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A new species of bent-toed geckos of the genus *Cyrtodactylus* Gray, 1827 from western Arunachal Pradesh, India

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Abstract

A new species of bent-toed geckos of the genus *Cyrtodactylus* is described from western Arunachal Pradesh. The new species is a member of the Indo-Burma clade and is embedded within the "*peguensis*" group, a relationship deduced contingent on a partial fragment of mitochondrial NADH subunit 2 gene. *Cyrtodactylus kamengensis* **sp. nov.** is morphologically similar to *C. himalayicus* from which it differs in bearing a distinct ventrolateral fold and 6–8 basal lamellae on digit IV of pes. Genetically, the new species is sister to the Indian lineage of the "*peguensis*" group containing *C. bhupathyi* and *C. gubernatoris*. The Indian lineage of the "*peguensis*" group diverged from its Burmese relatives during the mid-Oligocene likely followed by the beginning of the Himalayan uplift, highlighting the role of the Himalayas in the diversification of biota.

Key Words

biodiversity hotspot, Gekkonidae, Himalayas, northeast India, taxonomy

Introduction

The genus *Cyrtodactylus* Gray, 1827 currently contains 324 species of which more than 60 species are distributed across the Himalayas and Indo-Burma biodiversity hotspot (Agarwal et al. 2018a; Uetz and Hošek 2021), constituting nearly 20% of the diversity within the genus (Mirza et al. 2021). Most of the species of the genus are narrowly distributed (Wood et al. 2012; Agarwal 2016; Agarwal et al. 2016, 2018a, 2018b; Grismer et al. 2020) with a few exceptions of widespread species (Mirza et al. 2021). Phylogenetically, the genus is well resolved and distinct groups have been created, based on monophyly (Grismer et al. 2020, 2021).

Sixteen new species of *Cyrtodactylus* have been described in the last four years from the Himalayan Region, of which, 15 were described from northeast India and the genus might harbour more narrowly distributed species (Agarwal et al. 2018a; Kamei and Mahony 2021; Purkayastha et al. 2021). Arunachal Pradesh is amongst the

least explored states in India for its herpetofaunal diversity (Agarwal et al. 2010), evident from the description of several new species of reptiles from the State in the last five years (Bhosale et al. 2019, 2020; Captain et al. 2019; Das et al. 2020; Mirza et al. 2020, 2021). Currently, a single species of the genus *Cyrtodactylus* is recorded from Arunachal Pradesh, *C. arunachalensis* Mirza, Bhosale, Ansari, Phansalkar, Sawant, Gowande & Patel, 2021 (Mirza et al. 2021) in addition to at least two undescribed species (Agarwal et al. 2014), one of which is dealt with in the present paper.

As part of an ongoing project to document the herpetofauna of Arunachal Pradesh (Bhosale et al. 2019, 2020; Mirza et al. 2020, 2021; Gowande et al. 2021), we surveyed several localities across this Indian State. During the expedition, we collected specimens of *Cyrtodactylus* from Shergaon in West Kameng District in western Arunachal Pradesh. The specimens were identified to belong to an undescribed species, based on morphological as well as molecular data. The present paper deals with the description of the new species and with additional notes on the genus.

Material and methods

Fieldwork and collection

The study was conducted under permit nos. CWL/Gen/173/2018-19/Pt.V11/2421-33 and CWL/Gen/173/2018-19/Pt.V11/2434-43, issued by the Forest Department of Arunachal Pradesh. Specimens of the new species were collected in the field by hand, photographed and later, euthanised with halothane within 24 hours of capture, following ethical guidelines for animal euthanasia (Underwood and Anthony 2020). The specimens were fixed in 8% formaldehyde solution for two days and washed in water and transferred into 70% ethanol for conservation. Liver or tail tip tissues were obtained for molecular work and stored in molecular grade ethanol prior to specimen fixation. The specimens have been deposited in the collection of the Bombay Natural History Society (**BNHS**), Mumbai and the collection of the National Centre for Biological Sciences (**NCBS**), Bangalore.

Morphology

Specimens were measured with Mitutoyo™ digital calipers to the nearest 0.01 mm. Morphometric data and description style follow Mirza et al. (2021): measurements were taken as defined by Mahony and Kamei (2021), SVL, snout to vent length; TRL, trunk length measured from the posterior margin of the fore-limb insertion to the anterior margin of the hind-limb insertion; BW, body width; TL, tail length; TW, tail width; HL, head length; HW, head width; HH, head height; FL, forearm length; CL, crus length; OD, eye diameter; NE, nostril to eye distance; SE, snout tip to eye distance; EE, eye to ear distance; EL, maximum ear length; IN, internarial distance; IO, interorbital distance. We also counted mid-ventral scales rows across belly (MVSR; counted between ventrolateral folds or, when fold absent, as demarcated by relative scale shape and size of the flattened imbricate ventral scales versus granular dorsal scales), paravertebral tubercles (PVT, counted from the most anterior tubercle on the occiput to mid-sacrum), dorsal tubercle rows counted transversely across the body (DTR), supralabials and infralabials (SL and IL, counted from the labial in contact with the rostrum and mental on each side, respectively, to the angle of the jaw; numbers in parentheses following SL indicate count at mid-orbit) and noted the presence or absence of a ventrolateral fold. We counted precloacal pores (PcP, pores only in preclocacal region that form a more or less continuous series). Subdigital lamellae of first and fourth digits on right manus and pes were counted in two series, a basal series, that includes scales at least twice the diameter of palmar scales up to and including a single large scale at the digital inflection and an apical series, including lamellae distal to the digital inflection and not including the ventral claw sheath. Comparison was made with data for Indian species presented in Agarwal et al. (2018a, 2018b) and Grismer et al. (2018a, 2018b).

Nomenclatural acts registration

The electronic version of this article in portable document format represents a published work according to the International Commission on Zoological Nomenclature (ICZN) and, hence, the new names contained in the electronic version are effectively published under that Code from the electronic edition alone (see Articles 8.5–8.6 of the Code). This published work and the nomenclatural acts it contains have been registered in ZooBank, the online registration system for the ICZN. The ZooBank LSIDs (Life Science Identifiers) can be resolved and the associated information can be viewed through any standard web browser by appending the LSID to the prefix-http://zoobank.org/. Publication LSID: urn:lsid:zoobank.org:pub: 4D3E4F4B-5538-46B8-9C44-9F1C21DC6950. New species LSID: urn:lsid:zoobank.org:act: 121841D4-E95B-40A5-8D0B-9587461F535A.

Molecular analysis

Genomic DNA was isolated from the preserved liver or tail tissue of specimens using QIAGEN DNeasy kits following protocols directed by the manufacturer. A fragment of the mitochondrial NADH-ubiquinone oxidoreductase, subunit 2 (*ND2*) gene was amplified using primers Metf1 5'-AAGCTTTCGGGCCCATACC-3' and CO1R1 5'-AGRGTGCCAATGTCTTTGTGRTT-3' (Macey et al. 1997). Bi-directional sequencing was carried out with primers L4437 5'- AAGCTTTCGGGCCCATACC-3' and H5540 5'- TTTAGGGCTTTGAAGGC-3' (Macey et al. 1997). A 22.4 µl reaction was set for a bi-directional Polymerase Chain Reaction (PCR), containing 10 µl of Thermo Scientific DreamTaq PCR Master Mix, 10 µl of

molecular grade water, 0.2 µl of each 10 µM primer and 2 µl template DNA, carried out with an Applied Biosystems ProFlex PCR System. Thermo-cycle profile used for amplification were as follows: 95 °C for 3 minutes, (denaturation temperature 95 °C for 30 seconds, annealing temperature 60 °C for *ND2* for 45 seconds, elongation temperature 72 °C for 1 minute) × 36 cycles, 72 °C for 10 minutes, hold at 4 °C. PCR product was cleaned using QIAquick PCR Purification Kit and sequenced with an Applied Biosystems 3730 DNA Analyzer. In addition to this, *ND2* sequences of *Cyrtodactylus* spp. available on GenBank® were downloaded for molecular phylogenetic reconstructions following Grismer et al. (2021). Newly-generated and downloaded sequences were aligned in MegaX (Kumar et al. 2018) using ClustalW (Thompson et al. 1994) with default settings. The aligned dataset was subject to Maximum Likelihood (ML) phylogenetics on the IQ-TREE (http://iqtree.cibiv.univie.ac.at/) online portal (Minh et al. 2020). 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. Un-corrected pairwise *p*-distance (% sequence divergence) was calculated in MegaX (Kumar et al. 2018) with pairwise deletions of missing data and gaps.

Results

Molecular phylogenetics

The mitochondrial *ND2* sequences generated in the present study were found to be similar with that of a specimen sequenced by Agarwal et al. (2014) from Khellong, Arunachal Pradesh voucher number CES13/1464 (KM255196). The sequences generated by Agarwal et al. (2014) for the sample from Khellong were included in a large-scale phylogeny of the genus and the specimen was found to be a member of the '*peguensis*' group (Grismer et al. 2021). A phylogenetic analysis of the '*peguensis*' group (Grismer et al. 2021) with addition of the newly-generated sequences confirms that the samples from Khellong and Shergaon (present work) are genetically similar (Fig. 1) and show the similar relationships recovered in previous studies (Agarwal et al. 2014; Grismer et al. 2021; Kamei and Mahony 2021). Thereby, morphological and molec-

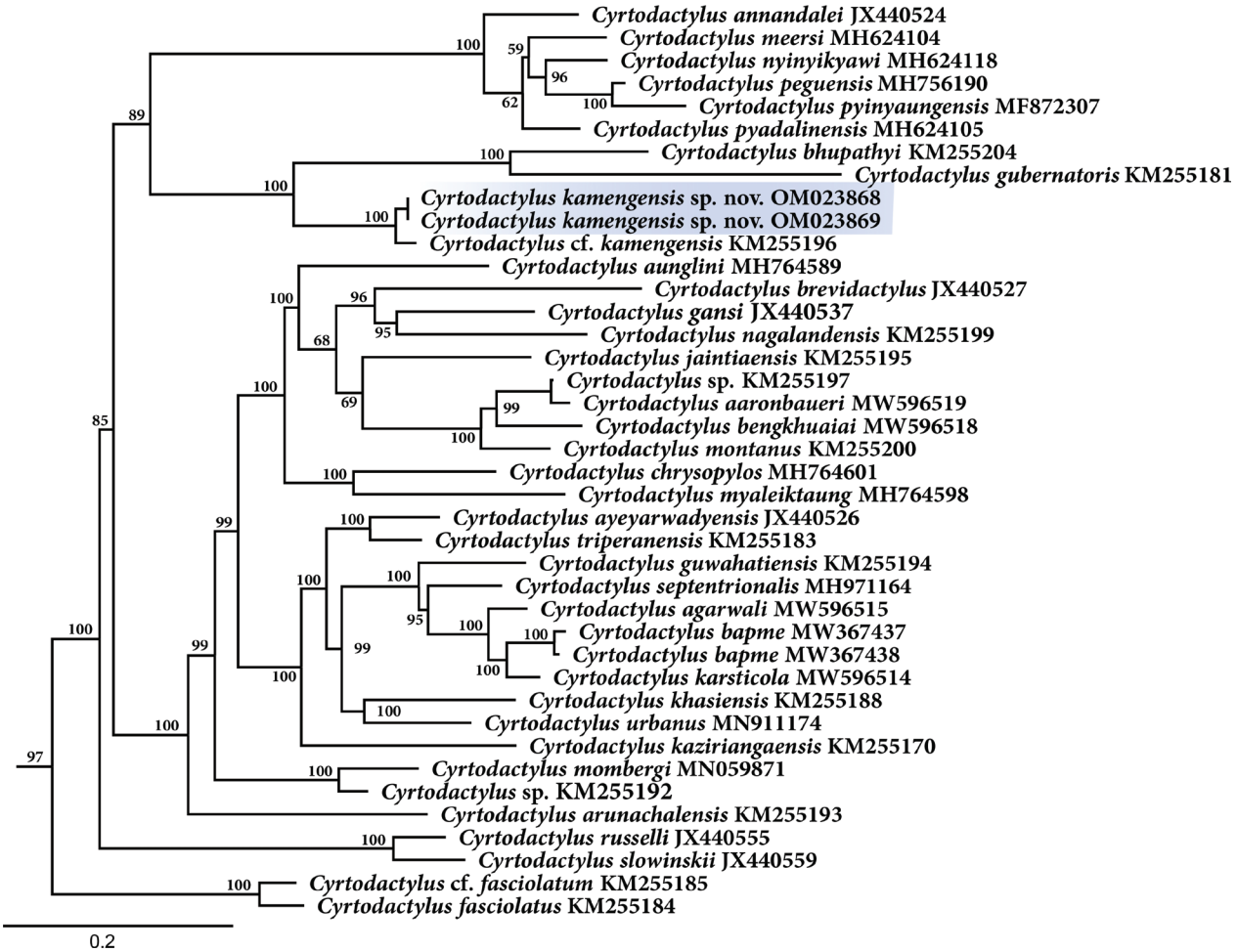

Figure 1. Maximum Likelihood phylogeny of selected members of the genus *Cyrtodactylus*, based on partial sequences of mitochondrial *ND2* gene generated through 1000 bootstraps through an ultrafast search method with GTR+F+I+G4 for each codon as model for sequence substitution. Numbers at nodes represent bootstrap support. See Suppl. material 1 for the complete tree (Suppl. material 1: Appendix I).

ular comparisons of the new species are restricted only to members of the '*peguensis*' group. The relationships recovered in the present study are slightly different from those of Grismer et al. (2021) as our study employed a single gene for the analysis. However, the sequences of the new population indicate it is a member of the Indian lineage (ML support 100, Fig. 1) of the '*peguensis*' group (Grismer et al. 2021). The Indian lineage of the '*peguensis*' group comprises of *C. bhupathyi* and *C. gubernatoris* to which the new species is sister (ML support 100, Fig. 1). The Indian lineage is sister to the Burmese taxa.

Systematics

Cyrtodactylus kamengensis sp. nov.

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Figs 2–5, Table 1

Cyrtodactylus khasiensis Agarwal et al. 2010: 89
Cyrtodactylus sp. Agarwal et al. (2014):147
Cyrtodactylus "KM255196" Mirza et al. (2021):21

Holotype. male, BNHS 3113, Shergaon, West Kameng District, Arunachal Pradesh (27.075528°N, 92.123500°E, elevation 950 m) collected by Mandar Sawant, Pushkar Phansalkar and Harshal Bhosale on 8 August 2021.

Paratypes. four males BNHS 3114 & BNHS 3115, and NCBS NRC-AA-0020 and NRC-AA-0021, from the same locality as holotype, collected on 8 August 2021.

Etymology. The specific epithet refers to the Kameng River in western Arunachal Pradesh close to which the new species was discovered.

Diagnosis. *Cyrtodactylus kamengensis* sp. nov. can be distinguished from all congeners by its moderate body size (SVL 70.2–78.6 mm, mean 73.84); 9–12 supralabials; 9–10 infralabials; 20–24 bluntly conical, feebly keeled dorsal tubercles; 49–58 paravertebral tubercles; 30–34 ventral scales between distinct ventrolateral folds; no precloacal groves; 7–11 precloacal pores in a continuous series; three to four rows of enlarged scales below pored scales, slightly larger than pored scales, femoral pores absent; 9–13 distal subdigital lamellae on digit IV of pes; subcaudal scalation of original tail without enlarged plates. Dorsum with paired irregular dark brown blotches on a light brown background.

Comparison. Molecular data for *ND2* gene suggest that *Cyrtodactylus kamengensis* sp. nov. is a member of the '*peguensis*' group (Grismer et al. 2021) and is here compared with members of this clade. Intraspecific uncorrected pairwise sequence divergence (*p*-distance) for samples across the two known localities for the species is 0–3% and an interspecific divergence of 19–26% calculated for *ND2* gene (Table 2). The new species, *C.*

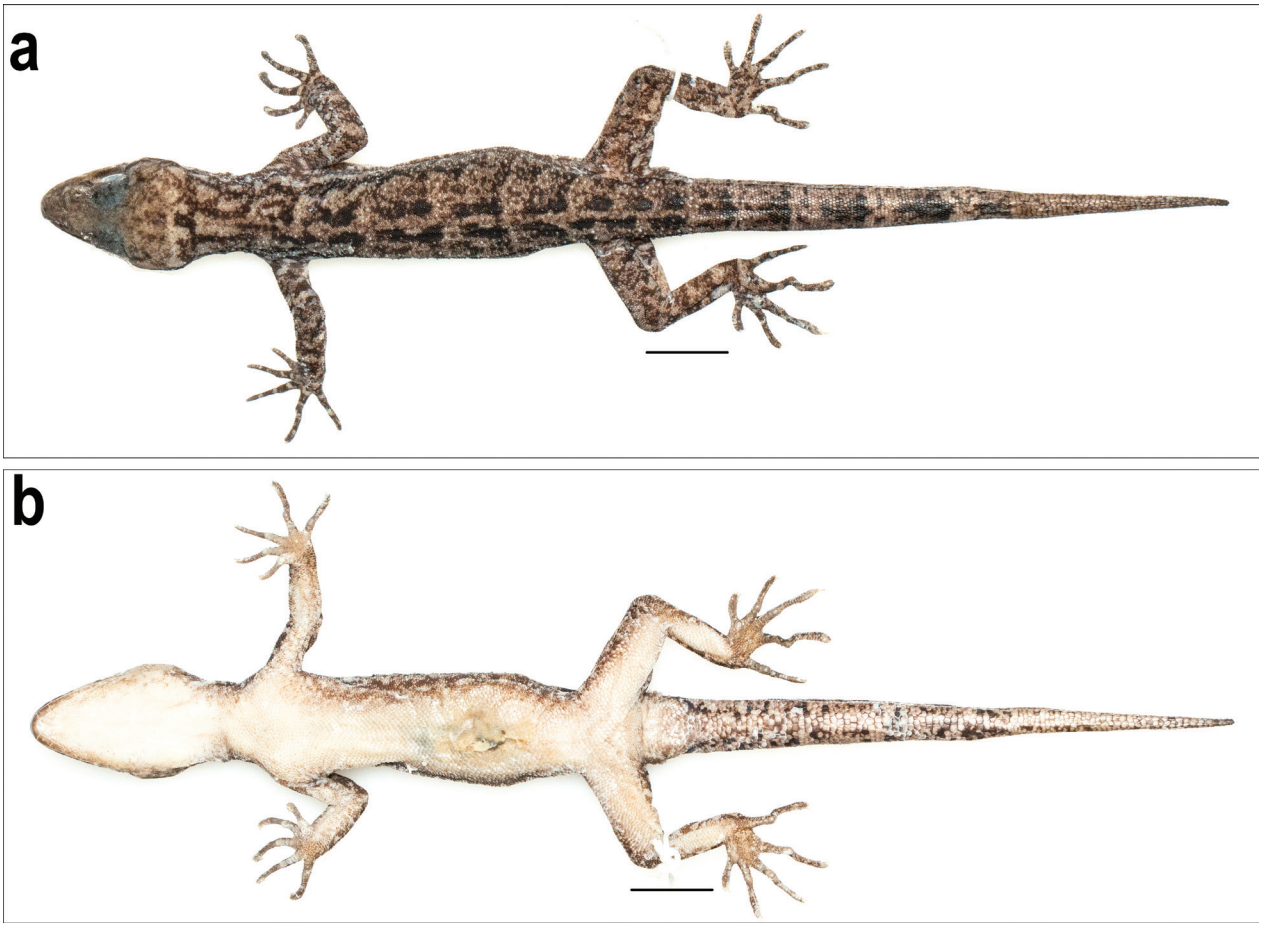

Figure 2. *Cyrtodactylus kamengensis* sp. nov. male holotype BNHS 3113 **a.** Dorsal view; **b.** Ventral view. Photo by Zeeshan A. Mirza. Scale bar: 10 mm.

kamengensis sp. nov. differs from members of the '*peguensis*' group as follows: dorsal tubercle in 20–24 rows (vs. 16–18 in *C. annandalei* Bauer, 24–25 in *C. bhupathyi* Agarwal, Mahony, Giri, Chaitanya & Bauer, 18 in *C. cayuensis* Li and *C. mandalayensis* Mahony, 15–18 in *C. pyinyaungensis* Grismer, Wood Jr, Thura, Zin, Quah, Murdoch, Grismer, Lin, Kyaw & Lwin, 17–19 in *C. peguensis* (Boulenger), 15–17 in *C. fasciolatum* (Blyth), 14–15 in *C. markuscombaii* (Darevsky, Helfenberger, Orlov & Shah), 13 in *C. meersi* Grismer, Wood, Quah, Murdoch, M Grismer, Herr, Espinoza, Brown & Lin); ventrolateral folds present (vs. absent in *C. annandalei*, *C. himalayicus* (Annandale); weak in *C. nyinyikyawi* Grismer, Wood, Quah, Murdoch, Grismer, Herr, Espinoza, Brown & Lin and *C. pyadalinensis*); 9–12 supralabials (vs. 7–8 in *C. annandalei*, *C. myintkyawthurai* Grismer, Wood, Quah, Murdoch, Grismer, Herr, Espinoza, Brown & Lin, *C. pyinyaungensis* Grismer, Wood Jr, Thura, Zin, Quah, Murdoch, Grismer, Lin, Kyaw & Lwin, *C. meersi*, *C. peguensis*) 7–11 precloacal pores in males, femoral pores absent (femoral as well as precloacal pores present in *C. myintkyawthurai*, *C. bhupathyi*, *C. pyadalinensis* and *C. meersi*); 49–58 paravetrebral tubercles (vs. 31 or 32 in *C. peguensis*, 32 in *C. meersi*, 28–32 in *C. myintkyawthurai* and 25–30 in *C. pyinyaungensis*). The dorsal colouration that is buff with paired irregular blotches distinguished the new species from Burmese members which bear pale to yellow blotches on the head with well-defined paired or fused blotches on the body. The new species is most similar to *C. himalayicus*, based on morphology in sharing overlapping numbers of precloacal pores, dorsal tubercle row number, ventral scales across belly and in lacking femoral pores. However, it differs from *C. himalayicus* as follows: ventrolateral fold present in *Cyrtodactylus kamengensis* sp. nov. vs. absent in *C. himalayicus*, 6–8 basal lamellae on digit IV of pes vs. 9 in *C. himalayicus*. Genetically, the new species is closer to *C. bhupathyi* and *C. gubernatoris*, from which it differs as follows: 30–34 ventral scales across belly vs. 37 or 38 in *C. bhupathyi*, 34–37 in *C. gubernatoris*; 53–58 paravertebral tubercles vs. 36–45 paravertebral tubercles in *C. gubernatoris*; 7–11 precloacal pores vs. 9 precloacal and 6–9 femoral pores in *C. gubernatoris*.

Description of holotype male BNHS 3113 (Figs 2–5). The holotype is in a generally good condition, except for minor folds of skin on flank (Fig. 2a) and ventral scales, all artefacts of preservation; tail tip removed as tissue sample for molecular analyses; part of the scales on the left lower side of the trunk was damaged during capture (Fig. 2b).

Adult male, SVL 78.6 mm. Head moderately long (HL/SVL ratio 0.17) and wide (HW/HL ratio 1.04), dorsoventrally depressed (HH/HW ratio 0.61), distinct from neck; loreal region slightly inflated, interorbital area flat, canthus rostralis not prominent; snout moderately short (SE/HL ratio 0.67), almost twice as long as OD (OD/SE ratio 0.48); scales on forehead, canthus rostralis and snout heterogeneous, those in the interorbital region small, rounded and granular; scales on snout and canthus rostralis slightly larger than those on forehead; scales of interorbital and occipital region heterogeneous, granular, those in occipital region mixed with

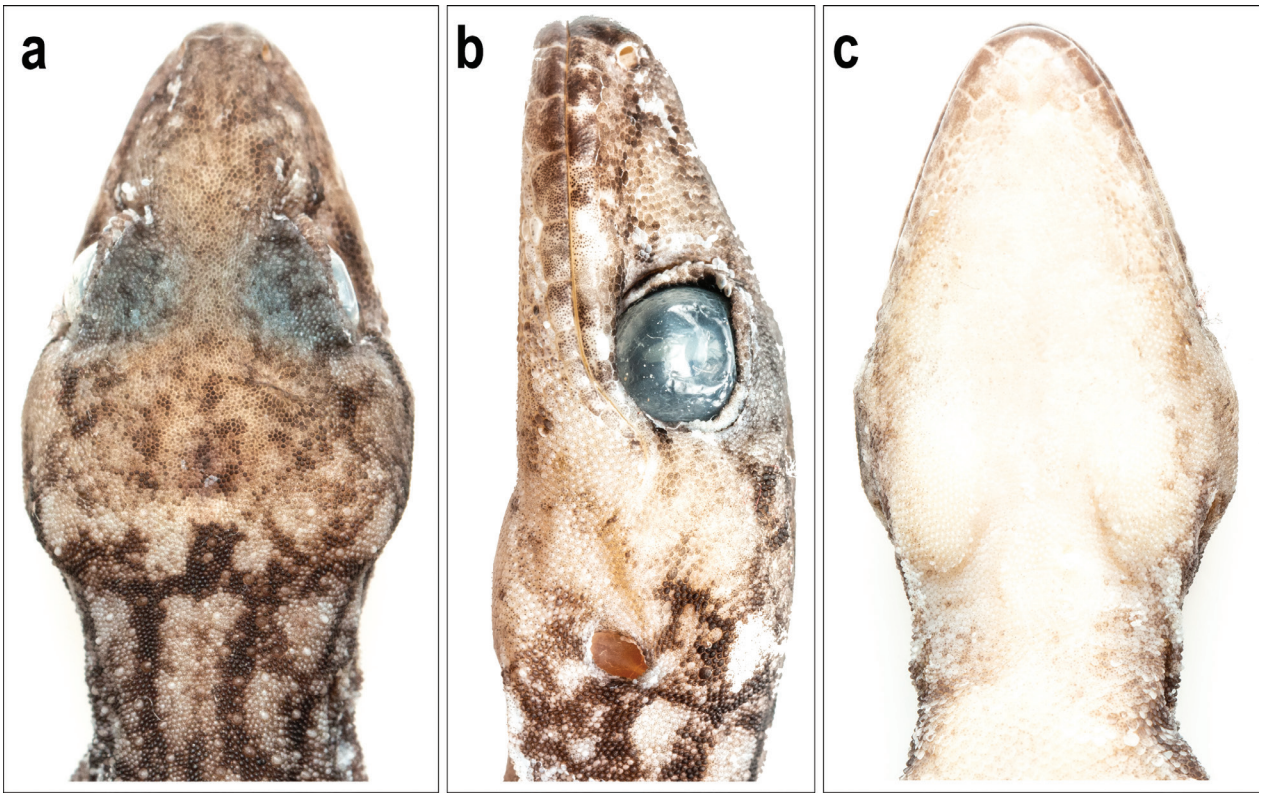

Figure 3. *Cyrtodactylus kamengensis* sp. nov. male holotype BNHS 3113 head **a.** Dorsal view; **b.** Lateral view; **c.** Ventral view. Photo by Zeeshan A. Mirza.

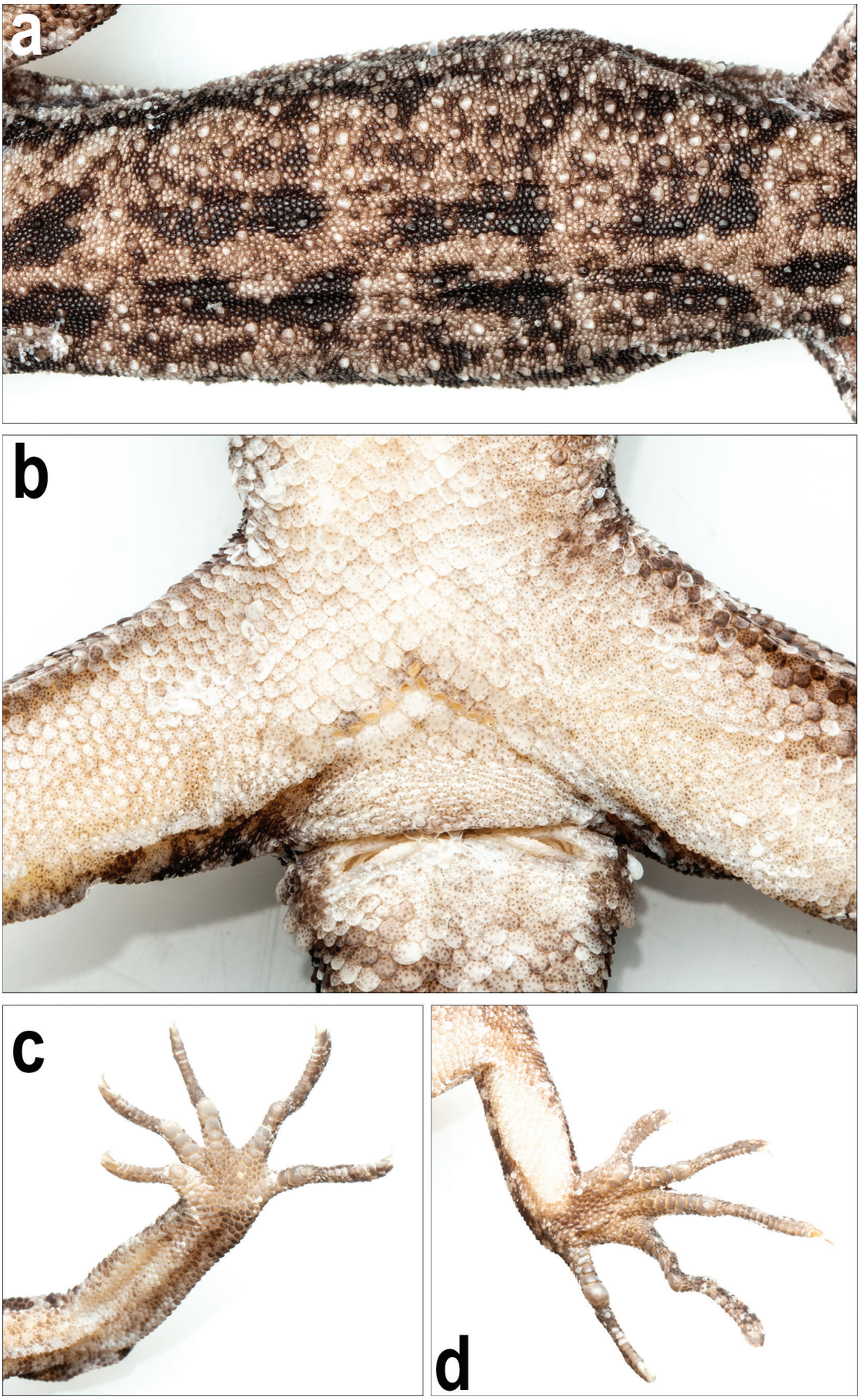

Figure 4. *Cyrtodactylus kamengensis* sp. nov. male holotype BNHS 3113 **a.** Dorsal view of trunk; **b.** Ventral view showing precloacal pores; **c.** Ventral view of left manus; **d.** Ventral view of left pes. Photo by Zeeshan A. Mirza.

Figure 5. *Cyrtodactylus kamengensis* sp. nov. male holotype BNHS 3113 in life. Photo Mandar Sawant.

slightly larger, rounded, conical tubercles (Fig. 3a–c), a row of large scale (two to three times larger than scales on the canthus rostralis) border the supralabials. Eye small (OD/ HL ratio 0.33); pupil vertical with crenulated margins; supraciliaries mucronate, decreasing in size towards posterior edge of orbit; ear opening oval, obliquely orientated, large; eye to ear distance slightly more than eye diameter. Rostral wider (2.7 mm) than deep (1.8 mm), partially divided dorsally by weakly developed rostral groove; single large supranasal on either side, separated by two small scales (internasals), which are approximately twice the size of enlarged granular scales on snout; rostral in contact with SL I, nasals, supranasals and an internasal; nostrils semicircular, laterally orientated, posterior half covered by nasal pad, each in broad contact with rostral and also surrounded by supranasal, SL I and three or four postnasals; one scale row separates orbit from supralabials; mental slightly wider (3.5 mm) than long (1.9 mm), triangular, two pairs of well-developed postmentals, inner pair longer (maximum length 2.3 mm) than and separating outer pair (maximum length 1.0 mm), outer pair in contact with the inner postmentals for part of its own length; inner postmentals bordered by mental, IL I, outer postmental and six gular scales; outer postmental bordered by inner postmental, IL I and IL II and four gular scales on either side; supralabials 12/12 (7 to mid-orbit), bordered by a row of large, flat, slightly elongated scales (Fig. 3c); infralabials 10/10, IL II to IL VII bordered by one row of chin-shields, largest anteriorly; interorbital scale rows across narrowest point of frontal bone approximately 30 scales. Body moderately slender, relatively short (TRL/SVL ratio 0.46) with distinct ventrolateral folds; dorsal scales heterogeneous, mostly rounded granular, intermixed with irregularly arranged small (2–3 times granule size) circular tubercles, bluntly conical and feebly keeled throughout (Fig. 4a), becoming more conical and smaller towards flanks, tubercles extend from frontal region to proximal one third of tail length; tubercles on nape smaller than those of dorsum, largest on flanks; enlarged tubercles on tail completely flat and weakly pointed and keeled; tubercles in approximately 21–22 irregular longitudinal rows at mid-body; 49 paravertebral tubercles; ventral scales much larger than dorsal scales, smooth, cycloid, imbricate to subimbricate, 30 mid-body ventral scale rows; gular scales smaller than ventrals and granular, except a few rows of larger, flat and juxtaposed scales, including a single row of chin-shields bordering mental, postmentals and infralabials (Fig. 3c). Eleven pitted precloacal scales in a continuous series; no precloacal groove (Fig. 4b). Six enlarged scales between pitted precloacal scales and vent, as large as the largest ventrals and first as well as second row of scales much larger than pitted precloacal scales, the other two rows are slightly smaller. Tail partly regenerated, dorsoventrally depressed, without distinct median furrow, tapering; tail tip removed for molecular analyses. Dorsal scales at base of tail granular, gradually becoming flatter, subimbricate posteriorly, increasing in size on lateral aspect, intermixed with 11–12 slightly enlarged tubercles near base of tail and reducing to two by fourth transverse row of tubercles (Fig. 2); ventral

Table 1. Meristic and morphometric details of the non-type specimens of *Cyrtodactylus kamengensis* sp. nov. in millimetres.

Specimens number	BNHS 3113	BNHS 3114	BNHS 3115	NCBS NRC AA0020	NCBS NRC AA0021
Sex	**male**	**male**	**male**	**male**	**male**
SVL (snout to vent length)	78.6	71.9	70.2	74.3	74.2
Ax-Gr length	35.8	33	26.4	32	29
BW (body width)	13.3	11.2	10.1	14.3	13
CL (from base of heel to knee)	14	13.1	13	12.3	13
TL (tail length)	72.3	39*	49.7	40.3*	66
TW (tail width)	6.4	5.5	6.8	6.4	5.5
HL (head length)	13.5	12	11.6	14.5	13.3
HW (head width)	14.1	12.7	11.2	14	13.3
HH (head height)	8.6	6.9	7.2	8.4	7.8
FL (base of palm to elbow)	11.7	11.2	11.3	11.5	9.3
OD (eye diameter)	4.4	3.9	4.4	–	4.5
NE (nose to eye)	6.5	6.1	6.5	5.8	5.3
SE (snout to eye)	9	7.3	8.5	8.1	7.5
EE (eye to ear)	6.4	5.1	5.4	5.8	5.5
EL (ear diameter)	1.2	1.5	0.9	1.5	1.4
IN (inter narial (nose) distance)	2.8	2.9	2.9	3.4	3.2
IO (inter-orbital/eyes)	6.2	5.5	4.9	5.3	6
Lamellae					
L manus	3(8)-4(9)-4(12)-5(12)-4(10)	3(7)-5(8)-5(11)-6(10)-5(10)	3(8)-5(9)-5(10)-6(11)-6(10)	4(8)-5(9)-5(10)-5(11)-4(9)	3(8)-4(9)-5(12)-6(11)-5(9)
R manus	3(7)-4(12)-5(13)-5(13)-4(10)	3(7)-6(10)-6(12)-6(11)-5(9)	3(8)-5(9)-5(11)-5(10)-5(9)	4(8)-5(9)-5(10)-5(10)-4(9)	4(8)-5(9)-6(11)-6(11)-5(9)
Left pes	3(9)-5(9)-6(13)-7(11)-4(9)	4(7)-6(9)-6(9)-8(11)-6(9)	3(8)-5(10)-6(12)-6(13)-8(12)	3(8)-5(9)-5(13)-7(11)-5(10)	4(8)-5(9)-6(11)-7(12)-6(10)
Right pes	3(10)-4(12)-6(11)-7(12)-6(11)	4(7)-6(8)-6(10)-7(9)-5(9)	3(8)-5(9)-6(12)-8(13)-5(11)	4(8)-5(9)-5(12)-7(11)-5(10)	4(8)-6(10)-6(12)-7(13)-5(11)
Supralabials Left/Right	12/12	11/9	12/11	11/11	10/11
Infralabials Left/Right	10/10	10/10	10/10	10/9	10/10
Pores	11	7	7	10	–
Ventral scales across belly	30	31	30	30	34
Dorsal tubercle rows	20	20	22	24	22
Paravertebral tubercles	49	58	54	53	53

scales larger that dorsal scales, imbricate, median row comprises irregularly enlarged subcaudals in one or two rows; three enlarged postcloacal tubercles at base of tail. Fore- and hind-limbs relatively slender; forearm (FL/SVL ratio 0.15) and crus (CL/SVL ratio 0.18) relatively short; digits relatively short, strongly inflected at each joint, all bearing robust, recurved claws; subdigital lamellae widened beneath basal phalanx; basal lamellae series on digits I–V: 3-4-5-5-4 (right manus) and 3-4-6-7-6 (right pes); distal lamellae series on digits I–V: 7-12-13-13-10 (right manus) and 10-12-11-12-11 (right pes) (Fig. 4c, d); interdigital webbing absent on manus, rudimentary between Digits I–V of pes; relative length of digits (measurements in mm in parentheses): IV (6.8) > III (6.4) > V (5.8) > II (4.9) > I (3.3) (right manus) and III (8.8) > IV (8.5) > V (7.9) > II (6.0) > I (3.0) (right pes); palmar and plantar scales smooth, rounded; scales on fore-limb heterogeneous, composed of flat, rounded, smooth sub-imbricate scales, gradually increasing in size on forearm, smaller scales appear granular, no enlarged tubercles, ventral portion covered mostly with smaller and granular scales; scales on hind-limbs heterogeneous, dorsal part of thigh and shank, with larger, conical granular scales, intermixed with scattered, enlarged, slightly conical, weakly-keeled tubercles, which are denser on shank than on thigh, anterior portion of thigh and ventral aspect of hind-limb with enlarged, smooth, imbricate scales, a few rows under thigh are slightly larger than those on abdomen.

Colouration in preservative. Background in a shade of buff with two rows of dark irregular blotches running from the nape to the flank; each of these blotches are placed fairly at an equal distance from each other. The nape bears a rudimentary bar composed of dark spots which continue into a parallel, irregular stripe along the dorso-lateral aspect of the trunk to its middle where it diffuses into individual spots. The paired blotches on the dorsum merge into alternating dark and light bands on the tail. The limbs bear dark unconnected reticulations. The ventral aspect is off white, lacking the diffusion of the dorso-lateral colouration into the lateral edges of the venter. Colouration in life: the overall colouration is a shade of faded brown with irregular dark reticulations on the head, the body bears a pair of dark brown irregularly-arranged blotches with paler posterior borders forming faded thin, white bars on the trunk and the original portion

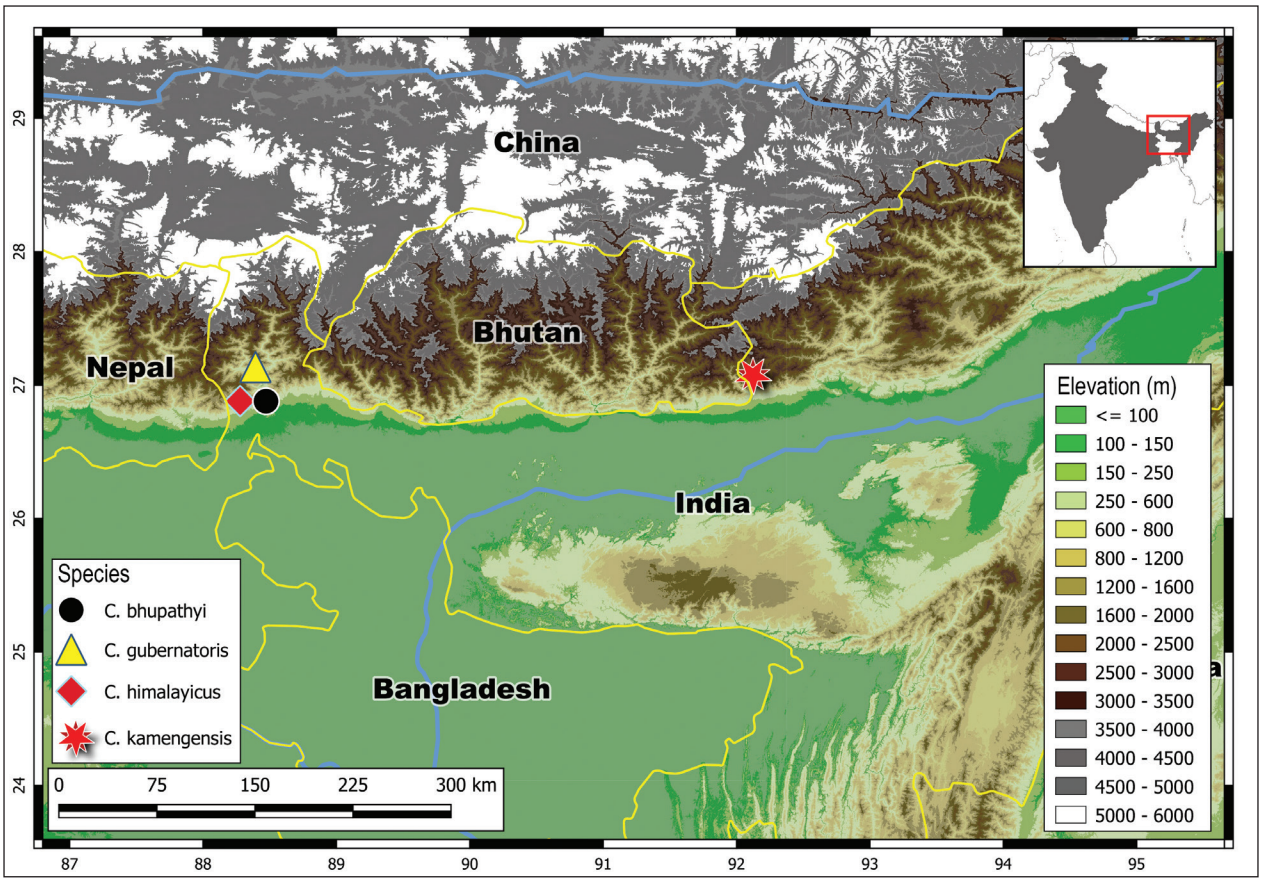

Figure 6. A map showing elevational profile of northeast India and distribution of the Indian members of the *Cyrtodactylus peguensis* group.

of the tail bears distinct alternate dark and light bands, while the regenerated part of the tail is ochre with dark mottling. The legs bear dark brown and yellowish-brown mottling on a paler background (Fig. 5).

Variation. the paratypes match the holotype in most aspects, except for details presented here and in Table 1: the number of postcloacal spurs and their size is variable in the species, ranging from 3 in most specimens to 4 (NCBS NRC AA-0020); the anterior two postcloacal spurs in the holotype are large, whereas only the first one in BNHS 3114 is large and in NCBS NRC AA-0020, all four are of equal size. The number of enlarged, non-pored scales between the precloacal pores and the vent range from 6–9.

Natural history and distribution notes: all the specimens of the new species were collected from near culverts along roads just after dusk. The species was found in sympatry with *Hemidactylus* cf. *malcolmsmithi* and *H. platyurus*. The species appears to be distributed at Shergaon (elevation ~ 1900 m) and Khellong (elevation ~ 500 m) in West Kameng District of Arunachal Pradesh (Fig. 6). Several individuals were observed on mud escarpments and tree trunks (not collected). The forest type at these localities is described as the East Himalayan moist temperate forest (elevation 1500–2600 m) and the Upper Assam Valley Tropical Wet Evergreen forest (below 800 m) by Champion and Seth (2005).

Discussion

The *Cyrtodactylus* sp. sequence from Khellong, Arunachal Pradesh bearing voucher number CES13/1464 (KM255196), presented in Agarwal et al. (2014), likely represents the new species. This assumption is based on geographic proximity (~ 29.1 km airline distance) and sequence similarity (p-distance 3%, Table 2). However, given that, we were unable to examine the specimen and owing to the slight molecular divergence, we refer to it as *Cyrtodactylus* cf. *kamengensis*. The Indian lineage of the '*peguensis*' group diverged from its Burmese relatives during the mid-Oligocene likely followed by the beginning of the Himalayan uplift (Agarwal et al. 2014) and *C. kamengensis* sp. nov. shared the most recent common ancestor with its Burmese relatives during early Miocene. The deep divergence between *C. kamengensis* sp. nov. (mid- to high elevation species) and *C. gubernatoris* + *C. bhupathyi* likely represented a case of Mountain and Lowland clades, with one lineage restricted to lower elevation regime, whereas the other spanning into higher elevation regimes (Agarwal et al. 2014). The Himalayas have played a pivotal role in shaping diversification of many taxa (Mani 1974; Agarwal et al. 2014; Price et al. 2014; Dahal et al. 2017) and conservation efforts are necessary to ensure protection to many relic lineages that thrive across this realm.

Table 2. Uncorrected p-distance for members of the clade containing the new species within the '*peguensis*' group.

		1	2	3	4	5	6	7	8	9	10	11
1	*C. annandalei* JX440524											
2	*C. bhupathyi* KM255204	0.26										
3	*C. gubernatoris* KM255181	0.27	0.17									
4	*C. meersi* MH624104	0.13	0.28	0.26								
5	*C. nyinyikyawi* MH624118	0.13	0.30	0.29	0.10							
6	*C. peguensis* MH756190	0.15	0.28	0.29	0.10	0.10						
7	*C. pyadalinensis* MH624105	0.13	0.26	0.27	0.09	0.09	0.09					
8	*C. russelli* JX440555	0.28	0.25	0.26	0.27	0.27	0.27	0.25				
9	*C.* cf. *kamengensis* KM255196	0.26	0.19	0.19	0.26	0.27	0.27	0.25	0.24			
10	*C. kamengensis* sp. nov. OM023868	0.26	0.19	0.20	0.26	0.26	0.26	0.25	0.24	0.03		
11	*C. kamengensis* sp. nov. OM023869	0.26	0.19	0.20	0.26	0.26	0.26	0.25	0.24	0.03	0.00	-

Table 3. Diagnostic characters for members of the *C. peguensis* group and *C. arunachalensis*. Abbreviations: PeP/PeFP precloacal pores/precloacal femoral pores, FP femoral pores, DTR dorsal tubercle rows, MVSR mid-ventral scale rows, SVL snout to vent length in mm.

Species	Supralabials	PcP/ PcFP	FP	DTR	MVSR	Enlarged subcaudals	SVL (max)	Ventrolateral fold
C. annandalei	7–8	11–12 (M,F)	10–11 (M), 0 (F)	16–18	43	yes	55	Absent
C. arunachalensis	9–11	6 to 10	0	24–26	37–38	no	81.7	Present
C. bhupathyi	10–11	10–11 (F)	4–7 (F)	24–25	37–38	yes	61	Present
C. gubernatoris	-	8–9 (M), 7–9 (F)	6–9 (M), 0 (F)	20–21	34–37	no	71	Present
C. himalayicus	-	10	0	19–21	33–44	no	65	Absent
***C. kamengensis* sp. nov.**	9–12	7–11(M)	0	20–24	30–34	no	78.6	Present
C. meersi	7–8	8(M)	12(M)	13	32	yes	36	Present
C. peguensis	7–8	8(M)	17–19(M)	17–19	36–37	yes	70	Present
C. pyadalinensis	-	14–15(M)	9–10(M)	19–21	40	yes	72.1	Present
C. pyinyaungensis	7–8	8(M)	17–18(M)	15–18	30–36	yes	71.7	Present

The new species is distributed in western Arunachal Pradesh (Fig. 6), close to the borders of Bhutan and the biotope of the region is similar, which suggests that the new species may be found in the adjoining areas of Bhutan as well. However, further work is necessary in this direction in addition to elucidating the phylogenetic relationship of the new species with *C. himalayicus*, with which it shares several morphological characters (Table 3).

The description of yet another new species of reptile from Arunachal Pradesh highlights how little exploration has been conducted in this region to document its reptilian fauna. The discovery of a new skink genus (Mirza et al. 2022), several species of snakes (Bhosale et al. 2019, 2020; Captain et al. 2019; Mirza et al. 2020) and a new *Cyrtodactylus* (Mirza et al. 2021) from Arunachal Pradesh warrant dedicated surveys to document its reptilian diversity.

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Supplementary material 1

Appendix I

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Data type: Phylogeny

Explanation note: Maximum Likelihood phylogeny of the genus *Cyrtodactylus* for dataset presented in Grismer et al. (2021).

Link: https://doi.org/10.3897/herpetozoa.35.e80610.suppl1