



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

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Abstract

We here describe a new species of bent-toed geckos from the northeastern Indian state of Arunachal Pradesh, which is widespread across the Dafla and Mishmi hills, occurring at elevations ranging from 179 m to 1400 m. The new species is recovered as sister to the *Cyrtodactylus khasiensis* clade based on a molecular phylogeny inferred from mitochondrial NADH-ubiquinone oxidoreductase, subunit 2 gene. Intraspecific uncorrected pairwise sequence divergence (*p*-distance) for the new species was found to be between 0 and 5%, whereas the interspecific divergence from the closely-related congeners was between 19 and 30%. The new species can be differentiated from members of the *C. khasiensis* clade using a suite of morphological characters: moderate body size (SVL 64.9–81.7); 8–11 supralabials; 8–10 infralabials; 24–26 bluntly conical, feebly keeled dorsal tubercles; 50–60 paravertebral tubercles; ~38 ventral scales between ventrolateral folds; no precloacal grooves; 6–10 precloacofemoral pores in a continuous series; 10–16 distal subdigital lamellae on IV of pes; subcaudal scalation of original tail without enlarged plates. This is the fourth reptile species described from Arunachal Pradesh from the expedition led by the team, and this further highlights the need for further herpetological investigations into the region.

Key Words

Bent-toed gecko, cryptic species, Himalayas, *ND2*, northeast India, widespread

Introduction

The genus *Cyrtodactylus* Gray, 1827 comprises of 306 species of which 57 species are distributed across the Himalayas and Indo-Burma biodiversity hotspot (Agarwal et al. 2018a) constituting nearly 10% of the diversity within the genus. Ten new species have been described in the last two years from Himalayan region, of which,

nine were described from northeast India and the genus might harbor more narrowly distributed species (Agarwal et al. 2018a). Arunachal Pradesh is among the least explored states in northeast India for its herpetofaunal diversity (Agarwal et al. 2010) and especially in case of the genus *Cyrtodactylus*. This is further highlighted by the fact that despite *Cyrtodactylus* being the most speciose gekkonid genus (Grismer et al. 2020), only six species

were known from northeast India and the adjoining regions, until multiple new species were described, and many synonyms were revalidated only recently (Agarwal et al. 2018a, b). Furthermore, a molecular phylogeny published by Agarwal et al. (2014) included sequences of *Cyrtodactylus* spp. representing three undescribed species from Arunachal Pradesh, which further hints towards the poor state of documentation of the northeast Indian *Cyrtodactylus* diversity.

In the course of herpetological exploration, we surveyed several localities across the Indian state of Arunachal Pradesh (Bhosale et al. 2019; Bhosale et al. 2020; Mirza et al. 2020). During the expedition, we collected specimens of *Cyrtodactylus* from three localities, which were later identified to belong to a single species based on morphological as well as molecular data. In the present communication, we describe this new species based on morphological and molecular analysis similar to the approach in Mirza et al. (2018).

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 by hand, photographed and later, euthanized with halothane within 24 hours of capture, following ethical guidelines for animal euthanasia (Leary et al. 2013). The specimens were fixed in 8% formaldehyde solution and later stored in 70% ethanol. Liver/tail tip tissues were collected 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 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 were recorded for the following to the nearest 0.1 mm following Agarwal et al. (2018a): SVL, snout to vent length measured from the tip of the snout to the cloacal opening; TRL, trunk length measured from the axilla to the groin; BW, body width measured at the widest part of the trunk; TL, tail length measured from the cloacal opening to the tip of the tail; TW, tail width widest portion of the tail; HL, head length measured from tip of the snout to the retro-articular process; HW, head width measured at the widest portion of the head; HH, head height; FL, forearm length measured from elbow to the base of the palm;

CL, crus length measured from the knee to the base of the palm; OD, eye diameter measured at the widest diameter of the eye; NE, nostril to eye distance measured from the nostrils to the anterior border of the eye; SE, snout tip to eye distance measured from the tip of the snout to the anterior border of the eye; EE, eye to ear distance measured from the posterior border of the eye to the anterior border of the tympanum; EL, 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 precloacal 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, b), Grismer et al. (2018) and Purkayastha et al. (2020).

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/>.

Molecular analysis

Genomic DNA was isolated from the preserved liver or tail tissue of five specimens using QIAGEN DNeasy kits following protocols directed by the manufacturer. A fragment of the mitochondrial NADH-ubiquinone ox-

idoreductase, 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 minutes) × 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. The newly generated sequences were added to the dataset for *Cyrtodactylus* spp. used by Grismer et al. (2020) to assess phylogenetic relationship. The dataset was aligned in MegaX (Kumar et al. 2018) using ClustalW (Thompson et al. 1994) with default settings and subjected to 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 and the analysis was run with an ultra-fast bootstrap option for 1000 iterations to assess clade support. Un-corrected pairwise *p*-distance (% sequence divergence) was calculated for members of the *khasiensis* clade in MegaX (Kumar et al. 2018) with pairwise deletions of missing data and gaps. Details of sequences generated in the present work and GenBank accession numbers are presented in supporting files (Appendix 1).

Results

Molecular phylogenetics

Molecular phylogeny was based on 1041 bp of *ND2* gene of which 312 are conserved, 726 are variable, 661 are parsimony informative sites and 65 singleton sites. The sequences collected from Pakke Tiger Reserve, Papum Pare District and Kamlang Tiger Reserve, at elevations ranging from 179 m to 1400 m clustered together, and the clade was recovered as sister to *Cyrtodactylus khasiensis* clade. This relationship was very-well supported (ML Bootstrap Values 99, BI posterior probabilities 1). Samples from across Arunachal Pradesh show a *p*-distance (sequence divergence) of 0–5% whereas show 19–30% sequence divergence from congeners. Molecular phylogenetic reconstructions and the pairwise distance suggest that the specimens collected from the aforementioned localities represent a new species, and with the integration of the morphological data, is here described.

Systematics

Cyrtodactylus arunachalensis sp. nov.

<http://zoobank.org/A159679A-30BB-45C8-A7CD-5AEB3EB1AE6>

Figs 1–4, Tables 1, 2

Cyrtodactylus sp. Agarwal et al. (2014): 147

Type material. *Holotype*. male, BNHS 2775, Seijosa near Pakke Tiger Reserve, East Kameng District, Arunachal Pradesh (26.966819°N, 93.01332°E, elevation 179 m) collected by Mandar Sawant, Pushkar Phansalkar, Harshal Bhosale and Zeeshan A. Mirza on 1 July 2019.

Paratypes. three males BNHS 2776 & NCBS NRC-AA-0006–NRC-AA-0007, one female BNHS 2777, from the same locality collected on 3 July 2019.

Material referred. three males, NCBS NRC-AA-0008–NRC-AA-0009 & BNHS 2778, from near Parshuram Kund near Kamlang Wildlife Sanctuary (27.887369°N, 96.376617°E, elevation 560 m) and Hawa Pass (27.916699°N, 96.332303°E, elevation 1217 m) collected by Mandar Sawant, Pushkar Phansalkar, Harshal Bhosale, Gaurang Gowande and Zeeshan A. Mirza; one female, BNHS 2779 from near Dakte – Hoj, Papum Pare District, Arunachal Pradesh (27.332567°N, 93.83775°E, elevation 980 m) collected by Mandar Sawant, Pushkar Phansalkar and Harshal Bhosale.

Etymology. The specific epithet is refers to the state of Arunachal Pradesh in northeast India where the species was discovered.

Diagnosis. *Cyrtodactylus arunachalensis* sp. nov. can be distinguished from members of the *khasiensis* group by its: moderate body size (SVL 64.9–81.7, mean 70.6); 8–11 supralabials; 8–10 infralabials; 24–26 rows of bluntly conical, feebly keeled dorsal tubercles; 50–60 paravertebral tubercles; ~38 ventral scales between ventrolateral folds; no precloacal grooves; 6–10 precloacofemoral pores in a continuous series; three to four rows of enlarged scales below pored scales, slightly larger than pored scales; 10–16 distal subdigital lamellae on IV of pes; subcaudal scalation of original tail without enlarged plates.

Comparison. Molecular data for *ND2* gene suggests that *Cyrtodactylus arunachalensis* sp. nov. is a member of the clade of species distributed south of Brahmaputra River (Agarwal et al. 2014) and is here compared with members of the clade. Intraspecific uncorrected pairwise sequence divergence (*p*-distance) for samples across the state in 0–5% and an interspecific divergence of 19–30% calculated for *ND2* gene. Precloacal pores 6–10, and no femoral pores (vs. 10–28 in *C. ayeyarwadyensis* Bauer, 16–29 in *C. gansi* Bauer, 29–37 in *C. tripuraensis* Agarwal, Mahony, Giri, Chaitanya and Bauer, 14 in *C. septentrionalis* Agarwal, Mahony, Giri, Chaitanya and Bauer, 11–12 in *C. jaintiaensis* Agarwal, Mahony, Giri, Chaitanya and Bauer, 26–39 precloacofemoral pores in *C. guwahatiensis* Agarwal, Mahony, Giri, Chaitanya and Bauer); 24–26 dorsal tubercle rows (vs. 19–23 in *C. khasien-*

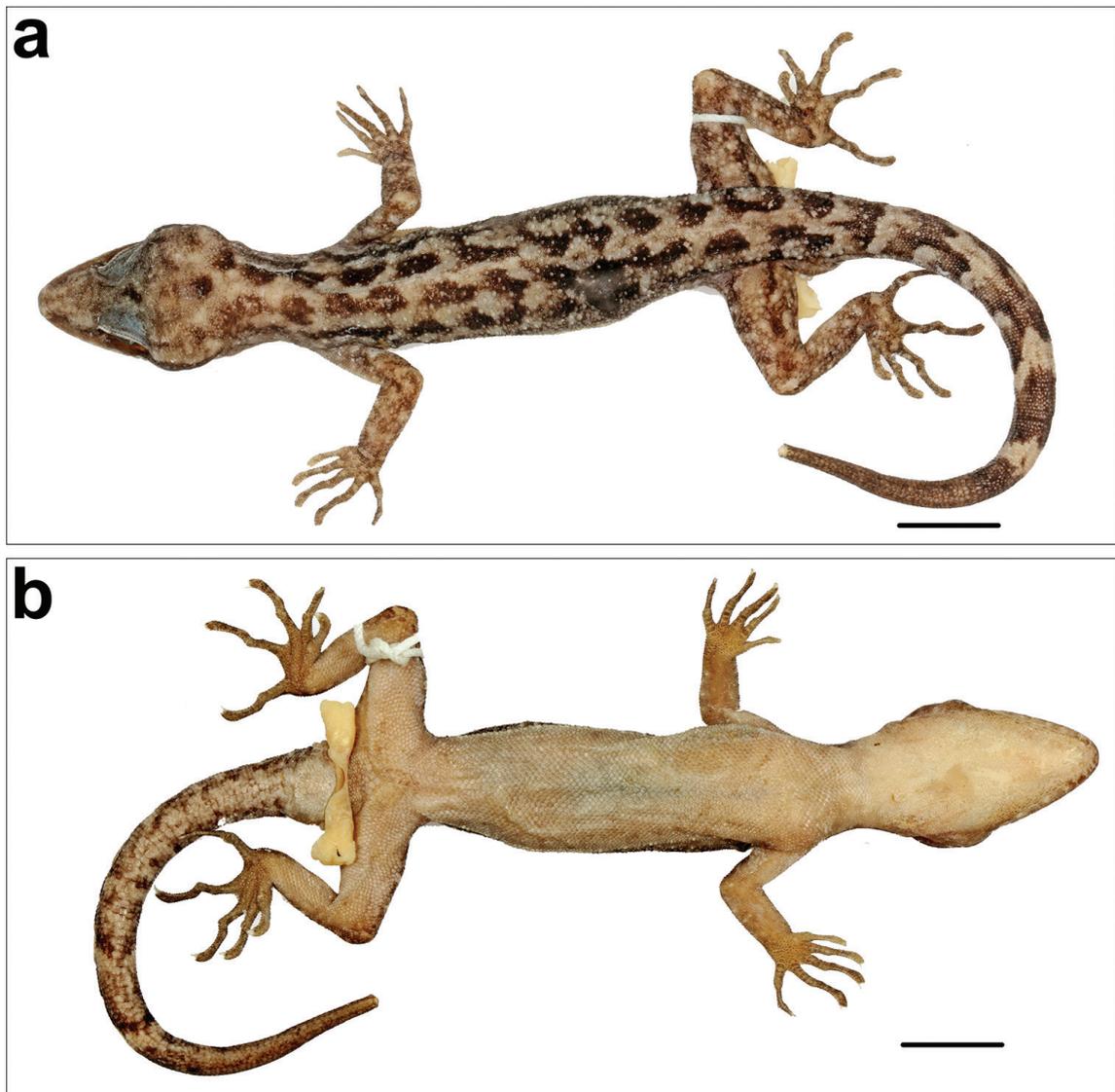


Figure 1. *Cyrtodactylus arunachalensis* sp. nov. male holotype BNHS 2775, (a) dorsal view, (b) ventral view. Scale bars: 10 mm.

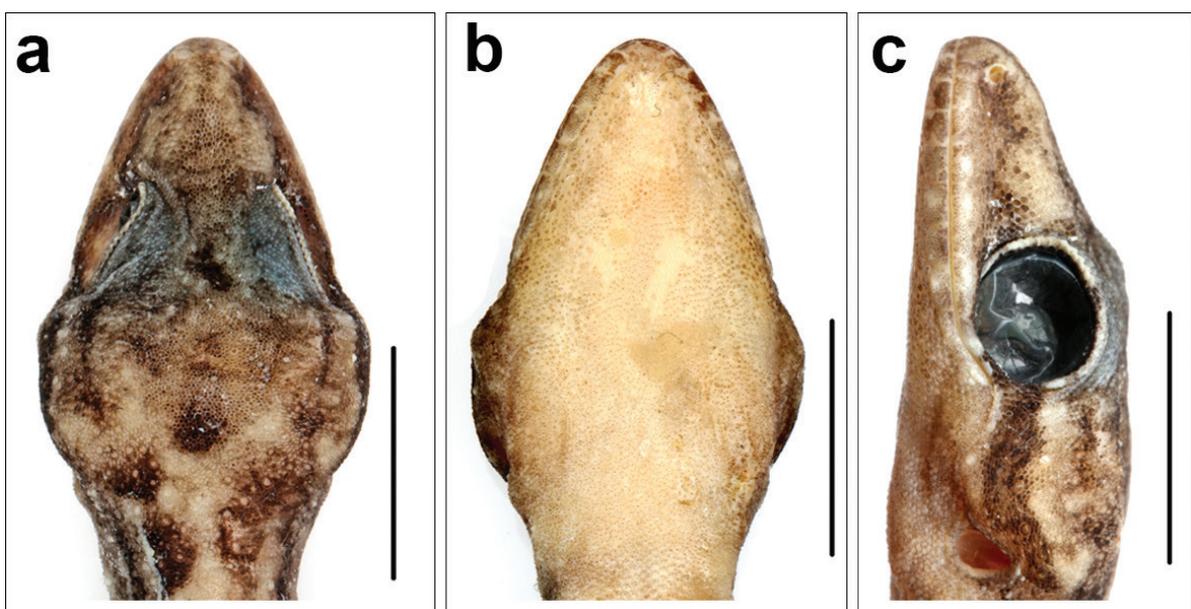


Figure 2. *Cyrtodactylus arunachalensis* sp. nov. male holotype BNHS 2775 head, (a) dorsal view, (b) ventral view, (c) lateral view. Scale bars: 5 mm.



Figure 3. *Cyrtodactylus arunachalensis* sp. nov. male holotype BNHS 2775 dorsal trunk showing arrangement of tubercles.

sis (Jerdon), 19–21 in *C. tripuraensis* Agarwal, Mahony, Giri, Chaitanya and Bauer, 16 in *C. chrysopylos* Bauer, 19–20 in *C. jaintiaensis*, 21–23 in *C. montanus* Agarwal, Mahony, Giri, Chaitanya and Bauer, 16–18 in *C. nagalandensis* Agarwal, Mahony, Giri, Chaitanya and Bauer); supralabials 8–11 (vs. 11–12 in *C. kazirangaensis* Agarwal, Mahony, Giri, Chaitanya and Bauer); 37–38 mid-ventral scale rows across belly (vs. 32–37 in *C. ayeyarwadyensis*, 30–34 in *C. urbanus* Purkayastha, Das, Bohra, Bauer & Agarwal, 41–49 in *C. aunglini* Grismer, Wood, Thura, Win, Grismer, Trueblood & Quah, 57 in *C. myaleiktaung* Wood, Thura, Win, Grismer, Trueblood & Quah); 50–57 paravertebral tubercles (30–35 in *C. guwahatiensis*, 37–43 in *C. kazirangaensis*, 34–42 in *C. khasiensis*, 38–42 in *C. septentrionalis*, 37–40 in *C. urbanus*).

Description of holotype male BNHS 2775. *Holotype* in generally good condition except for minor folds of skin on flank 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. 4A).

Adult male, SVL 71.6 mm. Head moderately long (HL/SVL ratio 0.25), and wide (HW/HL ratio 0.76), dorsoventrally depressed (HH/HW ratio 0.53), distinct from neck; loreal region slightly inflated, interorbital area flat, canthus rostralis not prominent; snout moderately short (SE/HL ratio 0.44), almost twice as long as OD (OD/SE ratio 0.75); scales on forehead, canthus rostralis and snout heterogenous, 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 homogenous, granular, those in occipital region mixed with slightly larger,

rounded, conical tubercles (Fig. 5A). Eye large (OD/HL ratio 0.33); pupil vertical with crenulated margins; supraciliaries mucronate, decreasing in size towards posterior edge of orbit; ear opening oval, obliquely oriented, large; eye to ear distance slightly more than eye diameter. Rostral wider (2.5 mm) than deep (1.7 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 oriented, posterior half covered by nasal pad, each in broad contact with rostral and also surrounded by supranasal, SL I, and three or four postnasals; three or four scale rows separate orbits from supralabials; mental slightly wider (2.5 mm) than long (1.8 mm), triangular, two pairs of well-developed postmentals, inner pair longer (maximum length 1.7 mm) than and separating outer pair (maximum length 1.0 mm), outer pair in contact with the inner postmentals for its entire 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 10/11 (8), bordered by a row of large, flat, slightly elongated scales (Fig. 5C); infralabials 8/9, 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. Body moderately slender, relatively short (TrL/SVL ratio 0.46) with weak 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. 4), becoming more conical

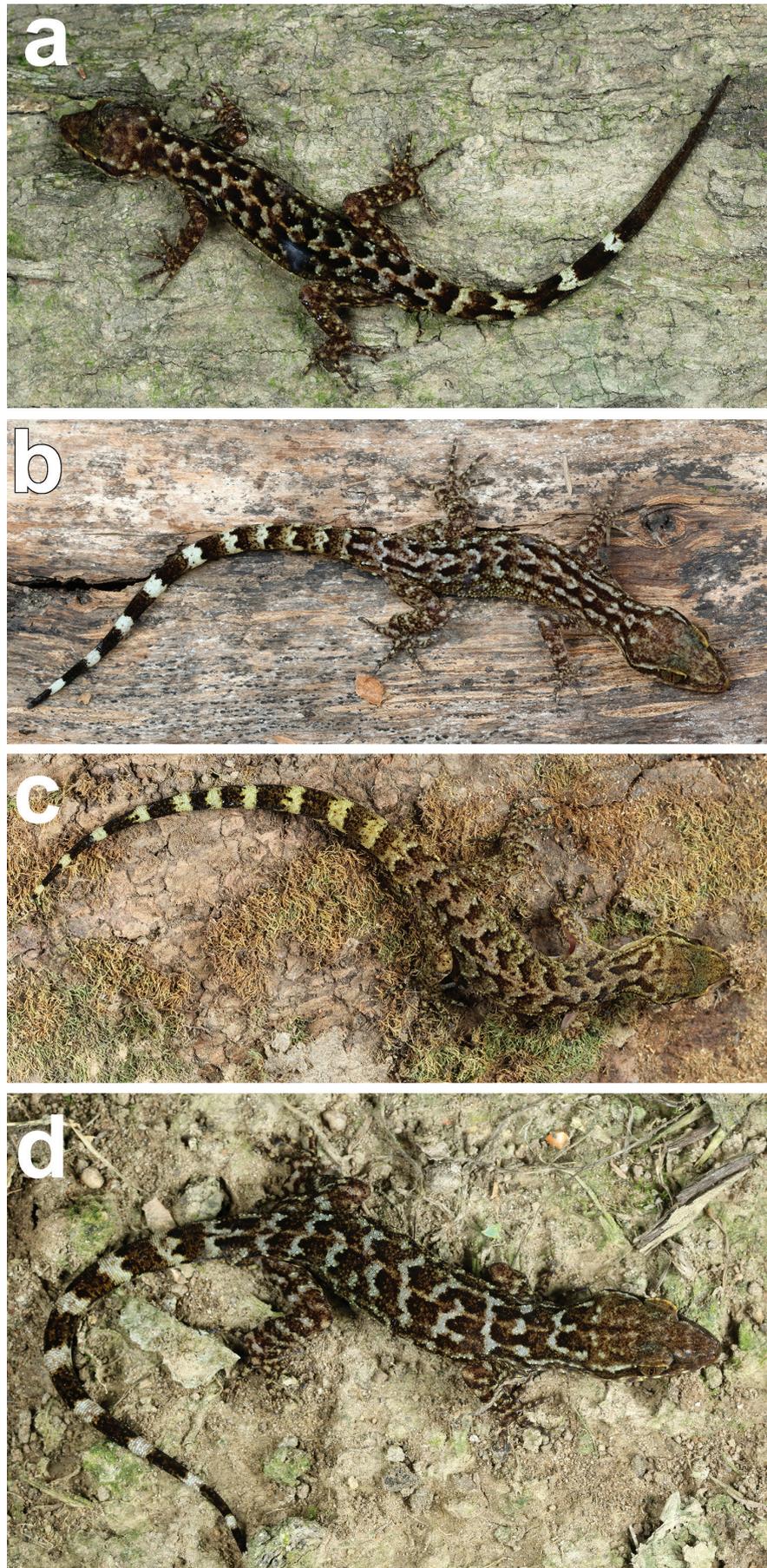


Figure 4. *Cyrtodactylus arunachalensis* sp. nov. in life (a) male holotype BNHS 2775, (b) paratype male BNHS 2777, (c) male NCBS NRC-AA-0008, (d) male BNHS 2778. Photographs by Zeeshan A. Mirza

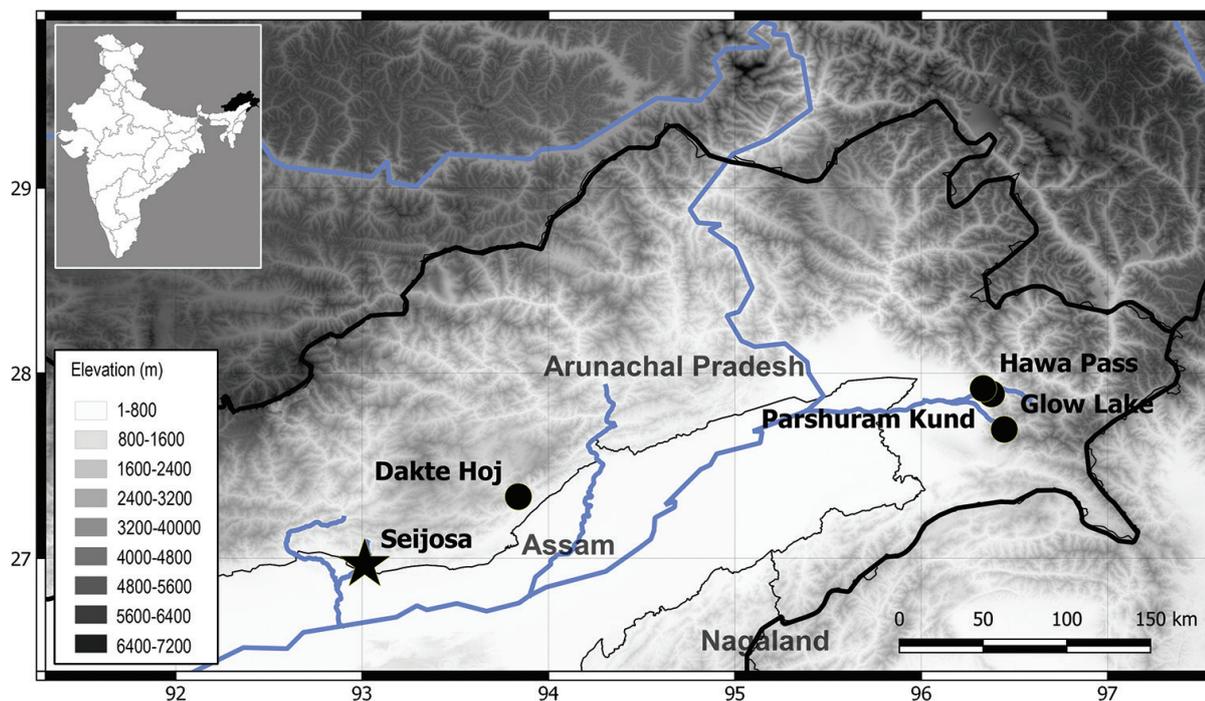


Figure 5. Map of northeast India showing the distribution of the new species, type locality denoted by the black star and other localities by solid black circles. Inset map shows location of Arunachal Pradesh in India.

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 24 irregular longitudinal rows at mid-body; 57–60 paravertebral tubercles; ventral scales much larger than dorsal scales, smooth, cycloid, imbricate to subimbricate, 37–38 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 chinshields bordering mental, postmentals and infralabials (Fig. 5C). Six pored precloacal scales in a continuous series; no precloacal groove. Three to four rows of enlarged post-precloacal 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. 4); ventral scales larger than dorsal scales, imbricate, median row comprises irregularly enlarged subcaudals in one or two rows; two enlarged postcloacal tubercles at base of tail. Fore and hindlimbs relatively slender; forearm (FL/SVL ratio 0.14) and crus (CL/SVL ratio 0.16) 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: 5-5-5-5-4 (right manus) and 5-6-

5-5-5 (right pes); apical lamellae series on Digits I–V: 11-12-13-10-9 (right manus) and 10-11-14-14-10 (right pes); interdigital webbing absent on manus, rudimentary between Digits I–V of pes; relative length of digits (measurements in mm in parentheses): V (4.4) < I (4.9) < IV (5.1) < III (6.3) < II (6.4) (right manus) and I (5.7) < II (6.1) < V (7.3) < III (7.5) < IV (8.4) (right pes); palmar and plantar scales smooth, rounded; scales on forelimb 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 hindlimbs 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 hindlimb with enlarged, smooth, imbricate scales, a few rows under thigh are slightly larger than those on abdomen (Fig. 4).

Colouration in preservative: Background in a shade of beige with four 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. These blotches merge into alternating dark and light bands on the tail. The limbs bear dark unconnected reticulations. The ventral aspect is off white lacking any mottling.

Variation. The paratypes and non-type specimens match the holotype in most aspects except for details presented here and in Table 1: the number of post cloacal spurs is variable in the species ranging from 2 in most specimens to 2/3 (BNHS 2778), 3/4 (BNHS 2776, NCBS NRC-AA-0006), 3/3 (BNHS 2777); tubercle rows on the first tail segment in the types series ranges from 11–13

Table 1. Meristic and morphometric details of the type series of *Cyrtodactylus arunachalensis* sp. nov. in millimeters.

Specimens number	BNHS 2775 Holotype	BNHS 2776 Paratype	BNHS 2777 Paratype	NCBS NRC-AA-0006	NCBS NRC-AA-0007
				Paratype	Paratype
Sex	male	female	male	male	male
SVL (snout to vent length)	71.58	74.92	68.78	64.87	64.93
Ax-Gr length	33.24	31.05	29.48	27.38	25.26
BW (Body width)	11.63	16.10	13.74	10.56	12.17
CL (from base of heel to knee)	11.42	13.12	11.51	11.10	11.19
TL (tail length)	61.85	76.10	22.10	69.52	–
TW (tail width)	5.01	5.26	6.97	5.23	–
Snout length	7.86	7.91	7.74	7.83	8.62
HL (head length)	18.10	18.10	17.81	16.10	16.86
HW (Head width)	13.78	12.83	12.68	11.42	10.66
HH (head height)	7.34	7.30	7.43	7.24	7.08
FL (base of palm to elbow)	10.29	7.99	10.32	8.85	10.06
OD (eye diameter)	4.02	4.84	5.19	5.76	4.75
NE (nose to eye)	5.83	5.44	5.73	3.45	6.00
SE (snout to eye)	8.06	8.73	7.83	7.35	7.99
EE (eye to ear)	5.98	6.24	6.05	5.44	5.46
EL (ear diameter)	2.26	2.47	1.86	1.46	1.84
IN (inter narial(nose) distance)	3.31	3.17	3.55	3.59	3.37
IO (inter-orbital/eyes)	6.48	7.63	7.65	6.67	7.09
Lamellae Right manus	5(11)-6(12)-5(13)-5(10)- 5(9)	4(9)-5(10)-6(14)-6(13)- 5(12)	4(9)-5(10)-5(14)-6(14)- 5(11)	6(8)-5(10)-5(12)-6(14)- 6(11)	4(8)-5(9)-5(13)-6(14)- 5(10)
Lamellae Right pes	3(10)-4(11)-6(14)-8(14)- 6(10)	3(10)-5(13)-8(14)-8(15)- 6(13)	4(10)-5(11)-5(14)-8(12)- 5(12)	4(10)-7(12)-6(14)-8(15)- 6(13)	4(10)-5(11)-7(14)-5(12)- 4(10)
Supralabials Left/Right	10/11	11/11	9/8	9/11	10/9
Infralabials Left/Right	8/9	9/9	10/10	9/10	8/9
Pores	6	–	8	7	10

Table 2. Meristic and morphometric details of the non-type specimens of *Cyrtodactylus arunachalensis* sp. nov. in millimeters.

Specimens number	NCBS NRC-AA-0008	NCBS NRC-AA-0009	BNHS 2778	BNHS 2779
	Sex	male	male	female
SVL (snout to vent length)	69.18	83.52	73.31	81.73
Ax-Gr length	32.17	38.59	32.39	32.45
BW (Body width)	11.04	18.18	13.23	17.15
CL (from base of heel to knee)	10.41	13.06	13.02	15.83
TL (tail length)	79.90	55.80	63.49	50.04
TW (tail width)	5.58	6.10	5.90	6.68
Snout length	8.80	9.10	8.20	9.9
HL (head length)	17.93	9.32	18.11	20.42
HW (Head width)	11.43	19.70	10.25	13.55
HH (head height)	6.68	14.56	7.92	9.44
FL (base of palm to elbow)	10.85	13.22	13.36	11.75
OD (eye diameter)	4.66	4.32	5.35	4.54
NE (nose to eye)	6.99	6.83	16.91	6.98
SE (snout to eye)	8.95	8.96	8.31	10.02
EE (eye to ear)	5.77	6.12	6.11	6.02
EL (ear diameter)	1.44	1.93	2.14	1.94
IN (inter narial(nose) distance)	2.56	4.12	3.27	3.56
IO (inter-orbital/eyes)	8.79	8.01	7.98	9.8
Lamellae				
L manus	5(10)-6(11)-5(12)-5(8)-5(9)	5(10)-4(10)-5(12)-5(13)-5(12)	4(10)-6(11)-5(12)-4(10)-6(17)	5(110)-5(11)-7(14)-6(14)-5(12)
R manus	5(8)-5(9)-5(13)-6(13)-5(10)	5(10)-5(10)-6(13)-5(12)-4(12)	5(9)-5(11)-5(9)-5(11)-5(9)	6(10)-5(13)-6(15)-6(15)-4(12)
Left pes	4(9)-5(9)-6(12)-8(10)-6(12)	3(8)-5(12)-6(14)-7(14)-5(13)	5(9)-5(11)-5(12)-7(11)-4(14)	5(11)-5(12)-6(16)-8(15)-6(14)
Right pes	4(9)-5(10)-6(14)-5(10)-5(11)	3(9)-5(12)-6(14)-7(14)-6(11)	4(9)-5(12)-7(12)-7(13)-4(10)	4(10)-5(12)-6(15)-8(15)-6(14)
Supralabials Left/Right	9/9	8/10	9/8	8/9
Infralabials Left/Right	8/9	10/10	10/10	10/10
Pores	9	8	8	–

however, NCBS NRC-AA-0008–NRC-AA-0009 & BNHS 2778 bear 15–16 tubercles rows. BNHS 2777 has 8 pre-cloacal pores, NCBS NRC-AA-0006 has 7, whereas NCBS NRC-AA-0007 has 10 pores. The coloration in the species is quite variable (Fig. 4).

Natural history notes. All the specimens of the new species were collected from near culverts along roads just after dusk. Other than the concrete culverts, individuals

were also observed on tree trunks, low branches, broad-leaved shrubs and rocky cliffs. The species was found in sympatry with *Hemidactylus* cf. *malcolmsmithi*, *H.* cf. *frenatus* and *H. platyurus*. The species appears to be distributed across the state and confirmed localities where it exists are Pakke Tiger Reserve, Papum Pare district and Kamlang Wildlife Sanctuary with recorded elevation ranging from 170 to 1400 m (Fig. 5).

2014) leading to underestimating the diversity within the genus. Current attempts made by researchers in the recent past have led to formal description of many of the populations from across northeast India (Agarwal et al. 2018a, b; Purkayastha et al. 2020) and also present a comprehensive phylogeny which can serve as the backbone for further research on the diversity and biogeography of the genus *Cyrtodactylus*.

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All DNA sequences generated in the current study have been deposited with NCBI.

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Appendix 1

Details of accession numbers for sequences generated in the present study:

BNHS 2777 “MT341522”

NCBS NRC-AA-0008 “MT341523”

NCBS NRC-AA-0009 “MT341524”

BNHS 2778 “MT341525”

BNHS 2775 “MT341526”

Supplementary material 1

Un-corrected pairwise sequence divergence (p-distance) for selected *Cyrtodactylus* for the mitochondrial *ND2* gene

Authors: Zeeshan A. Mirza, Harshal Bhosale, Faizan Ansari, Pushkar Phansalkar, Mandar Sawant, Gaurang Gowande, Harshil Patel

Data type: COL

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Link: <https://doi.org/10.3897/evolsyst.5.61667.suppl1>

Supplementary material 2

Details of accession numbers for sequences used in the present study from Grismer et al. (2020).

Authors: Zeeshan A. Mirza, Harshal Bhosale, Faizan Ansari, Pushkar Phansalkar, Mandar Sawant, Gaurang Gowande, Harshil Patel

Data type: GenBank accession numbers

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Link: <https://doi.org/10.3897/evolsyst.5.61667.suppl2>

Supplementary material 3

ML phylogeny of selected members of the genus *Cyrtodactylus*

Authors: Zeeshan A. Mirza, Harshal Bhosale, Faizan Ansari, Pushkar Phansalkar, Mandar Sawant, Gaurang Gowande, Harshil Patel

Data type: ML phylogeny

Explanation note: ML phylogeny of selected members of the genus *Cyrtodactylus* based on partial sequences of mitochondrial *ND2* gene generated through 1000 non-parametric bootstrap pseudoreplicates under the GTR+F+I+G4 model of sequence evolution. Numbers at nodes represent ML bootstrap support.

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