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A new species of skink from mountains of southern Vietnam (Reptilia, Squamata, Scincidae)

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Abstract: We provide an integrative taxonomic revision of miniaturized sphenomorphine skinks from Vietnam and Cambodia based on morphological analysis and COI DNA barcoding. Our data reveal a new species, *Sphenomorphus valentinae* **sp. nov**., from Chu Yang Sin National Park, Dak Lak Province, Vietnam. The new species is distinguished from other congeners by the following combination of morphological characters: long and short-legged skink with pentadactyl limbs; *SVL* 28.1–37.5 mm, *TAL* 49.4–62.3 mm; ear opening concealed; scales smooth; supranasal and postnasal absent; the lower eyelid movable and scaly; prefrontals two, separated; supraoculars four; supraciliaries eight; presuboculars two; primary temporals three; supralabials six, first fused with the nasal; infralabials four; chin shields in three pairs; nuchals not enlarged; paravertebral scales rows 50–55; ventral scales rows 52–56; midbody scale rows 18; five subdigital lamellas beneath the fourth finger; six subdigital lamellas beneath the fourth toe; dorsal surfaces brown-beige, iridescent, with dark spots forming four thin longitudinal lines; ventral surfaces from light brown to grayish pink; a light dorsolateral stripe ventrally edged with dark brown extends from the posterior edge of the eye to the tail. We also show that *Sphenomorphus sheai*, which was found in Quang Nam Province, Vietnam, represents a junior synonym of *Lygosoma veunsaiense*, which was found in Ratanakiri Province, Cambodia. We redescribe this taxon and tentatively regard it as *Sphenomorphus veunsaiensis* **comb. nov**. (Geissler, Hartmann & Neang, 2012). We provide new information on distribution and discuss the discrepancies in taxonomy and diagnostics of *S. veunsaiensis*, *S. tridigitus*, *S. tetradactylus*, and *Leptoseps poilani* in Indochina. Further field survey efforts and examination of available type materials are required to achieve a better understanding of the diversity of miniaturized sphenomorphine skinks in the region.

Keywords: *Sphenomorphus valentinae* **sp. nov**., *Lygosoma veunsaiense*, *Sphenomorphus sheai*, *Sphenomorphus tridigitus*, Indochina, Cambodia, Laos, Truong Son Mountains

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INTRODUCTION

Skinks (Scincidae Oppel, 1811) form the largest lizard family on the globe (Chapple et al., 2023). Within Indochina, currently 101 species of skinks are recognized as being valid (Poyarkov et al., 2023). However, this number does not reflect the actual number of species within the region. Beside others, there are two main challenges that made and make it extremely difficult to assess scincid actual species richness and the phylogenetic relationships between different taxonomic units, especially in tropical areas like Vietnam.

Firstly, during their evolution, skinks underwent extreme ecological and morphological diversification (Greer, 2007). In fossorial skinks, there have been more than 25 independent cases and stages of body elongation and limb reduction in relatively short time scales (Greer, 1990; Skinner et al., 2008). In Indochina, skinks with elongated bodies and short, reduced, or absent limbs occur in every of the present skink subfamilies except the Mabuyinae Mittleman, 1952. Their morphological similarities are a result of their convergent adaptation to a fossorial life mode and do not reflect their actual phylogenetic relationships. In studies that only considered morphological traits, this often led to false generic assignments and the establishment of para- or polyphyletic genera (e.g., *Lygosoma* Hardwicke & Gray, 1827; *Scincella* Mittleman, 1950; and *Sphenomorphus* Fitzinger, 1843).

Secondly, among all lizard families, skinks comprise the largest number of species, known only from their type specimens, and a comparatively high number of species with very small known distribution areas (Meiri et al., 2018). This causes a tremendous lack of information on their morphological variation. Therefore, we often misinterpret smaller differences in scale counts and other traits within a species' actual variation range. This resulted in a number of described synonyms, of which many are probably still to be uncovered, e.g., *Lygosoma corpulentum* Smith, 1921, and *Lygosoma carinatum* Darevsky & Orlova, 1996, both from southern Vietnam (Geissler et al., 2011).

The above-mentioned difficulties in skink taxonomy also might have played a role in the interpretation of morphological data from specimens from Vietnam and Cambodia, which were described as two species from two different genera: *Lygosoma veunsaiense* Geissler, Hartmann & Neang, 2012, and *Sphenomorphus sheai* Nguyen, Nguyen, Van Devender, Bonkowski & Ziegler, 2013. Both species were only described based on one single specimen and only based on a morphological dataset (Geissler et al., 2012; Nguyen et al., 2013). Some years later, Le et al. (2020) documented additional specimens from the Central Highlands (Tay Nguyen) Region of Vietnam, which they did assign to *S. sheai*. These recently collected specimens did largely agree with the diagnosis of *S. sheai* (Le et al., 2020). Interestingly, Le et al. (2020) also showed a broad morphological overlap of their material with specimens of another miniaturized skink species, *Sphenomorphus tridigitus* (Bourret, 1939), except for the number of digits. A newly discovered population of miniaturized skinks from Dak Lak Province in southern Vietnam showed similarities with all three above-mentioned species and led us to the new integrative taxonomic approach presented within this manuscript.

MATERIAL AND METHODS

Sample collection. Specimens of *Sphenomorphus* spp. were collected from montane evergreen tropical forests within the Chu Yang Sin National Park, Dak Lak Province, southern Vietnam, on April 15–28, 2024, by N. A. Poyarkov and A. M. Bragin; from montane evergreen forests within the An Toan Nature Reserve on May 05–16, 2024, by N. A. Poyarkov, A. M. Bragin, and S. X. Le; from montane evergreen forests within the Kon Ka Kinh National Park, Gia Lai Province, and Kon Chu Rang National Park, Gia Lai Province, on May 15 – June 5, 2016, April 15 – May 5, 2017, and April 15 – May 30, 2018, by N. A. Poyarkov and S. X. Le (Fig. 1). Geographic coordinates and elevation were obtained using a Garmin GPSMAP 60CSx and recorded in the WGS 84 datum. Specimens were collected by hand during the day (10:00–15:00 h) from leaf litter and under fallen tree logs. Specimens were photographed in life, and euthanized using MS-222 solution within 24 h after capture. Specimens were subsequently fixed in 4% buffered formalin for 24 h and later stored in 70% ethanol. Specimens were subsequently deposited in the herpetological collections of the Zoological Museum of Moscow University (ZMMU, Moscow, Russia) and the Joint Vietnam–Russia Tropical Science and Technology Research Centre (VRTC, Hanoi, Vietnam). **Other abbreviations:** Mt.: Mountain; NP: National Park; NR: Nature Reserve; Prov.: Province; Distr.: District; Comm.: Commune; a.s.l.: above sea level.

Specimen collection and animal use protocols were approved by the Institutional Ethical Committee of the Joint Vietnam–Russia Tropical Science and Technology Research Center (VRTC). Field work in Chu Yang Sin NP, including collection of animals in the field and specimen exportation, was authorized by the People's Committee of Dak Lak Prov., Vietnam (No. 487/SNgV-LSBG of March 28, 2024); field work in An Toan NR was authorized by the People's Committee of Binh Dinh Prov., Vietnam (No. 487/SNgV-LSBG of March 28, 2024); field work in Kon Ka Kinh NP and Kon Chu Rang NP was authorized by the Ministry of Natural Resources and Environment of Vietnam (No. 547/TCLN-BTTN of April 21, 2016), and by the People's Committee of Gia Lai Prov., Vietnam (Nos. 1951/UBND-NV of May 04, 2016; 142/SNgV-VP of April 11, 2017; 432/TCLN-BTTN of March 30, 2017; and 530/UBND-NC of March 20, 2018), all granted to VRTC.

Morphological data and analyses. Measurements were acquired using digital calipers (X-PERT Xp150) to the nearest 0.1 mm under the Olympus SZ61 and the Nikon SMZ460 dissecting microscopes with the Olympus SC180 digital camera. The morphological characters examined were modified from Ouboter (1986), Geissler et al. (2012), Nguyen et al. (2013), and Grismer et al. (2019, 2020) and included the following measurements: snout-vent length (*SVL*), from the tip of the rostral scale to the vent; tail length (*TAL*), from the vent to the tip of the tail; tail width (*TW*), measured at the base of tail; axilla-groin length (*AG*), measured from the posterior margin of the forelimb to the anterior margin of the hind limb; head length (*HL*1), from the tip of the snout to the angle of jaws from the lateral view; head length (*HL*2), from the tip of the snout to the posterior parietal from the dorsal view; interorbital distance (*IO*), distance between anterior edges of the orbits from the dorsal view; head width (*HW*), the widest point of the head posterior to the eyes; head height (*HH*), the highest part of the head posterior to the eyes; body width (*BW*), the widest point of the body closer to the hind limbs; internarial distance (*IN*), distance between inner edges of nares from the dorsal view; eyeball diameter (*ED*), the anterior to the posterior margins of the eyeball; eye-nostril length (*EN*), from the margin anterior of the orbit to the posterior margin of the nares; snout length (*SL*), from the tip of the snout to the anterior border of the orbit; snout-forelimb length (*SFIL*), from the tip of the snout to the anterior margin of the forelimb insertion on the body; forelimb length (*FIL*1), from the axilla (the insertion point of the forelimb on the body) to the base of the palm; forelimb length (*FIL*2), from the insertion point of the forelimb on the body to the tip of the fourth finger on an outstretched limb; hindlimb length (*HIL*1), from the groin (the insertion point of the hindlimb on the body) to the base of the heels; hindlimb length (*HIL*2), from the insertion point of the hindlimb on the body to the tip of the fourth toe on an outstretched limb. We also calculated the following ratios: *AG*/*SFIL*, *SVL*/*FIL*, *SVL*/*HIL*, *TaL*/*SVL*, *HL*/*SVL*, *FlL*/*SVL*, and *HlL*/*SVL* to make our data comparable with the data presented in Geissler et al. (2012) and Nguyen et al. (2013), respectively.

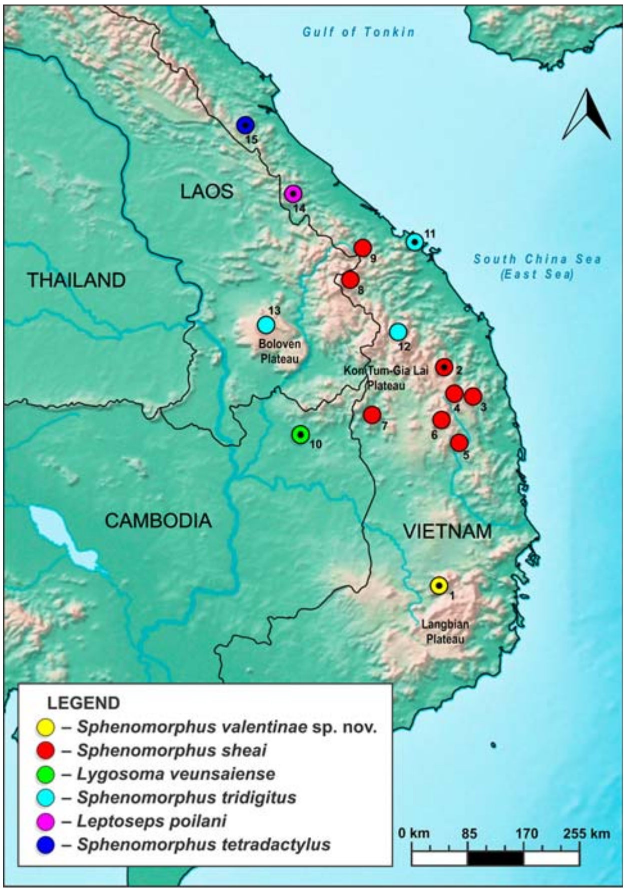

Fig. 1. Distribution of miniaturized sphenomorphine skinks in central Vietnam, Cambodia, and Laos. Dot in the center of an icon denotes type locality of a taxon; colors correspond to those used in Fig. 2. Base map created using simplemappr.net. Locality information: *1* – Chu Yang Sin NP, Dak Lak Prov., Vietnam (this study); *2* – Border between Quang Ngai and Kon Tum Provs., Vietnam (Nguyen et al., 2013); *3* – An Toan NR, Binh Dinh Prov., Vietnam (this study; ZMMU NAP-15989); *4* – Kon Chu Rang NP, Gia Lai Prov., Vietnam (this study; ZMMU NAP-06371); *5* – Tram Lap, Gia Lai Prov., Vietnam (Le et al., 2020); *6* – Kon Ka Kinh NP, Gia Lai Prov., Vietnam (this study; ZMMU NAP-05515–05517); *7* – Chu Mom Ray NP, Kon Tum Prov., Vietnam (this study; ZMMU NAP-04327); *8* – Tay Giang Protected Forest, Quang Nam Prov., Vietnam (this study; ZMMU NAP-12082); *9* – Sao La NR, A'Roang, A'Luoi Distr., Thua Thien-Hue Prov., Vietnam (this study; ZMMU NAP-14150); *10* – O'Kasieb Campsite, Veun Sai Dist., Ratanakiri Prov., Cambodia (Geissler et al., 2012); *11* – Bach Ma NP, Thua Thien-Hue Prov., Vietnam (Bourret, 1939; Le et al., 2020); *12* – Ngoc Linh NP, Dak Glei Dist., Kon Tum Prov., Vietnam (Le et al., 2020); *13* – Xepian, Boloven Highlands, Champasak Prov., Laos (Greer et al., 2006); *14* – Dong Tam Ve, now Bac Huong Hoa NR, Huong Hoa Distr., Quang Tri Prov., Vietnam (Bourret, 1937); *15* – Phong Nha-Ke Bang NP, Quang Binh Prov., Vietnam (Darevsky, Orlov, 2005; Luu et al., 2013)

Scale counts taken included: the number of supraoculars contacted by the frontoparietal (*F-SO*); the degree of contact of prefrontals with each other, and with the frontal (PF); the total number of nuchal scales (*Nu*) counted as the number of scales between opposing upper secondary temporals (*UST*) on each side of the head that contact the parietals; number of primary and secondary temporals (*PT* and *ST*, respectively); the character of overlapping of the lower secondary and the upper secondary temporal scales (*UST-LST*); the total number of supranasal and postnasal scales (SN-PN), supraciliaries (*SC*), supraoculars (*SO*), loreals (*L*, *AL*, *PL*), preoculars (*PR*), presuboculars (*PRS*), postoculars (*PO*), postsuboculars (*PSO*), supralabials (*SL*) and infralabials (*IF*), chin shields (*Cs*) on each side of the head; character of the scalation of the lower eyelid; number of midbody scale rows (*TMR*) counted as the number of longitudinal scale rows encircling the body at a point midway between the limb insertions; paravertebral scale rows (*Mds*) counted as the number of scales in a line from, but not including, the nuchal scales to a point on the dorsum opposite the vent; transverse dorsal scale rows (*ER*), counted between the upper edges of the body; ventral scale rows (*VR*) counted as a row of scales between the postmental and the precloacal scales; the number of enlarged precloacal scales (*PrC*); fourth toe and finger subdigital lamellas (*TL*4 and *FL*4, respectively); the number of fingers (*F*) and toes (*T*). Scalation features were counted bilaterally and are given in left/right order when different. The hemipenial structures were described following Vergilov et al. (2017).

Laboratory methods. For the newly-obtained samples of *Sphenomorphus* spp. from Vietnam and the holotype of *Lygosoma veunsaiense*, we analyzed a 654 bp fragment of the cytochrome oxidase I subunit (COI) mitochondrial DNA. We conducted the molecular analysis at the Department of Vertebrate Zoology, Faculty of Biology, Lomonosov Moscow State University (MSU), Moscow, Russia. We extracted the total genomic DNA using the standard phenol-chloroform extraction protocol (Sambrook et al., 1989). We performed PCR amplification using MyCycler BioRad, following the conditions described by Ivanova et al. (2006). For PCR and sequencing, we used the following primers: VF1d (5'-TTCTCAACCAACCACAARGAYATYGG-3', forward) and VR1d (5'-TAGACTTCTGGGTGGCCRAARAAYCA-3', reverse) (Ivanova et al., 2006). The PCR reaction volume was 20 μL, and it contained ca. 100 ng of template DNA, 0.3 pM/μL of each PCR primer, 1xTaq-buffer with 25 mM of MgCl2 (Silex, Moscow, Russia), 0.2 mM dNTPs, and 1 unit of Taqpolymerase (Silex, Moscow, Russia; 5 units/μL). The results of the amplification were examined using electrophoresis on a 1% agarose gel in the presence of ethidium bromide. The successful targeted PCR products were purified by the Diatom DNA PCR Clean-Up kit and outsourced to Evrogen® (Moscow, Russia) for sequencing; sequence data collection and visualization were performed on an ABI 3730xl Automated Sequencer (Applied Biosystems).

Phylogenetic analyses. We first used Seaview 5 (Gouy et al., 2021) to align annotated mitogenomes from seven Scincidae species, including representatives of the subfamilies Sphenomorphinae (genera *Sphenomorphus*, *Scincella*, *Tropidophorus* Jan, 1865, and *Isopachys* Lönnberg, 1916) and Lygosominae (genera *Lygosoma* and *Eutropis* Fitzinger, 1843), and the sequence of mitogenome of *Plestiodon liui* (Hikida & Zhao, 1989) (subfamily Scincinae), which was used to root the tree. The repetitive elements, the control region (CR), and tRNA sequences were then trimmed, as in most cases these fragments could not be properly aligned, resulting in a mtDNA alignment with a total length of up to 15.591 bp. Using the mitogenome alignment as an anchor, we then manually aligned sequences from partial sequences of COI obtained for the newly collected specimens of Sphenomorphus spp. and the holotype of *Lygosoma veunsaiense* and added these sequences to the alignment. In total, genetic information from 16 specimens of Scincidae was included in our phylogenetic analyses (summarized in Table 1).

Sequences were aligned using Seqman 5.06 and verified using BioEdit Sequence Alignment Editor 7.1.3.0 (Hall, 1999). Mean inter- and intraspecific uncorrected genetic *p*-distances and sequence characteristics were calculated in MEGA X (Kumar et al., 2018). We applied the Bayesian inference (BI) and maximum likelihood (ML) approaches to infer mtDNA-genealogy for the dataset. The BI approach was implemented using MrBayes v.3.1.2 software (Huelsenbeck, Ronquist, 2001; Ronquist, Huelsenbeck, 2003).

PartitionFinder v1.0.1 (Lanfear et al., 2012) was used to estimate the optimal nucleotide substitution models, resulting in HKY+G as the best-fit model for all three codon partitions of the COI gene, as suggested by the Akaike information criterion (AIC). In MrBayes, phylogenetic analysis was performed with two simultaneous runs, each with four chains, for five million generations; 10% of the generations were cut as burn in. The convergence of the runs was verified to make sure that the effective sample sizes (ESS) were all above 200 by examining the likelihood plots using TRACER v.1.5 (Rambaut, Drummond, 2007).

The ML tree was generated using the IQ-TREE webserver (Nguyen et al., 2015); preceded by the selection of substitution models using the Bayesian Information Criterion (BIC) in MODELFINDER (Kalyaanamoorthy et al., 2017), which supported TrN+I+G for COI codon positions 1 and 2, and GTR+F+I+G for position 3.

Table 1. Sequences and voucher specimens of *Sphenomorphus*-like skinks and outgroup taxa used in this study

Museum ID	GenBank AN	Species	Locality
Ingroup			
ZMMU Re-17931	PP931013	*Sphenomorphus valentinae* **sp. nov.**	Chu Yang Sin NP, Dak Lak Prov., Vietnam
ZMMU Re-17932	PP931014	*Sphenomorphus valentinae* **sp. nov.**	Chu Yang Sin NP, Dak Lak Prov., Vietnam
VRTC NAP-15987	PP931015	*Sphenomorphus valentinae* **sp. nov.**	Chu Yang Sin NP, Dak Lak Prov., Vietnam
ZMMU NAP-05515	PP931016	*Sphenomorphus sheai*	Kon Ka Kinh NP, Gia Lai Prov., Vietnam
ZMMU NAP-07141	PP931018	*Sphenomorphus sheai*	Kon Ka Kinh NP, Gia Lai Prov., Vietnam
ZMMU NAP-06168	PP931019	*Sphenomorphus sheai*	Kon Ka Kinh NP, Gia Lai Prov., Vietnam
ZMMU NAP-05516	PP931020	*Sphenomorphus sheai*	Kon Ka Kinh NP, Gia Lai Prov., Vietnam
ZMMU NAP-06371	PP931021	*Sphenomorphus sheai*	Kon Chu Rang NP, Gia Lai Prov., Vietnam
CBC 00808	PP931017	*Lygosoma veunsaiense*	O'Kasieb, Seun Sai Distr., Ratanakiri Prov., Cambodia
JAM 1892	JQ610821	*Lygosoma bowringii*	Johor State, Malaysia
–	MH020638	*Isopachys gyldenstolpei*	Myanmar
–	OM117612	*Tropidophorus hainanus*	Jinxiu, Guangxi Prov., China
–	MN786972	*Scincella modesta*	Nanjing Prov., China
–	MH329292	*Sphenomorphus incognitus*	Huangshan, Anhui Prov., China
–	MN938934	*Eutropis multifasciata*	–
Outgroup			
CB202004001	MT662111	*Plestiodon liui*	Wuxi, Jiangsu Prov., China

Confidence in nodal topology for BI analysis was estimated by calculating posterior probabilities (BI PP), and for ML analysis was assessed by 1000 ultrafast bootstrap replications (ML UFBS). The nodes with BI PP values >0.95 and ML UFBS values 95% or above were a priori regarded as strongly supported; BI PP values between 0.95 and 0.90 and ML BS values between 95% and 90% were regarded as moderately supported; while lower values were regarded as indicating not significant node support (Huelsenbeck, Hillis, 1993).

RESULTS

Phylogenetic relationships and genetic distances. We deposited the newly obtained COI sequences in GenBank under the accession numbers PP931013–PP931021 (see Table 1). Phylogenetic relationships among the miniaturized sphenomorphine skinks from Vietnam and Cambodia derived from the analysis of mtDNA alignment are presented in Fig. 2. ML- and BI-analyses resulted in essentially identical topologies and differed only in a few poorly supported nodes, which are not important for our study. Overall, our data provided strong support for the monophyly of the subfamily Sphenomorphinae by both analyses (99/1.0; hereafter the values correspond to ML UFBS and BI PP support values for a given node, respectively; see Fig. 2), while the monophyly of the subfamily Lygosominae was supported by BI-analysis but not in ML-tree (83/0.96). The genus *Sphenomorphus* was found to be paraphyletic, with *S. incognitus* occupying a distant phylogenetic position, while the miniaturized *Sphenomorphus*-like skinks from Vietnam and Cambodia were grouped with the limbless skink *Isopachys*, though with a moderate node support (89/0.92).

All samples of the miniaturized *Sphenomorphus*-like skinks from Vietnam and Cambodia examined in this study were grouped in a well-supported monophylum (100/1.0), which was comprised of two reciprocally monophyletic clades. The first clade (99/1.0) included three samples of *Sphenomorphus* sp. from Chu Yang Sin NP, Dak Lak Province, in the southern part of the Truong Son (Annamite) Mountains. The second clade (99/1.0) included samples from the highlands in the central part of the Truong Son Range in Gia Lai Province of Vietnam, which we identified as *S. sheai*. Surprisingly, the holotype of *Lygosoma veunsaiense* (CBC 00808) from Veunsai Distr., Ratanakiri Prov. of Cambodia, was found to be not a member of *Lygosoma* but a sphenomorphine skink and was deeply nested within the *S. sheai* clade, forming a sister lineage with the sample ZMMU NAP-06371 from Kon Chu Rang NP, Gia Lai Province in Vietnam (100/1.0).

Uncorrected genetic *p*-distances among the miniaturized *Sphenomorphus*-like skinks of Vietnam and Cambodia examined in the present study are summarized in Table 2. All three *Sphenomorphus* sp. samples from Chu Yang Sin NP shared the same COI haplotype. The genetic divergence between the latter population and its closest relatives varied from $p = 3.3\%$ (with *S. sheai*) to $p = 3.7\%$ (with *L. veunsaiense*). Genetic divergence between *S. sheai* and *L. veunsaiense* was minimal ($p = 0.8\%$), while the inter-group divergence among various COI haplotypes revealed within *S. sheai* reached $p = 0.5\%$.

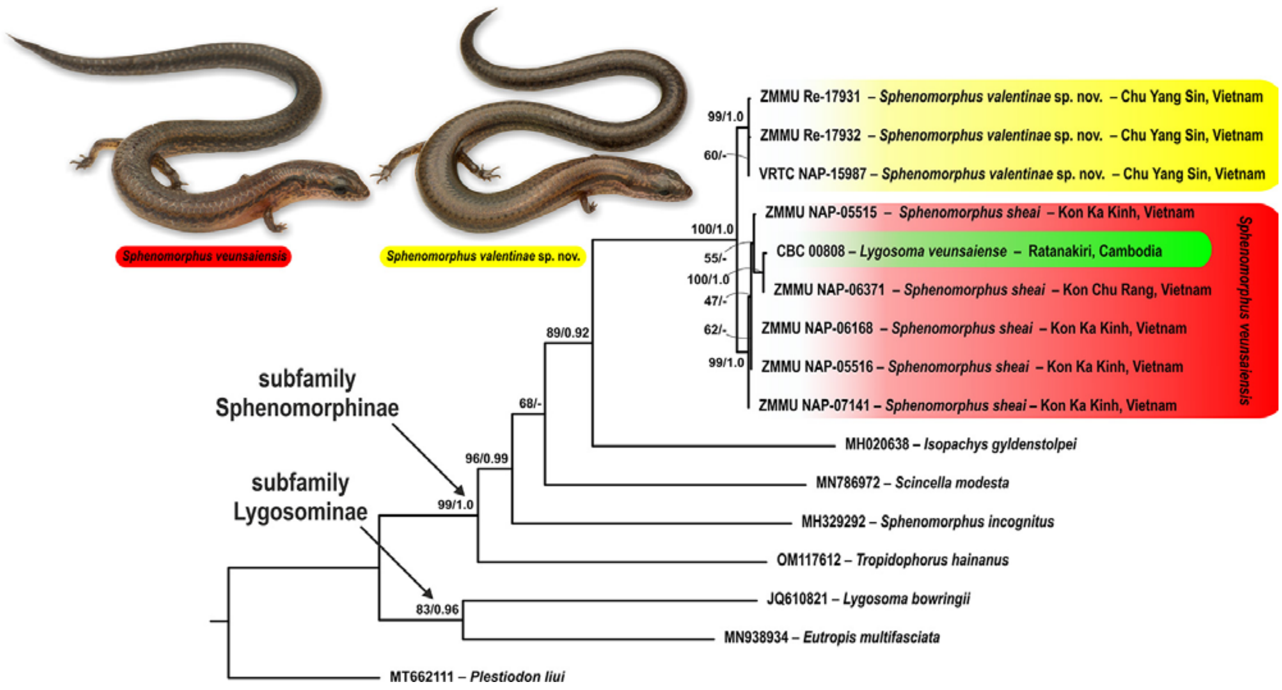

Fig. 2. Phylogenetic relationships among the miniaturized sphenomorphine skinks from Vietnam and Cambodia. ML-tree is derived from the analysis of up to 15.591 bp mtDNA alignment, including 654 bp fragment of COI mtDNA gene for the newly collected samples of *Sphenomorphus* and *Lygosoma*. Numbers at tree nodes correspond to ML UFBS / BI PP support values, respectively. Colors of the mitochondrial lineages in the tree correspond to the colors used in Fig. 1. Photos by A. M. Bragin

Taxonomy

Overall, the study of mtDNA data showed that the populations of the small *Sphenomorphus*-like skinks from Vietnam and Cambodia belong to a well-supported clade within the radiation of sphenomorphine skinks. It was also found that *Lygosoma veunsaiense* does not belong to the subfamily Lygosominae but to the subfamily Sphenomorphinae. Moreover, our analysis recovered two reciprocally monophyletic lineages with a moderate level of divergence in the COI mtDNA gene (p = 3.3–3.7%), one of which corresponds to the newly discovered population of *Sphenomorphus* sp. from Chu Yang Sin NP in Dak Lak Prov. of Vietnam, and the second one joins two populations of *S. sheai* from Gia Lai Prov. of Vietnam and the holotype of *Lygosoma veunsaiense* from Ratanakiri Prov. of Cambodia. A very shallow divergence in COI gene fragment between *Lygosoma veunsaiense* and *S. sheai* populations (p = 0.8%) clearly indicates the intraspecific level of differentiation among them; this result is further corroborated by the fact that the latter two species are almost indistinguishable from each other in external morphology as well, and the reported differences actually result from counting errors made in the original description of *Lygosoma veunsaiense* (Geissler et al., 2012; see discussion below).

Given the evidence from mtDNA-based genealogy and external morphology, we herein formally recognize *Sphenomorphus sheai* Nguyen, Nguyen, van Devender, Bonkowski & Ziegler, 2013 as a subjective junior synonym of *Lygosoma veunsaiense* Geissler, Hartmann & Neang, 2012. As this species was found to be a member of the subfamily Sphenomorphinae, here we tentatively assign it to the genus *Sphenomorphus* and propose a new combination for this taxon: *Sphenomorphus veunsaiensis* (Geissler, Hartmann & Neang, 2012) **comb. nov**.

The newly discovered population of miniaturized skinks from Chu Yang Sin NP in southern Vietnam is undoubtedly morphologically and genetically very closely related to *Sphenomorphus veunsaien-*

Table 2. Uncorrected p-distances (percentage) between the sequences of COI mtDNA gene of *Sphenomorphus*-like skinks included in the phylogenetic analyses

No.	Species	1	2	3	4
1	*Sphenomorphus valentinae* **sp. nov.**	**0.0**	0.7	0.8	1.4
2	*Sphenomorphus sheai*	3.3	**0.5**	0.3	1.3
3	*Lygosoma veunsaiense*	3.7	0.8	–	1.3
4	*Sphenomorphus incognitus*	20.0	19.7	19.5	–

sis. However, we argue that the observed levels of divergence in the COI mtDNA gene, along with concordant and stable differences in diagnostically important morphological characters (see below), suggest that this geographically isolated population (see Fig. 1) represents an independently evolving entity, which we formally describe as a new species below.

The assignment of both species to the genus *Sphenomorphus* is also supported by their morphology. The diagnostic features of both fit the diagnostic traits for *Sphenomorphus* from Southeast Asia as they were compiled by prefrontals present, parietals in contact behind interparietal, supranasals absent, lower eyelid scaly, dorsal scales smooth, medial pair of precloacals enlarged, the inner precloacals overlapping the outer ones, hindlimbs with five digits, scales on dorsal surface of fourth toe in two or more rows over at least half of digit, see Taylor (1963); Greer (1979, 1990); Shea, Greer (2002); Greer et al. (2006); Grismer (2008); Grismer et al. (2019, 2020); and Nguyen et al. (2011).

Family Scincidae Gray, 1825
Genus Sphenomorphus Fitzinger, 1843
Sphenomorphus veunsaiensis comb. nov.
(Geissler, Hartmann & Neang, 2012)

(Fig. 3, Table 3)

Lygosoma veunsaiensis Geissler, Hartmann & Neang, 2012 – Holotype. CBC 00808, adult male, collected by G. Csorba on 24 February 2010 at O'Kasieb campsite at 14°01'00.2'' N, 106°45'09.0" E, 114 m a.s.l., in disturbed semi-deciduous forest in Veun Sai District, Ratanakiri Province, Cambodia.

Sphenomorphus sheai Nguyen, Nguyen, Van Devender, Bonkowski & Ziegler, 2013 – Holotype: IEBR A.2013.22 (Field number ASU 10715), adult female, collected on 4 June 2012 by K. V. Nguyen and R. W. Van Devender from Camp 1 (14°37.098'N, 108°30.177'E, elevation 1,025 m a.s.l.; datum WGS84) from Kon Tum Plateau in the border area between Quang Ngai and Kon Tum provinces, southern Central Vietnam.

Etymology. The species epithet of *Lygosoma veunsaiensis* Geissler, Hartmann & Neang, 2012 was corrected to "*veunsaiense*" following the Latin declination rules, adjusting it to the neuter gender of the generic name *Lygosoma* (Chapple et al., 2023; Poyarkov et al., 2023). With the new generic assignment proposed herein, it has to be declined in correspondence to the masculine gender of the name *Sphenomorhus* as *Sphenomorphus veunsaiensis*.

Suggested Common Names: *Cambodian Dwarf Skink* (English); *Камбоджийский крохотный сцинк* (Russian); *Thằn lằn phê nô Cam-pu-chia* (Vietnamese); *Kambodschanischer Zwergskink* (German).

Revised diagnosis. *Sphenomorphus veunsaiensis* **comb. nov**. is differentiated from all other congeners by the following combination of characters: body elongated and small; prefrontals separated from each other; supraoculars four; enlarged nuchals in two pairs; lower eyelid scaly; supralabials six, first fused with nasal; primary temporals two; external ear openings absent; midbody scales in 20 to 22 rows; dorsal scales smooth, paravertebral scales 51 to 53, not widened; ventrals in 49 to 54 rows; limbs short, pentadactyl; scales on dorsal surface of base of fourth toe in three rows; lamellae under fourth toe six; subdigital lamellae on fourth finger five; subdigital lamellae on fourth toe six; light stripe present on outer edge of the dorsum; and a dark dorsolateral stripe present, from behind the eye to the tail base.

Distribution. At present, *Sphenomorphus veunsaiensis* **comb. nov.** is known to occur in montane

Fig. 3. Photos of *Sphenomorphus veunsaiensis* in life: *A*: *Lygosoma veunsaiense* (holotype, CBC 0808); and *B*: *Sphenomorphus sheai* (holotype, IEBR A.2013.22). Photos by G. Csorba (*A*) ; R. W. Van Devender (*B*), reproduced from Nguyen et al. (2012)

Table 3. Mensural data (in mm) from the type series *Sphenomorphus valentinae* **sp. nov**. and its close relatives *Sphenomorphus sheai* and *Lygosoma veunsaiense*

Specimen ID	Taxon				
	Sphenomorphus sheai	*Lygosoma veunsaiense*	*Sphenomorphus valentinae* **sp. nov.**		
	IEBR A.2013.22	CBC 00808	ZMMU Re-17931 (holotype)	ZMMU Re-17932 (paratype)	VRTC NAP-15987 (paratype)
Reference	Nguyen et al. (2013)	Geissler et al. (2012)	*this study*	*this study*	*this study*
Sex	♀	♂	♂	♂	♂
SVL	35.2	33.6	36.01	28.1	37.5
TAL	58.5	40.1*	58.9*	49.4	62.3*
AG	21.2	20.3	22.3	16.4	23.2
*HL*1	–	6.0	5.1	4.6	5.5
*HL*2	6	5.1	5.6	5	5.9
HW	4.2	3.7	3.8	3.5	3.9
SL	2.6	1.7	2.1	1.9	2.2
SFIL	10.8	11.1	12.3	10.5	12.9
*FIL*1	–	4.3	2.5	2.3	2.5
*FIL*2	5.1	4.9	4.1	3.5	3.8
*HIL*1	–	6.2	5.1	3.8	4.8
*HIL*2	7.5	7.9	7.8	5.5	6.9
AG/*SFIL*	–	1.83	1.82	1.56	1.8
SVL/*FIL*1	–	7.81	14.58	12.02	15.29
SVL/*HIL*1	–	5.42	7.06	6.12	6.81
TaL/*SVL*	1.66	1.66	–	1.76	–
*HL*2/*SVL*	0.17	–	0.16	0.18	0.16
*FlL*2/*SVL*	0.14	–	0.11	0.12	0.1
*HlL*2/*SVL*	0.21	–	0.22	0.19	0.18

Note. "–" – data unobtainable or not applicable; * – regenerated or incomplete tail. Abbreviations are listed in the Materials and Methods.

areas of the Central Truong Son (Annamites) Mountains, including the Kon Tum-Gia Lai Plateau in Vietnam (recorded in provinces Gia Lai, Kon Tum, Binh Dinh, Quang Ngai, Quang Nam, and Thua Thien-Hue) and the adjacent montane parts of north-eastern Cambodia (Ratanakiri Prov.).

Remark. Additional measurements and pholidosis characters of all known specimens of *Sphenomorphus veunsaiensis* are summarized in Table 3.

Sphenomorphus valentinae sp. nov.
Bragin, Geissler, Nguyen & Poyarkov

(Figs. 4–6, Tables 3, 4)

Holotype. ZMMU Re-17931 (field number NAP-15886), adult male, collected by A. M. Bragin and N. A. Poyarkov on April 17, 2024 from Chu Yang Sin National Park, Bong Krang Commune, Lak District, Dak Lak Province, southern Vietnam (12.38750°N, 108.34417°E; elevation 761 m a.s.l.). The holotype was found under the pine log on sandy soil near the path.

Paratypes. Two males, ZMMU Re-17932 (field number NAP-15952) and VRTC NAP-15987 (field number NAP-15987) collected by A. M. Bragin and N. A. Poyarkov on April 19th and 29th, 2024, respectively, from the same locality in the altitude range from an elevation of 840 to 1138 m a.s.l.

Etymology. The specific name "*valentinae*" is a Latinized patronymic noun in genitive singular; the name of the new species is given in honor of Dr. Valentina F. Orlova, the head and main curator of the Herpetology department of the Zoological Museum of Lomonosov Moscow State University (ZMMU), where she works since 1962. Dr. Orlova made a significant contribution to the studies of different groups of lizards, including skinks of Vietnam (e.g., Darevsky and Orlova, 1996).

Suggested Common Names: *Valentina's dwarf skink* (English); *Крохотный сцинк Валентины* (Russian); *Thằn lằn phê nô Va-len-ti-na* (Vietnamese); *Valentinas Zwergskink* (German).

Diagnosis. The new species, *Sphenomorphus valentinae* **sp. nov**., differs from other members of the genus *Sphenomorphus* by the combination of the following morphological characters: body size small (*SVL* 28.1–37.5 mm, *TAL* 49.4–62.3 mm); body gracile, elongated; limbs short, pentadactyl; ear opening concealed; head, body, and caudal scales smooth; supranasals and postnasals absent; lower eyelid movable and covered with scales; prefrontals two, separated by frontonasal; supraoculars four; supraciliaries eight; preoculars forming a group of three scales; presuboculars two; primary temporals three; supralabials six, first fused with nasal; infralabials four; chin

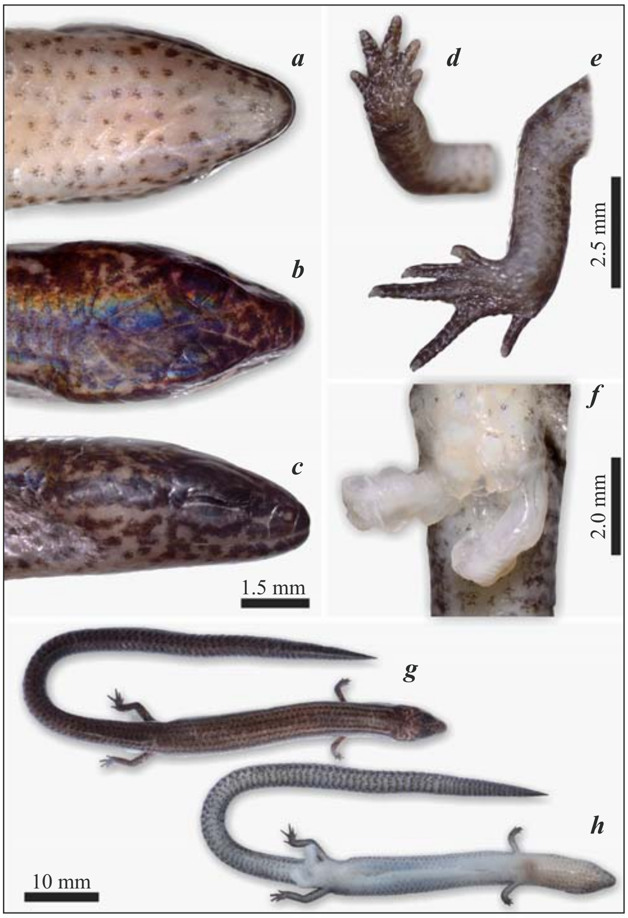

Fig. 4. Holotype of *Sphenomorphus valentinae* **sp. nov**. (ZMMU Re-17931; adult male) in preservative: *a* – ventral view of head; *b* – dorsal view of head; *c* – right lateral view of head; *d* – ventral view of left forelimb; *e* – ventral view of left hindlimb; *f* – view of hemipenes, fully everted; *g* – dorsal view of body; *h* – Ventral view of body. Scale bars: *a–c* – 1.5 mm; *d*, *e* – 2.5 mm; *f* – 2 mm; *g*, *h* – 10 mm. Photographs by A. M. Bragin

shields in three pairs; nuchals not enlarged, followed by four transverse dorsal scale rows located between dorsolateral dark stripes, all scales similar in size; paravertebral scales in 50–55 rows; ventral scales in 52–56 rows; midbody scale rows 18; the central subcaudal scale row enlarged; five subdigital lamellas under the fourth finger; six subdigital lamellas under the fourth toe; dorsal surfaces of body, head and tail brown-beige, iridescent, with dark gray spots forming four thin longitudinal lines disappearing on the tail; venter, lower flanks, ventral region of the neck and tail from light brown to grayish pink, with dark spots disappearing on the belly; light sand-colored dorsolateral stripe running from the posterior edge of the eye to the tail there; ventrally edged with a contrasting dark lateral stripe running along the body flanks to the tail base.

Description of the holotype. Adult male (see Figs. 4–6) specimen in a good state of preservation.

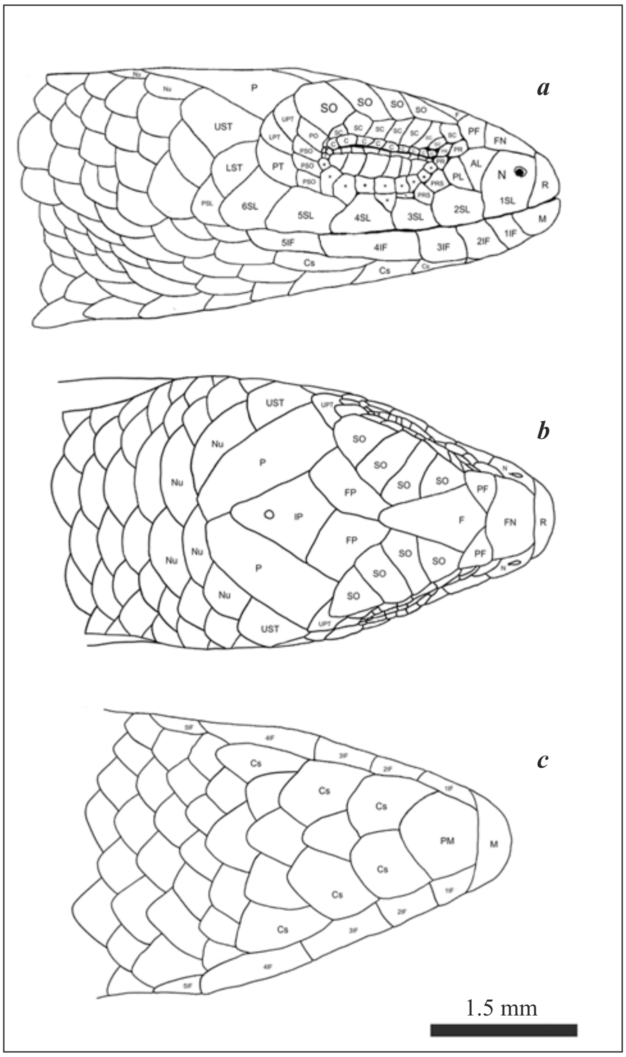

Fig. 5. Head scales nomenclature and their positional relationship and size illustrated by the adult male *Sphenomorphus valentinae* **sp. nov.** (holotype, ZMMU Re-17931): *a* – right lateral view; *b* – dorsal view; *c* – ventral view. Terminology follows Ouboter (1986), Nguyen et al. (2013), and Grismer et al. (2019). For abbreviations, see the Material and Methods sections. Illustration by A. M. Bragin

The specimen displays fully everted hemipenes. The specimen body straightened; tail bended on the left; limbs bent at the joints and straightened to the sides.

Body small (*SVL* 36.01 mm), tail incomplete (*TAL* 58.86 mm), head longer than wide (*HL*2/*HW* 1.47; *HL*2/*SVL* 0.16), limbs short (*FIL*2/*SVL* 0.11, *HIL*2/*SVL* 0.22). Head not distinct from neck; weak cervical interception present in front of axilla. Snout obtuse, rounded anteriorly; rostral wider than high, distinctly visible from above; supranasals absent; frontonasal wider than long, in contact with rostral, nasals, anterior loreals, and prefrontals; prefrontals separated from each other by the anterior edge of frontal; frontal narrowing posteriorly, longer than the distance to the tip of snout, in contact with frontonasal,

Fig. 6. Holotype of *Sphenomorphus valentinae* **sp. nov.** (ZMMU Re-17931; adult male) *in situ*. Photograph by A. M. Bragin

prefrontals, first and second supraoculars, and frontoparietals; frontoparietals in contact with each other anteriorly, and bordered by frontal, three posterior supraoculars, parietals, and interparietal; interparietal diamond-shaped with a small transparent parietal eye spot posteriorly; parietals in contact posteriorly; the posterolateral border of parietal edged by four scales on each side–by upper pretemporal anteriorly, by upper secondary temporal and two nuchals posteriorly; nuchal scales not enlarged. Nostril located in the center of nasal; postnasals absent; loreals two, anterior larger than posterior; preoculars forming a group of three small scales, one of which smaller; presuboculars two, of similar size; supraciliaries eight, first largest, first to third in contact with first supraocular; ciliaries nine, thin, non-convex scales; supraoculars four, second widest, fourth supraocular posterolaterally in contact with postocular and upper pretemporal; postocular single; postsuboculars three, identical in size, lower one in contact with fifth supralabial; primary temporal single, in contact with sixth supralabial; secondary temporals two, upper one very large, in contact with parietal, overlapped by parietal and lower secondary temporal; lower eyelid moveable, scaly, covered with one row of six opaque rectangular scales elongated dorsoventrally, separated from supralabials by one row of small scales, and by two rows of small scales at the level of the third and fourth supralabials; supralabials six, first (anterior) fused with nasal, fifth and sixth enlarged, fourth located below the eye; external ear openings concealed (see Fig. 5). Mental wider than long, rounded anteriorly, in contact with anterior infralabial on each side and with postmental; infralabials five, fourth longest; postmental undivided, in contact with mental, first infralabial and anterior pair of chin shields; three pairs of chin shields, anterior pair in contact with each other anteriorly, second pair separated from each other by a single gular scale and posterior pair separated from each other by three gular scales (see Fig. 5). Midbody scales in 18 rows; dorsal scales smooth, subequal to lateral and ventral scales, four scale rows between dorsolateral stripes; paravertebral scales 52, not widened; ventrals smooth, in 54 rows; precloacals four, inner scales overlapping outer ones, medial two enlarged, right scale overlapped by left scale; tail thick at base, median subcaudals widened. Limbs short, pentadactyl; second and fourth fingers equal in length, third longest; fore- and hindlimbs do not touch each other and are distinctly separated when adpressed along the body; scales on dorsal and ventral surfaces of the limbs smooth and imbricate; subdigital lamellas convex with a protrusion medially, forming grooves along the inner surface of the fingers; subdigital lamellas five under fourth finger and six under fourth toe.

Hemipenis with well-developed ornamentation consisting of a row of six convex transverse grooves on the asulcal surface of the anterior part of the truncus (see Fig. 4, *f*). Hemipenis weakly bilobed into two equally long, wide, short, wrinkled apexes. The length to-width ratio of the apexes ca. 1:1.5. Sulcus spermaticus bifurcation point located closely to that of the apexes. Sulcus spermaticus surrounded by wide, well-developed labia. The sulci open at the tips of the apexes of the hemipenis. Apexes of the same length (0.94 mm) and shorter than the body (truncus + pedicle) of the hemipenis (1.54 mm). The truncus of the hemipenis bears two ca. 0.84 mm long, clearly visible, flattened, symmetrical bulbous lobes; another pair of barely noticeable, flattened, asymmetrical lobes located at the base of the pedicle. The total length of the hemipenes is 2.48 mm.

Coloration in life (see Fig. 6). Dorsal surfaces of the head brown-beige with a bluish iridescence; the anterior part of the head to the frontoparietals and supraoculars covered with large dark spots; supralabials and infralabials light grayish-white to beige, with regularly distributed dark spots; scales posterior to the frontoparietals with irregular small bluish-gray and dark-gray spots, continuing to the dorsum where they form four thin longitudinal lines running along the dorsum and disappearing on the tail. Dorsum coloration is similar to that of the dorsal surfaces of the head; the dorsal surfaces of the tail are noticeably darker but also have iridescence; they are covered with

Table 4. Meristic data from the type series *Sphenomorphus valentinae* **sp. nov**. and its close relatives *Sphenomorphus sheai* and *Lygosoma veunsaiense*

Specimen ID		Taxon				
		Sphenomorphus sheai	*Lygosoma veunsaiense*	*Sphenomorphus valentinae* **sp. nov.**		
		IEBR A.2013.22	CBC 00808	ZMMU Re-17931 (holotype)	ZMMU Re-17932 (paratype)	VRTC NAP-15987
1		2	3	4	5	6
Reference		Nguyen et al. (2013)	Geissler et al. (2012)	*this study*	*this study*	*this study*
Sex		♀	♂	♂	♂	♂
PF	Prefrontals in contact or not	no	no	no	no	no
F–SO	Frontal in contact with which supraoculars	1, 2	1, 2	1, 2	1, 2	1, 2
SN–PN	Supranasals and postnasals	both absent	both absent*	both absent	both absent	both absent
SO	Total number of supraoculars	4	4	4	4	4
Nu	Total number of nuchals (enlarged)	4 (2 pairs)	0	0	0	0
L	Total number of loreals (*R*/*L*)	2/2	2/1	2/2	2/2	2/2
PR	Total number of preoculars	1	2	3	3	3
PRS	Total number of presuboculars	1	2	2	2	2
SC	Total number of supraciliaries	7	9	8	8	8
PO	Total number of postoculars	1	1	1	1	1
PSO	Total number of postsuboculars	3	1	3	3	3
PT	Total number of primary temporals	2+1 scale**	3**	1+2 pretemporals**	1+2 pretemporals**	1+2 pretemporals**
ST	Total number of secondary temporals	2	2	2	2	2
	Upper secondary temporal large (yes/no)	yes	yes	yes	yes	yes
UST–LST	The upper secondary temporal overlaps the lower one	no	–	no	no	no
SL	Total number of supralabials	6	6***	6	6	6
	Which supralabials below the eye	4th	4th	4th	4th	4th
	Supralabials separated from the eye by 1 rows of small scales	yes	yes	yes	yes	yes
	Largest supralabial	5, 6	5	5, 6	5, 6	5, 6
Transparent window		absent	absent	absent	absent	absent
External ear opening		absent	absent	absent	absent	absent
IF	Total number of infralabials	5	5	5	5	5
Cs	1st pair of chin shields in contact medially	yes	yes	yes	yes	yes
	2nd pair of chin shields separated by how many scales	1	1	1	1	1
	3nd pair of chin shields separated by how many scales	3	3	3	3	3
TMR	Midbody scale rows	20	22	18	18	18
Mds	Paravertebral scales	53	51	52	50	55
ER	Entire scale rows across the back	4	4	4	4	4
VR	Ventral scales	54	49	54	52	56
PrC	Total number of enlarged precloacals	2	2***	2	2	2
F	Number of fingers	5	5	5	5	5

Table 4. Continuation

1		2	3	4	5	6
T	Number of toes	5	5	5	5	5
FL4	Subdigital lamellae on 4th finger	5	5	5	5	5
TL4	Subdigital lamellae on 4th toe	6	6*****	6	6	6
F	Number of fingers	5	5	5	5	5
T	Number of toes	5	5	5	5	5
FL4	Subdigital lamellae on 4th finger	5	5	5	5	5
TL4	Subdigital lamellae on 4th toe	6	6*****	6	6	6

Note. “–” – data unobtainable or not applicable. Data recorded through “/” indicate the value on the right/left side of the head or bod. * – The original description of *L. veunsaiense* by Geissler et al. (2012) stated that supranasals are present and postnasals are absent in this species. Subsequent re-examination of the *L. veunsaiense* holotype by us (PG, TN) indicated that both supranasals and postnasals are absent in the holotype of *L. veunsaiense*. ** – The spread of values is explained by different interpretations of the scales in the postorbital region between the postoculars and secondary temporals: in Nguyen et al. (2013) there are two primary temporals and a large scale above them, behind the supraoculars; in Geissler et al. (2012) there are three primary temporals; in this study, following the scale nomenclature of Grismer et al. (2019), we interpret these scales as one primary temporal and two pretemporals. In this measurement, in any case, three large scales conditionally corresponding to the primary temporals are obtained. *** – This value is given as “*SL* = 5” in the original description of *L. veunsaiense* (Geissler et al., 2012); this discrepancy can be explained by the fact that the first supralabial, which is fused with the nasal, was not taken into account during the measurement in Geissler et al. (2012); we (PG, TN) double-checked the specimen CBC 00808 and confirm the corrected value “*SL* = 6”. **** – The original description of *L. veunsaiense* by Geissler et al. (2012) stated that the holotype has three enlarged precloacal scales; we rechecked this character and it appears that this value is due to a counting error; the holotype of *L. veunsaiense* has three enlarged precloacal scales. ***** – The original description of *L. veunsaiense* by Geissler et al. (2012) stated that the holotype has nine subdigital lamellae on the 4th toe; we rechecked this character and it appears that this value is due to a counting error. Abbreviations are listed in the Materials and Methods.

numerous gray spots, resulting in a darker gray-brown coloration. Dorsal stripes disappear at the tail base. Iris black; light sand-colored dorsolateral stripe running from the posterior edge of the eye to the base of the tail, fading posteriorly, ventrally edged with dark lateral stripe, which spreads from the loreals along the preoculars through the eye and posteriorly on the body flanks and further to the second third of the tail length. Ventrally dark lateral stripes are edged with thin sandy-beige lines. The ventral parts of the body flanks and ventral surfaces of the neck, belly, and tail are light brown to grayish-pink, with small dark spots present on the chin, neck, and tail but not on the belly. Ventral surfaces of the lower jaws, chin, and gulars grayish-pink with dark-gray mottling. On the ventral surface of the tail, the dark spots form irregular transverse stripes along the posterior edges of the subcaudal scales; the color of the posterior two-thirds of the tail length varies from grayish-white to pale blue. Dorsal surfaces of hands and feet grayish-brown; ventral surfaces of hands and feet are dusty gray.

Coloration in preservative (see Fig. 4). After three months of storage in ethanol, dorsal surfaces turned from brown-beige to grayish-brown; dark spots remained intact; the coloration faded slightly, with the pattern becoming more contrasting; dorsal, lateral, and dorsolateral stripes remained intact and were well-discernable; all the black markings on the head, trunk, tail, and limbs were well-discernable; while the ventral surfaces of the trunk, limbs, and tail faded from light grayish-pink to grayish-blue.

Variation. Tables 3, 4 summarize the differences in measurements and scalation among the members of the type series. Within the type series, we recorded variability in the number of paravertebral scales (from 50 to 55) and ventral scales (from 52 to 56), which seems to correlate with the size of a specimen (*SVL*) (see Table 3). There is some variability in the number of ciliars, ranging from nine ciliary scales in ZMMU Re-17931 and VRTC NAP-15987 to ten in ZMMU Re-17932. Since the type series is represented only by males, data on sexual dimorphism is lacking.

Comparisons. *Sphenomorphus valentinae* **sp. nov**. could be mistaken for several skink species of the genus *Lygosoma* Hardwicke & Gray, which also have elongated bodies, short limbs, and fewer than 26 midbody scale rows, but can be readily distinguished from these species by having 18 midbody scale rows, compared to *L. anguinum* Theobald (*TMR* 18 vs. 22), *L. lineolatum* Stolizcka (*TMR* 18 vs. 22), *L. popae* Shreve (*TMR* 18 vs. 24), *L. punctata* Gmelin (*TMR* 18 vs. 24–28), *L. quadrupes* Linnaeus (*TMR* 18 vs. 25–26), *L. siamense* Siler, Heitz, Davis, Freitas, Aowphol, Termprayoon & Grismer (*TMR* 18 vs. 26–28), *L. tabonorum* Heitz, Diesmos, Freitas, Ellsworth & Grismer (*TMR* 18 vs. 26–28). Moreover, *Sphenomorphus valentinae* **sp. nov**. further differs from all aforementioned species by the absence of supranasals (present in *Lygosoma*) and having the first supralabial fused with the nasal (not fused in *Lygosoma*).

Sphenomorphus valentinae **sp. nov**. also superficially resembles *Scincella apraefrontalis* Nguyen, Nguyen, Böhme & Ziegler in having identical midbody scale count (*TMR* 18 in both species), ear opening concealed, and the first supralabial fused with nasal; however, it can be readily distinguished from the latter species by the presence of two prefrontals (vs. absence) and by having a scaly movable lower eyelid lacking transparent window, which is present in *Scincella apraefrontalis* (Nguyen et al., 2010).

Sphenomorphus valentinae **sp. nov**. can be distinguished from most *Sphenomorphus* species from China and mainland Southeast Asia by having a small body size, characteristic elongated body proportions, and a small number of midbody scale rows (*TMR* 18 vs. > 22 in most other species). Few *Sphenomorphus* species have a number of midbody scale rows close to *Sphenomorphus valentinae* **sp. nov**., including *S. tridigitus* (*TMR* 18–20) and *S. tetradactylus* Darevsky & Orlov (*TMR* 20). *Sphenomorphus valentinae* **sp. nov**. can be distinguished from *S. tridigitus* and *S. tetradactylus* by having pentydactyl forelimbs (vs. forelimbs with three and four digits in *S. tridigitus* and *S. tetradactylus*, respectively).

Finally, the new species can be distinguished from its sister taxon *S. veunsaiensis* by having a lower number of midbody scale rows (*TMR* 18 vs. 20–22), the number and shape of three small preoculars (*PR* 3, small vs. 1, large), the number of presuboculars (*PRS* 2 vs. 1), the higher number of supraciliary scales (*SC* 8 vs. 7), and comparatively shorter forelimbs (*FIL*2/*SVL* 0.10–0.12 vs. 0.14).

Distribution. The new species is currently recorded only from the mid-elevation montane coniferous forests at elevations ranging from 760 to 1140 m a.s.l. at the type locality in Chu Yang Sin National Park, Bong Krang Commune, Lak District, Dak Lak Province, southern Vietnam (12.38750° N, 108.34417° E) (see Fig. 1).

Natural history notes and conservation status. At the type locality, skinks inhabit mid-elevation montane pyrogenic coniferous forests with thick pine litter formed by *Pinus kesiya* Royle ex Gordon. Tall pine trees (*Pinus kesiya*) dominated the upper canopy layer, while the following species formed the sparse lower canopy layer: *Castanopsis* sp. (D. Don) Spach, *Lithocarpus* sp. Blume (Fagaceae), *Litsea monopetala* (Roxb.) Pers. (Lauraceae), *Kydia calycina* Roxb. (Malvaceae), *Acronychia pedunculata* (L.) Miq. (Rutaceae), *Ficus* sp. L., *Artocarpus* sp. J. R. Forst. & G. Forst. (Moraceae), and *Elaeocarpus* sp. L. (Elaeocarpaceae). The understory was poorly developed. The herbaceous cover was also poorly developed due to developed pine litter and included species from the genera *Alpinia* Roxb., *Curcuma* L. (Zingiberaceae), and Poaceae gen. sp. Barnhart, as well as the fern *Brainea insignis* (Hook.) J. Sm. (Blechniaceae). Skinks were found both on gently sloping open sections of forest trails and along forest edges at elevations ranging from 760 to 840 m a.s.l. and on steep, heavily shaded slopes and in dry stream beds at elevations ca. 1140 m a.s.l. (Fig. 7). During the study period, daytime temperatures ranged from 24 to 27°C, and nighttime temperatures dropped to 19–20°C. Skinks were found both during the day and at night, primarily under medium-sized pine logs and rarely under small rocks. Along the forest trail, one specimen of *Sphenomorphus valentinae* **sp. nov**. was found hiding under a stone together with a crab of the genus *Dalatomon* sp. Dang & Ho. In the same area during the study period, we also recorded several reptile species: *Sphenomorphus yersini* Nguyen, Nguyen, Nguyen, Orlov & Murphy, *Sphenomorphus indicus* Gray, *Cyrtodactylus ziegleri* Nazarov, Orlov, Nguyen & Ho, *Pareas formosensis* van Denburgh, and *Trimeresurus vogeli* David, Vidal & Pauwels. The natural history of *Sphenomorphus valentinae* **sp. nov.** remains largely unknown. The remains of Cantharidae Imhoff (Coleoptera) larva, imago of Machaerotidae Stal (Hemiptera) spittlebug, and Theridiidae

Fig. 7. Habitats of *Sphenomorphus valentinae* **sp. nov.** at the type locality in Chu Yang Sin National Park, Dak Lak Province, Vietnam on ridges covered with middle mountain open pyrogenic coniferous forest formed by *Pinus kesiya* at an altitude of 760 m a.s.l. Photograph by A. M. Bragin

Sundevall spider were found in the stomach of the paratype VRTC NAP-15987. The discovery of the last two prey items may indicate that this skink forages not only within the pine or leaf litter but also on the surface of the ground and feeds on various small invertebrates. The new species likely tears its prey into several pieces before swallowing.

The habitat of *Sphenomorphus valentinae* **sp. nov.** is relatively stable since the current distribution of the lizard lies within the territory of Chu Yang Sin NP. Although the pine forests in the area are subjected to regular forest fires, this seems not to affect the burrowing and semifossorial lizards too much. We did not record any agricultural activity in the type locality except the collection of medical and edible plants by the locals, which likely also does not represent a direct threat to the lizards. However, given the sparse data on the distribution of the new species, *Sphenomorphus valentinae* **sp. nov**. should be considered a local endemic and therefore its conservation requires special attention.

DISCUSSION

Our study further highlights the importance of integrative transnational taxonomic approaches for studies of the skink fauna in Indochina. The description of *Sphenomorphus valentinae* **sp. nov.** increases the current number of *Sphenomorphus* species to 114. Of these, 16 species shave been recorded from Vietnam, including *S. annamiticus* (Boettger), *S. bacboensis* (Eremchenko), *S. buenloicus* Darevsky & Nguyen, *S. cryptotis* Darevsky, Orlov & Ho, *S. incognitus* (Thompson), *S. indicus* (Gray), *S. maculatus* (Blyth), *S. mimicus* Taylor, *S. phuquocensis* Grismer, Nazarov, Bobrov & Poyarkov, *S. tetradactylus*, *S. tonkinensis* Nguyen, Schmitz, Nguyen, Orlov, Böhme & Ziegler, *S. tridigitus*, *S. tritaeniatus* (Bourret), *S. yersini* Nguyen, Nguyen, Nguyen, Orlov & Murphy, and *S. veunsaiensis* (Le et al., 2020; Uetz et al., 2024; this study). As the genus *Sphenomorphus* is widely recognized as a paraphyletic group, the sheer quantity of included species in combination with significant morphological variation suggests that some of the species currently assigned to *Sphenomorphus* might actually be closely related to other scincid genera, as demonstrated in the present study. This outlines the urgent need for molecular phylogenetic and integrative systematic approaches to be applied to the studies of *Sphenomorphus* diversity in Indochina. Such studies will most likely eventually lead to a reconsideration of the general genus-level taxonomy of sphenomorphine skinks.

In our study, we tentatively assigned the species group of *S. veunsaiensis* and *S. valentinae* **sp. nov.** to the genus *Sphenomorphus*; however, further integrative studies are required to clarify their phylogenetic position and taxonomic affinities. As already shown by Le et al. (2020), the abovementioned species show an astonishing similarity with *Sphenomorphus tridigitus* (distributed in central Vietnam and the Bolaven Plateau, Laos). Moreover, morphologically, these taxa also broadly overlap with the other two poorly known sphenomorphine species, which were formerly assigned to the genus *Leptoseps*, namely *S. tetradactylus* (distributed in central Vietnam) and *Leptoseps poilani* (distributed in central Vietnam) (see Fig. 1). These species are known from only a few specimens and lack molecular data until now. To reassess this issue, future studies are required, including the reexamination of all available type materials and the collection of new specimens for molecular phylogenetic analyses. If all of these species appear to be closely related, this would make them an interesting model group for evolutionary studies, as they all show different stages of limb reduction, namely finger reduction (from five to three). As outlined in the introduction, this differentiation might have occurred over a relatively short geological timescale. If future studies find that they are not closely related, this would again represent an intriguing case of astonishing morphological similarity that evolved in parallel in different lineages of skinks.

Although our taxon sampling in molecular analyses is incomplete, the observed differentiation pattern has certain biogeographic implications. *Sphenomorphus valentinae* **sp. nov.** occurs in the northern foothills of the Langbian (Da Lat) Plateau, representing the southernmost part of the Truong Son (or Annamite) Range or the southern part of Tay Nguyen Region (Central Highlands) according to Vietnamese geographical tradition (see Fig. 1). The Truong Son Mountains are widely recognized as the local center of herpetofaunal diversity and endemism in Indochina (e.g., Poyarkov et al., 2021, 2023). At the same time, *Sphenomorphus veunsaiensis* and *S. tridigitus* are restricted to the central portion of the Truong Son Range and inhabit the Kon Tum-Gia Lai Plateau, the adjacent mountains of northeastern Cambodia, and the Boloven Plateau in southeastern Laos, while the records of *Leptoseps poilani* (Quang Tri Province) and *S. tetradactylus* (Quang Binh Province) are located in the northernmost portion of central Truong Son (see Fig. 1). The fact that *L. veunsaiense* from Cambodia and *S. sheai* from Vietnam were found to be conspecific is not surprising from a biogeographic perspective, as all known localities of this taxon are located within the Kon Tum-Gia Lai Plateau of central Truong Son. It's remarkable that the range of *S. tridigitus* partially overlaps with the known distribution of *S. veunsaiensis* (see Fig. 1), which further suggests that these two species may be very closely related or even represent a single taxon.

The discovery of a new *Sphenomorphus* species indicates that reptile fauna in Vietnam remains insufficiently studied, and future field surveys are needed to more accurately assess the country's herpetological diversity (Poyarkov et al., 2021, 2023). *Sphenomorphus valentinae* **sp. nov.** is currently only known from three specimens collected from Chu Yang Sin NP, Dak Lak Province, Vietnam. Due to their small size and fossorial habits, they appear to be quite elusive and difficult to detect in the field. The main threat to this species is habitat loss and degradation. The new species' actual extent of distribution, population trends and size, reproductive behavior, and ecology remain poorly known. Further study efforts are required to collect data on *Sphenomorphus valentinae* **sp. nov.** natural history, as well as to gain a better understanding of the diversity, taxonomy, and distribution of fossorial miniaturized sphenomorphine skinks in Indochina.

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НОВЫЙ ВИД СЦИНКА ИЗ ГОР ЮЖНОГО ВЬЕТНАМА (REPTILIA, SQUAMATA, SCINCIDAE)

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Аннотация. Представлена интегративная таксономическая ревизия миниатюризированных сцинков подсемейства *Sphenomorphinae* фауны Вьетнама и Камбоджи по данным морфологического анализа и ДНК-баркодинга по фрагменту гена COI митохондриальной ДНК. Выявлен новый для науки вид *Sphenomorphus valentinae* **sp. nov**., населяющий национальный парк Чуянгсин (провинция Даклак, южный Вьетнам). Новый вид отличается от остальных членов рода следующими признаками: тело удлиненное, конечности короткие, пятипалые; *SVL* 28.1 – 37.5 мм, *TAL* 49.4 – 62.3 мм; наружное слуховое отверстие отсутствует; чешуи гладкие; надносовые и задненосовые щитки отсутствуют; нижнее веко подвижное, покрыто чешуями; предлобных щитка два, они разделены; надглазничных щитков четыре пары; ресничных щитков восемь пар; предподглазничных щитков две пары; первичных височных щитков три; верхнегубных щитков шесть пар, первая из них сливается с носовыми щитками; нижнегубных щитков четыре пары, нижнечелюстных щитков три пары; загривковые щитки не увеличены; паравертебральные чешуи в 50 – 55 поперечных рядах; брюшные чешуи в 52 – 56 поперечных рядах; 18 чешуй вокруг середины туловища; подпальцевых пластинок под четвертым пальцем передней конечности пять, под четвертым пальцем задней конечности шесть; спинная поверхность тела коричнево-бежевая с радужным отливом и темными пятнышками, образующими четыре тонкие продольные линии; брюшная поверхность тела от светло-коричневого до серовато-розового; от заднего края глаз к основанию хвоста проходят светлые дорзолатеральные полосы, снизу окаймленные темно-коричневым. Также наши данные свидетельствуют, что *Sphenomorphus sheai*, описанный из вьетнамской провинции Куангнам, представляет собой младший синоним *Lygosoma veunsaiense*, описанной ранее из провинции Ратанакири в Камбодже; приводится расширенное описание этого вида, который мы предварительно рассматриваем как *Sphenomorphus veunsaiensis* **comb. nov**. (Geissler, Hartmann & Neang, 2012). Представлены новые данные по распространению и спорным вопросам диагностики и систематики *S. veunsaiensis*, *S. tridigitus*, *S. tetradactylus* и *Leptoseps poilani* на территории Индокитая. Для лучшего понимания разнообразия миниатюризированных сфеноморфидных сцинков региона необходимы дальнейшие полевые исследование вкупе с детальным изучением типовых экземпляров.

Ключевые слова: *Sphenomorphus valentinae* **sp. nov**., *Lygosoma veunsaiense*, *Sphenomorphus sheai*, *Sphenomorphus tridigitus*, Индокитай, Камбоджа, Лаос, хребет Чьонгшон

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