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The phylogeny of *Hemiphyllodactylus* Bleeker, 1860 (Squamata: Gekkonidae) with a description of a new species from the Mangin Range, Sagaing Region, northern Myanmar

L. Lee Grismer [ID][a], May Thu Chit[b], Parinya Pawangkhanant [ID][c], Roman A. Nazarov[d], Than Zaw[b] and Nikolay A. Poyarkov [ID][e,f]

[a]Herpetology Laboratory, Department of Biology, La Sierra University, Riverside, CA, USA; [b]Department of Zoology, University of Mandalay, Mandalay, Myanmar; [c]Rabbit in the Moon Foundation, Ratchaburi, Thailand; [d]Zoological Museum, Moscow State University, Moscow, Russia; [e]Faculty of Biology, Department of Vertebrate Zoology, Moscow State University, Moscow, Russia; [f]Laboratory of Tropical Ecology, Joint Russian-Vietnamese Tropical Research and Technological Center, Hanoi, Vietnam

ABSTRACT

Phylogenetic analyses of the 49 nominal species of the gekkonid genus *Hemiphyllodactylus* based on the mitochondrial gene NADH dehydrogenase subunit 2 and its flanking tRNAs resulted in a strongly supported tree composed of a number of regionally localised monophyletic lineages consistent with previous genus-wide analyses. One such lineage from Western Indochina is composed of three previously recognised clades plus an additional species from southern Thailand. An integrative taxonomic analysis of one of these clades (clade 3 from Western Yunnan, China) recovered a new species from the Mangin Mountain Range that represents the third independent origin of *Hemiphyllodactylus* in Myanmar (not counting the widespread parthenogenetic *H. typus*). *Hemiphyllodactylus zalonicus* sp. nov. from Mt. Zalon, Sagaing Region, is the first species of *Hemiphyllodactylus* known from the northern part of Ayeyarwady Basin and bears a 15.0–18.9% uncorrected sequence divergence from other clade members as well as having discretely non-overlapping meristic and mensural differences. This discovery brings the total number of *Hemiphyllodactylus* in Myanmar to at least 11 species.

Introduction

Hemiphyllodactylus is a rapidly growing gekkonid genus due to the discovery of new species and currently contains 49 species (Mohapatra et al. 2020; Do et al. 2020; Uetz et al. 2020) that collectively extend from Southern India and Sri Lanka to the Western Pacific (Grismer et al. 2013). All are small nondescript species which in Indochina are generally restricted to circumscribed upland areas (see Grismer et al. 2013; 2014a, 2020a; Eliades et al. 2019; Sukprasert et al. 2018, and references therein). *Hemiphyllodactylus* species are elusive and generally difficult to find in their native environments and as such, many species descriptions are based on a single or just a few specimens (Cobos et al. 2016; Eliades et al. 2019; Grismer et al. 2013; 2014b, 2015,

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CONTACT L. Lee Grismer ✉ lgrismer@lasierra.edu; Nikolay A. Poyarkov ✉ n.poyarkov@gmail.com

2018; Grismer et al. 2018a; 2020a, 2020b; Guo et al. 2015). On the other hand, lizards may be incredibly dense in rural situations where they are human commensals (Mohapatra et al. 2020; Grismer et al. 2020a). At present, at least 10 species of *Hemiphyllodactylus* are reliably recorded from Myanmar, though the real diversity of this genus in the region appears to be clearly underestimated (Grismer et al. 2020a).

Indochina is considered as the major centre of *Hemiphyllodactylus* diversity (Grismer et al. 2013). Our recent fieldwork at Mangin Mountain Range (also known as Mhankin Range in Burmese spelling) at Mt. Zalon (or Zalon Taung) near Ban Mauk, Sagaing Region in northern Myanmar, resulted in the discovery of yet another new species of *Hemiphyllodactylus* which represents the first record of the genus from the northern part of the Ayeyarwady Basin (Figure 1). Genetic data from the mitochondrial gene NADH dehydrogenase subunit 2 (ND2) and its flanking tRNAs do not place it in either of the known distantly related Burmese clades (Grismer et al. 2020a) but align it with the Chinese species *H. changningeneis* and *H. longlingensis* (clade 3 of Grismer et al. 2017) from the mountains of Western Yunnan Province in southwest China. As such, this new population represents a third Burmese lineage. However, the single specimen is vastly different in morphology from *H. changningeneis* and *H. longlingensis* and therefore is described as a new species herein.

Materials and methods

Sampling

Two specimens were collected in dipterocarp tropical forest at the foothills of Zalon Mountain in Ban Mauk District of Sagaing Region, northern Myanmar (Figure 1). Geographic coordinates and elevation were obtained using a Garmin GPSMAP 60CSx and recorded in WGS 84 datum. Tissue samples were taken from one specimen (ZMMU R-16635) and stored in 95% ethanol prior to preservation in 10% buffered formalin and
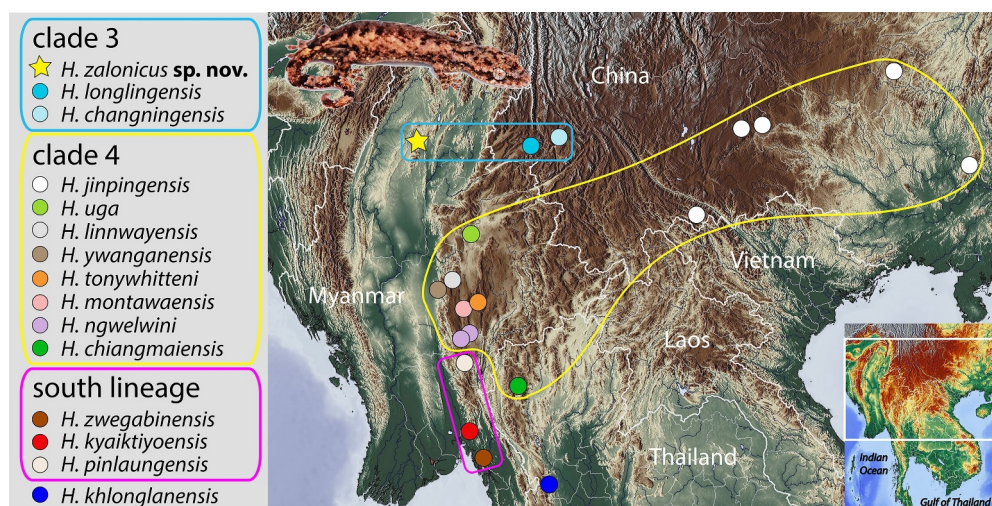

Figure 1. Distribution of the species of the Western Indochina lineage of the genus *Hemiphyllodactylus*.

subsequent storage in 70% ethanol. The specimens and tissue sample were subsequently deposited in the herpetological collections of the Zoological Museum of Moscow University (ZMMU, Moscow, Russia) and Zoology Department of University of Mandalay (ZDUM, Mandalay, Myanmar).

Phylogenetic analyses

We obtained 1,039 base pairs of NADH dehydrogenase subunit 2 (ND2) sequence data from 199 specimens from GenBank (see Grismer et al. 2017, Grismer et al. 2018a, 2020a) and a newly sequenced specimen from Sagaing, Myanmar for phylogenetic analyses. Four outgroup species, *Gehyra felmani* (Taylor), *G. mutilata* (Wiegmann), *Hemidactylus frenatus* Duméril & Bibron and *Lepidodactylus lugubris* Duméril & Bibron were used to root the tree based on Heinicke et al. (2011).

For molecular phylogenetic analyses, total genomic DNA was extracted from ethanol-preserved liver tissue using standard phenol-chloroform – proteinase K (final concentration 1 mg/ml) extraction procedures with consequent isopropanol precipitation (protocols followed Hillis et al. 1996). The isolated total genomic DNA was visualised in agarose electrophoresis in presence of ethidium bromide. The concentration of total DNA was measured in 1 µl using NanoDrop 2000 (Thermo Scientific) and consequently adjusted to ca. 100 ng DNA/µL.

The ND2 mitochondrial DNA gene was amplified using a double-stranded Polymerase Chain Reaction (PCR) under the following conditions: 1.0 µl genomic DNA (10–30 ng), 1.0 µl light-strand primer (10 µM), 1.0 µl heavy strand primer (10 µM), 1.0 µl dinucleotide pairs (1.0 µM), 2.0 µl 5x buffer (2.0 µM), 1.0 MgCl 10x buffer (1.0 µM), 0.10 µl Taq polymerase (5 u/µl) and 7.4 µl H_2O. PCR reactions were executed on a Bio-Rad T100™ Thermal Cycler under the following conditions: initial denaturation at 95°C for 2 min, followed by a second denaturation at 95°C for 35 s, annealing at 48°C for 35 s, followed by a cycle extension at 72°C for 35 s, for 31 cycles. The PCR products were visualised on a 1.0% agarose electrophoresis gel. Successful targeted PCR products were outsourced to Evrogen® (Moscow, Russia) for PCR purification and sequencing. Primers used for amplification and sequencing of the ND2 gene were L4437b (5'-AAGCAGTTGGGCCCATACC-3') and H5934 (5'-AGRGTGCCAATGTCTTTGTGRTT -3') (Macey et al. 1997). The obtained sequence for the specimen from Sagaing Region was deposited in GenBank (accession number MW039150); GenBank accession numbers for the remaining 198 specimens are listed in Grismer et al. (2017, Grismer et al. 2018a, 2020a, 2020b).

We used maximum likelihood (ML) and Bayesian inference (BI) to estimate the phylogenetic relationships among the sampled geckos in our sequence alignment. An ML phylogeny was estimated using the IQ-TREE webserver (Nguyen et al. 2015; Trifinopoulos et al. 2016) preceded by the selection of substitution models using the Bayesian Information Criterion (BIC) in ModelFinder (Kalyaanamoorthy et al. 2017), which supported HKY+F+ G4 as the best fit model of evolution for the tRNAs and TVM+F+ G4 for ND2 codon position 1, TVM+F + I+ G4 for position 2 and GTR+F + I+ G4 for position 3. One thousand bootstrap pseudoreplicates via the ultrafast bootstrap (UFB; Hoang et al. 2017) approximation algorithm were employed and nodes having ML UFB values of 95

and above were considered highly supported (Minh et al. 2013). A Bayesian inference (BI) analysis was carried out in Mr Bayes 3.2.3. (Ronquist et al. 2012) on XSEDE using the CIPRES Science Gateway (Cyberinfrastructure for Phylogenetic Research; Miller et al. 2010) employing GTR+I + G model of evolution to all partitions using default priors. Two independent Markov chain Monte Carlo (MCMC) simulations were performed each with four chains, three hot and one cold. We ran the MCMC simulation for 100 million generations, sampled every 10,000 generations and discarded the first 10% of each run as burn-in. Convergence and stationarity of all parameters from both runs were checked in Tracer v1.6 (Rambaut et al. 2014) to ensure effective sample sizes (ESS) were above 200. Post-burn-in sampled trees from both runs were combined using the sumt function in Mr Bayes and a 50% majority-rule consensus tree was constructed. Nodes with Bayesian posterior probabilities (BPP) of 0.95 and above were considered highly supported (Huelsenbeck et al. 2001; Wilcox et al. 2002). After removing taxa, not in the Indochina clade (see designation below) to which the new species belonged, MEGA7 (Kumar et al. 2016) was used to calculate uncorrected pairwise sequence divergence among and within the species.

Morphological analyses

For the descriptive work, colour data were taken from digital images of the holotype in life and in preservative. For purposes of comparison, the methodology involving the evaluation of mensural and meristic characters follows Zug (2010) and Grismer et al. (2018a, 2020a, 2020b). Mensural data were taken with Mitutoyo dial calipers to the nearest 0.1 mm under a Nikon SMZ 1500 dissecting microscope on the left side of the body where appropriate. Data recovered were snout-vent length (SVL), taken from the tip of the snout to the vent; trunk or axilla-groin length (AG), taken from the posterior margin of the forelimb at its insertion point on the body to the anterior margin of the hind limb at its insertion point on the body; head length (HL), measured from the posterior margin of the retroarticular process of the lower jaw to the tip of the snout; head width (HW), measured at the angle of the jaws; eye diameter (ED), the greatest horizontal diameter of the eyeball; snout-eye length (SN), measured from anteriormost margin of the eyeball to the tip of snout; nares-eye length (NE), measured from the anterior margin of the eyeball to the posterior margin of the external nares; and snout width (SW), measured between the external nares. Meristic character states evaluated were the number of scales contacting the nares (circumnasal scales, CN); the number of scales between the supranasals (=postrostrals or intersupranasals, IS); the number of scales contacting the medial edge of the infralabials and mental from the juncture of the second and third infralabials on both sides (CS); the number of supralabial (SL) and infralabial (IL) scales counted from the largest scale immediately posterior to the dorsal inflection of the posterior portion of the upper jaw to the rostral and mental scales, respectively; the number of longitudinal rows of ventral scales at mid-body contained within one eyeball diameter (VS); the number of longitudinal rows of dorsal scales at mid-body contained within one eyeball diameter (DS); the number of subdigital lamellae wider than long on the first finger (FL1)

and toe (TL1); lamellar formulae determined as the number of U-shaped, sub-digital lamellae (split and single) on the digital pads of digits II–V of the hands and feet; the total number of femoral pores (FP), precloacal pores (PP) or femoroprecloacal pores (i.e. the contiguous rows of femoral and precloacal pore-bearing scales [FPC]; given that the holotype is a female, the enlarged pitted homologous scales in the proximal femoral and precloacal regions were counted); and the number of cloacal spurs on each side of the hemipenal swelling or immediately posterior to the vent in females. Colour pattern characters evaluated were the presence or absence of dark pigmentation in the gonadal tracts and caecum; configuration of the dark markings on the dorsum (dorsal pattern); presence or absence of a dark pre- and/or postorbital stripe extending to at least the neck; the presence or absence of a linear series of white postorbital and dorsolateral spots on the trunk; and the presence or absence of light-coloured, anteriorly projecting arms of the light-coloured post-sacral marking.

Species delimitation

The general lineage concept (GLC: De Queiroz 2007) adopted herein proposes that a species constitutes a population of organisms evolving independently of other such populations owing to a lack of gene flow. By 'independently', it is meant that new mutations arising in one species cannot spread readily into another species (Barraclough et al. 2003; De Queiroz 2007). Under the GLC implemented herein, molecular phylogenies were used to recover monophyletic mitochondrial lineages of individual(s) (i.e. populations) in order to develop initial species-level hypotheses – the grouping stage of Hillis (2019). Discrete colour pattern data and morphological data were then used to search for unique characters and patterns consistent with the previous designations of the species-level hypotheses – the construction of boundaries representing the hypothesis-testing step of Hillis (2019) – thus providing independent diagnoses to complement the molecular analyses.

Results

The ML and BI analyses returned well supported, nearly identical topologies for all the known species of the genus that were concordant with genus-wide phylogenies in previous analyses (Grismer et al. 2013, 2017, 2018a; 2020a, 2020b). The Mt. Zalon specimen was recovered as a member of the *typus* group and embedded within a lineage of species from Western Indochina where it is nested in clade 3 with *Hemiphyllodactylus longlingensis* and *H. changningensis* to which it is the well-supported (BI 1.00/ML 94) sister species of the latter (Figure 2). The Mt. Zalon specimen and *H. chingningensis* differ by having an uncorrected pairwise sequence divergence of 15.0–15.3% (Table 1) and also differ in a number of discrete (i.e. non-overlapping ranges) of meristic and mensural characters (see comparisons). As such we hypothesise this specimen represents a new evolutionary lineage and describe it as a new species below.
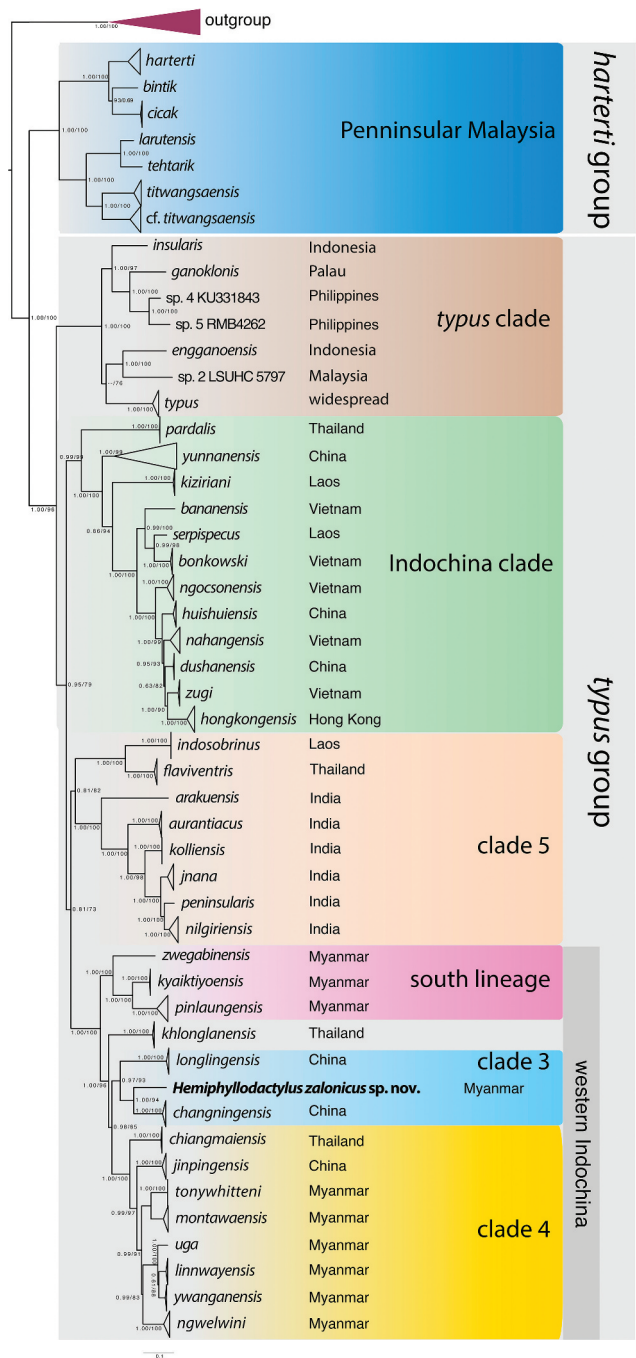
Figure 2. Maximum likelihood consensus tree of *Hemiphyllodactylus* with Bayesian posterior probabilities (BPP) and Ultrafast Bootstrap support (UFB) value coding at the nodes. Clade nomenclature follows Grismer et al. (2017, Grismer et al. 2018a, 2020a).

Table 1. Uncorrected pairwise sequence divergences between the mitochondrial ND2 lineages of *Hemiphyllodactylus* in clade 3.

Species	1	2	3	4	5	6	7	8	9	10
1. *H. zalonicus* sp. nov. ZMMU R-16635	*									
2. *H. changningensis* isolate YNCN06	0.150	*								
3. *H. changningensis* isolate YNCN12	0.153	0.003	*							
4. *H. changningensis* isolate YNCN14	0.152	0.005	0.005	*						
5. *H. changningensis* isolate YNCN40	0.152	0.002	0.002	0.003	*					
6. *H. longlingensis* isolate N30	0.184	0.182	0.182	0.184	0.180	*				
7. *H. longlingensis* isolate N31	0.189	0.184	0.184	0.185	0.182	0.012	*			
8. *H. longlingensis* isolate N32	0.187	0.182	0.182	0.184	0.180	0.010	0.002	*		
9. *H. longlingensis* isolate N33	0.185	0.184	0.184	0.185	0.182	0.008	0.003	0.002	*	
10. *H. longlingensis* isolate N34	0.145	0.013	0.013	0.015	0.012	0.182	0.187	0.185	0.184	*

Taxonomy

Family GEKKONIDAE Gray 1825
Genus *Hemiphyllodactylus* Bleeker, 1860

Hemiphyllodactylus zalonicus sp. nov. (Figure 3–4; Table 2)

ZooBank registration: http://www.zoobank.org/urn:lsid:zoobank.org:act:D2B420D6-B39E-4E2C-A8F9-8FAA3C443FB0

Holotype

Adult female (museum cat no. ZMMU R-16635; field ID NAP-09556) collected from the evergreen dipterocarp tropical forest on the slope of Zalon Mountain (Zalon Taung), ca. 1 km westwards from the Zalon Taung Pagoda, Zalon Taung National Forest, ca. 13 km northwards from Ban Mauk town, Ban Mauk District, Sagaing Region, northern Myanmar (GPS data N 24.51628°, E 095.81705° WGS; elevation 690 m a.s.l.) on 2 August 2019, at 18:00 h by P. Pawangkhanant, May Thu Chit and N.A. Poyarkov.

Paratype

Adult female (museum cat no. ZDUM-2019.12.29–038; field ID MTZ-00038), collected from a rock at the same locality as the holotype on 29 December 2019, at 23:30 h by May Thu Chit.

Diagnosis

Hemiphyllodactylus zalonicus sp. nov. can be distinguished from all other congeners by possessing the unique combination of having a maximum SVL of 37.7 mm, trunk not particularly elongate or gracile (AG/SVL ratio 0.49); eight to ten chin scales; enlarged post-mentals; five circumnasal scales; four intersupranasals (= postrostrals); 10 supralabials; eight infralabials; 18 longitudinal rows of dorsal scales and nine longitudinal rows of ventral scales at midbody contained within one eye diameter; 3333 digital formulas on hands and 3444 formulas on the feet; three subdigital lamellae on the first finger and four subdigital lamellae on the first toe; perforated femoroprecloacal scales; 16 perforated precloacal scales that extend part-way onto the proximal femoral region; one cloacal spur on each side; no plate-like subcaudal scales; a dark postorbital stripe extending to at least base of neck; no
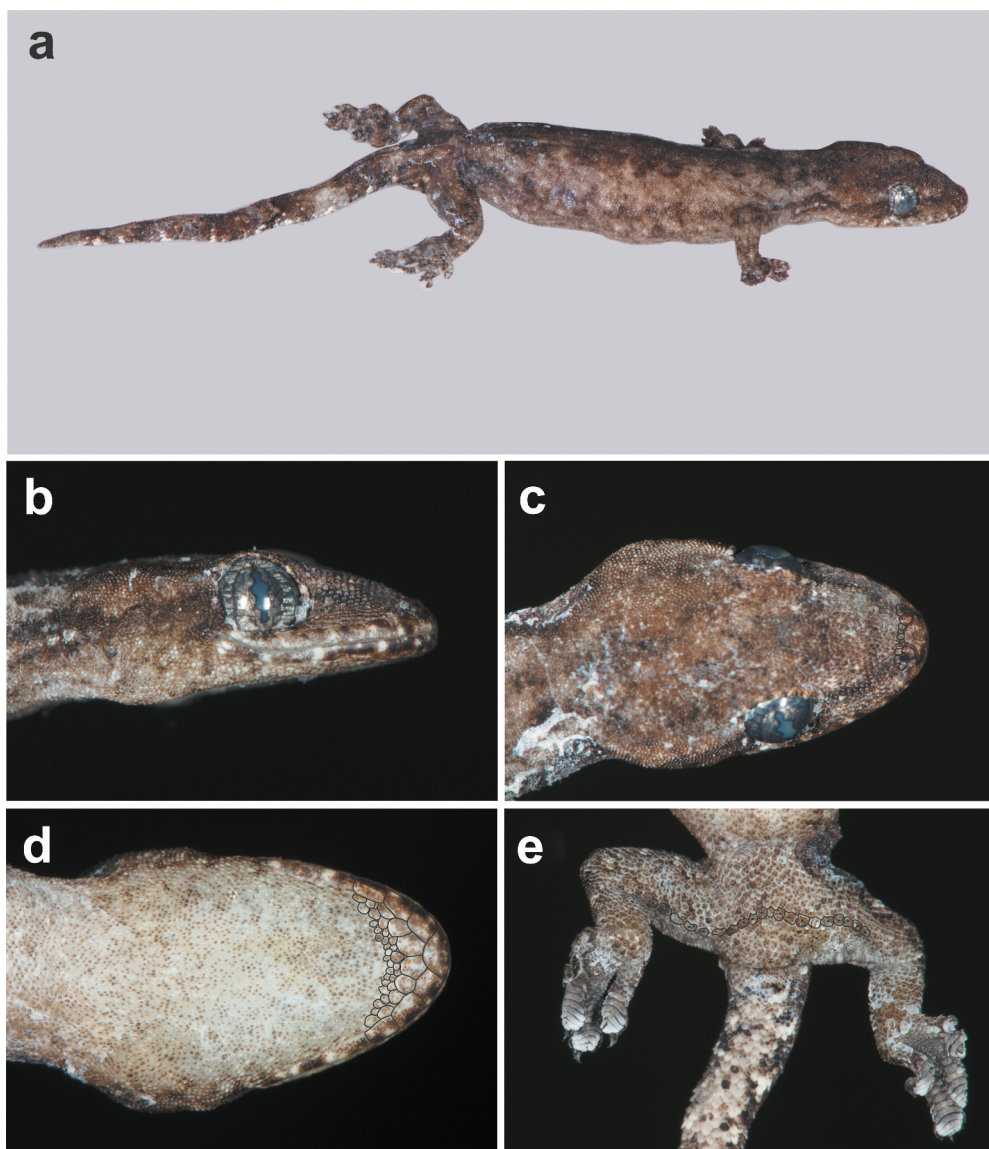
Figure 3. Adult female holotype of *Hemiphyllodactylus zalonicus* sp. nov. (ZMMU R-16635) from Zalon Mountain, Zalon Taung National Forest, Ban Mauk District, Sagaing Region, northern Myanmar, in preservative. (a) Dorsal view of body. (b) Lateral view of top head. (c) Dorsal view of top of head. (d) Gular region showing mental, postmental and chin scales arrangement. (d) Lateral view of head. (e) Precloacal and proximal femoral regions showing arrangement of enlarged, pitted scales. Photos by Roman A. Nazarov.

dorsolateral light-coloured spots or dark dorsolateral stripe on trunk; no dark ventrolateral stripe on trunk; dark paravertebral markings on trunk; no light-coloured postsacral marking bearing anteriorly projecting arms; and caecum and gonads pigmented. These characters are scored across all species in the Indochina clade, all Thai species and all other species of *Hemiphyllodactylus* from Myanmar in Grismer et al. (2017, Grismer et al. 2018a, 2020a, 2020b), Sukprasert et al. (2018), and Eliades et al. (2019).
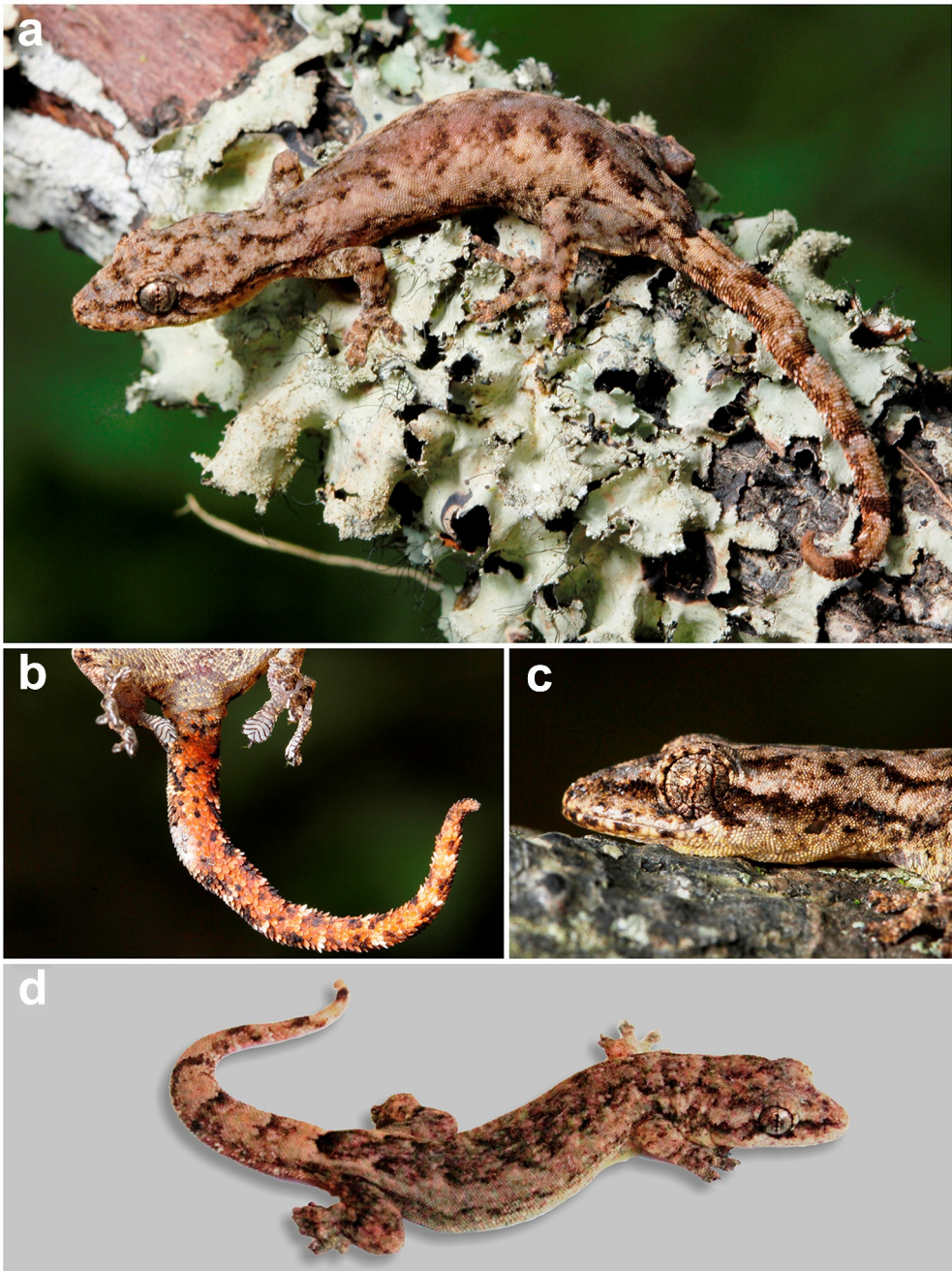
Figure 4. Type specimens of *Hemiphyllodactylus zalonicus* sp. nov. from Zalon Mountain, Zalon Taung National Forest, Ban Mauk District, Sagaing Region, northern Myanmar, in life. Holotype (ZMMU R-16635, female): (a) General dorsolateral view. (b) Ventral view of tail. (c) Lateral view of head. Paratype (ZDUM-2019.12.29–038, female): (d) General dorsolateral view. Photos by Parinya Pawangkhanant (a–c) and May Thu Chit (d).

Table 2. Meristic, mensural (in mm) and colour pattern data from the type series of *Hemiphyllodactylus zalonicus* sp. nov., *H. longlingensis* and *H. changninensis* of clade 3. Data for latter two species come from (Zhou et al. 1981) and Guo et al. (2015), respectively. Values in bold are potentially diagnostic with respect to *Hemiphyllodactylus zalonicus* sp. nov. (/) = data unavailable.

Character	*zalonicus* **sp. nov.**	*zalonicus* **sp. nov.**	*longlingensis*	*changningensis*
Specimen ID	ZMMU R-16635 (holotype)	ZDUM-2019.12.29–038 (paratype)		
Sex and age class	Adult female	Adult female		
Chin scales (CS)	8	10	7–9	7 or 8
Postmentals distinctly enlarged	Yes	Yes	Yes	Yes
Circumnasal scales (CN)	5\5	5\5	4 or 5	3 or 4
Intersupranasals (IS)	4	3	1–3	2 or 3
Supralabial scales (SL)	10	10	9 or 10	8–11
Infralabial scales (IL)	8	9	8–10	8–10
Dorsal scales (DS)	18	17	**10–14**	**11–15**
Ventral scales (VS)	9	10	6 or 7	6–8
Lamellar formula on hand	3333	3333	3444(3) 444(5)4	33(4)3(4) 3444
Lamellar formula on foot	3444	3444	44(5)4(5)4	3444 3333
Subdigital lamellae on first finger	3	3	4 or 5	3 or 4
Subdigital lamellae on first toe	4	4	4–6	3 or 4
Precloacal and femoral pore series separate or continuous	Perforated scales in continuous row	Perforated scales in continuous row	Continuous	Continuous
Total femoroprecloacal pores	16 perf. scales	20 perf. scales	16–27	19–22
Cloacal spurs on each side	1\1	1\1	1 or 2	1 or 2
Subcaudals enlarged, plate-like	No	No	No	No
Dark postorbital stripe	Yes	Yes	Yes	Yes
Adult females yellow	No	No	No	No
Dorsolateral light-coloured spots on trunk	No	No	No	No
Dark dorsolateral stripe on trunk	No	No	No	No
Dark ventrolateral stripe on trunk	No	No	No	No
Wide vertebral area generally unicolour	No	No	No	No
Dark dorsal transverse blotches/bands	No	No	Variable	No
Dark reticulate pattern on dorsum	No	No	Variable	Yes
Dark transverse zig-zag pattern on dorsum	No	No	variable	No
Dark paravertebral markings on body	Yes	Yes	Variable	**No**
Postsacral marking bearing light-coloured anteriorly projecting arms	No	No	Yes	No
Caecum pigmented	Yes	Yes	(/)	(/)
Gonads pigmented	Yes	Yes	(/)	(/)

(Continued)

Table 2. (Continued).

Character	*zalonicus* **sp. nov.**	*zalonicus* **sp. nov.**	*longlingensis*	*changningensis*
SVL	36.4	37.7	(/)	(/)
TL	25.7	34.0	(/)	(/)
AG	18.1	18.9	(/)	(/)
HL	8.5	8.4	(/)	(/)
SN	3.4	3.5	(/)	(/)
HW	5.8	5.7	(/)	(/)
NE	2.7	2.4	(/)	(/)
ED	2.0	2.6	(/)	(/)
SW	1.2	1.2	(/)	(/)
AG/SVL	0.49	0.50	0.47–0.52	0.46–0.51
HL/SVL	0.23	0.22	0.22–0.24	0.22–0.25
HW/SVL	0.15	0.15	**0.17–0.19**	**0.17–0.18**
NE/HL	0.31	0.28	**0.42–0.45**	**0.41–0.49**
ED/HL	0.23	0.30	0.22–0.25	0.21–0.25

Description of holotype

Adult female SVL 36.4 mm (Figure 3a); head triangular in dorsal profile (Figure 3c), depressed, distinct from neck; lores flat to slightly convex; rostrum moderate in length (NE/HL 0.13); prefrontal region weakly concave; canthus rostralis smoothly rounded, barely discernable; snout moderate, rounded in dorsal profile; eye large; ear opening elliptical, small (Figure 3b); eye-ear distance greater than diameter of eye; rostral wider than high, bordered posteriorly by large supranasals (Figure 3c); four equally sized intersupranasals (= postnasals); external nares bordered anteriorly by rostral, dorsally by supranasal and one internasal, posteriorly by two postnasals, ventrally by first supralabial (= circumnasals); 10 (R,L) rectangular supralabials tapering to below posterior margin of eye; nine (R,L) rectangular infralabials not tapering to below posterior margin of eye; scales of rostrum, lores, top of head, and occiput small, raised, those of rostrum largest; dorsal superciliaries flat, mostly square, subimbricate, largest anteriorly; mental triangular, bordered laterally by first infralabials and posteriorly by two postmentals (Figure 3d); postmentals in contact with first infralabial and bordered laterally by a slightly smaller chin shield; four or five lateral chin shields; gular scales small, subimbricate, grading posteriorly into slightly larger, subimbricate throat and even larger pectoral scales which grade into slightly larger, subimbricate ventrals.

Body moderate in stature, trunk not noticeably elongate (AG/SVL 0.49), dorsoventrally compressed; ventrolateral folds absent; dorsal scales small, granular, 18 dorsal scales at midbody contained within one eye diameter; ventral scales flat, subimbricate much larger than dorsal scales, nine ventral scales contained within one eye diameter; precloacal scales larger than abdominal scales; 16 perforated, slightly enlarged femoroprecloacal scales in an angular series, scale at apex lacks a pit; single enlarged tubercle (spur) on lateral margin of tail base (Figure 3e); forelimbs short, robust in stature, covered with flat, subimbricate scales dorsally and ventrally; palmar scales slightly raised, subimbricate; all digits except digit I well developed; digit I vestigial, clawless; distal subdigital lamellae of digits II–V undivided, angular and U-shaped, lamellae proximal to these transversely expanded; distal lamellar formula of digits II–V 3333 (R,L); three transversely expanded lamellae on digit I; claws on digits II–V well developed, unsheathed; distal portions of digits strongly curved, terminal joint free, arising from central portion of lamellar pad; hind limbs short, more robust than forelimbs, covered with slightly raised, juxtaposed scales dorsally and by larger, flat subimbricate scales anteriorly and ventrally; plantar scales slightly raised, subimbricate; all digits except digit I well developed; digit I vestigial, clawless; distal subdigital lamellae of digits II–V undivided, angular and U-shaped, lamellae proximal to these transversely expanded; distal lamellar formula of digits II–V 3444 (R,L); four transversely expanded lamellae on digit I; claws on digits II–V well developed, unsheathed; distal portions of digits strongly curved, terminal joint free, arising from central portion of lamellar pad; tail original, 25.7 mm in length, caudal scales occurring in whorls; dorsal caudal scales larger than dorsal body scales, flat, subcycloid, subimbricate; ventrolateral caudals slightly enlarged, weakly flared anteriorly; subcaudals flat, slightly larger than dorsal caudals, not plate-like. Morphometric data are presented in Table 2.
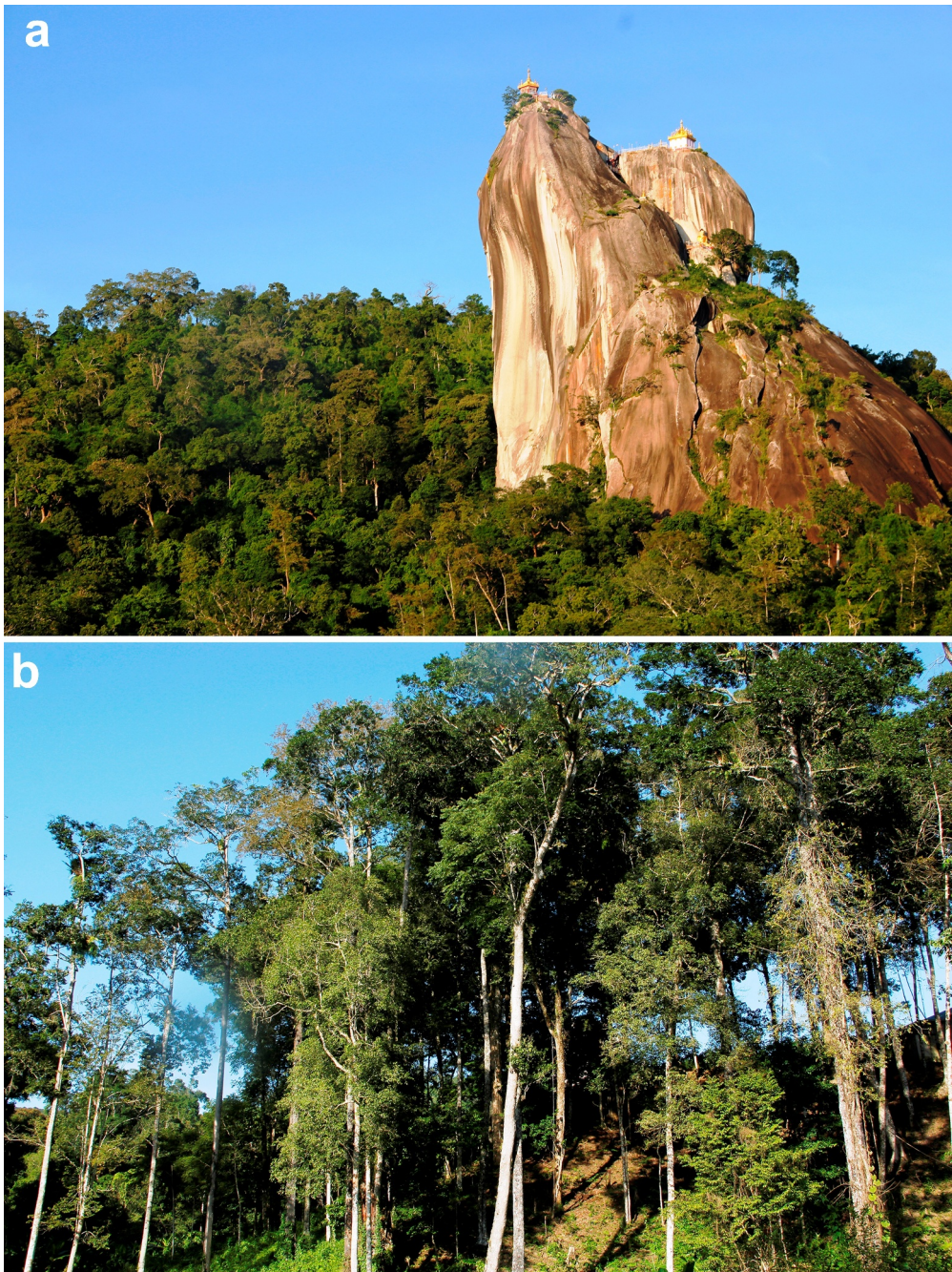
Figure 5. Habitat of *Hemiphyllodactylus zalonicus* sp. nov. at the type locality: Zalon Mountain, Zalon Taung National Forest, Ban Mauk District, Sagaing Region, northern Myanmar. (a) Zalon Mountain with Zalong Taung Pagoda. (b) Mixed semi-deciduous dipterocarp tropical forest on the Western slope of Zalon Mountain. Photos by Parinya Pawangkhanant.

Colouration in life

Dorsal ground colour light-brown except for vertebral region which is brownish grey (Figure 4a); top of head bearing dark-coloured, irregularly shaped markings; dark-coloured, diffuse stripe extends from rostral scale to forelimb insertion (Figure 4c); large, dark-coloured, diffuse, irregularly shaped, paravertebral marking on trunk; indistinct dark-coloured markings on ventral margin of trunk becoming more distinct posteriorly; dark-coloured, irregularly shaped markings on limbs; indistinct light-coloured postsacral band with broken, light-coloured anteriorly projecting arms; five indistinct, dark-coloured, caudal bands; gular, pectoral and abdominal regions beige with dark stippling; stippling dense in pelvic region and underside of limbs; subcaudal region reddish-orange bearing scattered black and white scales (Figure 4b). Colouration after a year in preservative much the same but not nearly as distinct, bright yellowish and reddish tints faded and overall colouration turned greyish-brown (Figure 3).

Variation

Measurements and counts of the paratype female ZDUM-2019.12.29–038 are presented in Table 2, photographs of the paratype in life are shown in Figure 4d. Morphologically, the paratype resembles the holotype in all major characteristics. ZDUM-2019.12.29–038 has a bright orange-red ventral surface of tail, a slightly more pronounced dark postocular stripe which continues posteriorly after the axilla; and more irregular dark-brown blotches on the dorsum (Figure 4d).

Distribution

Hemiphyllodactylus zalonics sp. nov. is at present known only from the type locality of Zalon Mountain, Ban Mauk District, Sagaing Region, northern Myanmar (Figure 1). Zalon Mountain (941 m a.s.l. at its peak) located in the center of Zalon Taung National Forest reserve, belongs to the northern portion of the Mangin Mountain Range – a low mountain chain located between the valleys of the Ayeyarwady (Irrawaddy) and Chindwin rivers, occupying the northern part of Sagaing Region and the southwest corner of Kachin Region in northern Myanmar. The actual extent of distribution of the new species is unknown, though its occurrence in other parts of the Mangin Range is anticipated.

Natural history

The holotype was collected at sundown (18:00 h) from a trunk of *Diospyros burmanica* Kurz (ca. 1.5 m above the ground), within the primarily dipterocarp tropical semi-deciduous forest at the foothill of Zalon Mountain (Figure 5a). The semi-deciduous forests around Zalon Mt. are composed of broad-leaved trees such as *Dipterocarpus alatus* Roxb. ex G.Don., *Shorea assamica* Dyer in J. D. Hooker, *Dyospiros burmanica*, *Swintonia floribunda* Griff., *Engelhardtia spicata* Lesch ex Blume, *Magnolia champaca* (L.) Baill. ex Pierre, *Schima* sp., *Terminalia alata* Heyne ex Roth, *Quercus lamellosa* Sm., *Castanopsis* sp., *Elaeocarpus* sp., *Ficus* spp. and others (Figure 5b). Holotype was collected while it was crawling on the

bark on tree trunk, hiding in bark crevices. There are several huts in the area where the new species was recorded; however, we have not seen other specimens on these buildings. The paratype was found at night (23:30 h) ca. 1 m above the ground on a large granite rock at the same locality as the holotype. Both are gravid females.

Etymology

The specific epithet *zalonicus* is a Latinised toponymic adjective in nominative singular given in reference to the type locality of Mt. Zalon (Zalon Taung) in Sagaing Region of northern Myanmar. We suggest the following common names: *Mt. Zalon Slender Gecko* (English), *Zalontaung Ein Myaung Twal* (Burmese).

Comparisons

The molecular analyses indicate that *Hemiphyllodactylus zalonicus* sp. nov. is nested within *Hemiphyllodactylus* clade 3 of Yunnan, China with *H. changningensis* and *H. longlingensis* from which it differs by an uncorrected pairwise sequence divergence of 15.0–15.3% and 14.5–18.9%, respectively (see Table 2 for comparative data). *Hemiphyllodactylus zalonicus* sp. nov. is most closely related to *H. changningensis* but differs from it by having 17–18 as opposed to 11–15 dorsal scales; and a narrower head (HW/SVL = 0.15 versus 0.17–0.18) and shorter snout (NE/HL = 0.28–0.31 versus 0.41–0.49). It differs from *H. longlingensis* by having more dorsal scales (17–18 versus 10–14), 16–20 perforated femoroprecloacal scales in the female versus 19–22 femoroprecloacal pores in males; and a narrower head (HW/SVL = 0.15 versus 0.17–0.19) and shorter snout (NE/HL 0.28–0.31 versus 0.42–0.45) (Table 2). These characters are scored across all species in the Indochina clade, all Thai species and all other species of *Hemiphyllodactylus* from Myanmar in Grismer et al. (2017, Grismer et al. 2018a, 2020a, 2020b), Sukprasert et al. (2018), and Eliades et al. (2019).

Discussion

A resurgence of herpetological fieldwork in Myanmar has resulted in a dramatic increase in the descriptions of new gekkonid lizards in the genera *Cyrtodactylus* Gray and *Hemiphyllodactylus* Bleeker (Uetz et al. 2020). Many of these descriptions are not just of single species but of entirely new clades containing multiple species, thus underscoring the still unexplored nature of vast regions of Myanmar (Grismer et al. 2017, 2018a, 2018b, 2018c, 2018d, 2018e, 2019a, 2019b, 2020a, 2020c).

The discovery of *Hemiphyllodactylus zalonicus* sp. nov. brings the total number of *Hemiphyllodactylus* in Myanmar to at least 11, though this is still likely an underestimate of the diversity of this genus given its high degree of site-specific endemism and that many upland areas remain not surveyed.

Isolated hilly areas within the Ayeyarwady Basin, including the Mangin and Kumon Ranges, are proving to be areas of gekkonid and, more generally, herpetofaunal endemism (Bauer 2002; 2003; Grismer et al. 2018d; 2019b, 2019c; Than Zaw et al. 2019; Poyarkov et al. 2019). *Hemiphyllodactylus zalonicus* sp. nov. is the most recently described species belonging to clade 3 (Figure 2) within a larger lineage from Western Indochina. It not only represents the first record of this genus from the Ayeyarwady Basin but represents the third independent origin of *Hemiphyllodactylus* in Myanmar (Figures 1, 2). The

south lineage (*sec*. Grismer et al. 2020a) is a newly described clade of species endemic to the southern extreme of the Shan Plateau and the northern end of the Salween Basin, Myanmar. Clade 4 (*sec*. Grismer et al. 2020a) is composed of six Burmese species endemic to the Shan Plateau and another from Chiang Mai, Thailand (*H. chiangmaiensis*) and one species (*H. jinpingensis*) scattered throughout mountains of southern and south-Western China. Large distribution gaps between closely related species in the three Western Indochinese clades suggest that many more species have yet to be discovered throughout the vast upland regions of Indochina.

The area around Zalon Mountain was recently regarded as a proposed Zalong Taung National Park, which should encompass the eastern slopes of Mangin Range north of Banmauk town, along with hilly catchment areas of Nam Ke Hu, Chaung Gyi and Hwe Taung Rivers between latitudes 24°27′N to 24°41′N and longitudes 95°45′E to 95°55′E. The Zalon Taung Pagoda, located on the top of Zalon Mountain (Figure 5a), is an important site for religious pilgrimage, and the number of local pilgrims has increased significantly in recent years, from 200,000 pilgrims in 2017 to over 400,000 pilgrims in 2018. In coming years more tourists will be attracted to this area (https://elevenmyanmar.com/). The planned development of tourist infrastructure in the area might lead to an increase of habitat loss and modification. Further intensified survey efforts and biodiversity assessments are urgently required for effective conservation management of yet unrealised herpetofaunal diversity of the Zalon Mountain area.

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Authors' contributions

NAP and LLG designed the study. MTC, TZ, PP, RAN and NAP collected data. NAP performed molecular analysis. RAN, MTC and NAP examined morphology. NAP and LLG supervised the analyses. LLG and NAP wrote the manuscript. MTC, TZ, RAN and NAP revised the manuscript. All authors read and approved the final manuscript.

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ORCID

L. Lee Grismer http://orcid.org/0000-0001-8422-3698
Parinya Pawangkhanant http://orcid.org/0000-0002-0947-5729
Nikolay A. Poyarkov http://orcid.org/0000-0002-7576-2283

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