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A new micro-endemic species of *Cyrtodactylus* Gray, 1827 (Squamata: Gekkonidae) from the lowlands of Northeast India, with additional morphological notes on *Cyrtodactylus khasiensis* Jerdon, 1870 based on topotypical specimens from Meghalaya, India

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Abstract. We provide additional morphological notes on *Cyrtodactylus khasiensis* Jerdon, 1870 sensu stricto based on topotypical specimens from Meghalaya, northeast India, thereby clarifying its diagnostic morphological traits and extending its distribution further westwards based on molecular data. In addition, based on an integrative systematic approach, we describe a new species of bent-toed gecko namely *Cyrtodactylus jayadityai* sp. nov. from the lowlands of North Tripura, northeast India. Genetically, the new species is a member of the '*C. khasiensis*' group and is a strongly supported sister to *C. tripuraensis* Agarwal, Mahony, Giri, Chaitanya & Bauer, 2018 from which it differs by a pairwise genetic distance of 4.7–5.2% in the mitochondrial ND2 gene. The investigation of morphological characters such as the precloacal-femoral pores in males and pre-cloacal pits in females further supports the distinctiveness of the new species and morphologically differentiates it from its congeners. This increases the number of *Cyrtodactylus* Gray, 1827 in northeast India to 31 species, underscoring the importance of the region as a hotspot for herpetofaunal research and conservation. At present, based on the current population status and distribution, we propose that the new species should be considered as Data Deficient (DD) under the IUCN Red List criteria.

Keywords. Systematics, mitochondrial gene, ND2, lizard, sister species.

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Introduction

The genus *Cyrtodactylus* Gray, 1827, belonging to the family Gekkonidae and commonly referred to as bent-toed geckos, represents one of the most species-rich lineages of vertebrates in the world, as it currently stands as the third most speciose vertebrate genus with more than 350 described species to date (Grismer *et al.* 2021; Uetz *et al.* 2025). The members of this genus are broadly distributed from South Asia through Southeast Asia to Melanesia, characterized by a remarkable ecological adaptability (Grismer *et al.* 2021) and diverse morphological features, many of which are tied to localized ranges and micro-endemism, making them one of the topics of great interest in reptilian systematics and evolution.

India is home to a significantly high number of *Cyrtodactylus* species, particularly across the Himalayas and northeastern India, the latter constituting a major portion of the Indo-Burma biodiversity hotspot. The Myanmarese radiation of *Cyrtodactylus*, which has been recognized as a principal component of the Indo-Burma radiation, was first identified by Wood *et al.* 2012 and currently expands into three major groups named the *fasciolatus*, *khasiensis* and *peguensis* groups (Grismer *et al.* 2021). At the turn of the 21st century, only ten species were described from this region but the improvement in molecular and systematic approaches have raised this number to more than 55 species within the Indo-Burma radiation. These lineages span a broad elevational range from below 50 m to approximately 1600 m a.s.l., with distributions extending from the Western Himalaya and northeastern India, through adjacent parts of Tibet, to areas of Myanmar east of the Salween River (Grismer *et al.* 2021; Uetz *et al.* 2025).

The *C. khasiensis* group sensu Grismer *et al.* (2021) diversified in a region located at the south of the Brahmaputra River approximately 28 Ma, with only three lineages distributed north of the river towards the Himalayan foothills (Agarwal *et al.* 2018b; Mirza *et al.* 2021; Grismer *et al.* 2022; Bhattarai *et al.* 2025). Furthermore, this group has recently gained significant research interest, particularly as the nominal species *C. khasiensis* formerly possessed a complex taxonomic history. This longstanding confusion was resolved by Agarwal *et al.* (2018a), who taxonomically stabilized the species using molecular data and clarified its status as an endemic taxon restricted to the Khasi Hills of Meghalaya. Since then, utilizing an integrative systematic approach, combining morphological characters and molecular phylogenetic analysis (mostly using mitochondrial ND2 gene), have allowed to describe within the past five years over two dozen new species predominantly belonging to the *khasiensis* group from the northeastern states of Assam, Arunachal Pradesh, Meghalaya, Nagaland and Mizoram (Agarwal *et al.* 2018a, 2018b; Purkayastha *et al.* 2020, 2021, 2022; Mahony & Kamei 2022; Mirza *et al.* 2021, 2022; Kamei & Mahony 2021; Bohra *et al.* 2022; Lalremsanga *et al.* 2022, 2023; Boruah *et al.* 2024; Bharali *et al.* 2025). Recently, on the basis of monophyly, Boruah *et al.* (2024), in agreement with Mahony and Kamei (2022), suggested splitting the broader '*khasiensis*' group into four nominal clades named the *khasiensis* clade, the *gansi* clade, the *mombergi* clade and the *cayuensis* clade (formerly the *arunachalensis* clade). Again, Bhattarai *et al.* (2025), in agreement with Agarwal *et al.* (2018b), proposed that the *khasiensis* clade can be subdivided into two principal assemblages, corresponding to lowland and highland subclades. In the present work, we adopt the cladistic partitioning outlined by Grismer *et al.* (2021). As a result, all the nominal *Cyrtodactylus* species from northeast India, except *C. kamengensis* (member of the *peguensis* group), are regarded as members of the broader '*khasiensis*' group sensu Grismer *et al.* 2021.

In this paper, we formally describe a new species of *Cyrtodactylus* from the lowlands of North Tripura following morphological, statistical and molecular phylogenetic analyses, increasing the number of *Cyrtodactylus* species in Tripura, northeast India, to three species. We also provide additional notes on the morphology of *C. khasiensis* based on topotypical specimens from Meghalaya and confirm its presence further westwards from its currently known locality (Sohra, East Khasi Hills District) towards South-West Khasi Hills District, Meghalaya close to India-Bangladesh border based on molecular data.

Material and methods

The study is a part of our ongoing initiative to document the biodiversity of Tripura and Meghalaya states of northeast India. A single adult specimen of *Cyrtodactylus tripuraensis* (MZMU 3796) and five adult specimens of *Cyrtodactylus* sp. (MZMU 3791, MZMU 3792, MZMU 3793, MZMU 3794 and MZMU 3795) were collected from the lowland forests of Gumti, Gomati District (23.42661° N, 91.81937° E) and Chamtilla Village, North Tripura District (24.2857070° N, 92.1758059° E; Fig. 1) respectively, between August 2024 and September 2025 after obtaining a permission for collection within Tripura State from the Chief Wildlife Warden of Environment, Forests and Climate Change Department, Government of Tripura [No.F.24 (12–19)/BD/For TBB]. Four adult specimens of *Cyrtodactylus khasiensis* sensu stricto bearing tag numbers MZMU 3797 (from Sohra, East Khasi Hills District; 25°15′2.48″ N, 91°41′52.86″ E), MZMU 3798 (from Umdohlun, South West Khasi Hills District; 25°21′58.67″ N, 91°16′11.43″ E), ADBU/GT/1 (from Sohra, East Khasi Hills District; 25°15′2.48″ N, 91°41′52.86″ E) and ADBU/GT/2 (from Sohra, East Khasi Hills District; 25°15′2.94″ N, 91°41′51.66″ E) were collected from the Khasi Hills of Meghalaya (Fig. 1) between April 2024 and September 2025. The collection was done after obtaining a permission for collection within Meghalaya State from the Chief Wildlife Warden of Environment, Forests and Climate Change Department, Government of Meghalaya (FOR.7/2021/216). Determination of sex was done based on the presence or absence of the pre-cloacal pores and the hemipenile bulge. After collection, the samples were euthanized using Lignocaine 2% and fixed as well as preserved in 95% ethanol. Specimens are deposited in the Departmental Museum of Zoology, Mizoram University (MZMU) India, and the Department of Zoology, Assam Don Bosco University (ADBU) India. A small portion of liver tissue was excised from the specimens and preserved in 100% ethanol for molecular analysis, prior to fixation. All measurements were recorded in mm with a Mitutoyo digital caliper to the nearest of 0.1 mm. Measurements were usually made on the right side of the specimens unless otherwise stated.

The following measurements and meristics were recorded, and abbreviations and terminology are as follows: BW = maximum body width; CL = crus length; DTR = dorsal tubercle rows (counted transversely across the trunk at midbody); EL = maximum ear length; ES = distance from the anterior border of the ear to the snout tip; FL = forearm length; HD = maximum head depth; HL = head length from the snout tip to the retroarticular process of the jaw; HW = maximum head width; IL = total infralabials; IN = internarial distance (distance between two nasal openings); IO = minimum interorbital distance between left and right supraciliary rows; JW = jaw width taken ventrally at the retroarticular process of the jaw; ML = Maximum mental length; MVSR = mid-ventral scale rows (counted between ventrolateral folds); MW = Maximum mental width; NO = distance between the posterior edge of the nostril and the anterior orbital border; OD = orbit diameter taken horizontally between the external eyeball borders; OE = distance between posterior orbital border and the anterior border of the ear; PcFP = precloacofemoral pores, a continuous series of pore-bearing scales that extends from the precloacal region onto the thighs; PcP = precloacal pores, a continuous series of pore-bearing scales on the precloacal region ventrally which never extend towards the thighs; PMIL = maximum length of inner postmental; PMIIL = maximum length of outer postmental; digits were measured from the proximal apex with the neighbouring digit to the tip (excluding the claw), and numbered from inner (1) to outer (5) as follows: on manus, F1, F2, F3, F4, F5; on pes, T1, T2, T3, T4, T5; PVT1 = paravertebral tubercles, counted from the most anterior tubercle on the occiput to the mid-sacrum; PVT2 = paravertebral tubercles on the trunk only, counted between the level of the axilla and the level of the groin; RL = maximum rostral length; RW = maximum rostral width; SL = total supralabials; SO = distance between the snout tip and the anterior orbital border; SVL = snout to vent length; TD = tail depth taken at first tail segment; TL = tail length; TRL = trunk length; TW = tail width taken at first tail segment. Two separate series for subdigital lamellae were counted on all digits of the right manus and right pes: a basal series, which includes scales of a width at least twice the diameter of the 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 or nonlamellar scales between the basal and apical lamellae series (counted separately), abbreviated as follows: on manus, F1L, F2L, F3L, F4L, F5L; on pes, T1L, T2L, T3L, T4L, T5L.

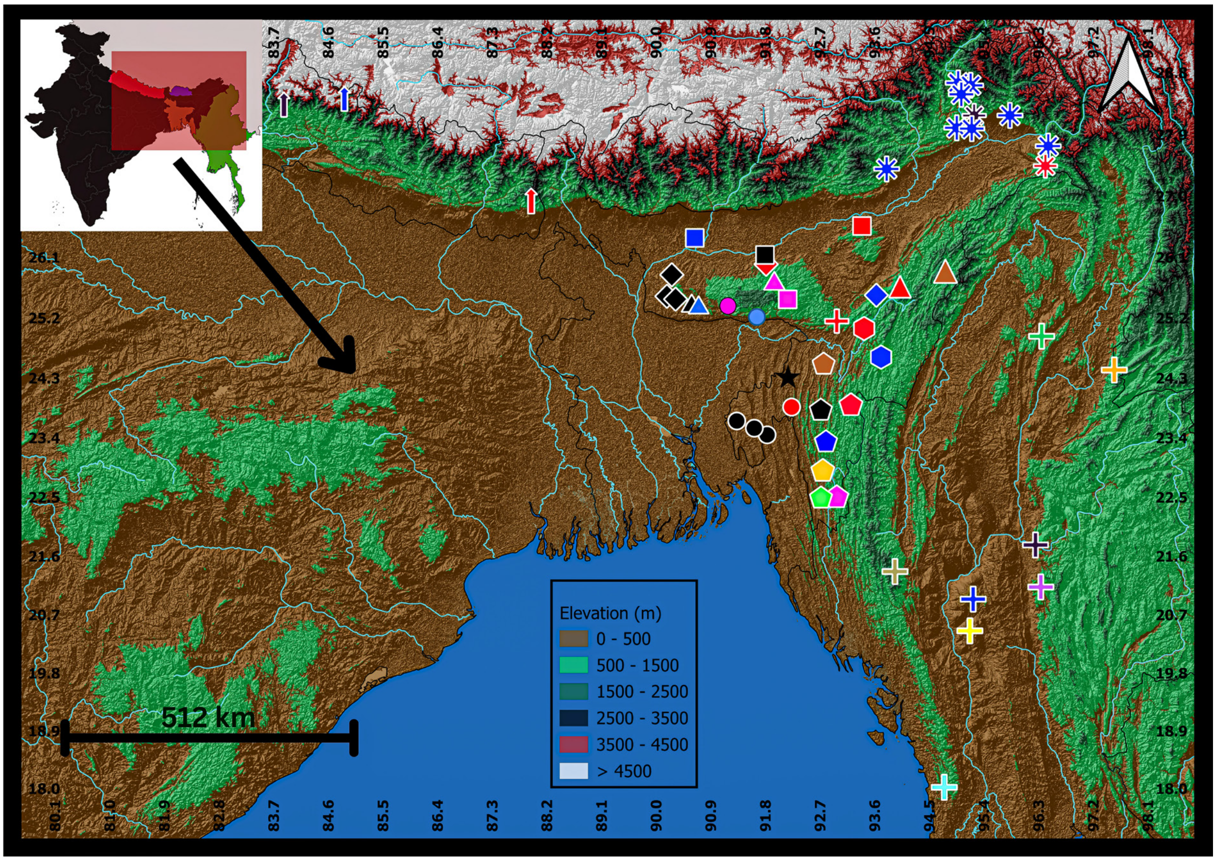

Fig. 1. Distribution of the species of the '*Cyrtodactylus khasiensis* clade' within the Indo-Burma and Himalayan belts. *C. jayadityai* sp. nov. (black star), *C. tripuraensis* (black circles), *C. montanus* (red circle), *C. aaronbaueri* (black pentagon), *C. bengkhuaiai* (blue pentagon), *C. siahaensis* (pink pentagon), *C. lungleiensis* (yellow pentagon), *C. ngopensis* (red pentagon), *C. vairengtensis* (maroon pentagon), *C. ngengpuiensis* (light green pentagon), *C. khasiensis* (blue circle and pink circle), *C. guwahatiensis* (black square), *C. kazirangaensis* (red square), *C. septentrionalis* (blue square), *C. jaintiaensis* (pink square), *C. nagalandensis* (red triangle), *C. urbanus* (red diamond), *C. bapme* (black diamonds), *C. karsticola* (blue triangle), *C. agarwali* (black triangle), *C. exercitus* (pink triangle), *C. namtiram* (red hexagon), *C. kiphire* (maroon triangle), *C. barailensis* (blue diamond), *C. manipurensis* (blue hexagon), *C. namdaphaensis* (red asterisks), *C. siangensis* (black asterisk), *C. vanarakshaka* (red cross), *C. martinstolli* (red arrow), *C. annapurnaensis* (black arrow), *C. karanshahi* (blue arrow), *C. cayuensis* (blue asterisks), *C. aunglini* (blue cross), *C. myaleiktaung* (black cross), *C. chrysopylos* (purple cross), *C. gansi* (brown cross), *C. mombergi* (green cross), *C. diaxiensis* (orange cross) and *C. ayeyarwadyensis* (light and bright sky blue cross).

The specimens were compared morphologically with all known species within the '*khasiensis* group' (Grismer *et al.* 2021) and other species from Northeast India and surrounding countries. Comparisons were made through examination of type as well as topotypical specimens (Appendix I and II), literature containing original descriptions and literature reviewing a species based on type specimens (e.g., Darevsky *et al.* 1998; Bauer 2003; Li 2007; Mahony 2009; Agarwal *et al.* 2018a, 2018b; Purkayastha *et al.* 2020, 2021; Mirza *et al.* 2021, 2022; Kamei & Mahony 2021; Bohra *et al.* 2022; Mahony & Kamei 2022; Lalremsanga *et al.* 2023; Boruah *et al.* 2024; Bhattarai *et al.* 2025; Bharali *et al.* 2025).

Molecular data

For this study, a single specimen of *Cyrtodactylus* sp. (GenBank no. PX425601) collected from Chamtilla Village, North Tripura District, Tripura, and another specimen of *Cyrtodactylus khasiensis* (GenBank no. PX425600) from Umdohlun, South West Khasi Hills District, Meghalaya, was sequenced. Genomic DNA was extracted from liver tissue preserved in ethanol (100%), using Tissue Kit (Qiagen) following manufacturer's instructions. A partial sequence of the mitochondrial NADH dehydrogenase subunit 2 (ND2) gene (1050 base pairs) was generated using the primer pair MetF1 and H5934 (Macey *et al.* 1997). Sequence chromatograms were quality checked, edited and assembled into contigs using Chromas and Sequence Scanner ver. 1.0 (Applied Biosystems). Comparative ND2 sequences comprising Indo-Burma clade members of *Cyrtodactylus* were obtained from GenBank (following Purkayastha *et al.* 2021; Kamei & Mahony 2021; Bohra *et al.* 2022; Lalremsanga *et al.* 2022; Mahony & Kamei 2022; Lalremsanga *et al.* 2023; Table 1). Sequence alignment was done using CLUSTALW (Thompson *et al.* 2002) in MEGA7 (Tamura & Nei 1993; Kumar *et al.* 2016) with default parameter settings followed by translation of mtDNA sequences to amino acids to verify no erroneous pre-mature stop codons were present. The best substitution model for the dataset was searched through Modelfinder (Kalyaanamoorthy *et al.* 2017) which identified TIM2+F+I+G4 for all the three codon positions. A partitioned ML phylogeny were reconstructed using the IQ-TREE option, ML analysis was run with an ultrafast bootstrap option for 10 000 replicates and 1000 iterations to assess clade support (Minh *et al.* 2013, Nguyen *et al.* 2015) implemented in the Phylosuite (Xiang *et al.* 2023). A sequence of *Cyrtodactylus condorensis* (KT013196) from GenBank was used as an outgroup before visualizing the final tree in FigTree (ver. 1.4.4). An ultrafast bootstrap value ranging from 95–100 represents a very strongly supported node. The uncorrected pairwise (p) genetic distance was calculated in MEGA 12 (Kumar *et al.* 2016) with pairwise deletion of missing data and gaps.

Statistical analysis

The newly obtained meristic variables of the new population were combined with raw morphological data of *C. tripuraensis* gathered from Agarwal *et al.* (2018a). The morphometric data were subjected to allometric adjustment using the equation: $X_{adj} = \log(X) - b[\log(BL) - \log(BL_{mean})]$; where Xadj = size corrected variable; X = unadjusted trait variable; b = regression coefficient; BL = standard measurement of body length/size (e.g., SVL); BLmean = the grand mean of all BLs (Thorpe 1975). The allometry adjusted morphometric data are provided in Supp. file 1. For meristic data, no adjustment/standardization was performed, and the raw data were utilized for statistical analyses. The combined dataset (sex pooled) that comprises raw meristic and allometry adjusted morphometric data was subjected to one-way analysis of variance (ANOVA), in order to discriminate the characters that differ between the new population and *C. tripuraensis*. A brown-Forsythe test was utilized as the alternative tests for the characters that violated the ANOVA assumptions. The sexually dimorphic characters such as PcP/PcFP were excluded in the statistical analyses and those individuals with missing characters were automatically excluded by the PCA. The statistically significant variables between the new population and *C. tripuraensis* were subsequently utilized for performing the concatenated Principal Component Analysis (PCA) of the raw meristic and allometry adjusted morphometric data to determine the clustering of the new specimens.

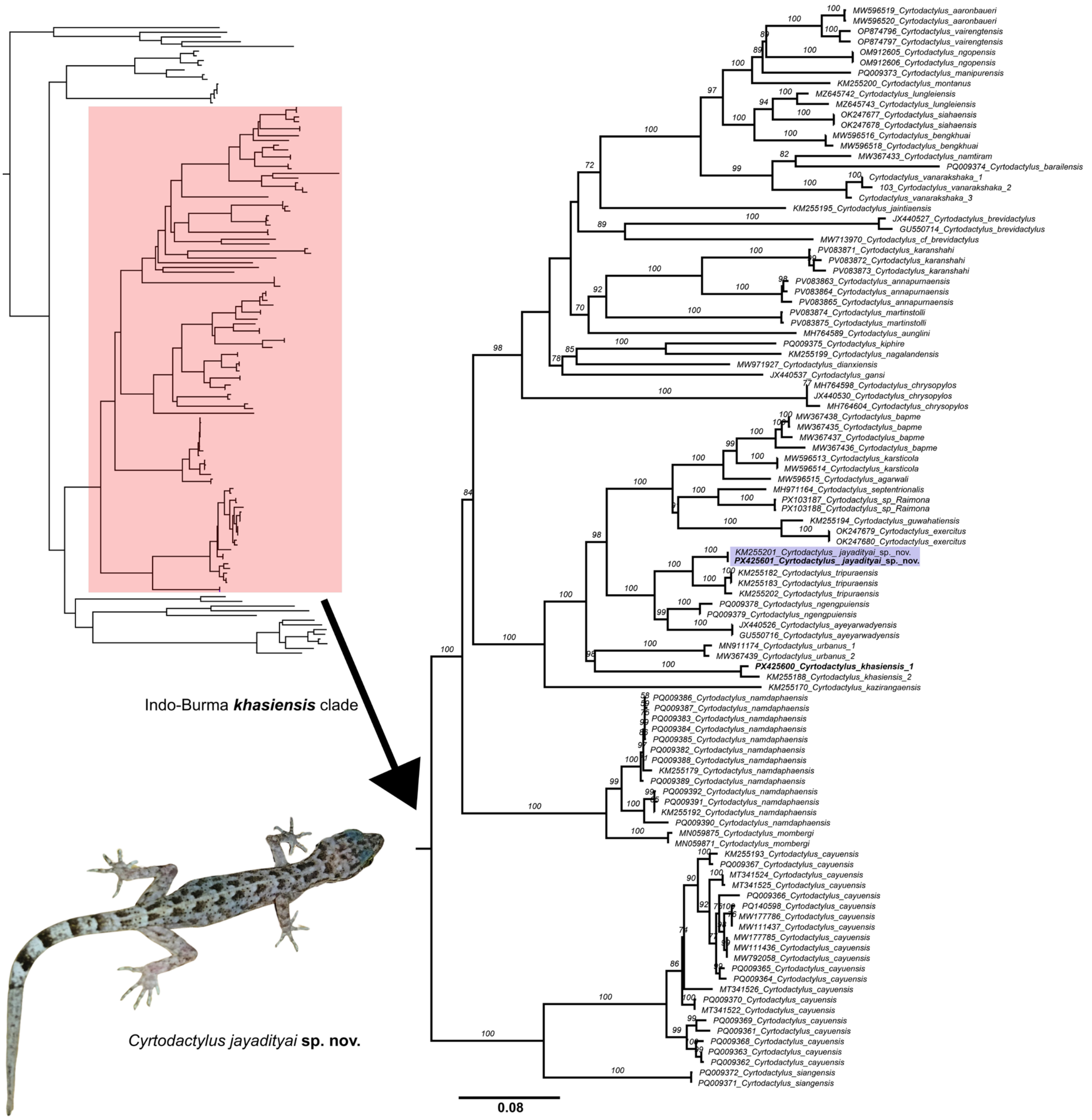

Fig. 2. Maximum-likelihood phylogeny showing the evolutionary relationships among the members of the ‘*Cyrtodactylus khasiensis*’ clade/group, based on the mitochondrial ND2 gene. *Cyrtodactylus jayadityai* sp. nov. is highlighted in blue and sequences obtained in this study are highlighted in bold. Values in the node represent ultrafast bootstrap support and preceding the species name is the GenBank accession number.

Table 1 (continued on next three pages). List of mitochondrial ND2 gene sequences used in this study (new sequences are highlighted in bold).

Species name	Voucher number	Accession number	Locality
Cyrtodactylus aaronbaueri	MZMU2020	MW596519	Tamdil National Wetland, Mizoram, India
Cyrtodactylus aaronbaueri	MZMU2015	MW596520	Durtlang, North Mizoram, India
Cyrtodactylus agarwali	MZMU2158	MW596515	Siju, South Garo Hills, Meghalaya, India
Cyrtodactylus annapurnaensis	NHM 2023/367	PV083863	Gandaki Province, Kaski District, Lwang, Nepal
Cyrtodactylus annapurnaensis	NHM 2023/368	PV083864	Gandaki Province, Kaski District, Lwang, Nepal
Cyrtodactylus annapurnaensis	NHM 2023/369	PV083865	Gandaki Province, Kaski District, Lwang, Nepal
Cyrtodactylus agarwali	MZMU2158	MW596515	Siju, South Garo Hills, Meghalaya, India
Cyrtodactylus aunglini	LSUHC 13948	MH764589	Pyin Oo Lwin District, Mandalay Region, Myanmar
Cyrtodactylus ayeyarwadyensis	CAS: 222812	GU550716	Myaung Mya Township, Ayeyarwady Division, Myanmar
Cyrtodactylus ayeyarwadyensis	CAS: 212459	JX440526	Mwe Hauk Village, Ayeyarwady Division, Myanmar
Cyrtodactylus bapme	BNHS2752	MW367437	Meghalaya State, East Garo Hills Dist., Daribokgre Hamlet, India
Cyrtodactylus bapme	BNHS2754	MW367438	Meghalaya State, West Garo Hills Dist., Jangrapara Village, India
Cyrtodactylus bapme	BNHS2755	MW367436	Meghalaya State, West Garo Hills Dist., Tura Peak, India
Cyrtodactylus bapme	BNHS2756	MW367435	Meghalaya State, East Garo Hills Dist., Daribokgre Hamlet, India
Cyrtodactylus bengkhuaiai	MZMU1985	MW596516	Sailam Community Reserved Forest, Mizoram, India
Cyrtodactylus bengkhuaiai	MZMU1986	MW596518	Sailam Community Reserved Forest, Mizoram, India
Cyrtodactylus brevidactylus	CAS214104	JX440527	Mandalay Division: Popa Mountain Park, Kyauk Pan Tawn Township, Myanmar
Cyrtodactylus brevidactylus	CAS214105	GU550714	Popa Mountain Park, Mandalay Division, Myanmar
Cyrtodactylus chrysopylos	CAS 22641	JX440530	Ywnagan Township, Taunggyi District, Shan State, Myanmar
Cyrtodactylus chrysopylos	LSUHC 13965	MH764598	Ywnagan Township, Taunggyi District, Shan State, Myanmar
Cyrtodactylus chrysopylos	LSUHC 13937	MH764604	Ywnagan Township, Shan State, Myanmar
Cyrtodactylus dianxiensis	KIZ059201	MW971927	Yunnan, China
Cyrtodactylus exercitus	MZMU2545	OK247680	Umroi, Meghalaya, India
Cyrtodactylus exercitus	MZMU2542	OK247679	Umroi, Meghalaya, India
Cyrtodactylus gansi	CAS 222412	JX440537	Chin State, Min Dat Township. Myanmar

Table 1 (continued). List of mitochondrial ND2 gene sequences used in this study (new sequences are highlighted in bold).

Species name	Voucher number	Accession number	Locality
Cyrtodactylus guwahatiensis	BNHS 2146	KM255194	Assam State, Kamrup Metropolitan Dist., Guwahati, India
Cyrtodactylus jaintiaensis	BNHS 2248	KM255195	Meghalaya State, Jaintia Hills Dist., near Jowai, India
Cyrtodactylus jayadityai sp. nov.	MZMU 3795	**PX425601**	Chamtilla Village, North Tripura district, Tripura, India
Cyrtodactylus jayadityai sp. nov.	BNHS 2230	KM255201	Rowa WLS, North Tripura district, Tripura, India
Cyrtodactylus karanshahi	NHM 2023/371	PV083871	Gandaki Province, Gorkha District, Manaslu Conservation Area, Philim, Nepal
Cyrtodactylus karanshahi	NHM 2023/372	PV083872	Gandaki Province, Gorkha District, Manaslu Conservation Area, Philim, Nepal
Cyrtodactylus karanshahi	NHM 2023/373	PV083873	Gandaki Province, Gorkha District, Manaslu Conservation Area, Philim, Nepal
Cyrtodactylus karsticola	MZMU2153	MW596514	Siju, South Garo hills, Meghalaya, India
Cyrtodactylus karsticola	MZMU2156	MW596513	Siju, South Garo hills, Meghalaya, India
Cyrtodactylus kaziriangaensis	BNHS 2147	KM255170	Golaghat Dist., Assam State, Kohora, India
Cyrtodactylus khasiensis	BNHS 2249	KM255188	Cherrapunjee Resort, East Khasi Hills Dist., Meghalaya State, India
Cyrtodactylus khasiensis	MZMU 3797	**PX425600**	Umdohlun, South West Khasi hills district, Meghalaya, India
Cyrtodactylus lungleiensis	MZMU2428	MZ645742	Lunglei Dist., outskirts of Lunglei town, Mizoram, India
Cyrtodactylus lungleiensis	MZMU2429	MZ645743	Lunglei Dist., outskirts of Lunglei town, Mizoram, India
Cyrtodactylus mombergi	LSUHC_14656	MN059871	Indawgyi Wildlife Sanctuary, Mohnyin Township, Kachin State, Myanmar
Cyrtodactylus mombergi	LSUHC_14734	MN059875	Indawgyi Wildlife Sanctuary, Mohnyin Township, Kachin State, Myanmar
Cyrtodactylus montanus	BNHS 2231	KM255200	Phuldungsei Village, North Tripura Dist., Tripura State, India
Cyrtodactylus nagalandensis	BNHS 2253	KM255199	Nagaland State, Kohima Dist., Khonoma, India
Cyrtodactylus namtiram	BNHS2751	MW367433	Manipur, India
Cyrtodactylus septentrionalis	BNHS 1989	MH971164	Assam State, Bongaigaon Dist., near Abhayapuri, India
Cyrtodactylus siahaensis	MZMU2445	OK247677	Siaha, Mizoram, India
Cyrtodactylus siahaensis	MZMU2446	OK247678	Siaha, Mizoram, India
Cyrtodactylus tripuraensis	BNHS2238	KM255183	Sepahijala district, Tripura, India
Cyrtodactylus tripuraensis	BNHS2236	KM255182	Sepahijala district, Tripura, India
Cyrtodactylus tripuraensis	BNHS2245	KM255202	Gumti, Gomati district, Tripura, India

Table 1 (continued). List of mitochondrial ND2 gene sequences used in this study (new sequences are highlighted in bold).

Species name	**Voucher number**	**Accession number**	**Locality**
Cyrtodactylus urbanus	VR/ERS/ZSI/688	MN911174	Assam, Kamrup (M) District, Guwahati, Basishta Temple, India
Cyrtodactylus urbanus	BNHS 2852	MW367439	Meghalaya State, Ri Bhoi Dist., Saiden, India
Cyrtodactylus vairengtensis	MZMU2905	OP874796	Mizoram, India
Cyrtodactylus vairengtensis	MZMU2904	OP874797	Mizoram, India
Cyrtodactylus barailensis	WII-ADR971	PQ009374	Athibung, Peren District, Nagaland, India
Cyrtodactylus kiphire	WII-ADR963	PQ009375	Forest office colony, Kiphire forest division, Kiphire District, Nagaland, India
Cyrtodactylus cayuensis	CES10/1465	KM255193	Arunachal Pradesh, Changlang District, Glaw Lake, India
Cyrtodactylus cayuensis	WII-ADR697	PQ009370	Potin, Lower Subansiri District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	WII-ADR3016	PQ009367	Glaw Lake, Kamlang Tiger Reserve, Lohit District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	WII-ADR454	PQ009368	Jengging, Upper Siang District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	WII-ADR473	PQ009369	Pasighat, East Siang District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	WII-ADR1218	PQ009361	Balek, East Siang District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	WII-ADR1683	PQ009364	Diffo river, Mehao WLS, Lower Dibang Valley District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	WII-ADR1681	PQ009365	Ezengo, Mehao WLS, Lower Dibang Valley District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	WII-ADR1682	PQ009366	Ezengo, Mehao WLS, Lower Dibang Valley District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	WII-ADR1199	PQ009362	Jengging, Upper Siang District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	WII-ADR1213	PQ009363	Ramsing, Mouling National Park, Upper Siang District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	NCBS NRC-AA-0009	MT341524	Near Parshuram Kund near Kamlang Wildlife Sanctuary, Arunachal Pradesh, India
Cyrtodactylus cayuensis	BNHS 2778	MT341525	Near Parshuram Kund near Kamlang Wildlife Sanctuary, Arunachal Pradesh, India
Cyrtodactylus cayuensis	BNHS 2777	MT341522	Pakke Tiger Reserve, East Kameng District, Arunachal Pradesh, India
Cyrtodactylus cayuensis	KIZYPX1446	MW111437	China
Cyrtodactylus cayuensis	CIB_X_08649	MW177786	China
Cyrtodactylus martinstolli 1	NHM 2023/356	PV083874	Koshi Province, Ilam District, Dobate, Nepal
Cyrtodactylus martinstolli 2	NHM 2023/359	PV083875	Koshi Province, Ilam District, Dobate, Nepal
Cyrtodactylus manipurensis	WII-ADR1596	PQ009373	Lamdan Kabui, Churachandpur District, Manipur, India

Table 1 (continued). List of mitochondrial ND2 gene sequences used in this study (new sequences are highlighted in bold).

Species name	Voucher number	Accession number	Locality
Cyrtodactylus siangensis	WII-ADR1581	PQ009371	Bodak, East Siang District, Arunachal Pradesh, India
Cyrtodactylus siangensis	WII-ADR1582	PQ009372	Bodak, East Siang District, Arunachal Pradesh, India
Cyrtodactylus sp.	ADBU/BB/1	PX103187	Gossaigaon, Kokrajhar district, Assam, India
Cyrtodactylus sp.	ADBU/BB/1	PX103188	Gossaigaon, Kokrajhar district, Assam, India
Cyrtodactylus namdaphaensis	WII-ADR1404	PQ009382	Deban, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR1416	PQ009386	Kamala valley, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR1417	PQ009387	Kamala valley, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR1415	PQ009385	Kamala valley, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR3293	PQ009383	Burma nallah, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR3294	PQ009384	Burma nallah, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR3067	PQ009388	Motijheel, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR3068	PQ009389	Motijheel, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR3060	PQ009390	Sinabrai, Kamlang Tiger Reserve, Lohit District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR3281	PQ009391	Hornbill, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	WII-ADR3282	PQ009392	Hornbill, Namdapha Tiger Reserve, Changlang District, Arunachal Pradesh, India
Cyrtodactylus namdaphaensis	CES13/1459	KM255192	Miao, Changlang Dist., Arunachal Pradesh State, India
Cyrtodactylus namdaphaensis	CES11/1349	KM255179	Arunachal Pradesh State, Changlang Dist., Miao, India
Cyrtodactylus ngengpuiensis	WII-ADR991	PQ009379	Ngengpui Wildlife Sanctuary, Lawngtlai District, Mizoram, India
Cyrtodactylus ngengpuiensis	WII-ADR1057	PQ009378	Ngengpui Wildlife Sanctuary, Lawngtlai District, Mizoram, India
Cyrtodactylus vanarakshaka	MZMU3031	PV554268	Assam, Dima Hasao, Dibarai, India
Cyrtodactylus vanarakshaka	MZMU4036	PV554269	Assam, Dima Hasao, Dibarai, India
Cyrtodactylus vanarakshaka	MZMU4037	PV554270	Assam, Dima Hasao, Dibarai, India

Institutional abbreviations

ADBU = Assam Don Bosco University, Sonapur, Assam, India
BNHS = Bombay Natural History Society, Mumbai, India
BPBM = Bernice Pauahi Bishop Museum, Honolulu, Hawaii, USA
CAS = California Academy of Sciences, San Francisco, USA
CES = Centre for Ecological Sciences, Bangalore, India
CUMZ = Chulalongkorn University Museum of Zoology, Bangkok, Thailand
FMNH = Field Museum of Natural History, Chicago, Illinois, USA
LSUHC = La Sierra University Herpetological Collection, La Sierra University, Riverside, California, USA
MVZ = Museum of Vertebrate Zoology, Berkeley, California, USA
MZMU = Departmental Museum of Zoology, Mizoram University, Aizawl, India
PMNH = Pakistan Museum of Natural History, Islamabad, Islamabad Capital Territory, Pakistan
UPC-NEI = The United Pentecostal Church of North East India, India
VR/ERS/ZSI = National Zoological Collection, North Eastern Regional Centre, Zoological 170 Survey of India, Shillong, India

Results

The ML phylogeny based on 1050 base pairs of the mitochondrial ND2 gene inferred a consistent topological tree revealing a new, distinct population of *Cyrtodactylus* within the monophyletic lineage of *C. khasiensis* group (Fig. 2; Table 2). Genetically, the new population directly forms a sister species of *C. tripuraensis* found in the southern parts of Tripura, with a very high bootstrap support and a pairwise genetic distance of 4.7–5.2% in the mitochondrial ND2 gene, indicating a moderate genetic divergence (Fig. 2; Table 2). Apart from genetics, morphological characters such as the pre-cloacal femoral pores

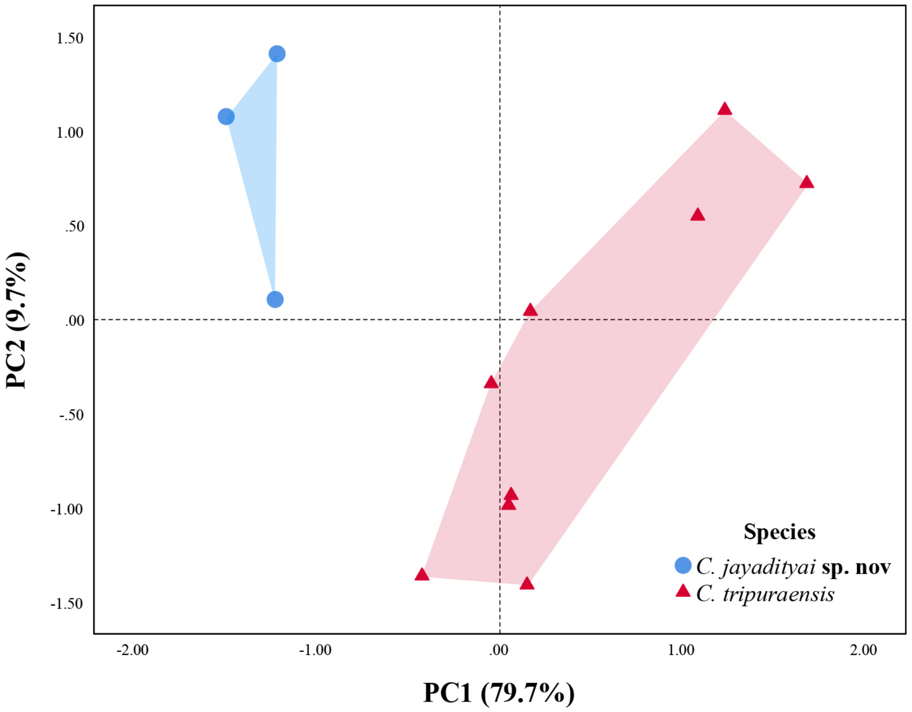

Fig. 3. Scatter plot with the first two PCs in the principal component analysis (PCA) of the morphological data of *Cyrtodactylus jayadityai* sp. nov. and *C. tripuraensis* superimposed by convex hull polygons.

Table 2. Uncorrected pairwise genetic distances between the new species and its closest congeners within the ‘*khasiensis*’ clade.

Sl no	**Species name**	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**
1	*Cyrtodactylus jayadityai* sp. nov.																
2	*Cyrtodactylus jayadityai* sp. nov.	0.000															
3	KM255183 – *Cyrtodactylus tripuraensis*	0.047	0.048														
4	KM255202 – *Cyrtodactylus tripuraensis*	0.048	0.052	0.006													
5	KM255182 – *Cyrtodactylus tripuraensis*	0.049	0.050	0.000	0.008												
6	PQ009379 – *Cyrtodactylus ngengpuiensis*	0.062	0.063	0.043	0.049	0.043											
7	PQ009378 – *Cyrtodactylus ngengpuiensis*	0.076	0.076	0.063	0.069	0.065	0.008										
8	GU550716 – *Cyrtodactylus ayeyarwadyensis*	0.100	0.097	0.079	0.103	0.081	0.049	0.069									
9	JX440526 – *Cyrtodactylus ayeyarwadyensis*	0.100	0.097	0.079	0.102	0.081	0.049	0.070	0.000								
10	MN911174 – *Cyrtodactylus urbanus 1*	0.117	0.140	0.127	0.156	0.129	0.107	0.125	0.153	0.153							
11	MW367439 – *Cyrtodactylus urbanus 2*	0.121	0.141	0.127	0.153	0.129	0.113	0.130	0.154	0.154	0.009						
12	MW367435 – *Cyrtodactylus bapme*	0.137	0.160	0.136	0.170	0.139	0.111	0.122	0.160	0.161	0.172	0.166					
13	MW367438 – *Cyrtodactylus bapme*	0.137	0.160	0.135	0.170	0.137	0.109	0.121	0.164	0.165	0.169	0.164	0.001				
14	MH971164 – *Cyrtodactylus septentrionalis*	0.139	0.157	0.126	0.160	0.128	0.119	0.127	0.164	0.165	0.149	0.145	0.126	0.125			
15	MW367437 – *Cyrtodactylus bapme*	0.141	0.164	0.136	0.173	0.138	0.111	0.126	0.158	0.158	0.174	0.168	0.015	0.013	0.131		
16	*Cyrtodactylus khasiensis* 1	0.145	0.156	0.134	0.160	0.137	0.102	0.133	0.164	0.165	0.149	0.149	0.182	0.180	0.166	0.190	
17	KM255188 – *Cyrtodactylus khasiensis* 2	0.147	0.161	0.139	0.182	0.141	0.110	0.137	0.179	0.179	0.159	0.157	0.195	0.193	0.179	0.198	0.019

(PcFP) as well as the number of poreless scales in the pre-cloacal-femoral region in males and the pitted scales in the pre-cloacal region in females strongly separate the new population from *C. tripuraensis* and other congeners within the *khasiensis* group (Tables 3–4). Furthermore, the differences between the new undescribed population from North Tripura and *C. tripuraensis* are statistically significant in the following variables: SVL ($p<0.01$), TRL ($p<0.01$), BW ($p<0.01$), TL ($p<0.001$), HW ($p<0.001$), HD ($p<0.01$), FL ($p<0.01$), CL ($p<0.01$), NO ($p<0.001$), SO ($p<0.001$), OE ($p<0.01$), IN ($p<0.01$), IO ($p<0.001$), IL(L) ($p<0.01$); as a result, we ordinate these statistically significant variables through a PCA analysis. The first two principal components (PCs) of the PCA explain 87.52% (PC1: 77.07%; PC2: 10.45%) of the variation amongst the new population and *C. tripuraensis*. All the variables used in the PCA are positively loaded with considerable high loadings (>0.8) in PC_1, except TL and IL (L) which are negatively loaded in PC_1 while having more effect on PC_2 (Fig. 3; Supp. file 2 and Supp. file 3). The specimens of these two populations form distinct groups in the morphospace with no overlaps (Fig. 3). We herein describe this isolated new population as *Cyrtodactylus jayadityai* sp. nov. from the lowlands of North Tripura, Northeast India, following morphological, statistical and molecular analyses.

We also provide further comments on the morphological characters of *C. khasiensis* sensu stricto based on topotypical specimens from the East Khasi Hills, Meghalaya, Northeast India. Moreover, one of our specimens of *C. khasiensis* from Umdohlun, South West Khasi Hills District, Meghalaya, is only ~1.9% genetically divergent from the only available ND2 data of *C. khasiensis* (KM255188) to date, which confirms the occurrence of *C. khasiensis* sensu stricto further westwards close to India-Bangladesh border.

Systematics

Phylum Chordata Haeckel, 1874
Class Reptilia Laurenti, 1768
Order Squamata Oppel, 1811
Family Gekkonidae Gray, 1825
Genus *Cyrtodactylus* Gray, 1827

Cyrtodactylus jayadityai sp. nov.
urn:lsid:zoobank.org:pub:9CEB1804-D1FB-4467-9272-82AA78FFD63A
Figs 4–9A; Table 3

Cyrtodactylus tripuraensis (non *C. tripuraensis*) – Agarwal *et al.* 2018a: 346–347, Table 3 (BNHS 2230, adult female) – 351, fig. 9A (BNHS 2230)

Diagnosis

Cyrtodactylus jayadityai sp. nov. (n = 5) is a small to moderately sized bent-toed gecko ranging in SVL from 47.8 mm to 54.9 mm (up to 70.7 mm including BNHS 2230), original TL ranging from 55.7 mm to 57.0 mm, having 9 to 12 supralabials and 9 to 11 infralabials. The dorsal tubercles are usually feebly keeled, bluntly conical and irregularly arranged in 19 to 21 rows (DTR) between the indistinct ventrolateral folds at the midbody; dorsal tubercles are usually four to five times the size of dorsal granular scales; 44 to 50 paravertebral tubercles (PVT1), originating from the most anterior tubercle on the occiput to the mid-sacrum; 30 to 31 paravertebral tubercles (PVT2) between the level of the axilla and the level of the groin and 37 to 43 mid-ventral scale rows (MVSR) between the indistinct ventrolateral folds. Males with a total of 18 to 28 pre-cloacal femoral pores (PcFP) (see 'Variation' section for further details) in two different arrangements: (1) a continuous series of 18 pre-cloacal pores or PcP (9 on each side) with no visible pitted scales (2) a discontinuous series of 22 to 28 pre-cloacal femoral pores or PcFP (11 to 15 PcFP on either side of which 7 to 13 occur continuously separated by 1 to 5 poreless scales from the remaining 2 to 4 pores) with no visible pitted scales; females with 0 to 14 continuous series of

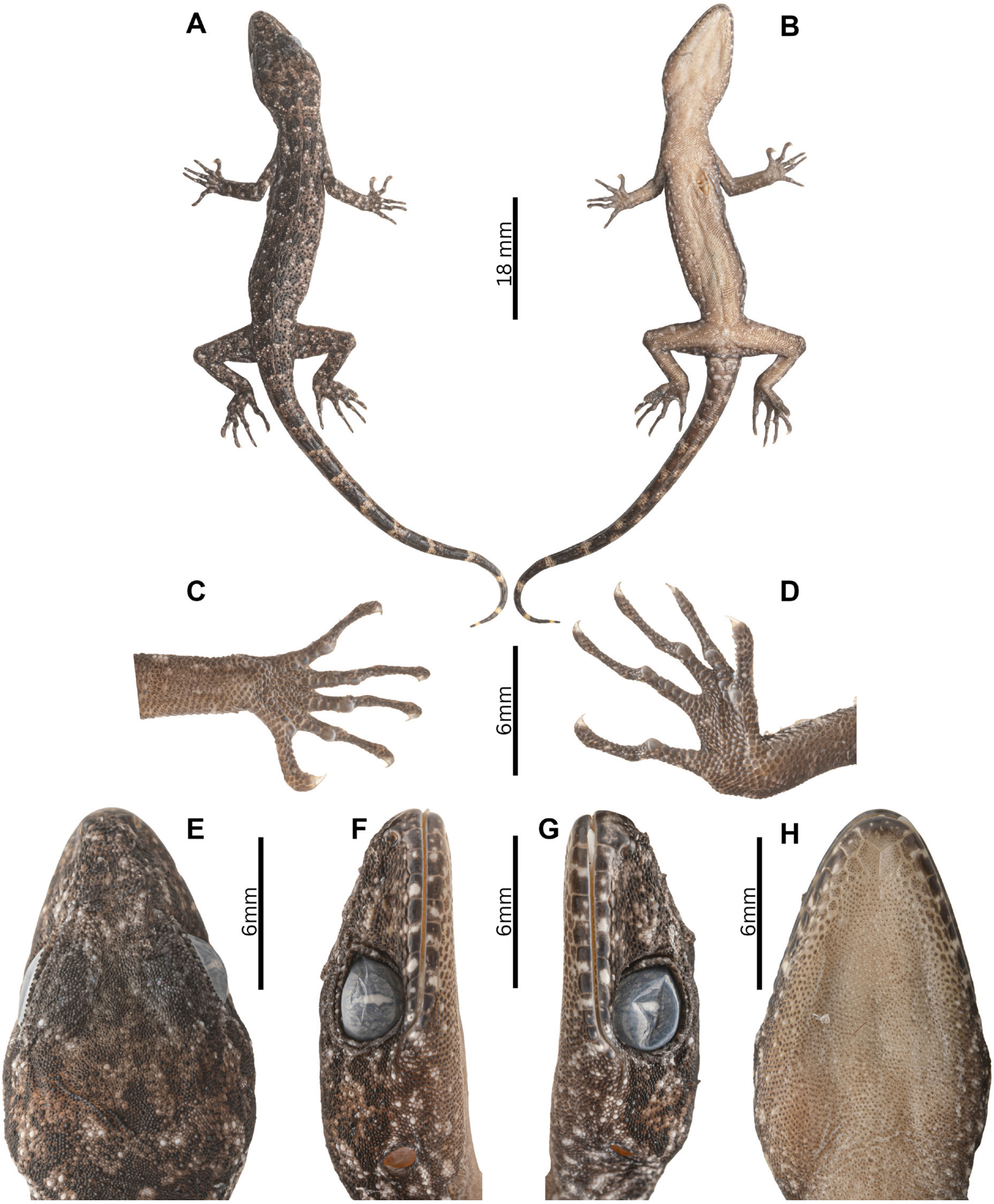

Fig. 4. *Cyrtodactylus jayadityai* sp. nov., holotype, ♂, in preservation (MZMU 3795). **A**. Dorsal view. **B**. Ventral view. **C**. Ventral view of the manus. **D**. Ventral view of the pes. **E**. Dorsal view of the head. **F**–**G**. Lateral views of the head. **H**. Ventral view of the head. Photos by Sanath Chandra Bohra.

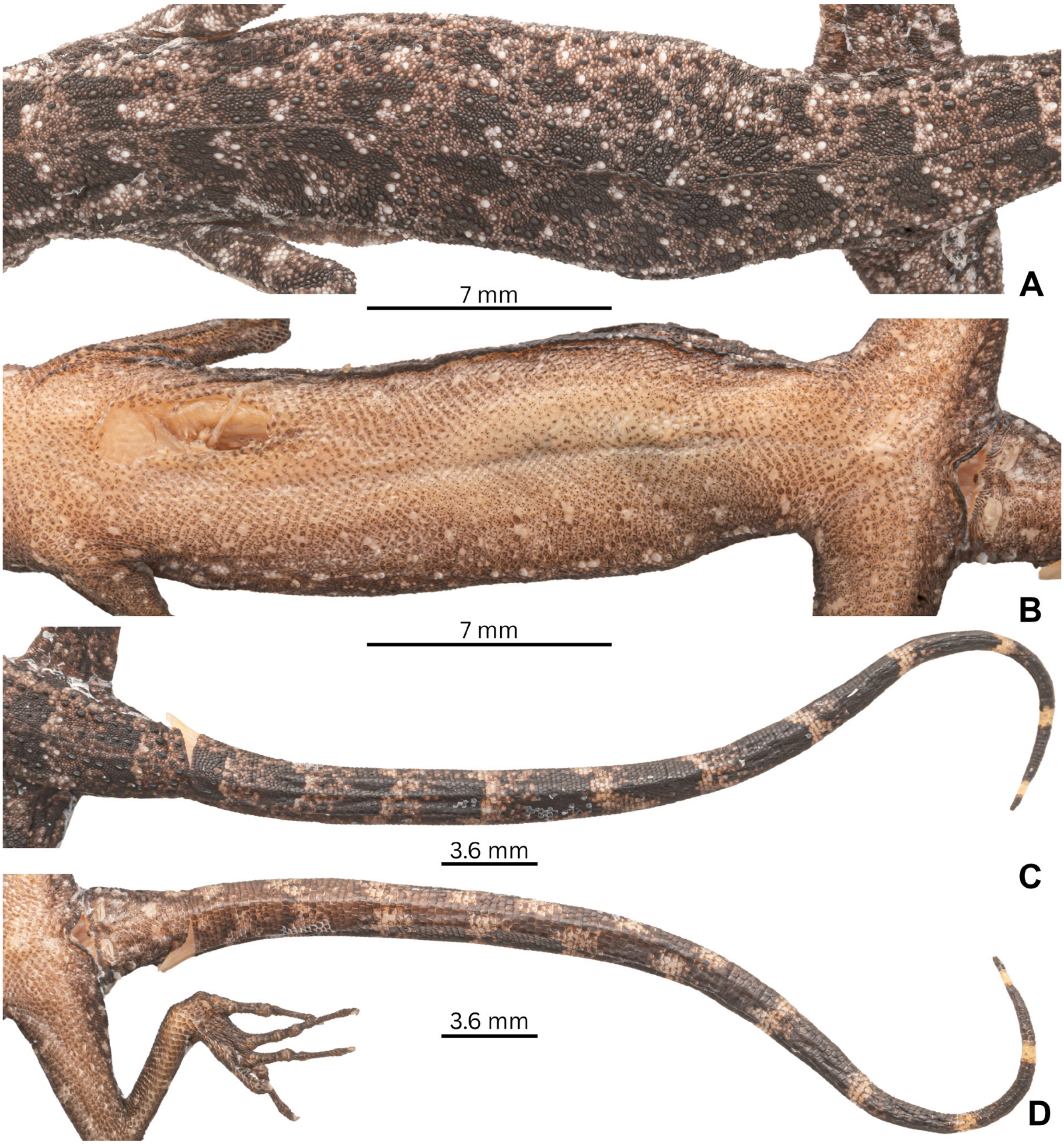

Fig. 5. *Cyrtodactylus jayadityai* sp. nov., holotype, ♂, in preservation (MZMU 3795). **A**. Dorsal view of the trunk showing distinct tubercles that are feebly keeled and bluntly conical. **B**. Ventral view of the trunk showing abdominal/ventral scales. **C**. Dorsal aspect of the tail showing alternate black and white bands. **D**. Ventral aspect of the tail showing alternate black and white bands. Photos by Sanath Chandra Bohra.

pre-cloacal pits (up to 19 continuous series of precloacal-femoral pits including BNHS 2230); 13 to 15 subdigital lamellae on finger IV (excluding non-lamellar scales between the proximal and apical lamellae series); 15 to 18 subdigital lamellae on toe IV (excluding non-lamellar scales between the proximal and apical lamellae series). The dorsum has a total of 9–10 paired dark brown blotches posteriorly edged with whitish punctuations, occurring on either side of the mid-vertebral region on the dorsum, somewhat parallel to each other, thereby forming a thin mid-dorsal line like appearance (the dark blotches close to the vertebral region are surrounded by another irregular row of somewhat lateral and similarly bi-colored, i.e., black and white blotches on either side). A continuous series of alternating dark and light transverse bands on the dorsum of the tail; not a single row of transversely enlarged, paired subcaudals on the ventral aspect of the tail; subcaudal scales are instead arranged in small, heterogeneous and irregular transverse series.

Etymology

The specific epithet is a patronym honoring Dr. Jayaditya Purkayastha (Help Earth, Guwahati, Assam, India), an Indian herpetologist known for his remarkable contributions in the field of herpetology, particularly regarding the systematics of natricid snakes (mainly *Fowlea*, *Hebius* and *Xenochrophis*) and the herpetofauna of the Indo-Burmese region.

Type material

Holotype

INDIA • ♂ adult; Tripura State, North Tripura District, Chamtilla village roadside mud bunds, surrounded by degraded mixed moist deciduous to semi-evergreen lowland forests; 24°17′8.55″ N, 92°10′32.90″ E, WGS 84; ca 56 to 60 m a.s.l.; 16 Aug. 2024, 11:30 h; Arnab Deb leg.; MZMU 3795 (Figs 4–5, 8A).

Paratypes

INDIA • 2 ♂♂ adult; same data as for holotype; MZMU 3791, MZMU 3792 • 2 ♀♀ adult; same data as for holotype MZMU 3793, MZMU 3794 (Figs 7, 8B–D).

Referred material (based on genetic data only)

INDIA • 1 ♀ adult; Tripura State, North Tripura District, Rowa Wildlife Sanctuary; 24.29062° N 92.16496° E; ca 56 m a.s.l., 2 Oct. 2010; A. Datta-Roy, T. Khichi, NPI Das and I. Agarwal leg.; BNHS 2230 (Agarwal *et al.* 2018a).

Description (holotype MZMU 3795)

Specimen is generally in good preservation condition (Fig. 4); the abdomen has a small incision made for tissue extraction and slightly shows signs of discoloration due to preservation.

Adult specimen (Figs 4–5) with a SVL of 50.9 mm.

HEAD. Length less than one-third of SVL (HL/SVL 0.3), longer than wide (HW/HL 0.56), distinct from neck and somewhat depressed (HD/HW 0.59); interorbital area flat, canthus rostralis broadly rounded; loreal region inflated with granular scales; snout less than half of the head length (SO/HL 0.38); dorsal scales on the forehead are almost homogeneous with the exception of few rows of scales close to the bony interorbital region (between the bony orbital sockets in the frontal region) and canthus rostralis that are comparatively smaller and slightly larger in size respectively; dorsal scales above the bony interorbital region (those occurring between the bony orbital sockets in the frontal region) are sub-equal/sub-homogeneous in size with the exception of very few slightly enlarged tubercle like scales scattered irregularly; dorsal scales just above the orbit are sub-equal in size and visibly larger than the ones occurring between the bony orbital sockets in the frontal region; dorsal scales beginning slightly anterior to the bony interorbital region of the head and extending to the nape are smaller than those on the forehead and canthus rostralis, somewhat blunt and juxtaposed; scales on the bony interorbital and occipital regions are almost homogeneous in size interspersed with small but distinct tubercles (the tubercles are usually two to three times the size of the dorsal scales on the head); eye slightly more than a quarter of the head length (OD/HL 0.26); vertical pupil with crenulate margins; supraciliaries small to moderate in size, blunt, somewhat oval and slightly circular, those present in the mid-portion (above the orbit) are the largest and are more prominent; ear opening oval, obliquely orientated, small (EL/HL 0.11); orbit to ear distance is slightly greater than the eye diameter (OE/OD 1.1); rostral wider than long (RL/RW 0.57), partially and dorsally divided (nearly invisible) by an indistinct rostral groove; a single enlarged supranasal on either side, separated by three small granular internasals which are in contact with the canthus rostralis and are slightly larger than the scales on the forehead, particularly frontal region; rostral in contact with the first supralabials, nasals, two supranasals and three internasals; nostrils semicircular, openings laterally orientated, posterior half covered by the nasal pad; each nasal is in broad contact with the rostral and surrounded by the supranasal, first supralabial, and five to six small post-nasal scales on either side (left and right) of the head; a single row of small granular scales separates the orbit from the supralabials. Mental scale is wider than long (ML/MW 0.7) and somewhat triangular; two well-developed postmentals on either side; the inner pair of postmentals (PMIL) are longer than the outer pair (PMIIL) (PMIIL/PMIL 0.55); the inner pair of postmentals are bordered by the mental, infralabial I, the outer postmental and eight gular scales whereas the outer pair is bordered by inner postmental, infralabials I and II, two to three gular scales and post mental III on either side; ten supralabials on either side of the head (the last one being the smallest and is somewhat sub-equal to the bordering granular scales), bordered by a row of small to medium sized lateral scales, somewhat flat and elongated; 10 infralabials on either side of the head (the first infralabial on the left side of the head is partially divided on its posterior half by a weak suture); a row of medium to slightly large sized gular scales (largest anteriorly) ventrally bordering infralabials II to VII; gular region with small and roughly homogeneous granular scales throughout except for a few scale rows bordering the postmentals and infralabials which are larger, flat and juxtaposed.

Body. Moderately slender, trunk length less than half of the snout to vent length (TRL/SVL 0.45); dorsal scales are mostly homogeneous, i.e., small irregularly rounded granule-like scales intermixed with irregularly arranged, bluntly conical and feebly keeled enlarged tubercles (four to five times the size of granular scales) becoming more conical towards the flanks, those tubercles on the dorsolateral region of the mid-dorsum appears to be the largest; large and distinct tubercles extend posteriorly from the occipital region of the head to the second dark segment of the tail and are smaller on the occiput as well as nape than those on the dorsum; 50 paravertebral tubercles, originating from the most anterior tubercle on the occiput to the mid-sacrum; 31 paravertebral tubercles between the level of the axilla and the level of the groin; ventrolateral folds are poorly developed, not denticulate but with a single row of continuous, projected smooth tubercle like scales; ventral scales smooth, cycloid, imbricate to sub-imbricate, much larger than dorsals; 41 mid-ventral scale rows between the ventrolateral folds; 22 distinct precloacal-femoral pores in a discontinuous series (11 pore-bearing scales on the right side of which nine occur in a continuous row separated by five non pore-bearing scales from the remaining two pore bearing ones; 11 continuous series of pore-bearing scales on the left side); a single row of ten enlarged sub-equal scales (nearly identical to the size of the pore-bearing scales) posteriorly bordering the pore-bearing scales in the pre-cloacal region; three post-cloacal spurs or tubercles on both the left and right sides of the tail base ventrally, particularly on the hemipenile bulge.

Legs. Forearm (FL/SVL 0.16) and tibia (CL/SVL 0.19) roughly moderate; digits narrow, without an adhesive pad, strongly inflected at each joint, all bearing robust, recurved claws; sub-digital lamellae transversely widened beneath the basal phalanx; basal lamellae 4-4-5-6-4 on the right manus, 4-5-5-8-5 on the right pes; distal lamellae (intervening rows of broken/non-lamellar granular scales between the basal and distal lamellae series in parentheses): 8(1)-8(0)-9(1)-9(2)-8(2) on the right manus, 9(1)-9(2)-10(3)-

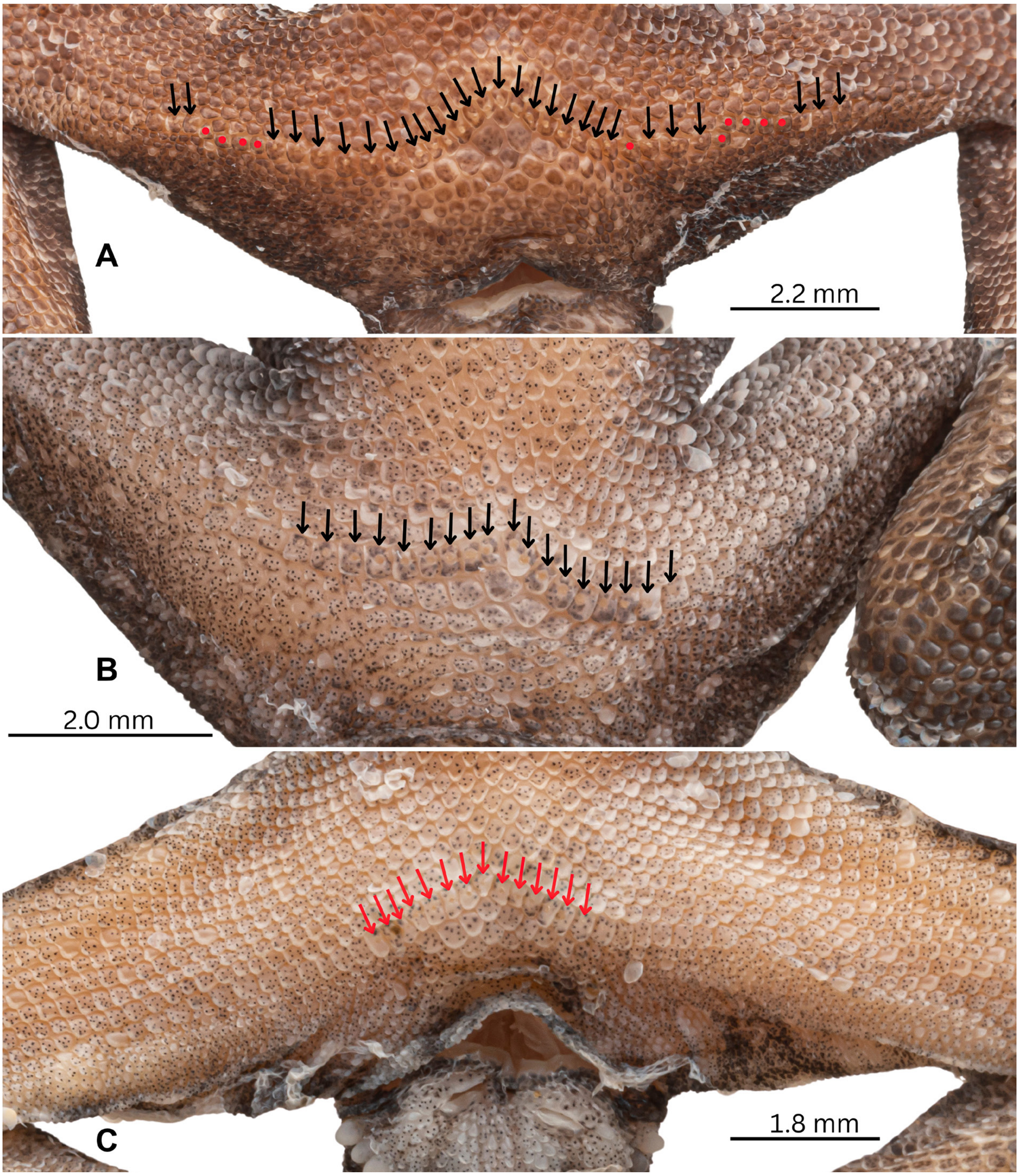

Fig. 6. The arrangements of pores and pits in the pre-cloacal and femoral region of *Cyrtodactylus jayadityai* sp. nov. **A**. Paratype, ♂ (MZMU 3791) showing distinct pre-cloacal femoral pores indicated by black arrows (the red dots indicate intermediate pore-less scales). **B**. Paratype, ♂ (MZMU 3792) showing distinct pre-cloacal pores indicated by black arrows. **C**. Paratype, ♀ (MZMU 3793) showing indistinct pre-cloacal pits indicated by red arrows. Photos by Sanath Chandra Bohra.

10(3)-11(2) on the right pes; interdigital webbing absent from both the manus and pes; relative length of digits I < II < V< III < IV on the right manus, I < II < V < III < IV on the right pes; scales on the palms and soles are smooth, weakly raised and somewhat subimbricate. Forelimbs usually comprising of flat, imbricate to subimbricate small granular scales; the dorsal granular scales on the forearms (of the forelimbs) are usually heterogeneous whereas those on the hind-arms (of the forelimbs) are somewhat homogeneous except for a few slightly enlarged granular scales; ventral portion of the forelimbs covered with smooth, somewhat homogeneous and sub-imbricate scales except for a few slightly enlarged ones close to the wrist and elbow; dorsal scales on the hind limbs are heterogeneous in size, dorsal surfaces of the thighs and shanks have slightly enlarged scales, intermixed with scattered, enlarged, conical, feebly keeled tubercles; a quarter of the dorsal portion of thighs anteriorly (not transversely but longitudinally) and ventral aspect of hind limbs has homogeneous, slightly enlarged, smooth, imbricate to sub-imbricate scales.

Tail. Original and complete, oval in cross section, dorsoventrally depressed; dorsal tubercles on the tail base (tail portion containing the hemipenis and the first dark segment of the tail) are enlarged, flat, strongly keeled and pointed; a few enlarged and keeled tubercles randomly scattered in and around the second dark segment of the tail, remaining dorsal caudal scales smooth, flat and somewhat homogeneous in size and shape; dorsal tubercles reaches up to second dark tail blotch; subcaudal scales on the ventral aspect of the tail smooth, sub-imbricate, small, visibly heterogeneous in size and arranged in irregular transverse series, although superficially granule-like in appearance; not a single row of transversely enlarged, paired subcaudals on the ventral aspect of the tail (Fig. 5D).

Coloration in life (Fig. 8A). Head is primarily dark (tan) brown in colour with a combination of dark and creamish patches scattered irregularly; a thin, narrow but distinct dark streak begins at the end of the posterior orbital margin and continues to the retroarticular process of the jaw dorso-laterally on either side of the head. Posterior region of the head (back of the occiput) has a pair of distinct dark-colored blotch bordered by white punctuations posteriorly and are slightly in contact with each other, thereby giving a transverse band like appearance close to the neck. Dorsal aspect of the body has shades of brown, somewhat slightly tan brown to beige brown intermixed with paired dark blotches and each dark blotch is posteriorly bordered by a small whitish spot, thereby forming a single bi-colored blotch; collectively rows of these bi-colored blotches run parallel to each other on either side of the vertebral region, thereby forming a total of ten distinct, somewhat paired bi-colored (white edged black) blotches on the dorsum; the paired, parallel blotches on the dorsum are barely in contact with each other, thereby giving a typical mid-vertebral or mid-dorsal line like appearance. Furthermore, the dark blotches close to the vertebral region are densely surrounded by another row of somewhat lateral and similar bi-colored (black and white) blotches on either side. Dorsal aspect of all the limbs with shades of brownish-grey, somewhat tan to beige brown intermixed with irregular dark and whitish blotches. Tail is complete, having 12 distinct alternate dark and whitish transverse bands (the dark bands are much larger than the whitish ones which are reduced to narrow transverse bands) dorsally which continue to the tail tip. Ventral region (excluding the underside of the tail) is mostly light, somewhat faded or beige in coloration, along with small, irregular creamish spots scattered irregularly close to the ventro-lateral edges of the abdomen, forelimbs as well as head and ventral aspect of hindlimbs as well. Ventral aspect of the tail with 12 distinct alternate dark and whitish transverse bands (the dark bands are much larger than the whitish ones which are reduced to narrow transverse bands; some of the whitish bands in the central region of the tail are broken into spots) which continue to the tail tip.

Coloration in preservative (Fig. 4). The specimen has become dull in preservative comparatively to its living condition.

Fig. 7. Paratype series of *Cyrtodactylus jayadityai* sp. nov. in preservation. Photos by Sanath Chandra Bohra.

Fig. 8. *Cyrtodactylus jayadityai* sp. nov. in life. **A**. Holotype, ♂, adult (MZMU 3795). **B**. Paratype, ♀, adult (MZMU 3794). **C**. Paratype, ♂, adult (MZMU 3792). **D**. Paratype, ♀, adult (MZMU 3793). **E – F**. Uncollected adult specimens. All the specimens were photographed by Arnab Deb from Chamtilla Village, North Tripura, northeast India.

Table 3 (continued on next page). Morphometrical and meristical data of *Cyrtodactylus jayadityai* sp. nov. from North Tripura, northeast India. Abbreviations: see Material and methods (NA stands for Not available).

Parameters	**MZMU3791**	**MZMU3792**	**MZMU3793**	**MZMU3794**	**MZMU3795**
Status	Paratype	Paratype	Paratype	Paratype	Holotype
SEX	M	M	F	F	M
SVL	54.9	47.8	50.6	50.4	50.9
TRL	24.7	21.9	22.0	24.04	23.0
BW	7.0	7.7	8.4	8.0	7.1
TL	N/A	55.7	N/A	57.0	56.6
TD	3.8	3.9	3.4	3.1	3.8
TW	4.2	4.0	3.6	3.6	3.6
HL	16.3	15.6	15.4	15.6	15.4
HW	8.2	8.4	8.3	8.2	8.7
HD	5.9	5.2	5.5	5.7	5.1
JW	5.2	5.8	5.3	5.3	5.0
FL	8.2	8.0	7.6	8.3	8.3
CL	9.6	9.5	9.5	9.7	9.6
OD	4.0	4.0	4.0	4.0	4.0
NO	4.3	4.3	4.1	4.3	4.2
SO	6.0	5.8	6.0	6.2	5.8
OE	4.4	4.4	4.5	4.4	4.4
EL	1.8	1.9	1.7	1.6	1.7
IN	1.4	1.2	1.1	1.1	1.8
IO	3.6	3.6	3.6	3.8	3.7
F1	3.7	3.4	3.6	3.4	3.3
F2	4.5	4.3	4.4	4.3	4.1
F3	5.2	4.9	5.2	5.3	5.1
F4	5.8	5.3	5.9	5.7	5.9
F5	4.6	4.8	4.5	4.4	4.7
T1	4.0	4.2	4.2	4.0	4.0
T2	5.5	5.7	5.9	5.3	5.7
T3	6.0	6.2	6.2	6.8	6.8
T4	7.3	7.5	7.3	7.7	7.7
T5	6.4	6.2	6.0	6.4	6.2
RL	1.3	1.3	1.3	1.5	1.3
RW	2	2.1	2.2	2.2	2.3
ML	1.3	1.2	1.2	1.5	1.4
MW	2.0	1.9	1.9	2.1	2.0
PMIL	1.1	1.1	1.2	1.1	1.1
PMIIL	0.6	0.5	0.6	0.6	0.6
PcP /PcFP	28	18	0 (14 pitted scales)	0 (0 pitted scales)	22
MVSR	42	43	43	37	41
DTR	21	21	21	20	19

Table 3 (continued). Morphometrical and meristical data of *Cyrtodactylus jayadityai* sp. nov. from North Tripura, northeast India. Abbreviations: see Material and methods (NA stands for Not available).

Parameters	MZMU3791	MZMU3792	MZMU3793	MZMU3794	MZMU3795
PVT1	47	47	48	44	50
PVT2	30	31	30	30	31
SL(L/R)	12,11	10,11	11,11	9,10	10,10
IL(L/R)	10,10	11,11	11,11	11,9	10,10
F1Lam	4(2)6	4(1)6	4(1)6	4(2)6	4(1)8
F2Lam	4(0)7	4(1)8	4(1)7	4(2)7	4(0)8
F3Lam	4(1)9	4(1)10	5(2)9	5(0)10	5(1)9
F4Lam	5(2)8	5(2)10	5(2)10	6(2)9	6(2)9
F5Lam	4(2)7	4(1)9	4(2)8	5(1)7	4(2)8
T1Lam	3(2)6	3(2)7	3(3)7	4(1)8	4(1)9
T2Lam	5(2)7	4(2)8	4(1)9	5(1)8	5(2)9
T3Lam	5(2)8	5(2)10	5(2)10	6(2)11	5(3)10
T4Lam	6(3)9	6(2)11	6(2)9	7(2)9	8(3)10
T5Lam	4(1)10	5(3)10	5(2)10	4(2)11	5(2)11
Dark dorsal spots	9	10	9	9	10

Variation

Please refer to Table 3 and Fig. 6 for variations within the new species. Most of the morphological characters in all the male and female paratypes are within the range of the holotype except for the precloacal regions.

Detail descriptions of the pre-cloacal regions and their variations: MZMU 3792 (an adult ♂) has a continuous series of 18 PcP (9 continuous pores on eich side with no poreless scales); MZMU 3791 (an adult ♂) has a total of 28 PcFP occurring in a discontinuous series (right side with 15 pores of which 13 are present in a continuous series followed by four poreless scales and then two additional pores whereas left side with 13 of which seven pores are present in a continuous row followed by a single poreless scale, then three pores, then five poreless scales and then a final series of three pores); MZMU 3794 (an adult ♀) and MZMU 3793 (an adult ♀) have 0 and 14 precloacal pits, respectively; BNHS 2230 (an adult ♀) has 19 pitted scales in the precloacal-femoral region as mentioned in Agarwal *et al.* (2018a) versus the holotype (MZMU 3795, an adult ♂) with a discontinuous series of 22 PcFP (right side with 11 pores of which nine are present in a continuous series followed by five poreless scales and then two additional pores whereas left side with a continuous series of 11 pores with no intermediate poreless scales).

Sexual dimorphism

Please refer to Table 3 for sexual dimorphism within the new species. Apart from the strong differences in the precloacal and femoral region, i.e., 18 to 28 PcFP in males versus 0 to 14 pitted (0 to 19 pitted scales including BNHS 2230) pre-cloacal scales in females, no other prominent differences were found between the two sexes (Fig. 6).

Comparisons

Genetically, *Cyrtodactylus jayadityai* sp. nov. is a sister to *C. tripuraensis*, both of them members of the'*khasiensis*' group and can be differentiated from each other by a pairwise genetic distance of at least 4.7 to 5.2% in the mitochondrial ND2 gene (Table 2) and certain non-overlapping morphological characters (Table 3).

Morphologically, *Cyrtodactylus jayadityai* sp. nov. differs from the closest members of the '*khasiensis*' group, including *C. tripuraensis*, for the combination of the following characters: (1) males with 18 PcP to 28 PcFP in a continuous to discontinuous series, respectively (versus 29 to 37 continuous series of PcFP in males of *C. tripuraensis*; 27 PcFP in a continuous series in males of *C. ngengpuiensis* Boruah, Narayanan, Lalronunga, Deepak & Das 2024); (2) females with 0 to 14 pitted scales (up to 19 pits including BNHS 2230) in the pre-cloacal region (versus 20 to 29 pitted scales in females of *C. tripuraensis*); (3) 19 to 21 rows of DTR at midbody (versus 22 to 24 rows in *C. ayeyarwadyensis* Bauer, 2002); (4) 37 to 43 MVSR between the indistinct ventro-lateral folds (versus 32 to 37 MVSR in

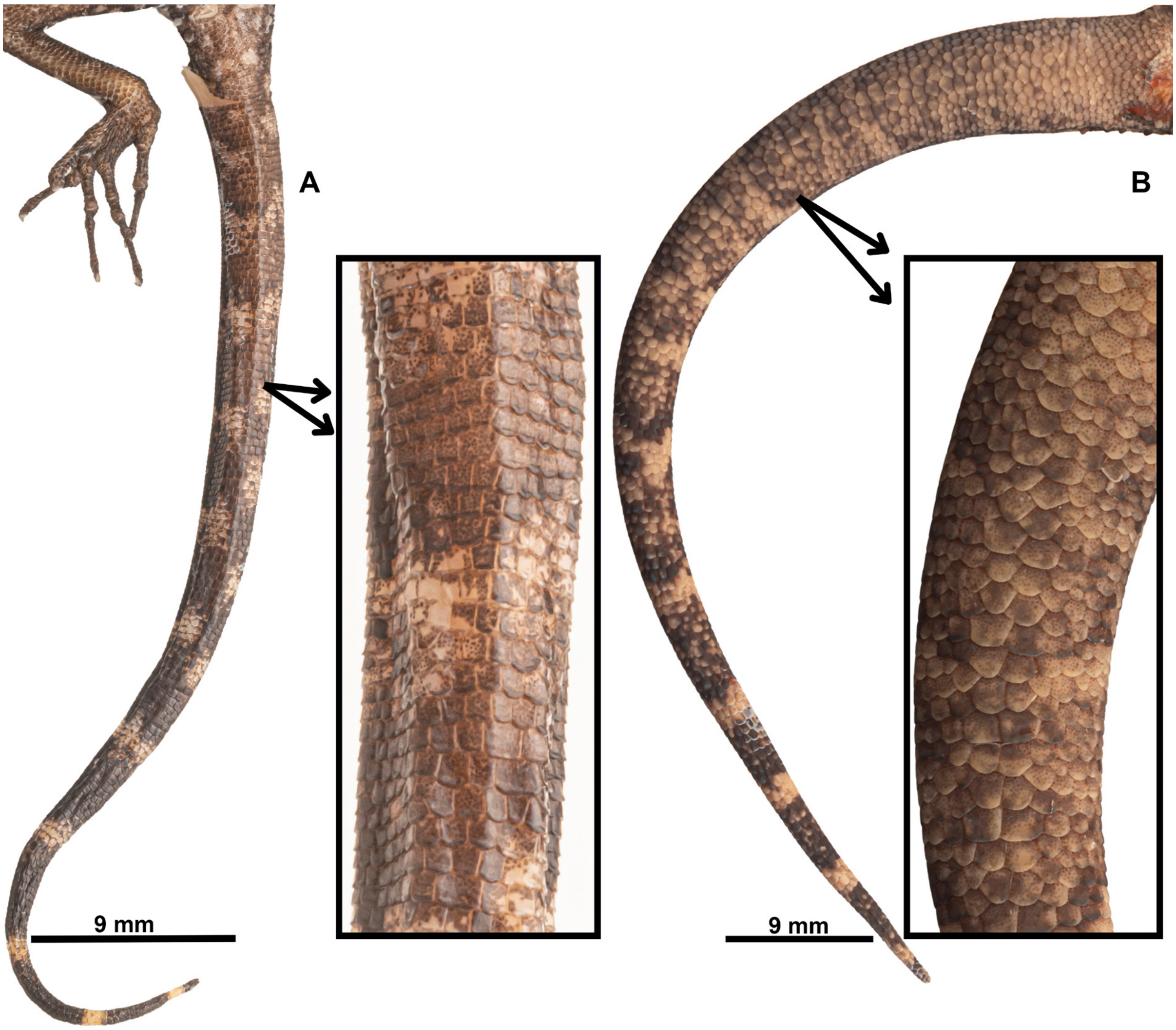

Fig. 9. Comparisons of the subcaudal scalation covering the underside of the tail between **A**. *Cyrtodactylus jayadityai* sp. nov. **B**. *Cyrtodactylus khasiensis.* Note the presence of small and visibly heterogeneous subcaudal scales arranged in irregular transverse series in both species. Photos by Sanath Chandra Bohra.

C. ayeyarwadyensis); (5) dorsum with a total of 9–10 small-sized, paired dark brown blotches posteriorly edged with whitish punctuations, occurring on either side of the mid-vertebral region on the dorsum, somewhat parallel to each other, thereby forming a thin mid-dorsal line like appearance (versus dorsum mostly with paired, enlarged irregular blotches on either side of the vertebral region that are parallel and strongly connected to each other alongside the presence of a distinct, thin dark dorso-lateral stripe on either side in *C. ngengpuiensis*; the paired dark blotches on either side of the vertebral region are at least 2 × longer in *C. tripuraensis*). For further morphological differences between *C. jayadityai* and its congeners in the '*khasiensis*' group, refer to the comparative data provided in Table 4.

Sequence divergence (Table 2)

Cyrtodactylus jayadityai sp. nov. is supported as a distinct species based on the mitochondrial ND2 gene, exhibiting 0% intraspecific divergence among the sequenced samples, with no current evidence of intraspecific phylogenetic splitting within the lineage. The new species shows an interspecific genetic distance of 4.7–5.2% from its closest congener *C. tripuraensis*, 6.2–7.6% from *C. ngengpuiensis*, and 9.7–10% from *C. ayeyarwadyensis*. Furthermore, it is more than 10% genetically divergent from all other congeners within the'*khasiensis*' group.

Natural history and biology

The individuals of *Cyrtodactylus jayadityai* sp. nov. predominantly inhabit small burrows and crevices along roadside mud bunds, often covered with moss and large tree roots connected to these bunds in association with mixed moist deciduous to semi-evergreen lowland forests (Fig. 10A–B) (56 to 100 m a.s.l.). These geckos exhibit strictly nocturnal behavior, with individuals regularly observed emerging from their retreats to forage between 20:00 h and 03:30 h. Most individuals were recorded at heights ranging from 1.5 to 1.8 m above ground level; however, some were observed as high as approximately 10 meters. Uncollected gravid females ranging in SVL from 49 mm to 60 mm were observed during the months of March to August, suggesting that breeding occurs during pre and peak monsoon. Notably, several individuals were also recorded during the peak winter month of January, despite ambient temperatures as low as 14°C. The species is sympatric with other gekkonid species, including *Hemidactylus frenatus* Duméril & Bibron 1836, *H. aquilonius* Mcmahan & Zug, 2007, *H. platyurus* Schneider, 1797 and *H.* cf. *brooki* Gray, 1845. Dietary observations suggest a preference for small to medium-sized arthropods like forest cockroaches and huntsman spiders. Behaviorally, individuals are generally shy and avoidant when approached, typically retreating into their burrows. However, when handled, they exhibit a strong biting behavior, indicating a possible defense mechanism against predators or threats.

Distribution

Based on the current data, *Cyrtodactylus jayadityai* sp. nov. is found only in a small patch of forests in the lowlands of North Tripura District covering an area of 8 to 12 km^2 ranging from the western (including Chamtilla Village) and southern boundaries of Rowa WLS towards its eastern boundary, further stretching into Indurail reserve forests close to Assam-Tripura border (Fig. 1).

Conservation status

Based on our current data of distribution, we consider this species Data Deficient (DD) as per the IUCN. However, the species restricted distribution (8 to 12 km^2) in fragmented and anthropogenically pressured habitats suggests that it may qualify for a threatened category (Endangered or Critically Endangered) if assessed formally, given its vulnerability to habitat alteration.

Suggested common name

Jayaditya's forest bent-toed gecko.

Remarks

Agarwal *et al.* (2018a) described *Cyrtodactylus tripuraensis* based on 11 specimens from Tripura, northeast India of which 10 were collected from Gomati and Sephaijala Districts (including type locality of *C. tripuraensis*) whereas the remaining one paratype (BNHS 2230) was collected from Rowa WLS, North Tripura District (very close to the type locality of the currently described new species). Our genetic data excised from MZMU 3795 (holotype of *Cyrtodactylus jayadityai* sp. nov.) collected from the North Tripura District has an intraspecific genetic divergence of 0% from BNHS 2230 (KM255201). As a result, we refer BNHS 2230 as additional material of *C. jayadityai* based on the existing genetic data. Together, these two samples (BNHS 2230 and MZMU 3795) of *C. jayadityai* are 4.7 to 5.2% divergent from all other samples of *C. tripuraensis* in the mitochondrial ND2 gene. To date, this specimen (BNHS 2230) has not been morphologically examined by us, so we decide not to include it amongst our type series (holotype and paratypes) of *C. jayadityai*. Apart from the size and its related parameters (e.g., SVL, HL, etc., as BNHS 2230 is a bit larger in size (Agarwal *et al.* 2018a)), the majority of the diagnostic morphological characters of BNHS 2230 as mentioned in Agarwal *et al.* (2018a) falls well within the range of the type series of the newly described species (Table 3). Furthermore, those diagnostic parameters show the slightest of variations between the type series (holotype and paratypes) and the referred material (BNHS 2230) of the new species is mentioned separately within brackets in the Diagnosis section of *C. jayadityai* to avoid any sort of confusion in the future.

Fig. 10. Habitat and microhabitat of collected specimens in northeast India. **A** – **B**. Chamtilla Village, North Tripura from where *Cyrtodactylus jayadityai* sp. nov. is being described. **C** – **D**. Sohra, East Khasi Hills, Meghalaya where *Cyrtodactylus khasiensis* thrives. Photos by Arnab Deb.

Table 4 (continued on next two pages). Comparisons of main morphological characters amongst species that are described within the 'Indo-Burmese *khasiensis* clade' to date. Abbreviations NA = Not Available; * = Discrepancies in scale-counting methods between cited sources and current criteria.

Species	**SVL (mm)**	**SL**	**IL**	**PcFP/PcP (male)**	**PcFP/ PcP (female)**	**DTR**	**PVT1**	**PVT2**	**MVSR**	**Enlarged plate-like subcaudals**	**Dark dorsal blotches (from nape to mid-sacrum)**	**Reference**
C. aaronbaueri	54.2–69.5	8–11	8–12	7–8	0 (6–8 pitted scales)	22–28	NA	36–39	35–40	no	9–11 (irregular and reticulated); no mid-dorsal line	Purkayastha *et al.* 2021
C. annapurnaensis	50.7 to 63.9 mm max.	10–11	9–11	3–4	0 (3 pitted scales)	18–21	NA	28–35	32–35	no	Dark irregular blotches	Bhattarai *et al.* 2025
C. agarwali	56.4–71.8	9–12	8–10	11–18	NA	21–25	NA	34–38	32–39	no	8–9 (distinct and paired)	Purkayastha *et al.* 2021
C. aunglini	68.6–81.6	*	*	12 –13	NA	21–26	NA	37–45	41–47	no	7–8 (distinct, some paired and some unpaired)	Grismer *et al.* 2018; Mahony & Kamei 2022
C. ayeyarwadyensis	62.1–71.8	*	*	10– 28	NA	22–24	NA	NA	32–37	no	9–11 (distinct and paired)	Bauer 2003
C. bapme	69.9–77.0	8–12	8–10	0	0 (0–13 pitted scales)	21–24	NA	32–37	30–39	no	7–9 (distinct and paired)	Kamei & Mahony 2021
C. barailensis	68.8	9 or 12	9	NA	10 pores	17	NA	32	36	no	Irregular and reticulated	Boruah *et al.* 2024
C. bengkhuaiai	54.9–72.5	9–11	7–11	5–7	0 (4–5 pitted scales)	22–26	NA	35–41	37–42	no	7–9 (distinct and paired)	Purkayastha *et al.* 2021
C. brevidactylus	71.4–88.0	10–12	10–11	8	8 pores	27–30	NA	38–42	35–46	no	3–4 large, dark dorsal blotches between nape and sacrum	Bauer 2002, Grismer *et al.* 2018
C. cayuensis	59.4–83.6	8–13	8–12	6–10	7–10 pores	15–26	NA	27–38	28–44	no	8–10 regular as well as irregular blotches	Mirza *et al.* 2021; Boruah *et al.* 2024
C. chrysopylos	64.9–83.8	*	*	8–13	0	16–20	NA	30–35	39–55	no	6–8, unpaired and transverse	Bauer 2002; Grismer *et al.* 2018
C. dianxiensis	73.8–79.9	9–12	8–11	7–8	0	17–19	NA	31 or 32	35–41	no	9–10, paired and distinct	Liu and Rao 2021; Zhang *et al.* 2024
C. exercitus	48.1–68.0	9–11	9–10	11–15	0 (11 pitted scales)	21–24	NA	32–34	35–37	no	Irregular	Purkayastha *et al.* 2022
C. gansi	46.5–62.4	*	*	16–29	13+1 pores	20–25	NA	NA	36–40	no	10 (distinct, transverse and unpaired)	Bauer 2003

Table 4 (continued). Comparisons of main morphological characters amongst species that are described within the ‘Indo-Burmese *khasiensis* clade’ to date. Abbreviations NA = Not Available; * = Discrepancies in scale-counting methods between cited sources and current criteria.

Species	SVL (mm)	SL	IL	PcFP/PcP (male)	PcFP/ PcP (female)	DTR	PVT1	PVT2	MVSR	Enlarged plate-like subcaudals	Dark dorsal blotches (from nape to mid-sacrum)	Reference
C. guwahatiensis	61.9–70.5	8–11	8–10	26–39	0	21–24	NA	35–38	30–35	no	8–10 (paired, not completely transverse)	Agarwal *et al.* 2018b; Purkayastha *et al.* 2020
C. jaintiaensis	87.0–96.2	8–9	9–10	11–12	12 pores	19–20	NA	30–34	40–42	no	Irregular and distinct, but paired	Agarwal *et al.* 2018b
C. karanshahi	53.2–74.5	10–12	10–11	7–8	NA	18–19	NA	32–36	39–42	no	Irregular, small blotches	Bhattarai *et al.* 2025
C. karsticola	63.7–70.7	10–11	9–10	34–38	0 (13 pitted scales)	21–24	NA	34–39	35–39	no	Irregular and distinct, but paired	Purkayastha *et al.* 2021
C. kazirangaensis	74.8–80.0	11–12	9–11	10–11	NA	22–23	NA	36–38	37–43	no	6–8, irregular and distinct	Agarwal *et al.* 2018b
C. khasiensis	57.0–81.1	9–13	8–11	10–12	0	19–23	42–53	NA	34–42	no	8–10 (paired and distinct)	Agarwal *et al.* 2018a
C. kiphire	63.9–64.7	10	9–12	6–7	NA	16	NA	26–29	35–36	no	Irregular blotches or reticulations	Boruah *et al.* 2024
C. lungleiensis	64.9–75.1	10–11	9–11	3–5	0 (5–7 pitted scales)	24–28	NA	32–40	37–43	no	Irregular blotches or reticulations	Lalremsanga *et al.* 2022
C. manipurensis	59.5	10	8–9	7	NA	21	NA	37	36	no	6 irregular blotches or reticulations	Boruah *et al.* 2024
C. mandalayensis	61.7	10/ 12	9/10	8	NA	18	NA	NA	32	no	Irregular	Mahony 2009
C. martinstolii	64.6–80.4	10–12	10–12	7–8	0 (8–9 pitted scales)	19–23	NA	30–37	35–40	no	Irregular but distinct dark blotches	Bhattarai *et al.* 2025
C. montanus	53.6–78.2	8–10	8–10	8–10	0	21–23	NA	37–43	36–42	no	Completely irregular dark blotches	Agarwal *et al.* 2018b
C. mombergi	64–74	*	*	10–11	0–9 pores	23–27	NA	35–42	31–39	no	Completely irregular dark blotches	Grismer *et al.* 2019
C. myaleiktaung	67.4	*	*	NA	0	NA	NA	NA	57	NA	7 (distinct and transversely wide)	Grismer *et al.* 2018
C. namtiram	65.8	8–9	10	12	NA	21	NA	33	36	no	6–7, irregular but distinctly paired blotches	Mahony & Kamei 2022

Table 4 (continued). Comparisons of main morphological characters amongst species that are described within the ‘Indo-Burmese *khasiensis* clade’ to date. Abbreviations NA = Not Available; * = Discrepancies in scale-counting methods between cited sources and current criteria.

Species	**SVL (mm)**	**SL**	**IL**	**PcFP/PcP (male)**	**PcFP/ PcP (female)**	**DTR**	**PVT1**	**PVT2**	**MVSR**	**Enlarged plate-like subcaudals**	**Dark dorsal blotches (from nape to mid-sacrum)**	**Reference**
C. nagalandensis	67.5–72.0	10–12	8–10	NA	0 (6 pitted scales)	16–18	NA	35–37	34–35	no	Completely irregular dark blotches	Agarwal *et al.* 2018b
C. ngopensis	62.6–68.6	10–11	9–11	6	0 (0–6 pitted scales)	19–20	NA	32–36	32–39	no	7–10 irregular dark blotches	Bohra *et al.* 2022
C. ngengpuiensis	53.9–74.1	9–12	8–11	27	10–16 pores	18–20	NA	29–34	38–39	no	Completely irregular dark blotches	Boruah *et al.* 2024
C. namdaphaensis	54.8–70.7	8–11	8–11	7–9	8–10 pores	17–19	NA	29–36	33–40	no	Completely irregular dark blotches	Boruah *et al.* 2024
C. septentrionalis	58–65.2	9–10	9	14	0 (14 indistinct pits)	23–24	NA	38–42	35–38	no	6–9 rows of paired dark blotches	Agarwal *et al.* 2018b
C. siangensis	70.1–72.1	8–12	9–12	NA	8 or 10 pores	15–16	NA	26–32	40–45	no	six or seven irregular and broken dark-brown bands	Boruah *et al.* 2024
C. siahaensis	42.6–72	9–11	9–11	7	0 (0–3 pitted scales)	22–24	NA	36–39	34–37	no	dark brown, irregular blotches	Purkayastha *et al.* 2022
C. urbanus	65.4–75.6	8–11	8–10	9–13	0	20–24	NA	30–40	30–39	no	dark brown, irregular blotches	Purkayastha *et al.* 2020; Kamei & Mahony 2021
C. vairengtensis	57.6–73.6	10–11	10–11	9–11	0 (0–9 pitted scales)	22–23	NA	34–39	35–41	no	dark brown, irregular blotches	Lalremsanga *et al.* 2023
C. tamaiensis	90	10	9	40	NA	21	NA	NA	37	no	dark brown, irregular blotches	Mahony 2009
C. vanarakshaka	53.1–65	9–11	9–10	10	0 (10 pitted scales)	21–22	52–55	35–36	38–41	no	dark brown, irregular blotches	Bharali *et al.* 2025
C. tripuraenensis	54.4–69.3	8–12	8–10	29–37 (male)	0 (20–29 pitted scales)	19–21	44–54	NA	35–43	no	7–10, paired and distinct	Agarwal *et al.* 2018a
***C. jayadityai* sp. nov.**	47.8– 54.9 (up to 70.7 including BNHS 2230)	9–12	9–11	18–28 (male)	0 (0–19 pitted scales)	19–21	44–50	30–31	37–43	no	9–10, paired and distinct	This study (data of BNHS 2230 taken from Agarwal *et al.* 2018a)

Additional notes on *Cyrtodactylus khasiensis*, Jerdon 1870 (Fig. 9B)

Cyrtodactylus khasiensis was described based on three specimens from the Khasi Hills of Meghalaya, northeast India (precise locality unknown) by Jerdon (1870) without the designation of a type specimen for the species. As a result, Agarwal *et al.* (2018a) designated BMNH 1906.8.10.4 (formerly ZSIK 6198) as a lectotype of *C. khasiensis* for the taxonomic stability of the species and also provided a detailed redescription of the species based on two paralectotypes and seven freshly collected specimens. Agarwal *et al.* (2018a) also provided the first mitochondrial genetic data of one of the topotypical specimens of *Cyrtodactylus khasiensis* sensu stricto. However, Agarwal *et al.* (2018a) mentioned that *C. khasiensis* had 'subcaudal scalation of original tail with median series of paired enlarged plates, covering underside of tail entirely toward tail-tip'.

Upon examination of three freshly collected adult specimens of *Cyrtodactylus khasiensis* sensu stricto from Sohra, East Khasi Hills (MZMU 3798, ADBU/GT/1 and ADBU/GT/2) of Meghalaya, we found that all of these specimens never possessed a distinct median series of paired enlarged plate-like subcaudals across the underside of tail as mentioned in Agarwal *et al.* (2018a). Rather, our collected topotypical specimens of *C. khasiensis* exhibit a small to medium, visibly heterogeneous and irregular transverse series of sub-imbricate subcaudal scales that are superficially granule-like in appearance across the ventral aspect of the tail, similar to all other described members of the '*khasiensis*' group. However, our *C. khasiensis* specimens also bear fewer rows (6 to 12 continuous or discontinuous rows) of subcaudal scales possessing a somewhat paired, median series of minutely to slightly enlarged scales when compared to its flanking/bordering smaller subcaudal scales. This suggests that Agarwal *et al.* (2018a) most likely used the terminology 'paired enlarged plates' for *C. khasiensis* to describe these very few rows of weakly enlarged, median series of somewhat paired subcaudal scales.

Many species within the '*khasiensis*' group (e.g., *Cyrtodactylus urbanus* Purkayastha, Das, Bohra, Bauer & Agarwal, 2020; *C. lungleiensis* Lalremsanga, Chinliansiama, Bohra, Biakzuala, Vabeiryureilai, Muansanga, Malsawmdawngliana, Hmar, Decemson, Siammawii, Das & Purkayastha, 2022; *C. guwahatiensis* Agarwal, Mahony, Giri, Chaitanya & Bauer, 2018 and *C. bapme* Kamei & Mahony, 2021) also exhibit a subcaudal scalation completely similar to *C. khasiensis* sensu stricto whereas in some species (e.g., *C. tripuraensis*, *C. jayadityai* sp. nov. and *C. siahaensis* Purkayastha, Lalremsanga, Litho, Rathee, Bohra, Mathipi, Biakzuala & Muansanga, 2022), all the subcaudal scale rows exhibit a small to medium, irregularly sized, heterogeneous scalation throughout the underside of the tail.

In terms of morphology, the case of the 'subcaudal scalation' within all the members of the *Cyrtodactylus khasiensis* group is completely overlapping across species. This is why we recommend not using 'subcaudal scalation' as a valid morphological character for differentiating new species with the congeners within the '*khasiensis*' group, since previously this character was used as a strong diagnostic feature by several workers in their 'comparisons and tables' section to differentiate their new species with the congeners, particularly *C. khasiensis* (Agarwal *et al.* 2018a, 2018b; Purkayastha *et al.* 2020, 2021, 2022; Mirza *et al.* 2021, 2022; Bohra *et al.* 2022; Lalremsanga *et al.* 2022, 2023; Boruah *et al.* 2024; Bharali *et al.* 2025).

Prior to this study, *Cyrtodactylus khasiensis* was known precisely only from the hills of East Khasi Hills District, Sohra, Meghalaya. Another collected adult male specimen (MZMU 3797) from Umdohlun, South West Khasi Hills District, Meghalaya, is only ~1.9% genetically divergent from the available mitochondrial ND2 data of *C. khasiensis* (KM255188). As a result, we confirm the occurrence of *C. khasiensis* sensu stricto further westwards from its currently known locality (Sohra, East Khasi Hills District) towards South-West Khasi Hills District close to India-Bangladesh border based on the molecular data.

Distribution and natural history

Based on our data, *C. khasiensis* is a Khasi Hills endemic species that predominantly lives on large as well as small rocks with or without mosses, in small burrows and crevices along roadside mud bunds, often covered with moss, as well as among large tree roots surrounded by tropical evergreen to montane forests in association with running hill streams (1292 to 1350 m a.s.l.). These geckos exhibit strictly nocturnal behavior, with individuals regularly observed emerging from their retreats to forage between 19:00 h and 03:30 h. Most individuals were recorded at heights ranging from one to three meters above ground level. Uncollected gravid females were observed during the months of late April to August, suggesting that breeding occurs during peak monsoon. The species is sympatric with other reptilian species including *Hemidactylus platyurus*, *Calotes zolaiking* Giri, Chaitanya, Mahony, Lalronunga, Lalrinchhana, Das, Sarkar, Karanth & Deepak, 2019, *C. maria* Gray, 1845, *Pareas monticola* Cantor, 1839 and *Lycodon septentrionalis* Günther, 1875. Dietary observations suggest a preference for small to medium-sized arthropods like forest cockroaches and beetles. Behaviorally, individuals are generally shy and avoidant when approached, typically retreating into their burrows. However, when handled, they exhibit a strong biting behavior, indicating a possible defense mechanism against predators or threats.

Conservation status

Based on our current data of distribution, we consider this species Data Deficient (DD) as per the IUCN.

Discussion

Our mitochondrial ND2 analysis places the new species from Northern Tripura as a distinct lineage, supported by both molecular divergence and diagnostic morphology within the broader *Cyrtodactylus khasiensis* group, a group that has undergone extensive diversification in the Indo-Burmese region during the Miocene (Grismer *et al.* 2021; Boruah *et al.* 2024). Within this radiation, most of the species are narrowly distributed, often restricted to specific lowlands or upland montane habitats (Purkayastha *et al.* 2021; Bohra *et al.* 2022; Boruah *et al.* 2024). Notably, the pairwise genetic distances separating the new species from its congeners are congruent with interspecific divergences elsewhere in the group, typically ranging from 3.8–6.0% in the mitochondrial ND2 gene between the closest congeners (Grismer *et al.* 2018; Purkayastha *et al.* 2022; Lalremsanga *et al.* 2022, 2023). Furthermore, species delimitation within various genus of geckos (e.g., *Cnemaspis* and *Cyrtodactylus*) has frequently relied on shallow but stable genetic distances when supported by distinct non-overlapping morphological traits, phylogenetic and evolutionary independence, as observed in several recently described taxa (Grismer *et al.* 2018; Purkayastha *et al.* 2022; Lalremsanga *et al.* 2023; Narayanan *et al.* 2023). The *Cyrtodactylus khasiensis* group, within which this new species nests, has emerged as one of the most speciose *Cyrtodactylus* lineages over the past decade. Encompassing over 35 recognized species, this group illustrates how the topographic complexity of regions like the Indo-Burmese and Himalayan transition zone promotes allopatric speciation by facilitating reproductive isolation. The use of advanced phylogenetics and rigorous species delimitation and diagnostic approaches (Grismer *et al.* 2021, 2022) continues to uncover further hidden diversity within this group, highlighting the essential role of integrative systematics in modern biological research. Moreover, regions having complex tectonic activity, elevational gradients and habitat heterogeneity increasingly emphasize the speciation of these geckos (Grismer *et al.* 2022).

Tripura itself is a part of a unique biogeographic zone, as it falls under the confluence of two major zones namely the hills of Indo-Burma towards its east forming a contiguous stretch of tropical montane-evergreen forests entering Mizoram (900 to 1500 m a.s.l.) and the lowlands of northern, western as well as southern parts of the state containing a heterogeneous mixed moist-dry deciduous/semi-evergreen forests (degraded in certain zones), expanding into certain regions of Bangladesh. This makes Tripura topographically intricate, thereby providing suitable microhabitats for both flora and fauna. The state's varied topography and mosaic of vegetation types generate extensive microhabitat heterogeneity, which likely drives genetic divergence via reproductive isolation, therefore fostering speciation. The phylogenetic position of *C. jayadityai* sp. nov., as inferred from the mitochondrial DNA sequences, further reinforces this hypothesis, as the new species is recovered as a well-supported sister to *C. tripuraensis*, both of which occupy distinct zones of Tripura's patchy lowland forests separated by an aerial distance of approximately 101 km, suggesting a possible allopatric distribution.

The newly described species occurs in the lowlands below 200 m a.s.l. in North Tripura District, not far from the Jampui hills bordering Mizoram, where *Cyrtodactylus montanus* is the only *Cyrtodactylus* observed within the niche to date. However, additional samplings are required to better understand the precise phylogeographic placement of the new species within this continuum. Moreover, considering the phylogenetic framework of *Cyrtodactylus* and the integrative systematic approach proposed by Grismer *et al.* (2021), it is plausible that further cryptic lineages within the *khasiensis* group still remain to be discovered and described, particularly in ecotonal zones near the forests along the Tripura/Mizoram-Bangladesh border. Furthermore, just like other regions of Tripura, even the lowland forests of extreme North Tripura are contiguous, stretching to Muraichhara in Bangladesh, which indicates the possibility of occurrence of *C. jayadityai* sp. nov. slightly further northwards. Agarwal *et al.* (2018a) further discusses that populations mentioned as *C. ayeyarwadyensis* from Kaptalmukh, Bangladesh requires genetic confirmation as Kaptalmukh is located ~100 km to the south of the type locality of *C. tripuraensis* (Gomati District, Tripura), indicating the possible presence of the latter (or related cryptic population) in the same continuous forests running further southwards. With forest cover increasingly fragmented and threatened by anthropogenic pressures, the documentation and formal description of cryptic taxa are crucial, both for achieving taxonomic resolution and for guiding conservation priorities. Although recent years have witnessed a rapid increase in the number of described *Cyrtodactylus* from northeast India, several areas remain inadequately surveyed, including Tripura. The discovery and recognition of another new micro-endemic species underscores the massive potential of Tripura to harbor its unique herpetofaunal diversity, which will be highlighted in the forthcoming works in the form of a checklist (Deb *et al.* in press). Prior to this, the only herpetofauna species described from Tripura state are *C. tripuraensis* and *C. montanus*, both of which were described back in 2018 (Agarwal *et al.* 2018a, 2018b).

We therefore highlight the urgency of continued, systematic field-based investigations in these biologically rich but historically neglected landscapes to promote research and conservation since micro-endemic species are often highly vulnerable to habitat degradation due to their restricted ranges and specialized microhabitats.

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Supplementary files

Supp. file 1. Allometry adjusted morphometric data of *C. jayadityai* sp. nov. and *C. tripuraensis*. https://doi.org/10.5852/ejt.2026.1048.3255.14399

Supp. file 2. Information of total variance explained by the Principal Components. https://doi.org/10.5852/ejt.2026.1048.3255.14401

Supp. file 3. Information of the loadings in Principal Component Analysis. https://doi.org/10.5852/ejt.2026.1048.3255.14403

APPENDIX 1

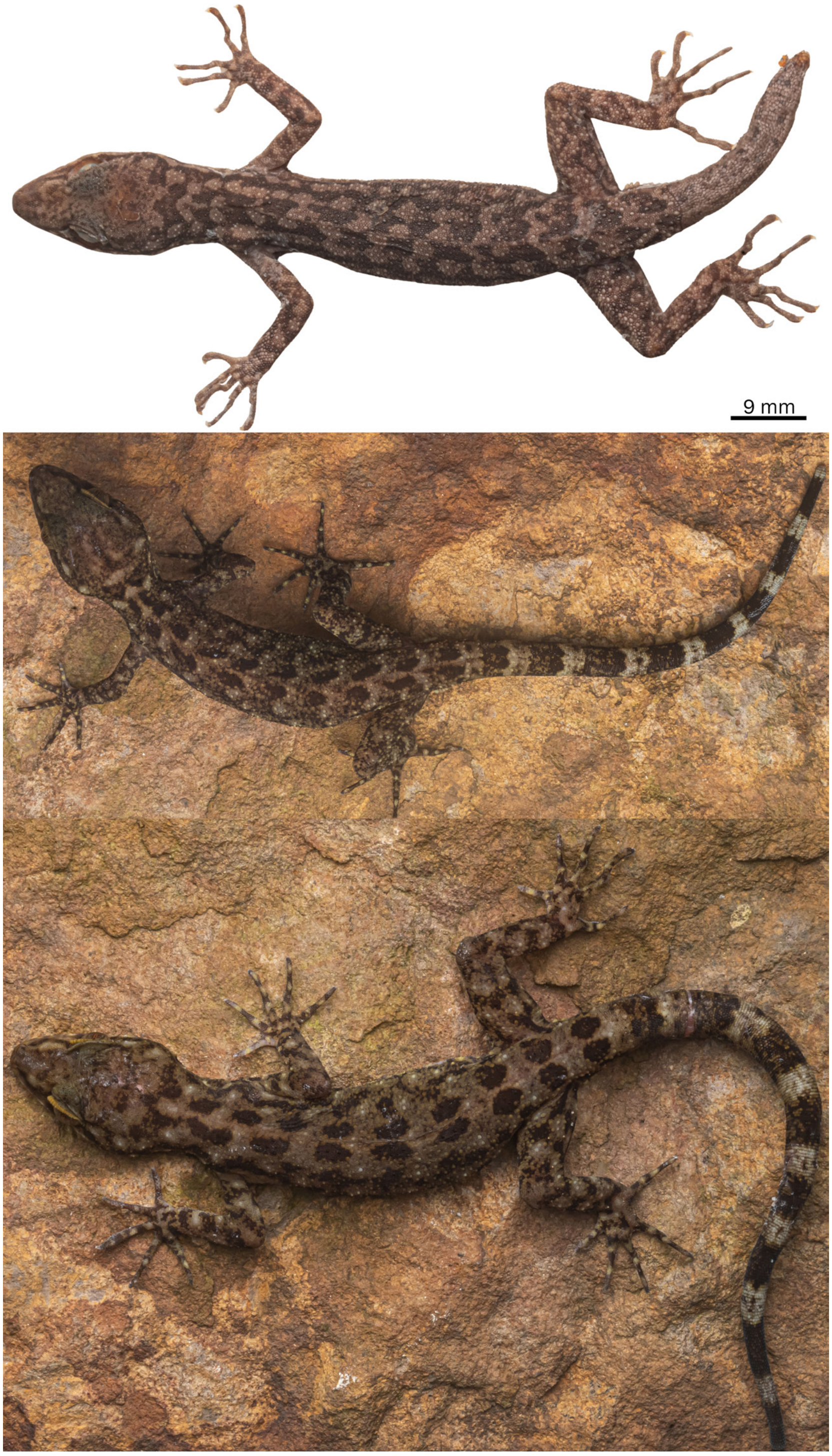

Fig. 1. Some of the topotypical specimens of *Cyrtodactylus khasiensis* Jerdon, 1870. from Umdohlun, South West Khasi Hills District (Top: MZMU 3797 in preservative) and Sohra, East Khasi Hills District (Middle and bottom: MZMU 3798 and ADBU/GT/1 respectively in life) of Meghalaya, northeast India. Photos by Sanath Chandra Bohra.

APPENDIX 2

List of museum specimens examined.

Cyrtodactylus aaronbaueri Purkayastha, Lalremsanga, Bohra, Biakzuala, Decemson, Muansanga, Vabeiryureilai, Chauhan & Rathee, 2021

Holotype

INDIA • ♂ adult; Durtlang, Aizawl District, Mizoram State; MZMU2015

Paratypes

INDIA • 3 ♂♂ adult; Mizoram University Campus, Aizawl District, Mizoram State; MZMU2012, MZMU2021, MZMU2032 • 1 ♀ adult; Tamdil National Wetland Saitual District, Mizoram State; MZMU2067 • ♂ adult; same collection data as for preceding; MZMU2020 • ♂ adult; Zawngtahlipui stream, Sihphir, Aizawl District, Mizoram State; MZMU2014 • 2 ♀♀ adult; Durtlang, Aizawl District, Mizoram State; MZMU2018, MZMU2056

Cyrtodactylus agarwali Purkayastha, Lalremsanga, Bohra, Biakzuala, Decemson, Muansanga, Vabeiryureilai, Chauhan & Rathee, 2021

Holotype

INDIA • ♂ adult; Outskirts of Siju village, South Garo Hills District, Meghalaya State; MZMU2160.

Paratypes

INDIA • 3 ♂♂ adult; Outskirts of Siju village, South Garo Hills District, Meghalaya State; MZMU2157, MZMU2159, MZMU2161 • 1 ♂ sub-adult; same collection data as for preceding; MZMU2158

Cyrtodactylus bengkhuaiai Purkayastha, Lalremsanga, Bohra, Biakzuala, Decemson, Muansanga, Vabeiryureilai, Chauhan & Rathee, 2021

Holotype

INDIA • ♂ adult; Sailam Community Reserved Forest outskirts of Sailam Village, Aizawl District, Mizoram State; MZMU1989

Paratypes

INDIA • 2 ♂♂ adult; Sailam Community Reserved Forest outskirts of Sailam village, Aizawl District, Mizoram State; MZMU1987; MZMU1990 • 3 ♀♀ adult; same collection data as for preceding; MZMU1985, MZMU1986, MZMU1988

Cyrtodactylus guwahatiensis Agarwal, Mahony, Giri, Chaitanya & Bauer, 2018

Referred materials

INDIA • 5 ♂♂ adult; Guwahati, Assam State, India; VR/ERS/ZSI/690, VR/ERS/ZSI/691, VR/ERS/ZSI/693, VR/ERS/ZSI/694, VR/ERS/ZSI/696 • 2 ♀♀ adult; same collection data as for preceding VR/ERS/ZSI/692, VR/ERS/ZSI/695

Cyrtodactylus karsticola Purkayastha, Lalremsanga, Bohra, Biakzuala, Decemson, Muansanga, Vabeiryureilai, Chauhan & Rathee, 2021

Holotype

INDIA • ♂ adult; Outskirts of Siju village, South Garo Hills District, Meghalaya State; MZMU2155

Paratypes

INDIA • 2 ♂♂ adult; Outskirts of Siju village, South Garo Hills District, Meghalaya State; MZMU2154, MZMU2156 • ♀ adult; same collection data as for preceding; MZMU2153

Cyrtodactylus urbanus Purkayastha, Das, Bohra, Bauer & Agarwal, 2020

Holotype

INDIA • ♂ adult; Basistha, Guwahati, Assam State; VR/ERS/ZSI/683

Paratypes

INDIA • 3 ♂♂ adult; Basistha, Guwahati, Assam State; VR/ERS/ZSI/686, VR/ERS/ZSI/685, VR/ERS/ZSI/687 • 3 ♀♀ adult; same collection data as for preceding; VR/ERS/ZSI/684, VR/ERS/ZSI/688, VR/ERS/ZSI/689

Cyrtodactylus exercitus Purkayastha, Lalremsanga, Litho, Rathee, Bohra, Mathipi, Biakzuala, & Muansanga, 2022

Holotype

INDIA • adult ♂; Umroi military cantonment area, Ri-Bhoi District, Meghalaya State; MZMU2542.

Paratypes

INDIA • 1 ♀ adult; Umroi military cantonment area, Ri-Bhoi District, Meghalaya State; MZMU2543 • 2 ♂♂ adult; same collection data as for preceding; MZMU2544 and MZMU2545

Cyrtodactylus siahaensis Purkayastha, Lalremsanga, Litho, Rathee, Bohra, Mathipi, Biakzuala, & Muansanga, 2022

Holotype

INDIA • ♂ adult; New Colony-I, Siaha District, Siaha Town, Mizoram State; MZMU2445

Paratypes

INDIA • 2 ♂♂ adult; New Colony-I, Siaha District, Siaha Town, Mizoram State; MZMU2444, MZMU2446 • 1 ♀ adult; same collection data as for preceding; MZMU2443 • 2 ♀♀ juvenile; same collection data as for preceding; MZMU244, MZMU2449

Cyrtodactylus ngopensis Bohra, Zonunsanga, Das, Purkayastha, Biakzuala & Lalremsanga, 2022

Holotype

INDIA • ♂ adult; Tuikhur veng, Chawngbawla section, Ngopa Town, Champhai District, Mizoram State; MZMU2553

Paratypes

INDIA • 1 ♂ adult; Tuikhur veng, Chawngbawla section, Ngopa Town, Champhai District, Mizoram State; MZMU2555 • 5 ♀♀ adult; same collection data as for preceding; MZMU2552, MZMU2554, MZMU2556, MZMU2557, MZMU2558

Cyrtodactylus vairengtensis Lalremsanga, Colney, Vabeiryureilai, Malsawmdawngliana, Bohra, Biakzuala, Muansanga, Das & Purkayastha, 2023

Holotype

INDIA • ♂ adult; Hall Veng, Vairengte, Kolasib District, Mizoram State; MZMU 2903

Paratypes

INDIA • 3 ♂♂ adult; Vairengte, Kolasib District, Mizoram State; MZMU2904, MZMU2901, MZMU2902 • 3 ♀♀ adult; same collection data as for preceding; MZMU2905, MZMU2626, MZMU2742

Cyrtodactylus lungleiensis

Holotype

INDIA • ♂ adult; Electric Veng, Zobawk, Lunglei District, Mizoram State; MZMU2432

Paratypes

INDIA • 2 ♂♂ adult; Lunglei District, Mizoram State; MZMU2431, MZMU2426 • 3 ♀♀ adult; same collection data as for preceding; MZMU2430, MZMU2427, MZMU2429

Cyrtodactylus tripuraensis Agarwal, Mahony, Giri, Chaitanya & Bauer, 2018

Additional material

INDIA • ♂ adult; Roadside loose soils in Gomati District, Tripura State; MZMU 3796