



Systematics and distribution of *Lankascincus fallax* (Peters, 1860) (Reptilia, Scincidae), an endemic litter-skink from Sri Lanka

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Abstract

Lankascincus fallax is an endemic, but widespread species of skink distributed throughout Sri Lanka, including all bioclimatic zones (elevations from 0 to 1,200 m a.s.l.). After thoroughly comparing morphology and morphometry between populations in different bioclimatic zones, we recognize it as a single morphospecies. We revise the systematics of *Lankascincus fallax* based on molecular and morphological data providing a comprehensive re-description of the adult syntype collected from either Ratnapura or Trinkomalee (sic), Sri Lanka. We provide the first-ever constructed phylogeny of *Lankascincus* representing five species (out of nine) based on GenBank data. In addition, we examined all the type specimens of the two synonymized species, *Sphenomorphus rufogulus* and *Lankascincus deraniyagalae*. We also provide a comprehensive discussion on the distribution of *L. fallax*.

Key words: biogeography, dry zone, endemic, rainforest, Sri Lanka, wet zone

Introduction

Lygosoma fallax Peters, 1860 was described based on two syntypes (ZMB 3762, 64361), with a single label indicating that those were collected from two localities in Sri Lanka: Ratnapura, Sabaragamuwa Province (in lowland wet zone) and Trinkomalie (=Trincomalee), Eastern Province (in lowland dry zone). Taylor (1950) described a similar species, *Sphenomorphus rufogulus* from Trincomalee based on a single specimen, which was eventually synonymized with *Lankascincus fallax* by Greer (1991). When the Sri Lankan endemic genus *Lankascincus* was erected to encompass most Sri Lankan species of small skinks of the genus *Sphenomorphus* Fitzinger, 1843, Greer (1991) described three new species and provided re-descriptions of three new combinations for the genus. Among Greer's (1991) three new taxa, another species similar to *L. fallax*, *L. deraniyagalae* was described from Punduloya (=Pundaluoya, mid-central highlands), and was synonymized with *L. fallax* by Batuwita (2019). In the same study, Batuwita (2019) included *Sphenomorphus megalops* (Annandale, 1906) in the genus *Lankascincus* and designated a neotype from Kitulgala (lower central highlands). Recently, Danushka *et al.* (2022) questioned the accuracy of Batuwita's (2019) identification of *L. megalops*, and Amarasinghe *et al.* (2022a) invalidated Batuwita's neotype designation for *L. megalops* with synonymising the nomen *L. megalops* with *L. fallax*. Thus, nine species of the

genus *Lankascincus* are currently known from the island (Batuwita 2019, Wickramasinghe *et al.* 2020, Kanishka *et al.* 2020, Amarasinghe *et al.* 2022a).

Lankascincus fallax is a widespread species, throughout the island including all the bioclimatic zones (wet, dry, and intermediate) from sea level up to 1,200 m a.s.l. (Batuwita 2019). After a thorough comparison of molecular, morphology, and morphometry, we here provide a detailed re-description of its adult syntype. We also map its distribution in Sri Lanka based on published records, observed specimens, and museum collections.

Material and methods

Specimen data. Specimens ($n=34$) were examined in the collections of the Natural History Museum, London, UK (NHMUK); Field Museum of Natural History, Chicago, USA (FMNH); National Museum of Sri Lanka, Colombo, Sri Lanka (NMSL); Wildlife Heritage Trust, Sri Lanka (WHT, currently deposited at NMSL), Museum für Naturkunde, Berlin, Germany (ZMB); and Zoologisches Museum Hamburg, Germany (ZMH). Museum acronyms follow Sabaj (2020). Morphometric and meristic data for species comparisons were obtained from examined specimens (see Appendix). Natural history data were taken from our field observations, as well as from published literature.

Morphological data were collected using Leica M50 or Carl Zeiss DRC 475003-9902 or AmScope SM-1BZ-RL ($\times 10$ – 90) microscopes, on the left side of each specimen. The following measurements were taken to the nearest 0.1 mm with a Mitutoyo digital calliper or an ocular micrometre (each measurement was taken three times and the mean recorded): snout–vent length (SVL, from tip of snout to anterior margin of vent), head length (HL, from posterior edge of the retro-articular process of the mandible to tip of snout), head width (HW, width of head at the temporo-mandibular articulation/angle of the jaws), head depth (HD, dorso-ventral distance between occiput and throat), snout length (ES, from anterior border of orbit to tip of snout), orbit diameter (ED, the greatest horizontal diameter of the orbit), tympanum–eye length (TYE, from posterior border of orbit to anterior border of tympanum), interorbital width (IO, shortest distance between dorso-medial margins of orbits), brachium length (UAL, on the dorsal surface from the axilla to the inflection of the flexed elbow), antebrachium length (LAL, on the dorsal surface from the posterior surface of the elbow while flexed 90 degree to the base of the heel), palm length [PLM, from wrist (carpus) to distal tip of longest finger], thigh length (FEL, from the anterior margin of the hind limb at its insertion point on the body to the knee while flexed), shank length (TBL, from the posterior surface of the knee while flexed to the base of the heel), foot length (FOL, from heel to tip of longest toe), body width (BW, greatest transversal width at midbody), body depth (BD, greatest dorso-ventral depth at midbody), axilla–groin length (AG, distance between axilla and groin), tail base width (TBW, greatest width at tail base), tail length (TL, from tip of tail to posterior margin of vent), total length (TOL = SVL + TL, from tip of snout to tip of tail), forelimb length (FLL = UAL + LAL + PLM), and hind limb length (HLL = FEL + TBL + FOL).

Supralabial (SUP) and infralabial (INF) scales were counted from the gape to the rostral and mental scales, respectively. Ventrals included all scales from the scale posterior to the postmental to the last scale bordering the vent, counted along the ventral midline. Paravertebral scales were counted from the post-parietal /nuchal to the level of the posterior margin of the thigh in a straight line immediately left of the vertebral column. Subdigital lamellae were counted from the first proximal enlarged lamella wider than the largest palm scale to the distal-most lamella at the base of the claw in the fourth toe. The total number of longitudinal scale rows was counted around the midbody (AG/2, at half-length of axilla–groin length). Sex was not determined unless the hemipenes were everted.

Morphometric analysis. Statistically informative tests were performed on 27 adult voucher specimens of *L. fallax* based on the distribution in two bioclimatic zones: wet zone ($n=16$) and dry zone ($n=11$). All the distribution records were based on the data associated with the museum specimens examined. These samples include (i) the adult syntype (ii) the holotype of the junior synonym, *Sphenomorphus rufogulus* from the dry zone, and (iii) syntypes of the synonym, *L. deraniyagalae* from the wet zone. Juveniles were excluded to avoid allometric bias. We performed separate Kruskal–Wallis one-way analysis of variance tests on six different morphometric characters (HL, HW, FOL, HLL, AG, and SVL) to detect any significant difference between the populations in the two bioclimatic zones. We used this test due to the small sample size (Zar 2010).

Variation in adult size was normalized using the following equation: $\log X_{\text{adj}} = \log(X) - \beta[\log(\text{SVL}) - \log(\text{SVL}_{\text{mean}})]$, where X_{adj} = adjusted value; X = measured value; β = unstandardized regression coefficient for each phenotype; and SVL_{mean} = overall average SVL of all phenotypes (Leonart *et al.* 2000, Chan & Grismer 2022)

before multivariate analyses on above morphometric characters. The scaled morphometric characters were treated as the dependent variable and the phenotypes as the predictor variable for multivariate analysis. The multivariate analysis uses Principal Component Analysis (PCA) to reduce the highly correlated multidimensional data matrix into a few uncorrelated variables, i.e., principal components (PC). We used the princomp function in the R statistical software program (v4.0.4; R Core Team 2021). Biplots of the first two principal component scores were used to examine the degree of relative influence of each morphometric character on the data set. All statistical analyses were conducted using the R statistical software program (v4.0.4; R Core Team 2021).

Genetic data. Molecular data for the fragments of the 16S rRNA mitochondrial gene was taken from the GenBank deposited data (Table 1). The samples of *Lankascincus fallax* represent both wet zone and dry zone populations to test whether there is any considerable genetic divergence between these populations. Sequences were aligned with ClustalW (Thompson *et al.* 2003) in Mega X (Kumar *et al.* 2018) with default parameters. The aligned dataset was subjected to Maximum Likelihood phylogeny on the IQ-TREE online portal (Minh *et al.* 2020). The Sequence substitution model was selected using the auto parameter with provision for FreeRate heterogeneity and the analysis was run with an ultrafast bootstrap option for 1000 iterations to assess clade support. The resultant tree was visualized and edited in FigTree v1.4.3 (Rambaut 2014). The *p*-distance (sequence divergence) was calculated in Mega X and a pairwise deletion approach was chosen to deal with gaps and or missing data.

TABLE 1. Locality data and sequence accession numbers of *Lankascincus* species used in phylogenetic analysis.

Species	Locality	Accession numbers
<i>Lankascincus taylori</i> 1	Sri Lanka	MT509018
<i>Lankascincus taylori</i> 2	Sri Lanka	MT509017
<i>Lankascincus taylori</i> 3	Sri Lanka	MT509016
<i>Lankascincus gansi</i> 1	Sri Lanka	MT509013
<i>Lankascincus gansi</i> 2	Sri Lanka	MT509012
<i>Lankascincus gansi</i> 3	Sri Lanka	MT509011
<i>Lankascincus fallax</i> 1	Sri Lanka (dry zone)	MT509020
<i>Lankascincus fallax</i> 2	Sri Lanka (dry zone)	MT509010
<i>Lankascincus fallax</i> 3	Sri Lanka (dry zone)	MT509009
<i>Lankascincus fallax</i> 4	Sri Lanka (wet zone)	MT509008
<i>Lankascincus fallax</i> 5	Sri Lanka (wet zone)	AY308240
<i>Lankascincus dorsicatenatus</i> 1	Sri Lanka	MT509015
<i>Lankascincus dorsicatenatus</i> 2	Sri Lanka	MT509014
<i>Lankascincus deignani</i>	Sri Lanka	MT509019
<i>Ristella rukrii</i>	India	AY308292

Results

Among the *Lankascincus* species groups and individual species defined by Kanishka *et al.* (2020), *L. fallax* is clearly distinguished by having two primary temporals (*vs* single in *L. taylori* group, *L. deignani* group, and *L. taprobanensis* Kelaart, 1854); last supralabial single (*vs* longitudinally split in *L. gansi* group, *L. dorsicatenatus* Deraniyagala, 1953); second supraocular subequal in transverse axis (*vs* wider in *L. gansi* group, *L. taylori* group, and *L. merrill* Wickramasinghe, Vidanapathirana & Wickramasinghe, 2020).

Morphometric analysis. The morphometric ratio mean comparison between the populations of dry and wet bioclimatic zones shows no significant difference: HL ($\chi^2=0.70$, $P=0.40$), HW ($\chi^2=12.52$, $P=0.22$), AG ($\chi^2=1.91$, $P=0.17$), FLL ($\chi^2=0.06$, $P=0.80$), HLL ($\chi^2=20.51$, $P=0.47$). Principal component analysis also showed no differences in morphometric characters between dry and wet bioclimatic zones with a distinct cluster (Fig. 1). Principal components 1 and 2 collectively explained only 61.6% of the variation in the morphometric data matrix (Table 2, Fig. 1) and in all three principal components, the dry and wet zone populations form a scattered distribution.

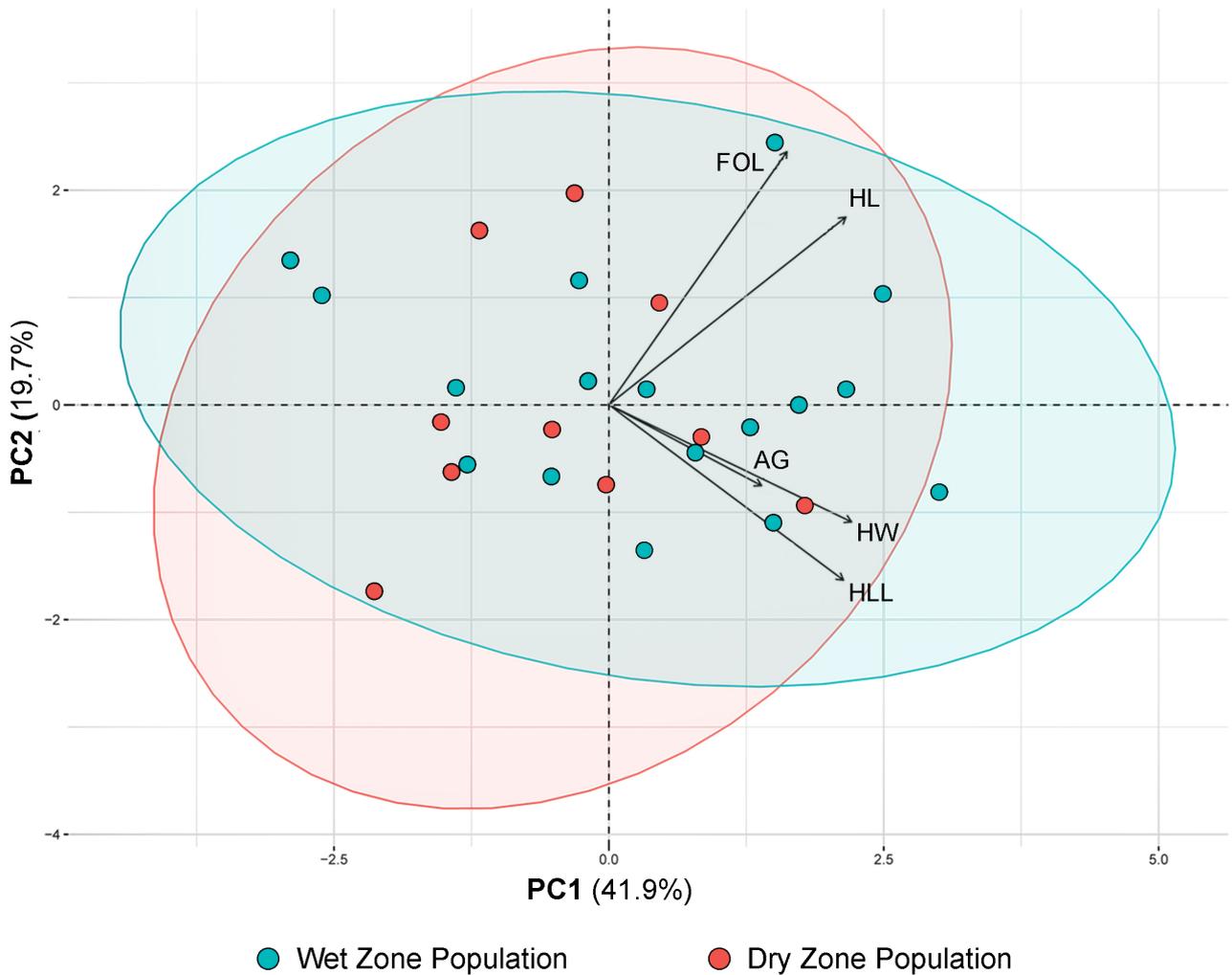


FIGURE 1. PC1 vs PC2 ordination plot of the morphometric variation of adult *Lankascincus fallax* (n=27) from two different bioclimatic (wet and dry) zones in Sri Lanka, each point represents a specimen, and the relative distances between two points represent the similarity.

TABLE 2. Principal Component Analysis (PCA) and loadings. Principal components (PC) 1 and 2 collectively explained nearly 61.6% of the variation. SVL = snout-vent length; HL = head length; HW = head width; AG = axilla-groin length; FLL = forelimb length; HLL = hind limb length.

PCA variable	PC1	PC2	PC3	PC4	PC5
Standard deviation	1.2313	1.1752	0.9440	0.8298	0.7233
Proportion of variance	0.3032	0.2762	0.1782	0.1377	0.1046
Cumulative proportion	30.3%	57.9%	75.8%	89.5%	100.0%
Loadings					
HL.scale	0.5177	-0.3595	-0.35838	-0.5633	-0.3960
HW.scale	-0.3821	-0.5993	-0.01178	-0.3780	0.5930
FOL.scale	0.5846	-0.2652	-0.26655	0.5548	0.4570
HLL.scale	-0.4826	-0.3553	-0.54221	0.4190	-0.4137
AG.scale	-0.1057	0.5611	-0.71159	-0.2371	0.3336

Phylogenetic relationship. The mitochondrial DNA tree recovered a clade consisting of five lineages (Fig. 2) corresponding to (1) *Lankascincus deignani* (Taylor, 1950); (2) *L. dorsicatenatus*; (3) *L. fallax*; (4) *L. gansi* Greer, 1991; and (5) *L. taylori* Greer, 1991. *Lankascincus fallax* and *L. deignani* are sister taxa and the lineage of *L.*

taylori is basal to these two species. Among the available *Lankascincus* samples, *L. dorsicatenatus* is basal to all the species of the genus. There is a 0.0–1.5% genetic distance (Table 3) between the wet and dry zone populations of *L. fallax*, but they are not divergent enough to be considered distinct taxonomic entities. On the other hand, for example, the genetic distance between the two wet zone species, *L. dorsicatenatus* and *L. gansi*, is 6.6–8.0. Thus, based on both morphometric and phylogenetic analysis we consider that *L. fallax* in both wet and dry zones represents a single species and we redescribe it below based on its adult syntype (ZMB 3762).

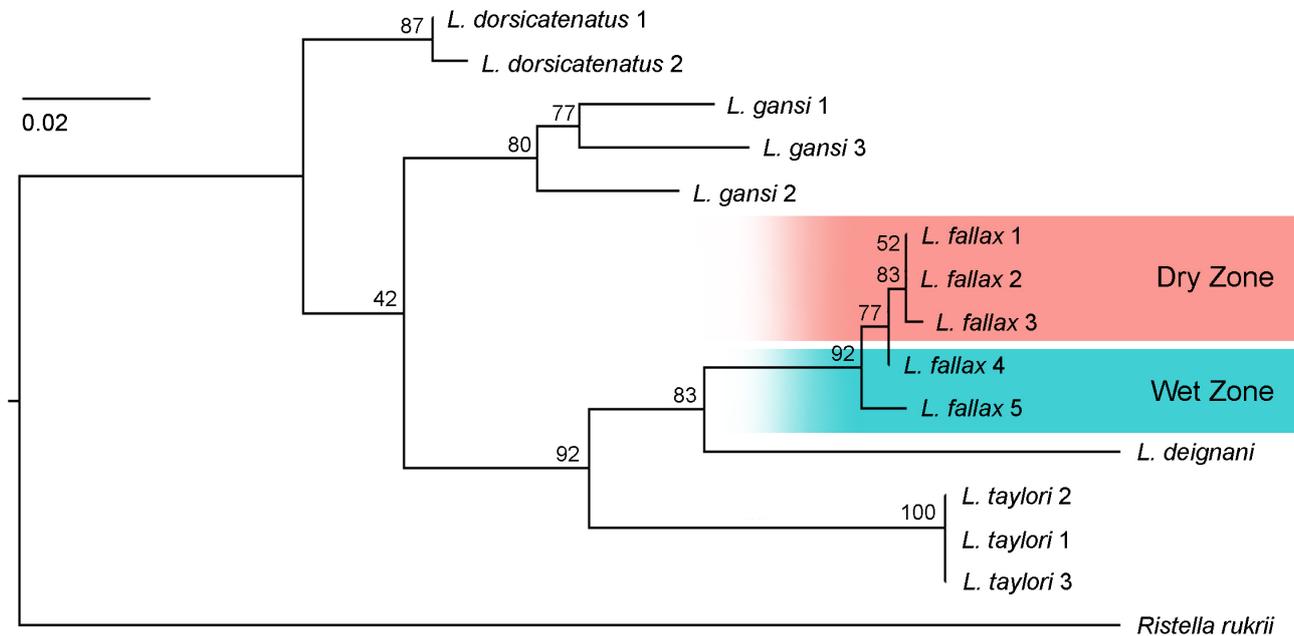


FIGURE 2. Maximum likelihood (ML) phylogeny of the members of the genus *Lankascincus* based on mitochondrial 16S rRNA gene (~500bp). Numbers at nodes represent branch supports (bootstrap) and color shadings represent wet and dry zone populations of *L. fallax*.

TABLE 3. Uncorrected pairwise *p*-distance (sequence divergence) for mitochondrial 16S rRNA gene calculated for members of the genus *Lankascincus*.

No. Samples	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1 <i>L. taylori</i> 1															
2 <i>L. taylori</i> 2	0.0														
3 <i>L. taylori</i> 3	0.0	0.0													
4 <i>L. gansi</i> 1	10.5	10.5	10.5												
5 <i>L. gansi</i> 2	9.8	9.8	9.8	4.3											
6 <i>L. gansi</i> 3	10.8	10.8	10.8	4.1	4.6										
7 <i>L. fallax</i> 1 (dry zone)	8.4	8.4	8.4	10.3	9.6	10.6									
8 <i>L. fallax</i> 2 (dry zone)	8.4	8.4	8.4	10.3	9.6	10.6	0.0								
9 <i>L. fallax</i> 3 (dry zone)	8.6	8.6	8.6	10.5	9.8	10.8	0.3	0.3							
10 <i>L. fallax</i> 4 (wet zone)	8.1	8.1	8.1	10.0	9.4	10.3	0.3	0.4	0.5						
11 <i>L. fallax</i> 5 (wet zone)	8.3	8.3	8.3	10.2	9.6	10.5	1.3	1.3	1.5	1.0					
12 <i>L. dorsicatenatus</i> 1	9.4	9.4	9.4	7.2	6.6	7.5	9.2	9.2	9.4	8.9	9.1				
13 <i>L. dorsicatenatus</i> 2	9.9	9.9	9.9	7.7	7.1	8.0	9.7	9.7	9.9	9.4	9.6	0.5			
14 <i>L. deignani</i>	11.0	11.0	11.0	12.9	12.3	13.2	7.6	7.6	7.8	7.3	7.5	11.8	12.3		
15 <i>Ristella rukrii</i>	20.2	20.2	20.2	18.1	17.4	18.4	20.0	0.0	20.2	19.8	20.0	14.2	14.7	22.7	

Systematics

Although neither the original description of *Lygosoma fallax* nor the accompanying specimen labels specify which syntype is from Trincomalee (dry zone) and which is from Ratnapura (wet zone), it is clear that both of its syntypes are the same species which is a clearly distinguished widespread species, and there is no taxonomic problem there, hence there is no taxonomic need for designating a lectotype (Art 74.7.3 of the Code). Therefore, here we provide a redescription based on its adult syntype ZMB 3762.

Lankascincus fallax (Peters, 1860)

(Figs. 3–6, 8; Table 4)

Lygosoma fallax Peters, 1860

Lygosoma megalops Annandale, 1906

Sphenomorphus rufogulus Taylor, 1950

Lankascincus deraniyagalae Greer, 1991

Lankascincus deraniyagalae—Somaweera & Somaweera 2009

Lankascincus fallax—Greer 1991, Somaweera & Somaweera 2009, Batuwita 2019, Kanishka *et al.* 2020

Lankascincus megalops—Batuwita 2019 [partim], Kanishka *et al.* 2020 [partim]

‘*Lankascincus megalops*’—Amarasinghe *et al.* 2022a [partim]

Syntypes ($n=2$). An adult male, ZMB 3762 (SVL 38.1 mm) and A juvenile, ZMB 64361 (SVL not measured) collected from Trinkomalee (=Trincomalee, Eastern Province) and Ratnapura (Sabaragamuwa Province) by Prof. L.K. Schmarida, date unknown.

Description of the syntype, ZMB 3762. Male, SVL 38.1 mm. Head moderately large (HL 14.7% of SVL), wide (HW 98.2% of HL), indistinct from neck; snout short (ES 44.6% of HL, ES 44.6% of HW), shorter than orbit diameter (ES 96.1% of ED), slightly convex in lateral profile.

Rostral shield large, posterior margin convex in contact with frontonasal caudally; nasal non-fused, nostril large, no supranasal or postnasal scale; frontonasal larger than prefrontals, in contact laterally with anterior loreal; prefrontals separate from each other by connection of frontonasal with frontal, in contact with anterior and posterior loreals laterally, 1st supraciliary, 1st supraocular and frontal posteriorly; frontal longer than frontonasal and prefrontal combined, shorter than fused (single) frontoparietal and interparietal length combined; supraoculars four, 1st longer than width in longitudinal axis, 2nd wider than length in longitudinal axis, first two supraoculars in contact with frontal, 3rd in contact with frontoparietal, 4th in contact with frontoparietal, parietal, upper pretemporal and last supraciliaries; frontoparietals fused, larger than interparietal, in contact with 2nd–4th supraoculars; parietals large, touching each other behind interparietal, in contact with 4th supraocular and upper pretemporal anteriorly, upper secondary temporal and body scales laterally; loreals two, anterior loreal touching prefrontal, frontonasal, nasal, 1st and 2nd supralabial, and posterior loreal; posterior loreal larger than anterior loreal, touching prefrontal, anterior loreal, 2nd supralabials, two preoculars, and 1st supraciliary; preoculars two, lower preocular larger, touching upper preocular, posterior loreal, 3rd supralabial and palpebral scales; eye large, orbit diameter smaller as tympanum-eye length, ED 74.2% of TYE, pupil rounded; interorbital distance broad, IO 66.0% of HW; supraciliaries eight (nine on right side), placed between supraocular and upper palpebrals; upper palpebrals 15, placed between eye and supraciliary row; lower palpebrals 16, placed between eye and subocular row; suboculars eight, smaller than supralabials, touching 3rd–6th supralabials ventrally, lower postoculars, primary temporals, and lower pretemporal scale posteriorly; last subocular touching lower and upper primary temporal, lower pretemporal, lower anterior and posterior postoculars; anterior postoculars two, upper one larger than lower; posterior postoculars two, subequal to anterior postoculars in size, touching pretemporals; pretemporals two, lower pretemporal larger than upper, touching parietals, upper primary temporal and upper secondary temporals; primary temporals two, upper one larger and in contact with secondary temporals; lower primary temporal touching 7th–8th suboculars, 6th and 7th supralabials; upper primary temporal touching last upper-supralabial, and upper and lower secondary temporals; secondary temporals two, upper one larger than the lower, upper one touching parietal and upper tertiary temporal; tertiary temporals three, equal in size, touching lower secondary temporal and upper posterior supralabial.

Supralabials 7, the last supralabial split on the left side (not split on right, a rare aberrant phenomenon), 5th at mid-orbit point; post-supralabials one; mental wider than postmental in transverse axis, shorter in longitudinal axis,

touching 1st infralabial only; infralabials five, single post-infralabial; chinshields three pairs, first pair meeting in midline, first chinshield touching 1st and 2nd infralabials, second pair touching 2nd and 3rd infralabials; gular scales cycloid, imbricate.

Body moderately elongate, dorsal scales smooth, cycloid; paravertebrals 46; 28 transverse scale rows at mid-body; ventrals 51, smooth, imbricate; median precloacals enlarged; forelimbs short, hind limbs relatively long, LAL 66.6% of TBL; thigh short and 78.5% of shank length; fourth finger with eight smooth lamellae; fourth toe with 14 smooth lamellae; relative length for fingers and toes both $4 > 3 > 5 > 2 > 1$, scales of palm and sole elevated.

Tail autotomized and detached, complete, shorter than body (TL 88.4% of SVL), round in cross-section.

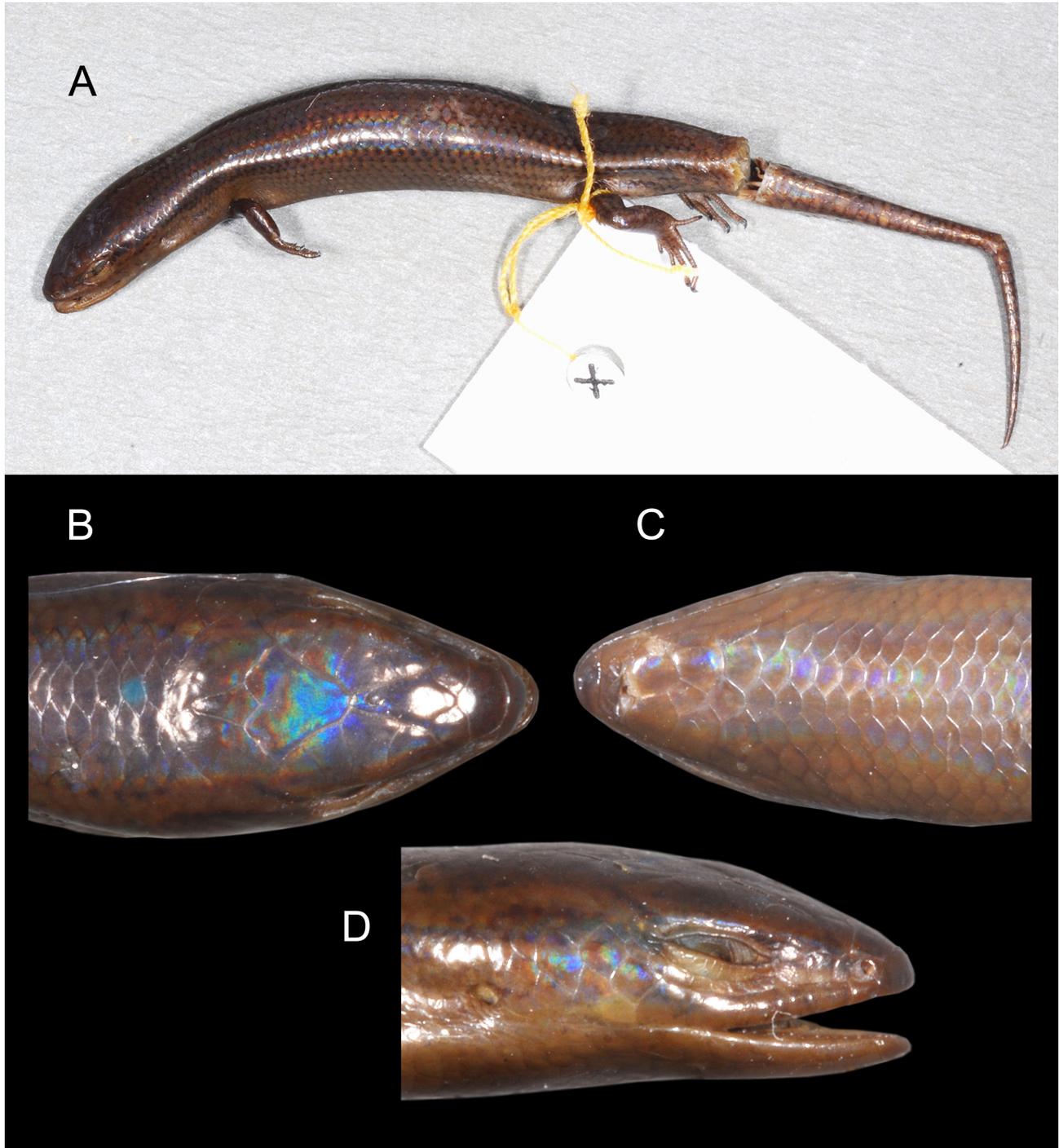


FIGURE 3. *Lankascincus fallax*, syntype male (ZMB 3762), (A) full body; head in (B) dorsal view, (C) ventral view, (D) lateral view; not to scale. Photo F. Tillack.



FIGURE 4. *Lankascincus fallax*, males in breeding coloration (not collected) from (A) Galle (lowland wet zone), and (B) Ampara (lowland dry zone).

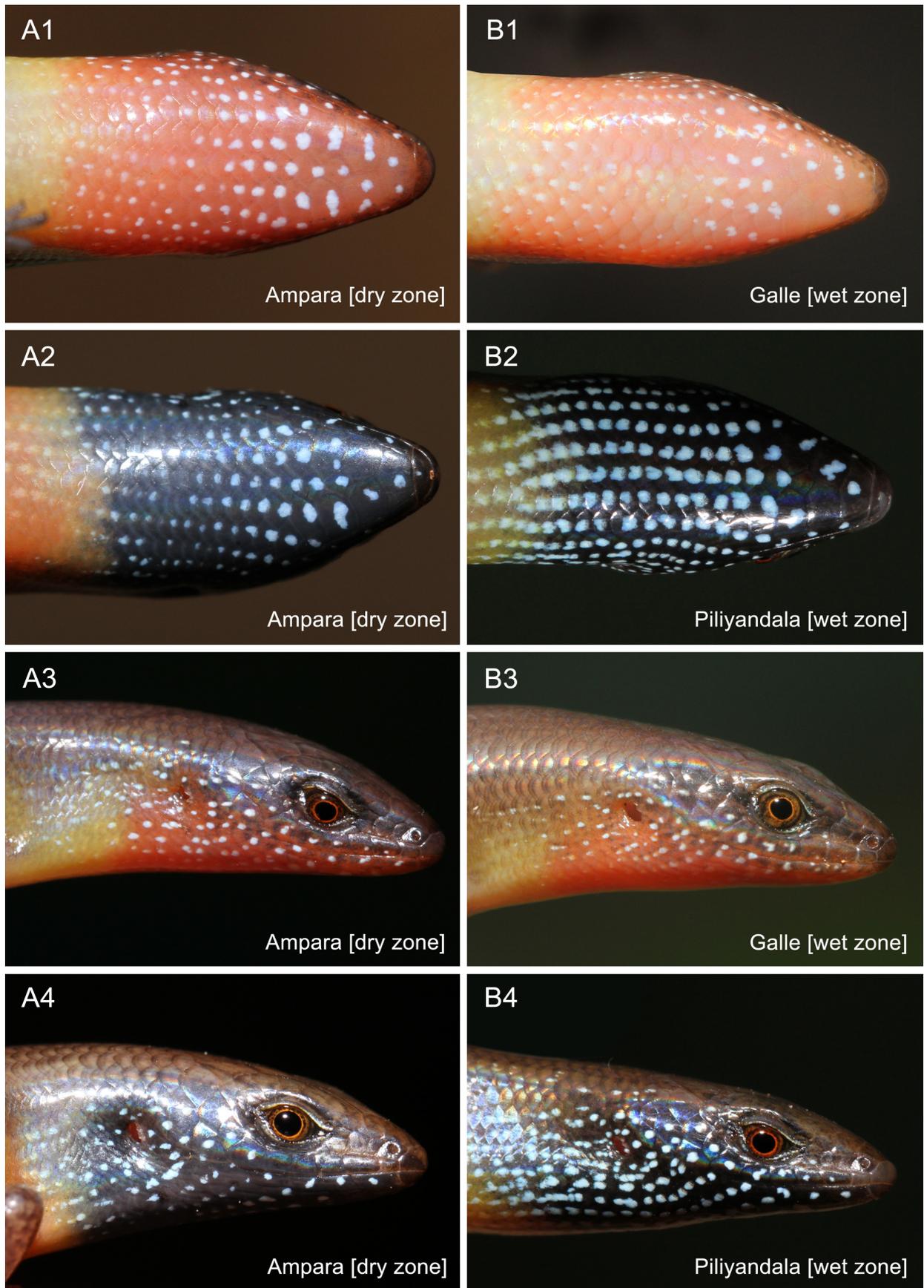


FIGURE 5. Color variation of males *Lankascincus fallax* in lowland populations (not collected, identified using photographs) from (A) dry zone and (B) wet zone.



FIGURE 6. Lateral view of head and neck of a juvenile *Lankascincus fallax* (not collected) from a home garden at Piliyandala, Western Province (lowland wet zone).

Coloration of syntype ZMB 3762. In preservative, the dorsal surface of the head, body, limbs, and tail is uniformly dark brown, with several indistinct darker longitudinal lines on the dorsum, anterior dorsal head darker; lower parts of the lateral head, temporal region, and throat light brown; neck color same as other ventral surfaces; light brown.

Variation. See Table 4. Body scalation in most examined specimens is as described above for the syntype, but the separation of prefrontals from each other by contact of frontal with frontonasal differs in comparative material. Among the materials at ZMH ($n=15$), the prefrontals are completely separated from each other ($n=1$), slightly in contact ($n=4$), and broadly in contact ($n=10$).

Comparison. See Tables 4 and 5 in Kanishka *et al.* (2020).

Coloration in life. Based on live individuals (not collected), males have dorsum iridescent brown, laterally iridescent light brown; hind limbs bronze brown with light markings; dorsal head dark brown, anteriorly black; the color of lower parts of the lateral head, temporal region, and throat highly variable (Fig. 5), but mostly dark greyish brown, in some populations it can be yellowish orange, scarlet orange, or red; neck color same as the throat; white flecks present on labials, lower temporal region, throat, and neck spread up to the shoulders; venter cream or light brown in most of the females and non-breeding males, in most of the breeding males the venter is bright yellowish. Juveniles are lighter in color, mostly yellowish; the anterior throat is yellow, and posteriorly dark greyish brown, including the neck (Fig. 6).

Distribution and natural history. This species is distributed throughout the island including all the bioclimatic zones from sea level to 1,200 m a.s.l. (Karunaratna & Amarasinghe 2010, 2012; Karunaratna *et al.* 2013; Batuwita 2019). See the map (Fig. 7) for confirmed locality data based on museum specimens and personal observations.

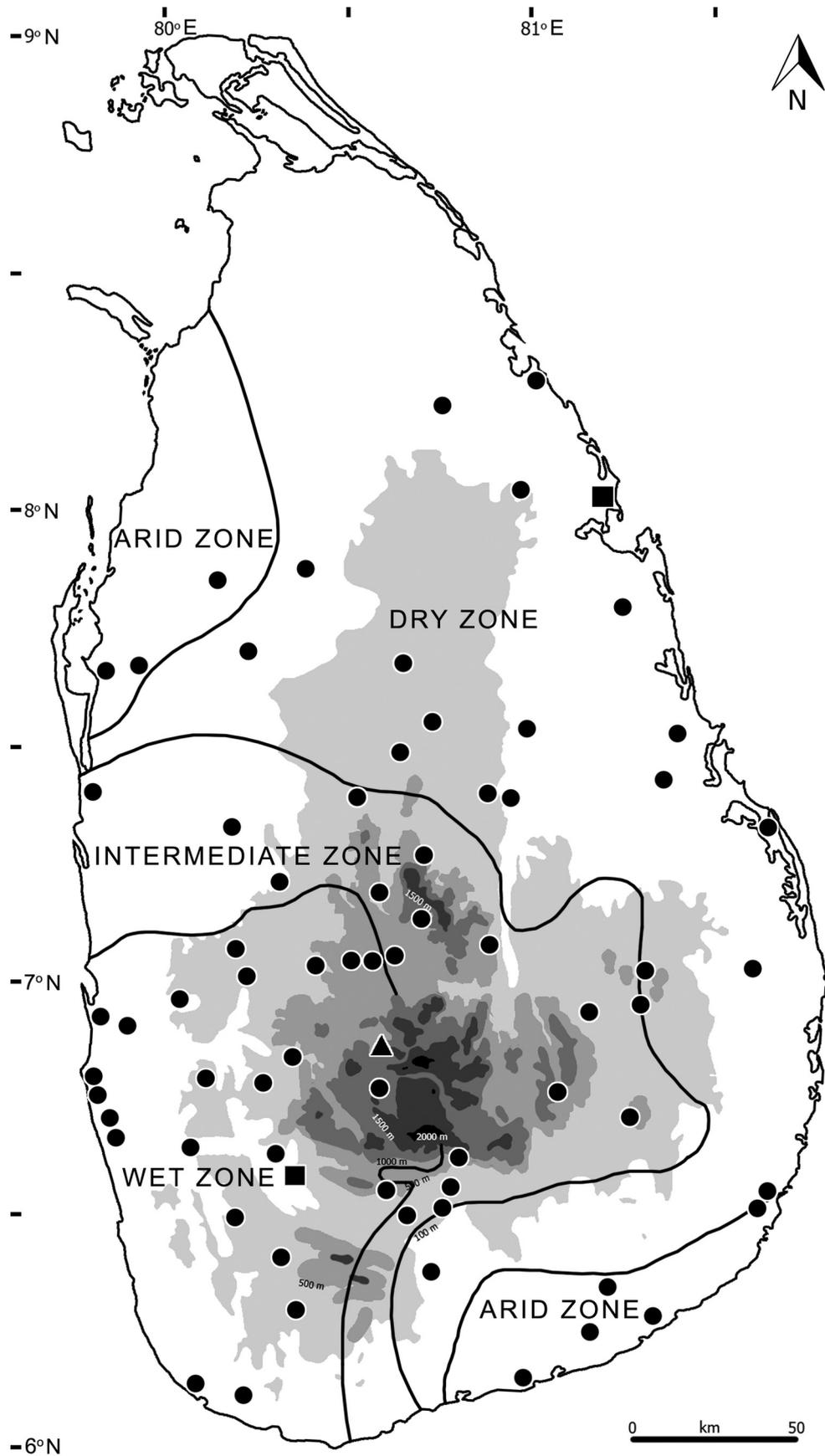


FIGURE 7. Current distribution map (based on museum specimens and personal observations) of *Lankascincus fallax* (circles), the two syntype localities of *L. fallax* are marked with squares; the holotype locality of *L. deraniyagalae* (synonym of *L. fallax*) is marked with a triangle.

TABLE 4. Selected morphometric (in mm) and meristic characters of syntypes, synonym types, and other specimens of *L. fallax* (Peters, 1860); “—” not evaluated; “+” distal part of the tail broken.

Character	<i>Lankascincus fallax</i>							
	<i>Lygosoma fallax</i>	<i>Sphenomorphus</i>	<i>Lankascincus deraniyagalae</i>				<i>Lankascincus fallax</i>	
	Peters, 1860	<i>rufogulus</i>	Greer, 1991				(Peters, 1860)	
	Syntype	Holotype	Holotype	Paratypes		males	females	
ZMB 3762	FMNH	NHMUK	NHMUK	NHMUK	NHMUK	(n=15)	(n=3)	
	male	120229	95.7.23.28C	95.7.23.28B	95.7.23.28D	95.7.23.28E		
snout-vent length	38.1	40.4	40.9	40.3	38.0	39.9	35.1–43.5	38.4–40.2
head length	5.7	7.1	10.0	8.8	8.1	11.1	6.7–8.9	7.0–7.4
head width	5.6	6.0	6.6	5.8	6.3	6.5	3.3–6.3	4.7–5.6
head depth	4.3	4.6	5.0	5.0	4.7	4.8	3.2–5.6	3.4–4.2
brachium length	2.9	3.1	3.1	3.3	3.7	3.5	2.4–3.6	2.5–2.9
antebrachium length	2.8	3.4	3.2	3.9	3.2	3.2	1.8–3.8	2.6–3.0
palm length	2.9	2.6	1.0	3.8	2.3	2.6	1.3–2.9	1.4–1.9
thigh length	3.3	4.6	4.2	5.0	3.9	3.5	3.1–4.9	4.0–4.9
shank length	4.2	4.1	4.1	5.1	4.0	3.4	3.2–9.7	5.3–5.9
foot length	5.0	5.9	5.2	5.97	4.8	5.6	3.8–5.1	4.1–4.5
body width	5.9	7.4	9.2	7.5	7.4	8.2	4.5–8.3	6.0–7.5
body depth	5.8	5.7	5.1	4.8	6.2	5.1	4.2–6.9	4.4–6.4
axilla–groin length	20.4	23.3	23.8	24.8	19.5	20.1	19.6–24.1	20.9–23.3
tail base width	3.7	4.4	3.6	4.4	4.8	5.2	3.5–4.9	3.6–4.3
tail length	33.7+	40.1+	36.5+	9.6+	3.1+	38.4	32.5–72.5	38.0–47.0
supralabials	7	7	7	7	7	7	7	7
infralabials	5	5	5	5	5	5	5	5
suboculars	8	7	5	8	5	5	7–9	8
paravertebrals	46	47	46	48	51	49	46–53	48–52
midbody scale rows	28	28	28	26	26	25	24–28	24–28
ventrals	51	51	58	51	58	57	48–58	49–51
lamellae finger IV	8	10	11	11	12	damaged	8–12	10
lamellae toe IV	14	16	18	16	17	9	13–17	14, 15
Locality	Trincomalee (dry zone: lowland)		Pundaluoya (wet zone: highlands)			throughout the island		

A diurnal skink occurring in every terrestrial habitat, except forests. They mostly occur on forest edges, in home gardens, agricultural lands, and occasionally, even within highly disturbed human habitation. However, this species is associated with understory vegetation, including grasses, fallen leaves, rocks, fallen logs or debris, and decaying leaf litter. It shelters at night among roots, tree buttresses, tree trunks, and tussocks (Somaweera & Somaweera 2009). It prefers less shady habitats but with open canopy areas. This species is not sympatric with any other *Lankascincus*, as the rest of the species are mostly forest dwellers, sometimes found in well-shaded home gardens.

Conservation status. The updated distribution data shows that *L. fallax* is the most common species of the genus, and is widely distributed. It is abundant outside forests, and never found inside them. With an area of occupancy (AOO) of 1,375 km² (we recorded this species from 70 sites; Fig. 7) within a 40,784 km² extent of occurrence (EOO), we did not determine any severely fragmented locations as we observed the species from home gardens even in urban habitats, and we haven’t noticed any continuing population decline in EOO, AOO, area, extent or quality of habitat, number of locations/subpopulations, or even number of mature individuals. Therefore, the application of the IUCN Red List criteria (IUCN Standards and Petitions Subcommittee 2019), *L. fallax* can be considered as a “Least Concern” (LC) species.

Discussion

Even though *Lankascincus fallax* has long been known as a widespread species, the high morphological variability created speculation and doubt in its taxonomy. This may be why Taylor (1950) was confident enough to describe *Sphenomorphus rufogulus* (currently a junior synonym) from Trincomalee, one of the type localities of *L. fallax*. To distinguish *S. rufogulus* from *Lygosoma fallax*, Taylor (1950) used the differences in throat color in live breeding males for the separation of his species. Although throat color might be a unique character for some species, for example in complexes such as in the *L. gansi* group (see *L. cf. gansi* and Table 5 in Kanishka *et al.* 2020), for *L. fallax* it is highly variable (see Greer 1991; Wickramasinghe *et al.* 2007; and Fig. 5). Interestingly, this variability is also represented in genetic data (Fig. 2, Table 3) showing higher infraspecific genetic divergence among *L. gansi* (4.1–4.6%) compared to *L. fallax* (0.0–1.5%) in the 16S rRNA mtDNA gene. Throat color can be a unique character for subpopulations of a particular species (e.g., *Eutropis*; see Amarasinghe *et al.* 2022b), but might not be good enough to distinguish some of *Lankascincus* species; it is debatable that subpopulations can yet evolve to the point where they can obtain distinct species level (e.g., see the case for *L. cf. gansi* in Kanishka *et al.* 2020). On the other hand, the color variations are linked to the adult life stages and associated with sex (see Fig. 5; also, Jayamanna *et al.* 2022) and reproductive seasonality (Ukuwela 2009), mostly disappearing in preserved specimens (personal observations, also see Greer 1991). However, the unique color patterns that are linked to particular subpopulations remain even post-preservation (personal observations, also see Kanishka *et al.* 2020).

Based on the morphological examinations we performed across a large number of preserved and live specimens, the morphometric analysis, and phylogenetic evidence we undertook enabled us to confidently treat *L. fallax* as a single species, widely distributed throughout the island from sea level (observed in shady places beside the beach) up to 1,200 m elevations in the central highlands (highest elevation recorded at Talawakelle, Central Province). The locality data on each of the labels of the syntypes clearly states the locations as “Ratnapura and Trinkomalie” (=Trincomalee), while the type locality of *L. rufogulus* is also Trincomalee. The locality Ratnapura is in the south-western wet zone and Trincomalee is in the north-western dry zone (Fig. 7). However, based on museum and live specimens, we were not able to find any distinct morphological differences between the populations in Trincomalee and Ratnapura to separate the syntypes according to their locality. Furthermore, the morphometric (Fig. 1, Table 2) and phylogenetic (Fig. 2, Table 3) analyses clearly show that there is no significant difference between the populations in the wet and dry bioclimatic zones. However, the recently described *L. merrill*, most probably a member of the *L. fallax* group (it also shares morphological characters of the *L. gansi* group; fide Kanishka *et al.* 2020), it might have evolved from the common ancestor of *L. gansi* + *L. fallax*. Therefore, it would be interesting to investigate deep phylogenetic relationships among the morphological complexes defined by Kanishka *et al.* (2020).

Some individuals of this highly variable skink species bear paired frontoparietals (*vs* fused in the syntypes as well as the holotype of *Sphenomorphus rufogulus*). We observed that variation occurs among populations throughout the island, but this is very rare. The majority of the individuals have fused frontoparietals in every population, but only less than 5% of the individuals have paired frontoparietals, this is probably an aberrant phenomenon. We believe such aberrant specimens collected from Pundaluoya (the central highlands) led Greer (1991) to describe it as *L. deraniyagalae*, which he considered a distinct species on that basis only. However, it was synonymized by Batuwita (2019) as it has no other distinguishable morphological characters to separate it from *L. fallax*. We also agree with Batuwita’s (2019) taxonomic action, as we also observed *L. fallax* individuals with paired frontoparietals (Greer’s *L. deraniyagalae*) even from the lowland dry zone (see Fig. 8).

Greer (1991) described *L. deraniyagalae* based on eight specimens: the holotype (NHMUK 95.7.23.28c) and three paratypes (NHMUK 95.7.23.28b,d,e) from Pundaluoya (submontane area) with paired frontoparietals; three paratypes (MCZ R39837–9) from Dimbulla Queensland Estate (montane area), and one paratype (SMF 15460) from Galle (lowland wet zone). However, the montane paratypes of *L. deraniyagalae* from Dimbulla Queensland Estate (near Talawakele) have been later identified as *L. sripadensis* Wickramasinghe, Rodrigo, Dayawansa & Jayantha, 2007 (fide Batuwita 2019). We re-examined the paratype series of *L. deraniyagalae* from Pundaluoya (type locality) currently housed at NHMUK (see Table 4) which agrees with its holotype and confirms the synonymy with *L. fallax*. However, it is still recommended to do a molecular assessment using specimens with and without fused frontoparietals for further clarification.

Apart from the variation of frontoparietals (fused and split), we observed another variation of prefrontals (in contact and separate) even within the same populations. Therefore, the arrangement of frontoparietal and prefrontal scales may not be a suitable character to distinguish the *Lankascincus* species. For further understanding of individual variations in some isolated or cryptic populations, we suggest a future reinvestigation, including a phylogenetic study with the missing samples of other nominal taxa.

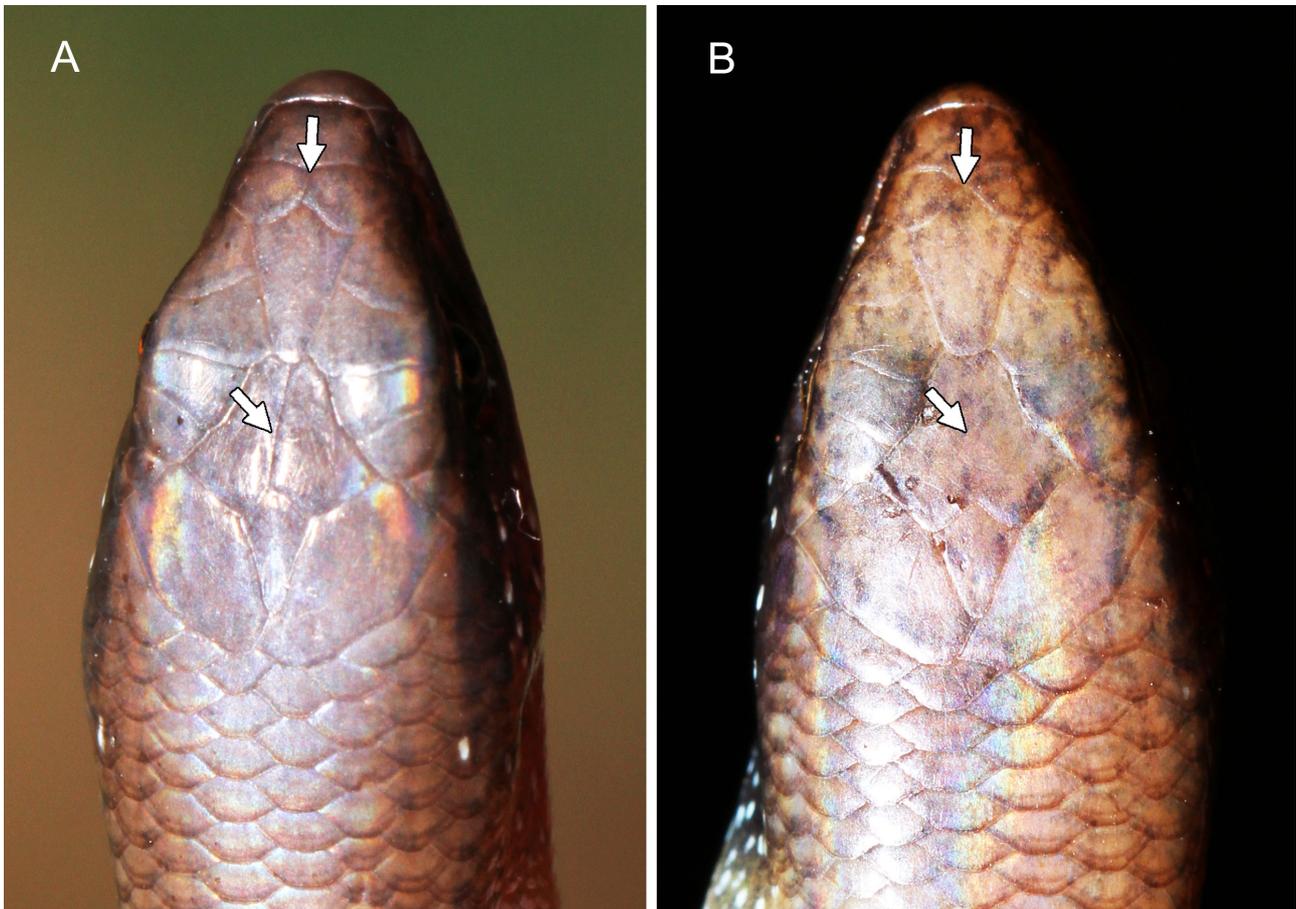


FIGURE 8. Two *Lankascincus fallax* males from one population in Ampara, lowland dry zone (not collected), with arrows indicating (A) paired frontoparietal and a wide contact in prefrontals (B) fused frontoparietal and separated prefrontals separated.

Acknowledgments

We thank M.O. Rödel and Frank Tillack at ZMB, Germany for the loan of specimens under their care. Nanda Wickramasinghe (former director), Sanuja Kasthuriarachchi (director), Lankani Somaratne, Chamalka Kothalawala, Chandrika Munasinghe, Rasika Dasanayake, Ravindra Wickramanayake, P. Gunasiri, and all the staff (worked since 2005) at NMSL are acknowledged for facilitating the in-house study of specimens under their care; Nimalka Sanjeevani, Dilum Samarasingha, Imesh Jayalath, Sampath Senaviratne, Himesh Jayasinghe, Suranjan Karunarathna, Hiranya Sudasinghe, Tharindu Ranasinghe, Divanka Randula, Madura De Silva and Mendis Wickramasinghe for valuable assistance in numerous stages of the study. We also thank Ivan Ineich (MNHN), David Chapple (Monash University, Melbourne), and anonymous reviewers for their valuable comments.

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APPENDIX I: Other specimens examined

- Lankascincus gansi* (14 ex.): Sri Lanka:** Udugama (type locality): NMSL 0397-SB; Kanneliya near Udugama: WHT 6670; Dediyaigala near Udugama: WHT 6664; Haycock-Hiniduma: WHT 0151; Kombala-Kottawa Forest Reserve (Hiyare): WHT 6661, 6676; Kottawa: WHT 6672; Nawinna: WHT 6776; Rumassala: WHT 6576, NMSL 0154; Yagirala: WHT 6752. *Lankascincus* cf. *gansi*: Sri Lanka: Gannoruwa, Kandy: WHT 6780; Kithulgala: NMSL 0186b, WHT 6613.
- L. taylori* (4 ex.): Sri Lanka:** Pundaluoya: NHMUK 1872.3.23.4A (holotype), 1872.3.23.4b,c (paratypes), WHT 6707.
- L. sripadensis* (7 ex.): Sri Lanka:** Sripada Sanctuary (Adam's peak): NMSL 2007.05.01 (holotype), 2007.05.02 (paratype); Agra Arboretum: WHT 2238, 6566, 6636, NMSL uncat. 125–126.
- L. dorsicatenatus* (15 ex.): Sri Lanka:** Angamma, Nivithigala: NMSL RSK 307 (paratype); Kuruwita Batadombalena: WHT 6619 (neotype); Nawinna: WHT 6774, 6779; Koskulana, Panapola: WHT 6737, 6745; Owilkanda, Mathale: WHT 6736; Nainakanda, Wathura: WHT 6719, 6728–29; Hanthana: NMSL (SB) 0391; Mathale Owilikanda: WHT 6736; Nainakkanda, Wathura: WHT 6729, NMSL uncat. 120; Batadombalena, Kithulgala: NMSL uncat.
- L. deignani* (3 ex.): Sri Lanka:** Kombala-Kottawa Forest Reserve (Hiyare): WHT 6524 (holotype of *L. greeri*), 6525 (paratype of *L. greeri*); NMSL uncat. (1 ex.).
- L. fallax* (34 ex.): Sri Lanka:** Trincomalee: ZMB 3762 (syntype), FMNH 120229 (holotype of *Sphenomorphus rufogulus*); Ratnapura: ZMB 64361 (syntype); Pundaluoya: NHMUK 1895.723.28c (holotype of *L. deraniyagalae*), 1895.723.28b (paratype of *L. deraniyagalae*); Kandahena Estate, Passara: WHT 1579; Puwakpitiya: WHT 2055, NMSL uncat. 9, 11–13; Mahamewna Uyana: NMSL uncat. 30–31; Polonnaruwa: WHT 6735; Mathale: NMSL uncat. 01; Yala block I: NMSL uncat. 34; Kitulampitiya, Galle: NMSL uncat. 66; Mahawalathenna, Balangoda: NMSL uncat. 197; Yongamulla, Yakkala: ZMH R08082–87, R08100–01, R08116–17; Mundal Lake, Chilaw: ZMH R08115; Andapolakanda, Malsiripura, ZMH R08118; Monaragala: ZMH R08118; Badulla: ZMH R08119; Peradenya: ZMH R12151; Colombo: ZMH R12151.
- L. taprobanensis* (7 ex.): Sri Lanka:** Nuwara Eliya (?): NHMUK 1946.8.26.11 (syntype); Horton plains: NMSL 2007.22.01–02, WHT 2014, 2097, 2097a–b.
- L. merrill* (5 ex.): Sri Lanka:** Enasalwatte Estate, Sinharaja: NMSL 2011.01.01 (holotype), 2011.01.02, DWC 2011.05.01–02; Mahawalathenna: WHT 6747.
- L. sameerai* (6 ex.): Sri Lanka:** Morningside: WHT 6720 (holotype), 1608 (paratype); Silverkanda, Deniyaya: WHT 6593 6741, 6749a–b.