68	21.49	21.66	3.98	–										
13	MK990602 *Scincella badenensis*	21.30	14.59	14.75	12.58	12.58	11.01	17.82	17.96	19.53	19.23	17.74	17.88	–									
14	MK990603 *Scincella badenensis*	21.30	14.59	14.75	12.58	12.58	11.01	17.82	17.96	19.53	19.23	17.74	17.88	0.00	–								
15	MK990605 *Scincella nigrofascia*	19.57	16.78	16.63	14.62	14.62	3.53	16.42	16.72	20.33	20.33	16.80	16.80	9.91	9.91	–							
16	MT742256 *Scincella baraensis*	23.12	20.13	20.13	19.65	19.81	18.86	16.13	16.28	18.91	19.07	20.46	21.50	18.47	18.47	17.87	–						
17	MT742257 *Scincella baraensis*	23.12	20.13	20.13	19.65	19.81	18.86	16.13	16.28	18.91	19.07	20.46	21.50	18.47	18.47	17.87	0.00	–					
18	OP927028 *Scincella ochracea*	21.28	21.64	21.80	19.78	20.55	19.75	22.77	22.00	20.88	21.64	21.92	21.91	19.80	19.80	19.67	20.10	20.10	–				
19	**PQ666442 *Scincella truongi* sp. nov. HUS.2024.01**	**22.53**	**19.76**	**19.76**	**17.91**	**17.30**	**18.21**	**18.27**	**17.95**	**21.29**	**21.30**	**20.93**	**22.15**	**17.57**	**17.57**	**18.18**	**20.72**	**20.72**	**22.01**	–			
20	**PQ666443 *Scincella truongi* sp. nov. IEBR R.6329**	**22.53**	**19.76**	**19.76**	**17.91**	**17.30**	**18.21**	**18.27**	**17.95**	**21.29**	**21.30**	**20.93**	**22.15**	**17.57**	**17.57**	**18.18**	**20.72**	**20.72**	**22.01**	**0.00**	–		
21	OP927026 *Scincella ouboteri*	19.74	21.03	20.88	19.02	19.95	19.31	21.37	20.76	21.65	21.80	21.12	21.73	19.34	19.34	18.76	19.80	19.80	8.68	**21.11**	**21.11**	–	
22	OP927027 *Scincella ouboteri*	19.91	21.03	20.88	19.02	19.79	19.31	21.07	20.46	21.34	21.80	20.82	21.43	19.04	19.04	18.76	19.65	19.65	8.38	**20.81**	**20.81**	0.30	–

PCR products were subjected to electrophoresis through a 1% agarose gel, 1st BASE (Selangor, Malaysia). Gels were stained for 10 min in 1X TBE buffer at 2 pg/ml of ethidium-bromide and visualized under UV light. Successful amplifications were purified to eliminate PCR components using GeneJET™ PCR Purification Kit (Thermo Fisher Scientific, Lithuania). Purified PCR products were sent to Macrogen Inc. (Seoul, South Korea) for sequencing. Sequences generated in this study were edited using Geneious v. 7.1.8 (Kearse et al. 2012).

After sequences were aligned by Clustal X v. 2 (Thompson et al. 1997), data were analyzed using maximum parsimony (MP), as implemented in PAUP*4.0b10 (Swofford 2001), and Bayesian inference (BI), as implemented in MrBayes v. 3.2.7 (Ronquist et al. 2012). For MP analysis, heuristic analysis was conducted with 100 random taxon addition replicates using tree-bisection and reconnection (TBR) branch swapping algorithm, with no upper limit set for the maximum number of trees saved. Bootstrap support was calculated using 1000 pseudo-replicates and 100 random taxon addition replicates. All characters were equally weighted and unordered. For the maximum likelihood (ML) analysis, we used IQ-TREE v. 2.3.4 (Nguyen et al. 2015a) with a single model and 10,000 ultrafast bootstrap replications. The optimal model for nucleotide evolution was determined using jModeltest v. 2.1.4 (Darriba et al. 2012).

For Bayesian analyses, we used the optimal model selected by jModeltest with parameters estimated by MrBayes v. 3.2.7a. Two independent analyses with four Markov chains (one cold and three heated) were run simultaneously for ten million generations with a random starting tree and sampled every 1000 generations. Log-likelihood scores of sample points were plotted against generation time to determine stationarity of Markov chains. Trees generated before log-likelihood scores reached stationarity were discarded from the final analyses using the burn-in function. The posterior probability values for all clades in the final majority rule consensus tree were provided. The optimal model for nucleotide evolution was set to GTR+I+G for ML and single-model Bayesian analyses as selected by jModeltest v. 2.1.4. The cutoff point for the burn-in function was set to 25% of generated trees. Nodal support was also evaluated using bootstrap replication (BP) as estimated in PAUP, ultrafast bootstrap (UBP) in IQ-TREE v. 2.3.4, and posterior probabilities (PP) in MrBayes v. 3.2.7. BP ≥ 70, PP and UBP ≥ 95 were regarded as strong support for a clade (Hillis and Bull 1993; Ronquist et al. 2012; Nguyen et al. 2015a). Uncorrected pairwise divergences were calculated in PAUP*4.0b10.

Morphological examination

Measurements were taken with a digital caliper (Electronic Digital Caliper) to the nearest 0.1 mm. The following morphological characteristics were recorded (after Nguyen et al. 2010a; Grismer and Quah 2015; Pham et al. 2024):

SVL snout-vent length (from tip of snout to cloaca);
TaL tail length (from cloaca to tip of tail);
AG distance from posterior junction of forelimb and body wall to anterior junction of hindlimb and body wall (with the limbs held at right angles to the body);
HL head length (from tip of snout to posterior margin of parietal or interparietal, depending on the longest distance);

HW head width (at the widest portion of temporal region);
HH head height (at the deepest portion of temporal region);
SL snout length (from anterior margin of eye to tip of snout);
STL distance from snout to anterior border of tympanum;
SFIL snout-forelimb length (from tip of snout to anterior junction of forelimb and body wall to the tip of fourth finger, with the limb held at right angles to the body);
END distance from anterior margin of eye to posterior border of nostril;
EL eye length (distance between anterior and posterior corners of eyelid);
WIN Window length (distance between anterior and posterior corners of window)
TYD maximum diameter of tympanum;
FIL forelimb length (from anterior junction of forelimb and body wall to the tip of fourth finger, with the limb held at right angles to the body);
HIL hindlimb length (anterior junction of hindlimb and body wall to the tip of fourth finger, with the limb held at right angles to the body).

Scalation

Paravertebral scales counted as the number of scales in a line from posterior edge of parietals to dorsal point opposite posterior margin of the medial precloacals; transverse ventral scale rows counted as the number of scales from first gular scale to anterior margin of precloacals, number of subdigital lamellae under fourth finger and fourth toe. Bilateral scale counts were given as left/right. Sex identification was performed by inspection of presence or absence of hemipenes.

Morphological comparisons were based on data from the following literature: Gray (1838), Boulenger (1887), Günther (1896), van Denburgh (1912), Stejneger (1925), Barbour (1927), Schmidt (1927), Smith (1935), Taylor (1963), Zhao and Huang (1982), Darevsky and Nguyen (1983), Ouboter (1986), Wang and Zhao (1986), Inger et al. (1990), Darevsky and Orlov (1997), Chen et al. (2001), Darevsky et al. (2004), Bourret (2009), Nguyen et al. (2010a, b, c, 2011), Pham et al. (2015, 2024), Neang et al. (2018), Nguyen et al. (2019, 2020), Koizumi et al. (2022), and Jia et al. (2023, 2024).

Results

Phylogenetic analyses

The aligned matrix of the molecular data contained 668 characters with no gaps, of which 247 were parsimony informative. The MP analysis produced two most parsimonious trees (Tree length = 864, Consistency index = 0.42, Retention index = 0.63). The new species from Son La Province was weakly placed as the sister taxon to a clade consisting of *S. baraensis* + *S. doriae* + *S. melanosticta* (BP < 50, UBP = 60, PP = 77) (Fig. 2). The three species are distributed either in southern Vietnam or broadly in the region. In terms of genetic divergences, the new species is separated from *S. baraensis*, *S. doriae* and *S. melanosticta* by 20.72%, 17.95–18.27%, and 21.29–21.30%, respectively. Genetically, it differs from the remaining species of *Scincella* included in the study by at least an uncorrected pairwise sequence divergence of ~17.3% (from *S. rufocaudata*) based on a fragment of the mitochondrial COI gene (Table 2).

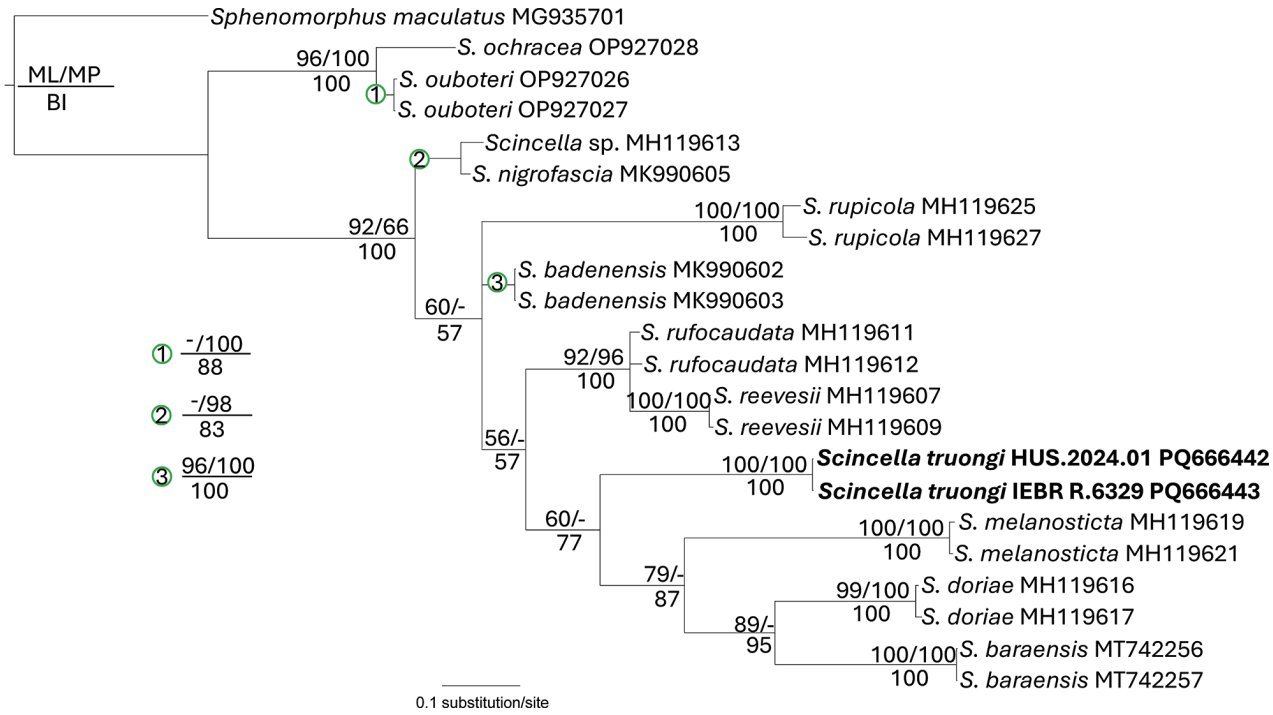

Figure 2. Phylogram based on the Bayesian analysis. Numbers above and below branches are ML ultrafast bootstrap/MP bootstrap values and single-model Bayesian posterior probabilities (> 50%), respectively. Dash indicates unsupported node. Letters and numbers after species names are GenBank accession records.

Table 2. Morphological characteristics of *Scincella truongi* sp. nov. from Son La Province, Vietnam.

	IEBR R.6329	IEBR R.6330	HUS. 2024.01	HUS. 2024.02	HUS. 2024.04	HUS. 2024.03	Min-Max
Type status	**Holotype**	**Paratype**	**Paratype**	**Paratype**	**Paratype**	**Paratype**	
Sex	**Female**	**Male**	**Female**	**Female**	**Female**	**Female**	
Measurements (in mm)							
SVL	54.86	49	51.66	54.01	59.4	53.7	49.0–59.4
TaL (*generated)	35*	32.8*	39.6*	36.1*	100.8	91.8	91.8–100.8
AG	32.15	25.29	29.4	31.15	34.3	31.4	25.3–34.3
SL	3.6	4	3.86	4	4.2	3.9	3.6–4.2
STL	9.8	9.98	9.38	10	9.98	9.3	9.3–10
SFIL	18.35	17.86	18.2	19.35	19.52	18.1	17.9–19.5
END	2.73	2.7	2.43	2.43	2.38	2.4	2.4–2.7
EL	3.11	2.9	2.72	3.2	3.24	2.7	2.7–3.2
HL	9.1	9.64	8.94	9.6	9.61	8.8	8.8–9.6
HW	6.57	6.19	5.89	7.1	7.05	6.6	5.9–7.1
HH	4.76	4.68	4.76	5	5.5	5.5	4.7–5.5
TYD	1.5	1.32	1.39	1.37	1.43	1.3	1.3–1.5
FIL	12.83	13	13.43	13.64	13	12.3	12.3–13.6
HIL	18.3	17.9	19.63	19.11	17.34	18.3	17.3–19.6
WIN	1.07	0.99	0.99	0.98	0.94	0.98	0.94–1.07
Scalation							
Supraoculars	4	4	4	4	4	4	4
Nuchals	3	3	3	3	3	3	3
Loreals	2	2	2	2	2	2	2
Preocular	1	1	1	1	1	1	1
Presuboculars	2	2	2	2	2	2	2

	IEBR R.6329	IEBR R.6330	HUS. 2024.01	HUS. 2024.02	HUS. 2024.04	HUS. 2024.03	Min-Max
Type status	**Holotype**	**Paratype**	**Paratype**	**Paratype**	**Paratype**	**Paratype**	
Sex	**Female**	**Male**	**Female**	**Female**	**Female**	**Female**	
Supraciliaries	7	7	7	7	7	7	7
Postoculars	3	3	3	3	3	3	3
Postsuboculars	2	2	2	2	2	2	2
Primary temporals	2	2	2	2	2	2	2
Secondary temporals	2	2	2	2	2	2	2
Supralabials (R/L)	7	7/8	7	7	7	7	7–8
Auricular lobules							
Infralabials	7	7	7	7	6	7	6–7
Chin shields (pairs)	3	3	3	3	3	3	3
Midbody scale rows	28	28	28	28	28	28	28
Paravertebral scales	67	60	65	63	66	65	60–67
Ventrals in transverse rows	68	60	64	70	64	65	60–70
Precloacals (enlarged)	2	2	2	2	2	2	2
Lamellae on finger IV	10	10	10	10	10	10	10
Lamellae on toe IV	15	14	14	14	15	13	13–15

Taxonomic account

***Scincella truongi* sp. nov.**

https://zoobank.org/09E36087-F43A-4D13-8918-C6F3AD27881E

Figs 3, 4

Material examined. *Holotype*. • IEBR R.6329 (Field number PAT.133) (Figs 3, 4A, B, 5A–D), adult female, collected on 3 April 2013 by A.V. Pham and D.A. Nguyen in evergreen forest near Ta Co Village (20°59'13.6"N, 103°37'19.4"E, at an elevation of 1660 m a.s.l.), Sop Cop Commune, within Sop Cop Nature Reserve, Sop Cop District, Son La Province, Vietnam. ***Paratypes*.** • IEBR R.6330 (Field number PAT. 129), adult male; HUS.2024.01 (PAT.130) (Fig. 6), adult female; HUS.2024.02 (PAT.131), adult female; HUS.2024.03 (PAT 134) (Fig. 7); and adult female, HUS.2024.04 (PAT. 164), adult female, bear the same data as the holotype.

Diagnosis. The new species can be distinguished from other species of *Scincella* by a combination of the following characteristics: size medium (SVL up to 594 mm); primary temporals two; external ear opening without lobules; loreals two; supralabials seven or eight; infralabials six or seven; nuchals in three pairs; midbody scales in 28 rows; dorsal scales smooth, in six rows across the back; paravertebral scales 60–67, not widened; ventral scales in 60–70 rows; ten smooth lamellae beneath finger IV and 13–15 beneath toe IV; toes not reaching to fingers when limbs adpressed along body; dorsal surface of body and tail bronze brown with few black spots, a dark stripe running from nostril to eye and extending from posterior corner of eye along upper part of flank to the middle of the tail.

Description of holotype. Size medium (SVL 54.86 mm), tail regenerated (TaL 35 mm); head longer than wide (HL 9.1 mm, HW 6.57 mm, SVL/HL 6.02); snout obtuse, round anteriorly; rostral wider than high, distinctly visible from above; supranasals absent; frontonasal wider than long, in contact with rostral, nasals, anterior loreals, and frontal; prefrontals not in contact with each other; frontal narrowing posteriorly, approximately 1.8 times longer than the distance to the tip of snout, in contact with prefrontals, first and second supraoculars,

Figure 3. Holotype of *Scincella truongi* sp. nov. (IEBR R.6329) in life, adult male. Photographs: AVP.

and frontoparietals; frontoparietals in contact with each other anteriorly, bordered by frontal, three supraoculars, parietals, and interparietal; interparietal lozenge-shaped, transparent spot posteriorly absent; parietals in contact posteriorly, posterolateral border surrounded by three scales on each side; nuchal scales in three pairs; nostril in center of nasal, in contact with rostral, frontonasal, loreal, first supralabial; loreals two, anterior loreal higher but narrower than posterior one; preocular one; presuboculars two, in contact with lower preocular, third and fourth supralabials; supraciliaries seven; supraoculars four, the first longest, the second widest, fourth supraocular followed by a small postsupraocular; postoculars three, anterior one in contact with seventh supraciliary, postsupraocular, and upper postsubocular; postsuboculars two, lower one in contact with sixth supralabial; primary temporals two, lower one in contact with sixth and seventh supralabials; secondary temporals two, upper very large, in contact with posterolateral, border of parietal, overlapped by lower one; lower eyelid with an undivided opaque window (central disc), separated from supralabials by two rows of granular scales; supralabials seven, fifth below the eye; external ear opening present, anterior margin with indistinct lobules, tympanum deeply sunk; mental wider than long, round anteriorly, in contact with anterior infralabials and postmental; infralabials seven, first small; postmental undivided, in contact with mental, first and anterior portion of second infralabials on each side, and first pair of chinshields; chinshields in three pairs, first pair in contact with each other medially, second pair separated from each other by a gular scale, and third pair separated from each other by three scales; midbody scales in 28 rows; dorsal scales smooth, in six rows across the back; paravertebral scales 67, not widened; ventral scales smooth, in 68 rows; precloacals four, inner scales overlapping outer ones, central two enlarged, left one overlapped by right one; tail thick at base, medial subcaudals widened vertical length of tail. Limbs relatively developed (SVL/FIL 4.28, SVL/HIL 3.0), pentadactyl, dorsal

Figure 4. Holotype of *Scincella truongi* sp. nov. (IEBR R.6329) in preservative **A** dorsal view **B** ventral view. Photographs: AVP.

surface of digits covered by two scale rows on basal and by a single row on terminal phalanges; subdigital lamellae keeled, in one row under the digits, ten under fourth finger and 15 under fourth toe; toe and finger separated when adpressed along body, adpressed forelimb reaching to eye (Table 3).

Coloration in life. Dorsal surface of body and tail bronze brown with black spots; a dark stripe running from nostril to eye and extending from posterior margin of eye along upper part of flank and tail middle; lateral side of the head and flank with a few white spots; chin, throat and venter cream, outer edge of ventral scales dark grey; underside of fore and hind limbs lightly brown; ventral surface of tail greyish cream (Figs 3, 6, 7).

Variation. IEBR R.6330 has 7/8 supralabials; infralabials 6/6 in paratype (HUS.2024.04); paravertebral scales 60 in IEBR R.6330, 65 in HUS.2024.01 and HUS.2024.03, 63 in HUS.2024.02, 66 in HUS.2024.04; ventrals in transverse rows 60 in IEBR R.6330, 64 in HUS.2024.01 and HUS.2024.04, 70 in HUS.2024.02, 65 in HUS.2024.03; lamellae on toe IV 14 in IEBR R.6330, 64 in HUS.2024.01 and HUS.2024.02, 15 in HUS.2024.04, 13 in HUS.2024.03.

Distribution. *Scincella truongi* sp. nov. is currently known only from the type locality in Son La Province, Vietnam (Fig. 1).

Natural history. Specimens were found on the ground in leaf litter of evergreen forest during the daytime between 8:00 and 16:00. The surrounding habitat was evergreen forest with large, medium, and small hardwoods mixed with shrubs. Air temperatures at the sites ranged from 26.0–34.0 °C and relative humidity was 50–70%. Other reptile species encountered at the sites included

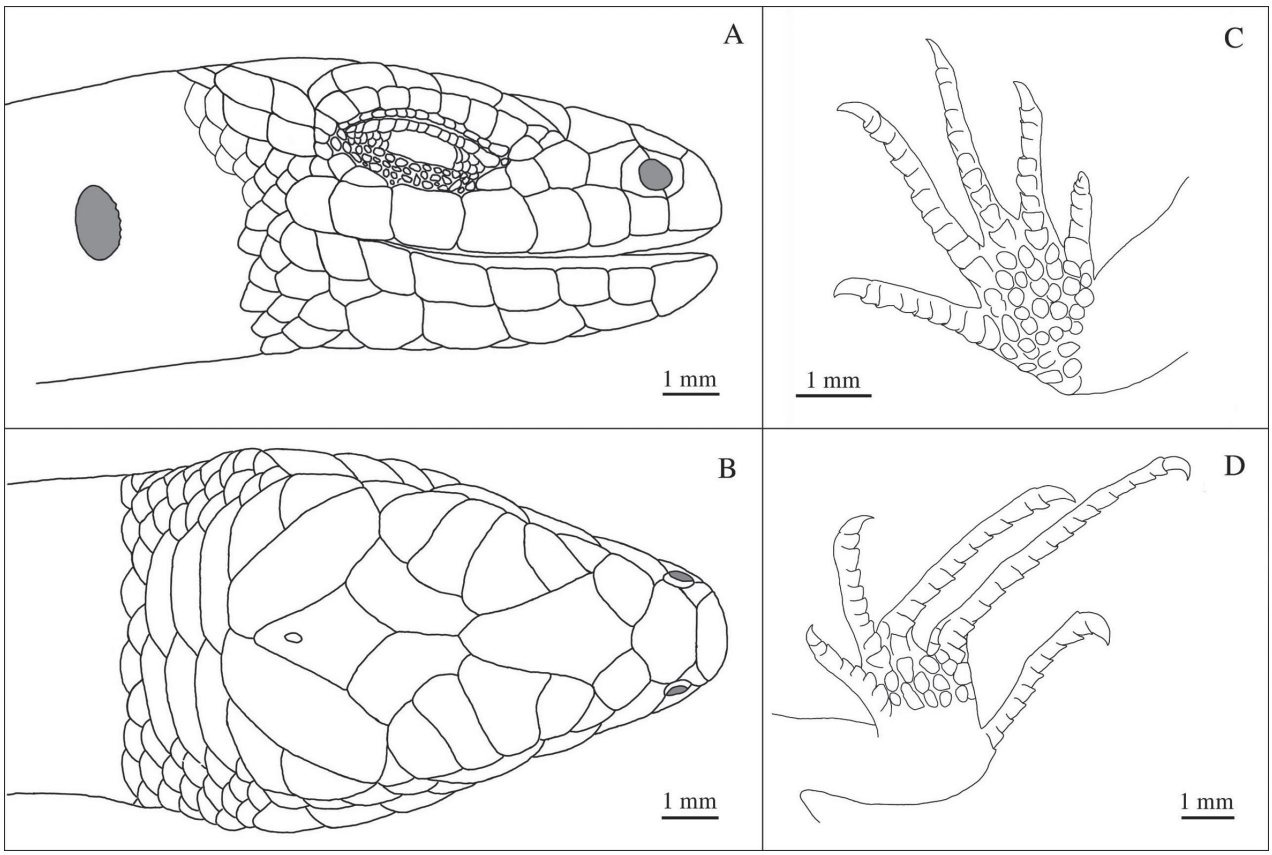

Figure 5. Holotype of *Scincella truongi* sp. nov. (IEBR R.6329): Head **A** lateral view **B** dorsal view **C** hand **D** foot. Photographs: TNH.

Acanthosaura lepidogaster (Cuvier), *Sphenomorphus indicus* (Gray), and *Pareas hamptoni* (Boulenger).

Etymology. We name the new species in honor of Prof. Dr. Truong Quang Nguyen from the Institute of Ecology and Biological Resources, Vietnam Academy of Science and Technology, in recognition of his great contributions to the herpetofaunal exploration of the Indochina region. We recommend "Truong's Smooth Skink" as the common English name and "Thằn lằn cổ trường" as the common name in Vietnamese for the new species.

Comparisons. We compared the new species with other known taxa in the genus *Scincella* from Asia based on examination of specimens and data obtained from the literature.

Morphologically, the new species resembles *Scincella ochracea* and *S. ouboteri* two other species known from northwestern Vietnam. However, they are distinguished from *S. ochracea* by having a larger size in the new species (males with maximum SVL 49.0 mm, *n* = 1 vs 45.4 mm, *n* = 7 and females with maximum SVL 59.4 mm, *n* = 4 vs 51.0 mm, *n* = 8), external ear opening without lobules (vs present), prefrontal in separate (vs contact), fewer midbody scale rows (28 vs 30–32), fewer lamellae beneath toe IV (13–15 vs 15–17), and different dorsal color pattern (dorsum with black spots vs with a dark discontinuous stripe) and from *S. ouboteri* by having fewer midbody scale rows (28 vs 30–32), fewer lamellae beneath toe IV (13–15 vs 18–20), toes separating fingers when limbs adpressed along body (vs overlap), and different dorsal color pattern (dorsum with black spots vs with two silver grey stripes, wide dark stripes) (Table 3).

Table 3. Morphological comparison between *Scincella truongi* sp. nov. and two similar taxa from northwestern Vietnam.

Selected characters	*Scincella truongi* sp. nov.	*S. ouboteri*	*S. ochracea*
	n = 6	*n* = 10	*n* = 15
SVL	49.0–59.4	40.9–58.6	42.3–51.0
TaL	91.8–100.8	52.9–76.9	62.3–75.0
AG	25.3–34.3	22–34.3	20.8–30.0
SL	3.6–4.2	3.5–4.3	2.4–3.4
STL	9.3–10	8.0–10.2	7.0–8.7
SFIL	17.9–19.5	14.9–20.1	12.4–16.2
END	2.4–2.7	2.1–2.6	1.8–2.2
EL	2.7–3.2	2.2–3.0	1.7–2.9
HL	8.8–9.6	7.8–9.5	6.9–8.2
HW	5.9–7.1	5.4–7.5	4.8–5.8
HH	4.7–5.5	4.0–5.3	3.6–4.4
TYD	1.3–1.5	1.5–2.0	1.3–1.6
FIL	12.3–13.6	9.9–13.5	7.6–10.4
HIL	17.3–19.6	16.4–19.5	13.9–16.6
Scalation			
Supraoculars	4	4	4
Nuchals	3	2–4	0–3
Loreals	2	2	2
Supraciliaries	7	7	7–8
Primary temporals	2	2	1
Secondary temporals	2	2	2
Supralabials (R/L)	7–8	7	7–8
Auricular lobules		3–4	3–4
Infralabials	6–7	6–7	5–6
Chin shields (pairs)	3	3	3
Midbody scale rows	28	32	30–32
Paravertebral scales	60–67	65–73	61–67
Ventrals in transverse rows	60–70	65–71	66–71
Precloacals (enlarged)	4	4	4–4
Lamellae on finger IV	10	10–12	9–11
Lamellae on toe IV	13–15	18–20	15–17

Scincella truongi sp. nov. has two primary temporals and thus differs from the following species in the genus *Scincella*: *S. apraefrontalis*, *S. baraensis*, *S. darevskii*, *S. devorator*, *S. melanosticta*, *S. monticola*, *S. punctatolineata*, and *S. rara*, which have only one primary temporal. The new species has toes not reaching fingers when limbs being adpressed along body, which differs from the following species, where toes and fingers do overlap: *S. baraensis*, *S. badenensis*, *S. dunan*, *S. formosensis*, *S. macrotis*, *S. melanosticta*, *S. reevesii*, and *S. rupicola*. In addition, the new species has the external ear opening without lobules and thus differs from the following taxa (external ear opening with lobules): *S. boettgeri*, *S. darevskii*, *S. ouboteri*, and *S. reevesii*.

The new species differs from *S. apraefrontalis* by having more midbody scale rows (28 vs 18), more paravertebral scales (60–67 vs 52), more ventral scales (60–70 vs 50), dorsal scales not enlarged (vs distinctly enlarged), more lamellae beneath toe IV (13–15 vs 8 or 9), and the presence of prefrontal (vs absent); from *S. baraensis* by having fewer dorsal scale rows on back (6 vs 8), fewer midbody scale rows (28 vs 30), and fewer lamellae beneath toe IV (13–15 vs 18–20); from *S. badenensis* by having more nuchal pairs (3 vs 0–1), fewer midbody scale rows (28 vs 32–36), and fewer lamellae beneath toe IV (13–15 vs 18–20);

Figure 6. Paratype of *Scincella truongi* sp. nov. (HUS.2024.01) in life, adult female. Photographs: AVP.

Figure 7. Paratype of *Scincella truongi* sp. nov. (HUS.2024.03) in life, adult female. Photographs: AVP.

from *S. barbouri* by having fewer paravertebral scale (60–67 vs 70–79) and fewer nuchal pairs (3 vs 4 or 5), and more supraciliaries (7 or 8 vs 5 or 6); from *S. boettgeri* by having more nuchal pairs (3 vs 2); from *S. capitanea* by having fewer midbody scale rows (28 vs 30–32) and smaller body size (49.0–59.4 mm vs 78.5 mm); from *S. darevskii* by having fewer lamellae beneath toe IV (13–15 vs 17) and fewer supraoculars (4 vs 5); from *S. devorator* by having fewer lamellae beneath toe IV (13–15 vs 17–19) and different dorsal color pattern (dorsum with black spots vs with two silver grey stripes, wide dark stripes); from *S. doriae* by having fewer

nuchal pairs (3 vs 4 or 5) and fewer midbody scale rows (28 vs 30–32); from *S. dunan* by having prefrontal in separate (vs contact) and and different dorsal color pattern (dorsum with a few black spots vs with many black spots); from *S. huanrenensis* by having fewer ventral scales (60–70 vs 75–89); from *S. liangshanensis* by having different dorsal color pattern (dorsal surface bronze brown with black spots (vs light brown with central dark brown) and more midbody scale rows (28 vs 23–27); from *S. macrotis* by having more nuchal scales (3 pairs vs 2) and fewer midbody scale rows (28 vs 31 or 32); from *S. melanosticta* by the presence of nuchal scales (3 pairs vs absent), fewer lamellae beneath toe IV (13–15 vs 16–22), fewer midbody scale rows (28 vs 34–38), and fewer dorsal scale rows on back (6 vs 10); from *S. modesta* by having more supraciliaries (7 or 8 vs 5–7), upper margin of lateral longitudinal striation relatively straight (vs wavy); prefrontal in separate (vs contact), and different lateral color pattern (upper margin of lateral with a dark stripe vs lateral dark with light spots); from *S. monticola* by having more midbody scale rows (28 vs 22–26), more paravertebral scales (60–67 vs 52–59), more dorsal scale rows on back (6 vs 4), and more ventral scales (60–70 vs 52–58); from *S. nigrofasciata* by having more nuchal scales (3 pairs vs 0 or 1), fewer midbody scale rows (28 vs 32–33), and fewer dorsal scale rows on back (6 vs 8); from *S. potanini* by having more midbody scale rows (28 vs 27) and fewer lamellae beneath toe IV (13–15 vs 17); from *S. przewalskii* by having more supralabials (7 vs 6), fewer midbody scale rows (28 vs 32–34), and fewer lamellae beneath toe IV (13–15 vs 17); from *S. punctatolineata* by having larger body size (SVL 49.0–59.4 mm vs 37.6–40.2 mm) and more nuchal scales (3 pairs vs 0–2); from *S. rara* by having more midbody scale rows (28 vs 24), more paravertebral scales (60–67 vs 53), and a single row of lamellae beneath toes II–IV (vs double rows); from *S. reevesii* by the presence of nuchals scales (3 pairs vs 0 or 1), fewer midbody scale rows (28 vs 29–35), and fewer dorsal scale rows on back (6 vs 8); from *S. rufocaudata* by the presence of nuchal scales (3 pairs vs absent), fewer dorsal scale rows on back (6 vs 10), and fewer midbody scale rows (28 vs 30–34); from *S. rupicola* by having fewer midbody scale rows (28 vs 34–36), fewer dorsal scale rows on back (6 vs 8), and the presence of nuchals scales (3 pairs vs 0 or 1); from *S. schmidti* by having more midbody scale rows (28 vs 26) and more lamellae beneath toe IV (13–15 vs 11); from *S. tsinlingensis* by having fewer paravertebral scales (60–67 vs 70–90) and fewer ventral scales (60–70 vs 70–90); from *S. vandenburghi* by having more lamellae beneath toe IV (13–15 vs 12) and upper margin of lateral longitudinal striation relatively straight (vs wavy); from *S. victoriana* by having more midbody scale rows (28 vs 26) and dorsal scales smooth (vs keeled); and from *S. wangyuezhaoi* by having fewer ventral scales (60–70 vs 71–89) and different dorsal color pattern (bronze-brown with black spots vs dark bronze-brown).

Discussion

Over the last five years, six additional species have been described within the genus *Scincella* (Uetz et al. 2024). Three of the species, i.e., *S. badenensis*, *S. baraensis*, and *S. ouboteri*, were newly discovered and recorded in Vietnam (Nguyen et al. 2019, 2020; Pham et al. 2024). Our discovery brings the number of *Scincella* species in Son La Province to three, and in Vietnam to 16. In terms of morphology, *S. truongi* closely resembles the distantly related *S. ochracea* and *S. ouboteri* but the new species differs from *S. ochracea* by having a larger

body size, external ear opening without lobules, separated prefrontal, fewer midbody scale rows, fewer lamellae beneath toe IV, and different dorsal color pattern and from *S. ouboteri* by having fewer midbody scale rows, fewer lamellae beneath toe IV, toes not reaching fingers when limbs being adpressed along body, and different dorsal color pattern. In the phylogenetic tree, the new species was recovered as an independent lineage with no clear sister taxon.

The new species is currently only found in Sop Cop Nature Reserve, a protected area established in 2002 in Son La Province. Although the new species has a small known range with an estimate of less than 50 km^2, which has been experiencing severe habitat degradation primarily as a result of road construction and timber logging it is unclear whether these activities will significantly threaten its population, but it likely adversely affects it. We recommend listing the species as Data Deficient based on the IUCN Red List categories and criteria. Further research is needed to clarify the population status of this species and to determine specific anthropogenic threats at the site.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

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Data availability

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

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