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Two new cryptic species of *Hemidactylus* (Reptilia: Gekkonidae) allied to *H. treutleri* from Telangana, India

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Abstract. We describe two new species of the genus *Hemidactylus* Goldfuss, 1820, namely *Hemidactylus cairnicola* sp. nov. and *H. koyaorum* sp. nov., from Nalgonda and Warangal districts of Telangana State, India, respectively, based on an integrative assessment of external morphology and mitochondrial NADH dehydrogenase subunit 2 (ND2) gene sequences. Both taxa are assigned to the *Hemidactylus brookii* group and belong to the *murrayi* clade, within which they show closest affinity to *H. treutleri* Mahony, 2009. Mitochondrial sequence divergence reveals substantial genetic differentiation from *H. treutleri*, with the species of Nalgonda exhibiting an uncorrected pairwise distance of 9.5–14.5%, and the species of Warangal differing by 7.0–13.5%. The two newly described species are also genetically distinct from each other, showing an uncorrected p-distance of 9.5–10.0%. These levels of divergence, in conjunction with consistent morphological differences, support the recognition of both taxa as distinct species.

Keywords. Central Plateau, Deccan Peninsula, *Hemidactylus murrayi*, morphology.

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Introduction

The genus *Hemidactylus* Goldfuss, 1820 represents one of the most species-rich gekkonid lineages, with 62 species currently documented from India (Patel *et al.* 2026; Uetz *et al.* 2026). For several decades, the taxonomy of Indian *Hemidactylus* remained largely unchanged until a series of descriptions by Giri (2008), Giri & Bauer (2008), Giri *et al.* (2009), and Mahony (2009) brought four new species to light. Subsequent advances were limited until Agarwal *et al.* (2011) added another species to the genus. A major revision came with the expanded ND2 phylogeny presented by Agarwal *et al.* (2019), which included 26 species of the *brookii* and *prashadi* groups and resolved four clades within the *brookii* group and six within the *prashadi* group. Since then, integrative taxonomic studies have revealed substantial cryptic diversity in *Hemidactylus* spp., with 20 additional species described from India (Agarwal *et al.* 2020; Chaitanya *et al.* 2019; Khandekar *et al.* 2020, 2021, 2023; Lajmi *et al.* 2020; Adhikari *et al.* 2022; Das *et al.* 2022; Kumar *et al.* 2022; Pal & Mirza 2022; Mohapatra *et al.* 2023, 2025a; Narayanan *et al.* 2023; Sayyed *et al.* 2023, 2025).

During the course of our fieldwork, we identified two previously undocumented lineages belonging to the *H. brookii* group in the districts of Nalgonda and Warangal in Telangana. Both lineages fall within the *murrayi* clade, which currently comprises nine described species: *H. treutleri* Mahony, 2009, *H. murrayi* Gleadow, 1887, *H. chikhaldaraensis* Agarwal, Bauer, Giri & Khandekar, 2019, *H. sankariensis* Agarwal, Bauer, Giri & Khandekar, 2019, *H. chipkali* Mirza & Raju, 2017, *H. mahonyi* Adhikari, Achyuthan, Kumar, Khot, Shreeram & Ganesh, 2022, *H. srikanthani* Adhikari, Achyuthan, Kumar, Khot, Shreeram & Ganesh, 2022, *H. rishivalleyensis* Agarwal, Thackeray & Khandekar, 2020, and *H. varadgirii* Chaitanya, Agarwal, Lajmi & Khandekar, 2019. In this paper, we formally describe the two morphologically and genetically distinct lineages as new species.

Material and methods

Sampling

Morphological data were collected from a total of eleven specimens of the two new species, three of which were collected from Nalgonda and eight from Warangal districts in Telangana (Fig. 1). The specimens were hand collected and euthanized with halothane following ethical guidelines for animal euthanasia (Leary *et al.* 2013). Tissues from the liver were collected and stored in molecular grade ethanol for molecular work and for fixation of the specimens, 8% formaldehyde solution was injected into the body and later stored in 70% ethanol after overnight soaking in the formaldehyde solution. Specimens were deposited in the Reptilia section of the Zoological Survey of India, Kolkata (ZSI-R) and Freshwater Biology Regional Centre of ZSI, Hyderabad (FBRC-ZSI).

Morphological and meristic data

Comparative data on described species of *Hemidactylus* from peninsular India were taken from examined type specimens of *H. treutleri* and earlier literature (Mirza & Raju 2017; Agarwal *et al.* 2019, 2020; Chaitanya *et al.* 2019; Adhikari *et al.* 2022). Comparisons were restricted to species in the *H. murrayi* clade. Mensural and meristic data were taken using a Tomlov digital microscope, on the right side of the body where possible. Measurements were taken with a Mitutoyo digital vernier calliper (to the nearest 0.01 mm) and were converted to the nearest decimal of 0.1 mm.

Abbreviations for measurements

We obtained the following meristic and mensural characters following Mahony (2009) and Mohapatra et al. (2025a):

1st finger (LamF1), 2nd (LamF2) …	= number of subdigital lamellae under 1st finger (LamF1), 2nd finger (LamF2) …
1st toe (T1), 2nd toe (T2) …	= number of subdigital lamellae under 1st toe (T1), 2nd toe (T2)…
1st PC	= first postmental contact region
1st PML	= first postmental length
2nd PML	= second postmental length
AGL	= axilla-to-groin length, measured from posterior edge of forelimb insertion to anterior edge of hind-limb insertion)
BW	= body width (maximum width of body)
CL	= crus length (from base of heel to knee)

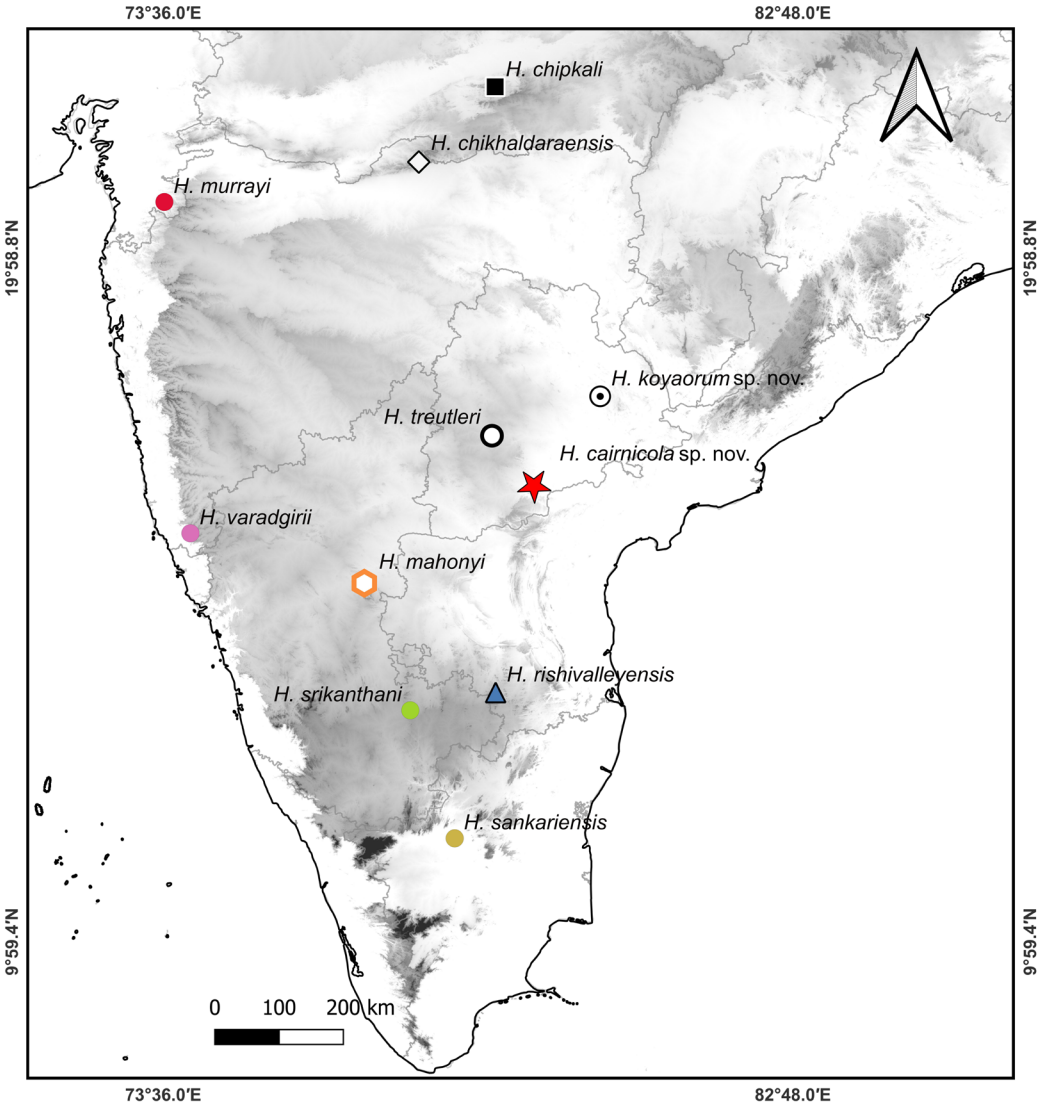


Fig. 1. Type localities of the members of the *Hemidactylus murrayi* clade in India including *H. cairnicola* sp. nov. and *H. koyaorum* sp. nov.

DTR = longitudinal dorsal tubercle rows
ED = eye diameter (greatest diameter of eye)
EE = eye to ear distance (distance from anterior edge of ear opening to posterior margin of eye)
EL = ear length (longest dimension of ear)
EN = eye to nare distance (distance between anterior most point of eye and nostril)
ES = eye to snout distance (distance between anterior most point of eye and tip of snout)
FL = forearm length (from base of palm to elbow)
FP = femoral pores
HD = head depth (maximum height of head, from occiput to underside of jaws)
HL = head length (distance between retroarticular process of jaw and snout-tip)
HW = head width (maximum width of head)
IL = number of infralabials
IN = internarial distance (distance between nares)
IO = interorbital distance (shortest distance between left and right supraciliary scale rows)
ML = mental length (maximum length of the mental scales)
MVSR = meristic data recorded were number of transverse ventral scale rows across midbody between ventrolateral folds
SBFP = number of poreless scales between femoral pores
SL = number of supralabials
TL = tail length from vent to tip of tail
TW = tail width, measured at widest point of tail
VS = number of longitudinal ventral scales (between mental and cloaca, excluding the postmentals)

Statistical analyses

Morphological data analyses were conducted in R software (R Core Team 2021), with graphical representations produced using the ggplot2 package (Wickham 2009). Patterns of morphometric variation and similarity among populations were examined through Principal Component Analysis (PCA). A total of 18 morphometric variables (excluding ear length, EL) were included in the PCA, based on measurements obtained from 16 individuals. Allometric effects within the morphometric dataset were calculated and corrected using the GroupStruct R package (Chan & Grismer 2022), following the allometric equations proposed by Thorpe (1975, 1983). Multivariate analyses were performed using the R package MASS (Venables & Ripley 2002). Permutational multivariate analysis of variance (PERMANOVA) and multivariate homogeneity of group dispersions (PERMDISP) were performed using the betadisper function in the the R package vegan ver. 2.5–3 (Oksanen *et al.* 2020) to evaluate within-group morphological dispersion among species and to test statistical differences among species centroids based on the numeric morphometric dataset (Skalski *et al.* 2018).

Molecular data

Genomic DNA was extracted from ethanol-preserved liver tissue using the DNeasy Blood and Tissue Kit (Qiagen, Hilden, Germany) following the manufacturer's protocol. The complete mitochondrial NADH dehydrogenase subunit 2 (ND2) gene was amplified using the primers MetF1 and H5934, and a 1041 bp fragment was sequenced using the MetF1 primer (Macey *et al.* 1997). Polymerase chain reaction (PCR) amplification was performed with an initial denaturation at 95°C for 2 min, followed by 32 cycles of denaturation at 94.5°C for 35 s, annealing at 50°C for 35 s, and extension at 72°C for 2 min 30 s, with a final extension at 72°C for 10 min. Sequencing was outsourced to Eurofins India Pvt. Ltd. (Hyderabad, India). Newly generated sequences were concatenated with corresponding ND2 sequences from 13 species of the *Hemidactylus brookii* group, including all members of the *H. murrayi* clade, with *Hemidactylus kalinga* and *H. flaviviridis* as the outgroup (Table 1). Raw chromatograms were manually checked and edited using Chromas ver. 2.6.6 (http://technelysium.com.au/wp/chromas), and sequence

alignment was performed using ClustalW (Thompson *et al.* 1994) with default parameters. Uncorrected pairwise genetic distances (p-distances) were calculated in MEGA ver. 7 (Kumar *et al.* 2016) using the pairwise deletion option and built a maximum likelihood (ML) tree using IQ-TREE ver. 3.1.3 (Wong *et al.* 2026) with ModelFinder selected HKY+G+I as the best-fit nucleotide substitution model. Statistical support for nodes was evaluated using 10 000 ultrafast bootstrap pseudoreplicates. BEAST ver. 1.7 (Drummond *et al.* 2012) was used to construct a Markov chain Monte Carlo (MCMC)-based Bayesian consensus tree (Fig. 2). The best nucleotide substitution model, HKY + I, was used for Bayesian inference analyses. MCMC chains were run for 10 million generations, logging every 1000 generations, with 10% of each run discarded as burn-in. The runs were evaluated using Tracer ver. 1.6, and resulting phylogenetic trees were visualized in FigTree ver. 1.4.0 (http://tree.bio.ed.ac.uk/software/figtree/).

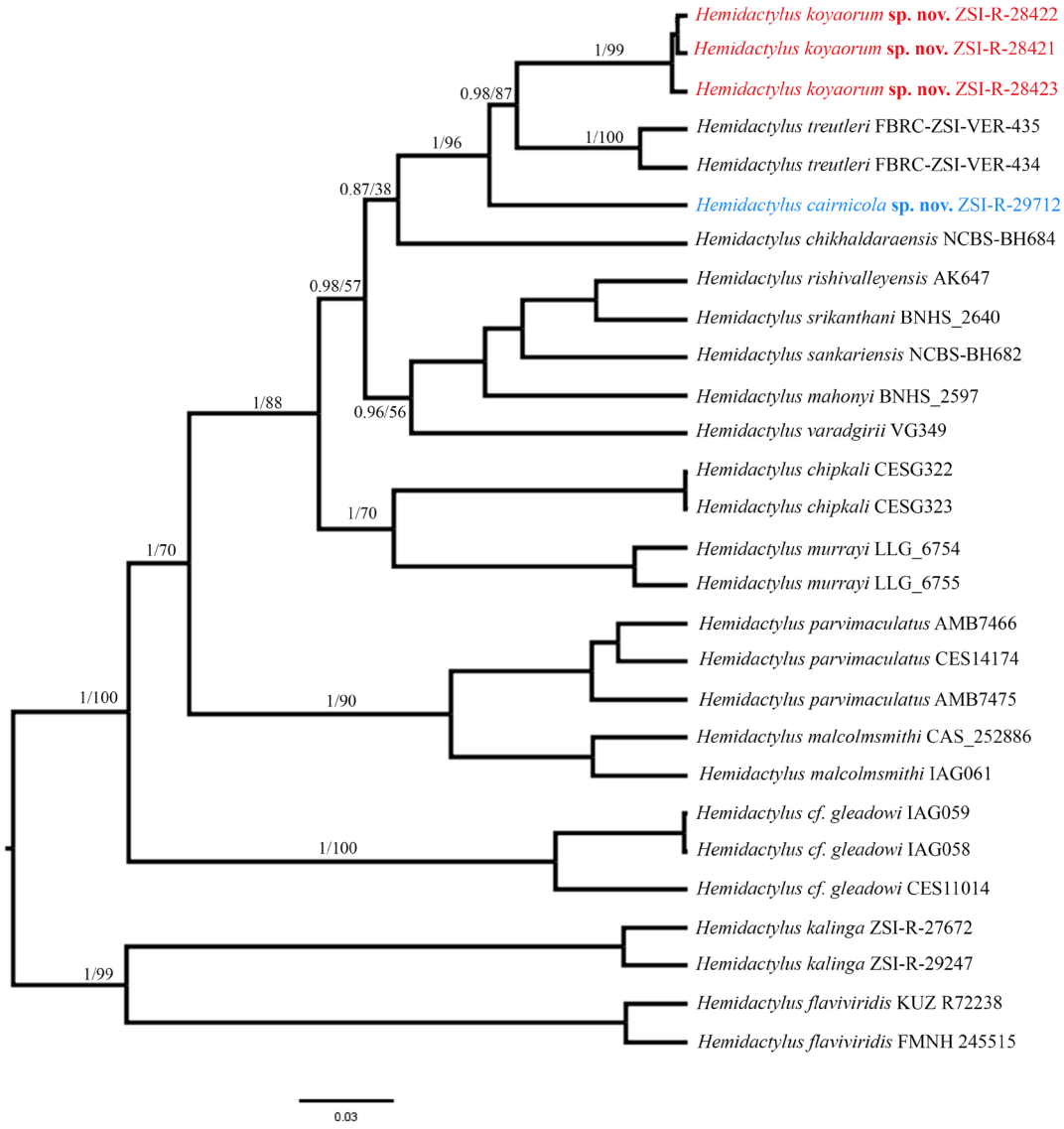


Fig. 2. Phylogenetic tree of the *Hemidactylus murrayi* clade based on the mitochondrial ND2 gene along with members of closely related other clades. Values at the nodes represent Bayesian posterior probabilities (PP) and Maximum Likelihood ultrafast bootstrap (UFB) support. *Hemidactylus kalinga* Mohapatra, Ray, Das, Bhupathi, Sarkar, Mohalik, Nair & Dutta, 2025 and *H. flaviviridis* Rüppell, 1835 were used as outgroups.

The aligned dataset was also subjected to phylogenetic analysis using the Maximum Likelihood (ML) framework in MEGA ver. 7 (Kumar *et al.* 2016) with an ultra-fast search method and 1000 bootstrap replicates.

Results

Phylogenetic relationships

The two newly identified lineages are nested within the *Hemidactylus murrayi* clade; *H. cairnicola* sp. nov. (this is the Nalgonda population) being sister to *H. treutlerti* and *H. koyaorum* sp. nov. (this is the Warangal population) being sister to the former two species. Together these three taxa are sister to all remaining members of the *H. murrayi* clade. Uncorrected pairwise genetic distances based on ND2 sequences indicate that the Warangal and Nalgonda lineages differ from *H. treutleri* by 7.0–13.5% and 9.5–14.5%, respectively, and by 9.5–10.0% from each other. Both lineages exhibit >15% divergence from other members of the *H. murrayi* clade (Table 2).

Taxonomy

Phylum Chordata Haeckel, 1874
Class Reptilia Laurenti, 1768
Order Squamata Oppel, 1811
Family Gekkonidae Gray, 1825
Subfamily Gekkoninae Gray, 1825
Genus *Hemidactylus* Goldfuss, 1820

Hemidactylus cairnicola sp. nov.
urn:lsid:zoobank.org:act:709DB863-B953-4669-ABE9-78BD994A19ED
Figs 1–4, 5A–B, 8–10; Tables 1–3, 5–6

Hemidactylus treutleri – Narayana *et al.* 2014 (in part).

Diagnosis

A medium-sized *Hemidactylus*, SVL up to 49.0 mm (n = 3). Dorsal pholidosis heterogeneous, composed of subcircular granular scales intermixed with enlarged, fairly regularly arranged, strongly keeled, conical tubercles in 13–15 longitudinal rows, extending from occiput to tail base, that are heterogeneous in shape and size. Ventrolateral fold present; about 31–32 scale rows across belly; longitudinal ventral scales 137–145. Digits with enlarged scansors, lamellae in straight transverse series with 0–1 undivided lamellae, six or seven lamellae beneath the first digit and nine or 10 beneath the fourth digit of manus and pes. Males with seven or eight femoral pores on each side, separated by eight poreless scales.

Etymology

The specific epithet '*cairnicola*' is proposed to highlight the species' characteristic association with traditional stone cairns at and around the type locality. Field observations showed that individuals were almost exclusively encountered within the narrow crevices and interstitial spaces of these man-made stone piles, which provide stable microclimatic refugia and secure shelter. This consistent habitat preference distinguishes the species from sympatric congeners that inhabit natural rock outcrops, tree bark, or human dwellings. The name therefore reflects a defining ecological trait of the new species and emphasizes the role of culturally constructed stone cairns in sustaining local gecko diversity.

Table 1. Sequences of the mitochondrial ND2 gene used in this study.

Sl. No	Species	GenBank Accession No.	Voucher	Locality
1	*Hemidactylus treutleri* Mahony, 2009	MH454770	CES14216	India, Telangana, Rangareddy District, Hyderabad, Gaganpahad
2	*H. treutleri*	PZ830930	FBRC-ZSI-VER-434	India, Telangana, Rangareddy District, Hyderabad, Himayat Sagar
3	*H. treutleri*	PZ830931	FBRC-ZSI-VER-435a	India, Telangana, Rangareddy District, Hyderabad, Himayat Sagar
4	*H. koyaorum* sp. nov.	PZ944181	ZSI-R-28421	India, Telangana, Warangal District, Pakhal Wildlife Sanctuary, Pakhal Nature Trail
5	*H. koyaorum* sp. nov.	PZ944182	ZSI-R-28424	India, Telangana, Warangal District, Pakhal Wildlife Sanctuary, Pakhal Nature Trail
6	*H. koyaorum* sp. nov.	PZ944183	FBRC-ZSI-VS-30	India, Telangana, Warangal District, Pakhal Wildlife Sanctuary, Haritha Resort
7	*H. cairnicola* sp. nov.	PZ944184	ZSI-R-29712	India, Telangana, Nalgonda District, Pedda Vagu Reservoir, Vardhamani Gudem
8	*H. varadgirii* Chaitanya, Agarwal, Lajmi & Khandekar, 2019	MK569849	VG349	India, Maharashtra, Sindhudurg, Amboli
9	*H. varadgirii*	MK569848	AQ473	India, Maharashtra, Sindhudurg, Amboli
10	*H. mahonyi* Adhikari, Achyuthan, Kumar, Khot, Shreeram & Ganesh, 2022	OM912578	BNHS 2597	India, Karnataka, Bellary, Joga
11	*H. rishivalleyensis* Agarwal, Thackeray & Khandekar, 2020	MT773220	AK647	India, Andhra Pradesh, Chittoor, Rishi Valley
12	*H. srikanthani* Adhikari, Achyuthan, Kumar, Khot, Shreeram & Ganesh, 2022	OM912580	BNHS 2640	India, Karnataka, Tumkur, Devarayanadurga
13	*H. chikhaldaraensis* Agarwal, Bauer, Giri & Khandekar, 2019	MK569807	NCBS-BH684	India, Maharashtra, Amravati, Gawilgarh Fort
14	*H. sankariensis* Agarwal, Bauer, Giri & Khandekar, 2019	MK569844	NCBS-BH682	India, Tamil Nadu, Erode, Sankari
15	*H. chipkali* Mirza & Raju, 2017	MK569808	CESG322	India, Madhya Pradesh, Hoshangabad, Pachmarhi
16	*H. chipkali*	MK569809	CESG323	India, Madhya Pradesh, Hoshangabad, Pachmarhi
17	*H. murrayi* Gleadow, 1887	EU268365	LLG 6754	Malaysia, Pulau Pinang, Empangon Air Hitam
18	*H. murrayi*	EU268366	LLG 6755	Malaysia, Pulau Pinang, Empangon Air Hitam
19	*H. malcolmsmithi* Constable, 1949	MK569842	IAG061	India, Maharashtra, Amravati, Chikhaldara
20	*Hemidactylus malcolmsmithi*	KM975948	CAS 252886	India, Himachal Pradesh, Hamirpur, Sujanpur
21	*H. parvimaculatus* Deraniyagala, 1953	MH454766	CES14174	India, Andhra Pradesh, Visakhapatnam, Araku forest guest house
22	*H. parvimaculatus*	GQ458056	AMB7466	Sri Lanka, Kandy
23	*H. parvimaculatus*	GQ458055	AMB7475	Sri Lanka, Mampuriya
24	*H.* cf. *gleadowi*	MH454761	CES11014	India, Karnataka, Bagalkot
25	*H.* cf. *gleadowi*	MK569810	IAG059	India, Maharashtra, Amravati, Chichghat
26	*H.* cf. *gleadowi*	MK569811	IAG058	India, Maharashtra, Buldhana, near Lokhanda
27	*H. kalinga* Mohapatra, Ray, Das, Bhupathi, Sarkar, Mohalik, Nair & Dutta, 2025	MK569846	ZSI-R-27672	India, Odisha State, Kandhamal District, Kalinga Ghati

Table 2. Pairwise uncorrected ND2 sequence divergence (p-distances) in percentage, among the *Hemidactylus murrayi* clade in India along with members of closely related other clades and the outgroups.

Sl. No	Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	*Hemidactylus treutleri*	0–4													
2	*H. koyaorum* sp. nov.	7–13.5	0–0.5												
3	*H. cairnicola* sp. nov.	9.5–14.5	9.5–10												
4	*H. mahonyi*	12–13.5	12	13.5											
5	*H. srikanthani*	13–14.5	13.5	13.5	9.5										
6	*H. chikhaldaraensis*	14.5–15	13.5	15.5	14.5	15.5									
7	*H. varadgirii*	10.5–17	13–14	14	11.5	12–12.5	15								
8	*H. rishivalleyensis*	13–19	15.5–16	14.5	10	5.5	15	13							
9	*H. sankariensis*	15.5–16	14.5	14.5	11	9.5	18	14	11						
10	*H. murrayi*	14–21	16.5–17.5	17.5	15.5	15–16	16–18	17	17–18	17–18	0–3				
11	*H. malcolmsmithi*	16–24	21.5–22	22	19.5	20.5	19	22	23	21	20–20.5	21–21.5			
12	*H. parvimaculatus*	18–25	20–22	20–21	17.5–19	17.5–19.5	17–18	20–21	20–21	19–20	20–20.5	19.5–21	0–5		
13	*H.* cf. *gleadowi*	18.5–25.5	21–22.5	22–23.5	18–19	20.5–21	19–20	21–22	21–22	19–20	22–24	20–22	24–22.5	0–6	
14	*H. kalinga*	22.5–27.5	22–24	22–24	21.5–22	23.5	21–22	23–24	25	26	25–25.5	24–24.5	24–26	25–26	0

Type material

Holotype

INDIA • ♂; Telangana State, Nalgonda District, near Vardhamani Gudem Bus Shelter, Guntu Madgu, between Pendlipakala and Pedda Vagu Reservoirs; 16.653509° N, 79.017558° E; alt. 262 m; 13 Oct. 2025; Bharath Bhupathi and B. Laxmi Narayana leg.; ZSI-R, ZSI-R-29712 (Fig. 3).

Paratypes (n = 2; Fig. 4)

INDIA • 1 ♂; same data as for holotype; FBRC-ZSI, FBRC-ZSI-VS-31 • 1 ♀; same data as for holotype; FBRC-ZSI, FBRC-ZSI-VS-32.

Other material examined

INDIA • 1 ♀; same data as for holotype; ZSI-R, ZSI-R-29713.

Description (holotype)

The male holotype is in good condition. The tail is bent to the left and partly regenerated. There is a 2.8 mm long incision in the ventral region (for tissue collection).

Medium-sized gecko (SVL 49.0 mm) with large head (HL/SVL ratio 0.33), slightly elongate (HW/HL ratio 0.66), depressed (HD/HL ratio 0.34), distinct from neck. Loreal region slightly inflated. Snout short (ES/HL ratio 0.38); scales on snout, canthus rostralis granular, larger than those on interorbital and occipital region; scales on occipital region heterogenous, comprising small granular scales intermixed with enlarged tubercles. Eye small (ED/HL ratio 0.21); pupil vertical with serrated margins; supraciliaries small, those at anterior end of orbit elongate, lacking spines. Ear opening deep, oval (greatest height 1.2 mm); eye to ear distance greater than diameter of eyes (EE/ED ratio 1.18). Rostral incompletely divided dorsally by weakly developed rostral groove; rostral in contact with supralabial I, nostril, one small internasal and two semi-circular supranasals; nostrils subcircular, oriented dorsally, not touching supralabial I, each nostril surrounded by rostral, three postnasals, and one supranasal; two rows of scales separate orbit from supralabials. Mental triangular, slightly higher (2.4 mm) than broad (2.3 mm), two pairs of postmentals, inner pair slightly shorter (2.3 mm) than mental and in extensive contact with each other (0.9 mm) behind mental; outer postmental fairly smaller than inner postmental (1.3 mm). Inner postmentals bordered by mental, infralabial I and II, outer postmental and three gular scales; outer postmentals bordered by inner postmental, infralabial II and III and seven gular scales on either side, of which outer row continues as single row of enlarged scales below infralabials. Supralabials nine (right), 10 (left); infralabials nine.

Body relatively stout, not elongate (AGL/SVL ratio 0.37), with distinct ventrolateral folds. Dorsal pholidosis heterogeneous, composed of uniform, rounded, granular scales intermixed with enlarged, posteriorly keeled, conical tubercles with oval outline, extending from occiput onto tail; 15 rows of tubercles across midbody; each enlarged tubercle surrounded by more or less 13 small granules, two or three granules separate adjacent enlarged tubercles; enlarged tubercles similar in size except those on most medial rows less than half size of adjacent tubercle; enlarged tubercles on nape smaller. Ventral scales larger than dorsal granules, smooth, and largest on femoral region; midbody scale rows across belly 31; longitudinal ventral scales from mental to cloaca 139; gular region with granular scales smaller than ventrals.

Scales on palm and sole smooth, granular, rounded; dorsal aspect of forearm predominantly bearing smooth scales larger than scales of dorsum of body, with very few small tubercles; scales on shoulder smooth without any tubercles; those on dorsal aspect of thigh heterogeneous with a few granular scales similar to those on dorsum, intermixed with much larger trihedral tubercles slightly larger than enlarged dorsal tubercles; scales on back of thigh without any tubercles; large trihedral tubercles on dorsal aspect

of crus smaller than those on dorsum of thigh, intermixed with a few granular scales. Seven femoral pores on left side and eight on right in enlarged row of ventral scales, separated medially by eight poreless scales. Fore- and hind limbs relatively short, stout; forearm short (FL/SVL ratio 0.13); tibia short (CL/SVL ratio 0.17); digits moderately short, strongly clawed; terminal phalanx of all digits curved, arising angularly from distal portion of expanded lamellar pad or scansor; lamellae beneath each toe in straight transverse series, divided except for one to two basal scansors on digit I and single distal on all digits and some single basal ones too: 7-9-9-9-9 (right manus), 7-9-9-9-9 (left manus), 7-9-10-10-9 (right pes), 7-9-10-10-8 (left pes). Relative length of digits (measurements in mm in parentheses): IV (3.5) > III (3.1) > V (3.0) > II (2.8) > I (2.3) (left manus); IV (3.8) > V (3.7) > III (4.2) > II (3.8) > I (2.1) (left pes). Two postcloacal spurs on each side, which are smooth and much smaller than dorsal tubercles at mid-body. Tail depressed, flat beneath, verticillate, with well-defined median furrow; length of regenerated tail as long as snout-vent length (TL/SVL ratio 1.0); dorsal and lateral scales on tail subimbricate, granular, larger than granules on dorsum, with a series of much enlarged, strongly pointed and keeled conical tubercles; ventral scales enlarged, imbricate, median row (subcaudal plates) covering almost entire base of tail after ten rows of smaller scales.

Coloration (Fig. 5A). In life, dorsal coloration light brown to grey, variable as per background habitat; head bordered with five or six dark spots followed by three larger spots on nape; a pair of preocular streaks and pair of postocular streaks present; lower postocular streak merges with discontinuous lateral line on both sides of body passing through tympanum; dorsal body and tail with dark irregular spots; fore- and hindarms of same color; base of phalanges with darker stripes; regenerated tail darker than original tail; ventrum lighter than body color and unpatterned. In preservative, major color patterns retained.

Variation

Mensural data for the type series is given in Table 3. There are two paratypes (one male and one female) ranging in SVL from 42.7 mm to 44.7 mm. They agree with the description of the holotype in most of the morphological characters except as follows: supralabials 10–12; ventral scales across midbody 32; longitudinal ventral scales 137–145; dorsal tubercle rows 13–15.

Comparison with members of the *murrayi* clade

Hemidactylus cairnicola sp. nov. was phylogenetically recovered as part of the *murrayi* clade and can be distinguished from other members of this clade based on the combination of following characters: MVSR 31 or 32 (vs 33 or 34 in *H. treutleri*, 33 in *H. murrayi*, 33–35 in *H. sankariensis*, 28–30 in *H. chipkali*, 37 or 38 in *H. srikanthani*); male with seven or eight FP and eight SBFP (vs 16 or 17 FP and seven SBFP in *H. srikanthani*, 10–12 FP and nine or 10 SBFP in *H. rishivalleyensis*, 15 FP and four SBFP in *H. sankariensis*, nine or 10 FP and four to six SBFP in *H. varadgirii*, six SBFP in *H. murrayi* and *H. mahonyi*, seven SBFP in *H. chikhaldaraensis* and *H. treutleri*); 13–15 DTR (vs 16–20 in *H. murrayi*, 15 or 16 in *H. treutleri*, 15–17 in *H. sankariensis* and 17 or 18 in *H. varadgirii*); sub-digital lamellae beneath digit I of manus six or seven (vs five in *H. chipkali*, five or six in *H. mahonyi* and *H. varadgirii*); sub-digital lamellae beneath digit I of pes six (vs five in *H. chipkali* and seven in *H. srikanthani* and *H. chikhaldaraensis*); sub-digital lamellae beneath digit IV of manus nine or 10 (vs seven in *H. chipkali*, eight or nine in *H. mahonyi*, eight in *H. varadgirii* and *H. sankariensis*); sub-digital lamellae beneath digit IV of pes 10 (vs seven or eight in *H. chipkali* and *H. varadgirii*, nine in *H. treutleri*, 11 in *H. chikhaldaraensis* and 7–9 in *H. sankariensis* and *H. murrayi*).

Additionally, *H. cairnicola* sp. nov. can be easily distinguished from its closest species *H. treutleri* by: outer postmentals bordered by infralabial II and III (vs infralabial II only); VS 137–145 (vs 133–136) and SVL up to 49.0 mm (vs 70.2 mm).

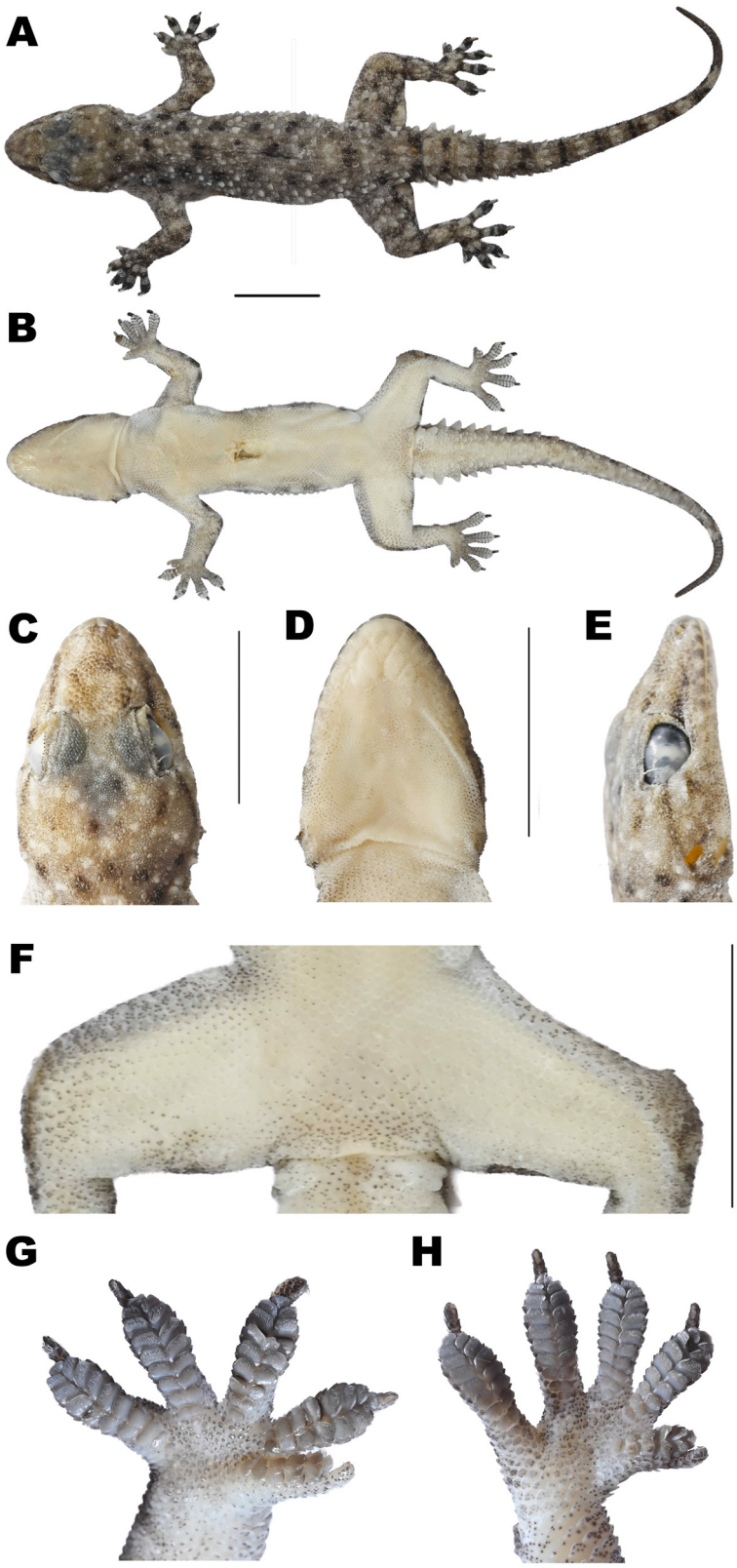


Fig. 3. *Hemidactylus cairnicola* sp. nov., holotype, ♂ (ZSI-R-29712). **A**. Body, dorsal view. **B**. Body, ventral view. **C**. Head, dorsal view. **D**. Head, ventral view. **E**. Head, lateral view. **F**. View of cloacal region. **G**. Right front limb. **H**. Right hind limb. Scale bars = 10 mm.

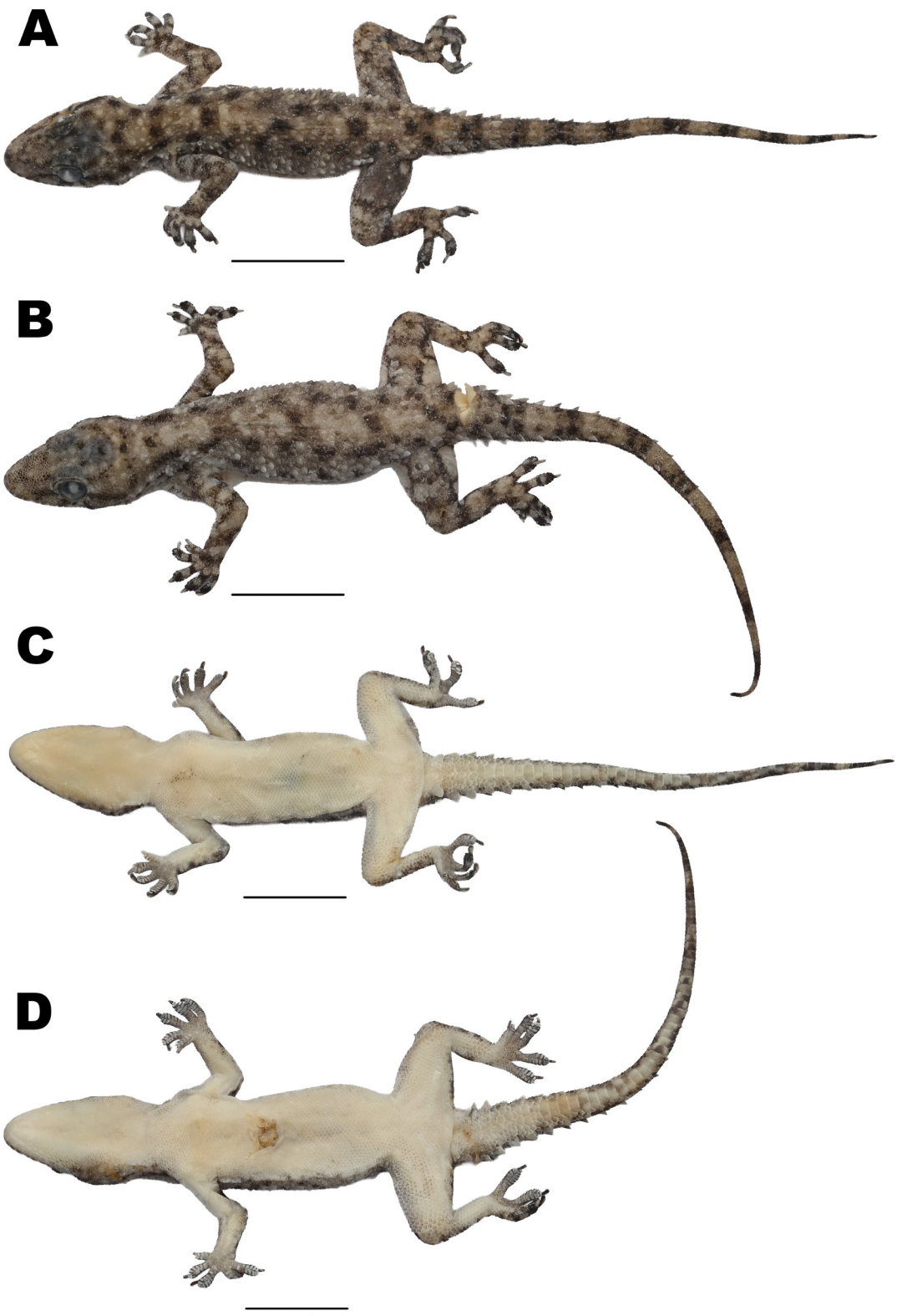


Fig. 4. Full body view of the paratypes of *Hemidactylus cairnicola* sp. nov. **A**. Paratype, ♂ (FBRC-ZSI-VS-31), dorsal view. **B**. Paratype, ♀ (FBRC-ZSI-VS-32), dorsal view. **C**. Paratype, ♂ (FBRC-ZSI-VS-31), ventral view. **D**. Paratype, ♀ (FBRC-ZSI-VS-32), ventral view. Scale bars = 10 mm.

Table 3. Morphological and meristic data for type specimens of *Hemidactylus cairnicola* sp. nov.

Voucher No.	**ZSI-R-29712**	**FBRC-ZSI-VS-31**	**FBRC-ZSI-VS-32**
Sex	male	male	female
SVL	49.0	44.7	42.7
AGL	18.0	16.7	16.2
BW	11.2	10.4	9.1
TL	49.0 (regenerated)	50.2	49.4
TW	6.5	5.6	4.9
HL	16.0	14.1	14.4
HW	10.6	9.5	9.0
HD	5.5	5.3	5.0
FL	6.3	6.4	6.0
CL	8.2	7.6	7.4
ED	3.4	3.0	2.7
IO	5.5	5.1	5.0
EN	5.0	5.1	4.7
ES	6.0	6.0	6.2
EE	4.0	4.1	3.7
EL	1.2	1.3	1.3
IN	1.4	1.3	1.4
ML	2.4	1.8	2.0
1st PML	2.3	1.9	2.0
1st PC	0.9	1.1	0.9
2nd PML	1.3	1.4	1.3
MVSR	31	32	32
VS	139	145	137
LamF1 (L/R)	7/6	6/7	6/6
LamF2 (L/R)	8/8	9/9	8/8
LamF3 (L/R)	9/9	9/9	8/9
LamF4 (L/R)	10/10	9/9	9/9
LamF5 (L/R)	10/9	9/9	9/9
LamT1 (L/R)	6/6	6/6	6/6
LamT2 (L/R)	9/9	9/9	9/*
LamT3 (L/R)	10/10	10/10	9/9
LamT4 (L/R)	10/10	10/10	10/10
LamT5 (L/R)	9/9	9/9	9/9
FP	7/8	7/7	–
SBFP	8	8	–
SL (L/R)	10/9	10/12	12/11
IL (L/R)	9/9	9/9	9/9
DTR	15	15	13

Distribution and natural history

Hemidactylus cairnicola sp. nov. is currently known only from its type locality in the Nalgonda District, Telangana, India. The species inhabits rocky outcrops (Fig. 5B) within a matrix of rocky scrub forest and adjacent agricultural landscapes, often in close proximity to human settlements, including Lambada thandas (traditional, often isolated, habitations of the Banjara/Lambada tribe, primarily found in Telangana, Andhra Pradesh, and Karnataka state of India) and small villages. Individuals were frequently encountered on black rock cairns and exposed rock surfaces, where their dorsal coloration provides effective camouflage against the substrate. The species occurs sympatrically with several other reptiles, including *Hemidactylus* cf. *frenatus* Duméril & Bibron, 1836 and *H.* cf. *giganteus* Stoliczka, 1871 (Gekkonidae Gray, 1825); *Eutropis macularia* (Blyth, 1853) and *E. nagarjuni* (Sharma, 1969) (Scincidae Gray, 1825); *Psammophilus blanfordanus* (Stoliczka, 1871) and *Sitana thondalu* Deepak, Khandekar, Chaitanya & Karanth, 2018 (Agamidae Gray, 1827); and the snake *Eryx johnii* (Russell, 1801) (Boidae Gray, 1825). *Hemidactylus cairnicola* sp. nov. appears to be primarily nocturnal, with individuals observed basking and resting on rock surfaces during daylight hours during winters and rainy days. However, it retreats into rock crevices during periods of inactivity and becomes active at night, when it forages for insects. The dominant plant species associated with its habitat include *Gyrocarpus*

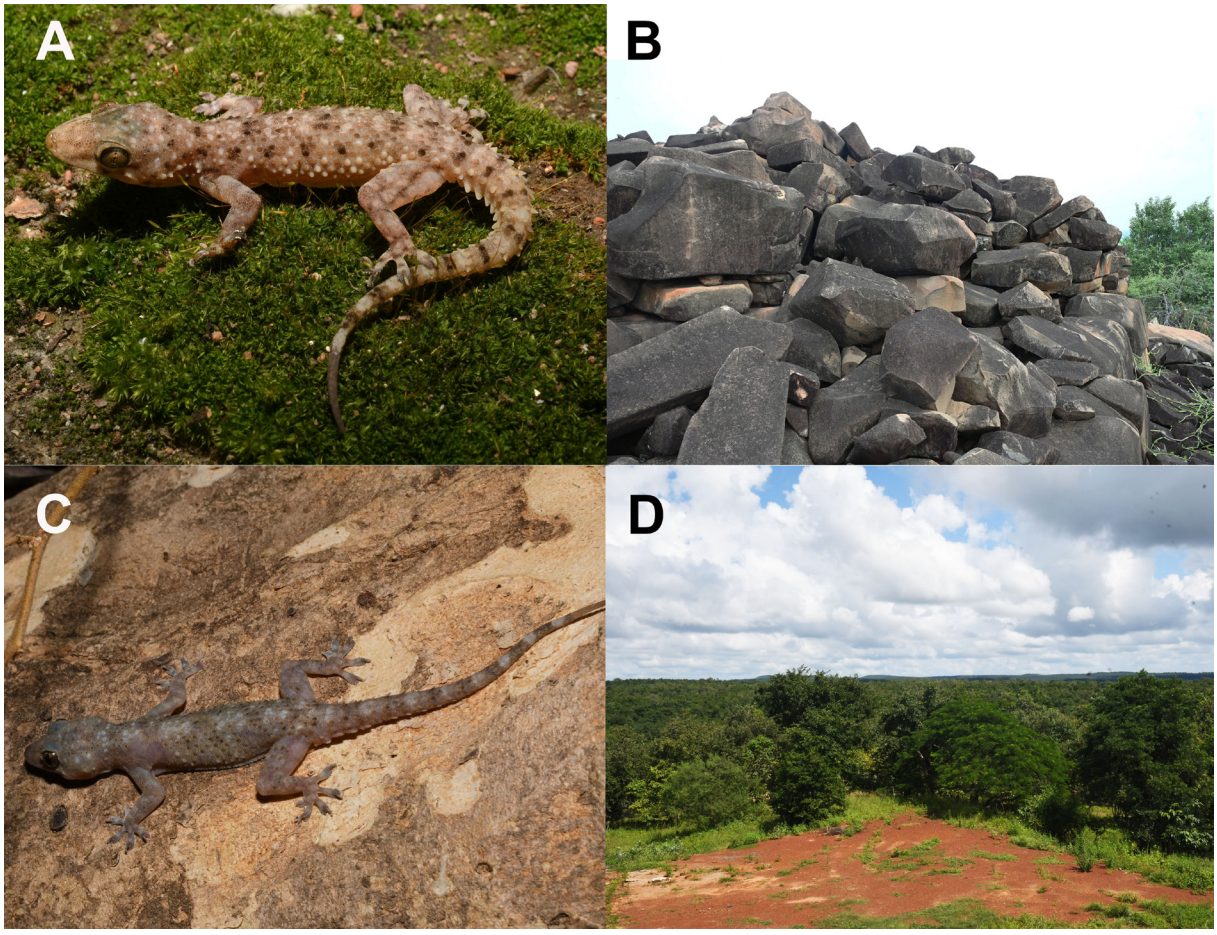


Fig. 5. A–B. *Hemidactylus cairnicola* sp. nov. **A**. Live uncollected individual. **B**. Habitat of *H. cairnicola* sp. nov. at the type locality in Nalgonda District, Telangana. **C–D**. *H. koyaorum* sp. nov. **C**. Live uncollected individual. **D**. Habitat of *H. koyaorum* sp. nov. at the type locality in Warangal District, Telangana.

americanus Jacq., *Chloroxylon swietenia* DC., *Mundulea sericea* (Willd.) A.Chev., *Albizia amara* (Roxb.) Boiv., *Dodonaea viscosa* Jacq., and *Canthium coromandelicum* (Burm.f.) Alston.

Hemidactylus koyaorum sp. nov.
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Figs 1–2, 5C–D, 6–10; Tables 1–2, 5–6

Diagnosis

A medium-sized *Hemidactylus*, SVL up to 55.6 mm (n = 8). Dorsal pholidosis heterogeneous, composed of subcircular granular scales intermixed with enlarged, fairly regularly arranged, strongly keeled, conical tubercles in 15 or 16 longitudinal rows, extending from occiput to tail base, that are heterogeneous in shape and size. About 27–34 scale rows across belly; longitudinal ventral scales 120–133; ventrolateral fold present. Digits with enlarged scansors, lamellae in straight transverse series, almost all divided, 6 or 7 lamellae beneath first digit and 9 or 10 beneath fourth digit of manus and pes. Males with 7–9 femoral pores on each side separated by 6 or 7 poreless scales.

Etymology

The specific epithet '*koyaorum*' is formed from the Latin plural genitive suffix '*-orum*', and is intended to honor the Koya people, an indigenous tribal community of central and south-eastern India known for their deep cultural ties to the forests and hills of the region. The name thus means "of the Koya". It acknowledges the tribe's longstanding stewardship of the landscapes in which this species occurs and recognizes their cultural heritage and traditional ecological knowledge.

Holotype

INDIA • ♂; Telangana State, Warangal District, Pakhal nature trail; 17.9603° N, 79.9850° E; alt. 277 m; 13 Sep. 2022; Pratyush P. Mohapatra and party leg.; ZSI-R, ZSI-R-28421 (Fig. 6).

Paratypes (n = 7; Fig. 7)

INDIA • 1 ♀; same data as for holotype; ZSI-R, ZSI-R-28422 • 1 ♂; same data as for holotype; ZSI-R-28423 • 1 ♂; same data as for holotype; ZSI-R, ZSI-R-28424 • 1 ♂; same data as for holotype; ZSI-R-28425 • 1 ♀; same data as for holotype; ZSI-R, ZSI-R-28426 • 1 ♂; Telangana State, Warangal District, Pakhal Wildlife Sanctuary; 17.9337° N, 79.9828° E; alt. 279 m; 13 Sep. 2022; Pratyush P. Mohapatra and party leg.; ZSI-R, ZSI-R-28428 • 1 ♂; Telangana State, Warangal District, in front of Haritha Resort, near Pakhal lake; 17.9482° N, 79.9808° E; alt. 278 m; 28 Mar. 2024; Bharath Bhupathi leg.; FBRC-ZSI, FBRC-ZSI-VS-30.

Other material examined

INDIA • 1 ♀; Telangana State, Warangal District, Pakhal Wildlife Sanctuary; 17.9337° N, 79.9828° E; alt. 279 m; 13 Sep. 2022; Pratyush P. Mohapatra and party leg.; ZSI-R, ZSI-R-28427.

Description (holotype)

The holotype is in good condition with a curved tail. It is a male specimen. The head is slightly bent to the right. The tail is bent to the left and partly regenerated.

Medium-sized gecko (SVL 55.1 mm) with large head (HL/SVL ratio 0.32), slightly elongate (HW/HL ratio 0.67), depressed (HD/HL ratio 0.36), distinct from neck. Loreal region slightly inflated. Snout short (ES/HL ratio 0.41); scales on snout, canthus rostralis granular, larger than those on interorbital and occipital region, small scales on occipital region mostly homogenous without any tubercles. Eye small (ED/HL ratio 0.2); pupil vertical with serrated margins; supraciliaries small, those at anterior end

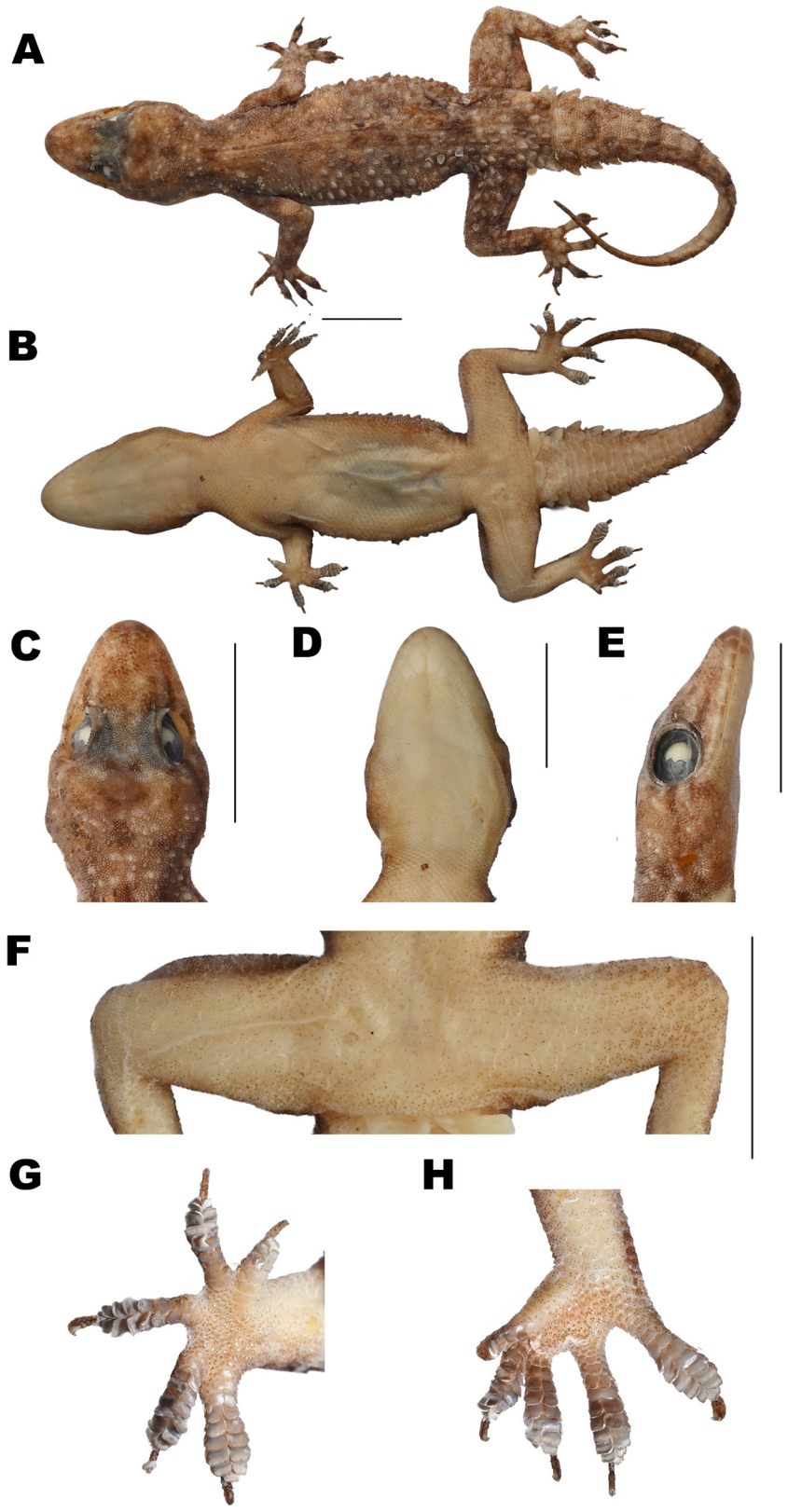


Fig. 6. *Hemidactylus koyaorum* sp. nov., holotype, ♂ (ZSI-R-28421). **A**. Body, dorsal view. **B**. Body, ventral view. **C**. Head, dorsal view. **D**. Head, ventral view. **E**. Head, lateral view. **F**. View of cloacal region. **G**. Right front limb. **H**. Right hind limb. Scale bars = 10 mm.

of orbit elongate, lacking spines. Ear opening deep, oval (greatest height 1.3 mm); eye to ear distance greater than diameter of eyes (EE/ED ratio 1.32). Rostral incompletely divided dorsally by weakly developed rostral groove, which fails to meet anterior of snout; rostral in contact with supralabial I, nostril, one small internasal and two semi-circular supranasals; nostrils subcircular, oriented dorsally, not touching supralabial I, each nostril surrounded by rostral, three postnasals, and one supranasal; two rows of scales separate orbit from supralabials. Mental triangular, broader (3.0 mm) than high (2.5 mm), two pairs of postmentals, inner pair slightly longer (2.8 mm) than mental and in extensive contact with each other (1.6 mm) behind mental; outer postmental fairly smaller than inner postmental (1.7 mm). Inner postmentals bordered by mental, infralabial I and II, outer postmental and three gular scales; outer postmentals bordered by inner postmental, infralabial II and 8 gular scales on either side, of which outer row continues as a single row of enlarged scales below infralabials. Supralabials 11 (right), 10 (left); infralabials nine (right), eight (left).

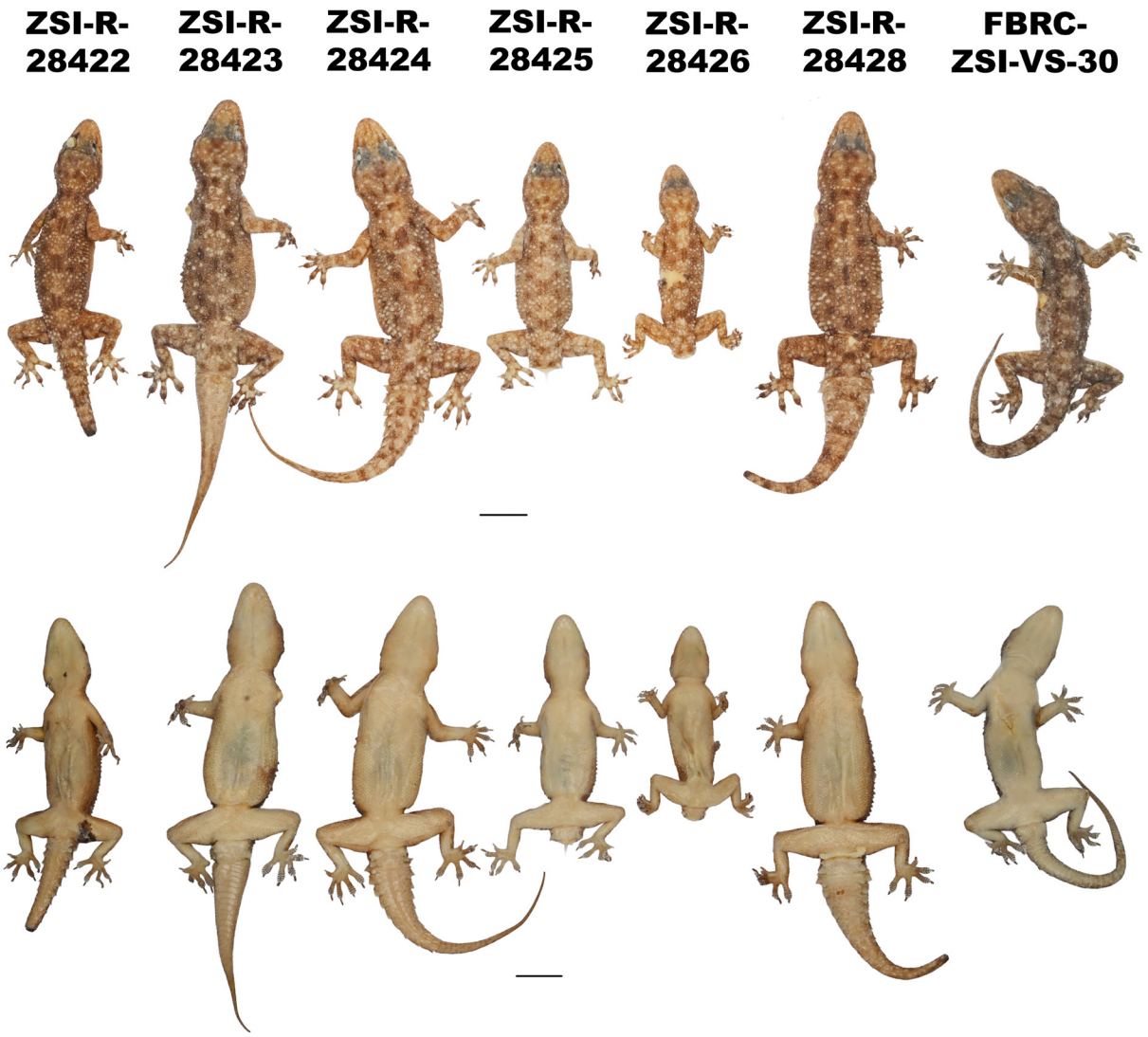


Fig. 7. Full body views of the paratypes of *Hemidactylus koyaorum* sp. nov., dorsal and ventral views. Scale bars = 10 mm.

Body relatively stout, not elongate (AGL/SVL ratio 0.42). Dorsal pholidosis heterogeneous, composed of uniform, rounded, granular scales intermixed with enlarged, posteriorly keeled, conical tubercles with oval outline, extending from occiput onto the tail; 15 rows of tubercles across midbody; each enlarged tubercle surrounded by 11–15 small granules, two or three granules separate adjacent enlarged tubercles; enlarged tubercles similar in size except those on most medial rows less than half size of adjacent tubercle; enlarged tubercles on nape slightly smaller; some part of dorsum regenerated. Ventral scales larger than dorsal granules, smooth, slightly larger on femoral and largest on precloacal region; midbody scale rows across belly 27; longitudinal ventral scales from mental to cloaca 123; gular region with granular scales smaller than ventrals.

Scales on palm and sole smooth, granular, rounded; dorsal aspect of forearm predominantly bearing smooth scales larger than scales of the dorsum of body, with very few small tubercles; scales on shoulder smooth without any tubercles; those on dorsal aspect of thigh heterogeneous with a few granular scales similar to those on dorsum, intermixed with much larger trihedral tubercles slightly larger than enlarged dorsal tubercles; scales on back of thigh without any tubercles; large trihedral tubercles on dorsal aspect of crus smaller than those on dorsum of thigh, intermixed with a few granular scales. Seven femoral pores on each side in slightly enlarged row of scales, separated medially by seven poreless scales. Fore- and hind limbs relatively short, stout; forearm short (FL/SVL ratio 0.14); tibia short (CL/SVL ratio 0.16); digits moderately short, strongly clawed; terminal phalanx of all digits curved, arising angularly from distal portion of expanded lamellar pad or scansor; lamellae beneath each toe in straight transverse

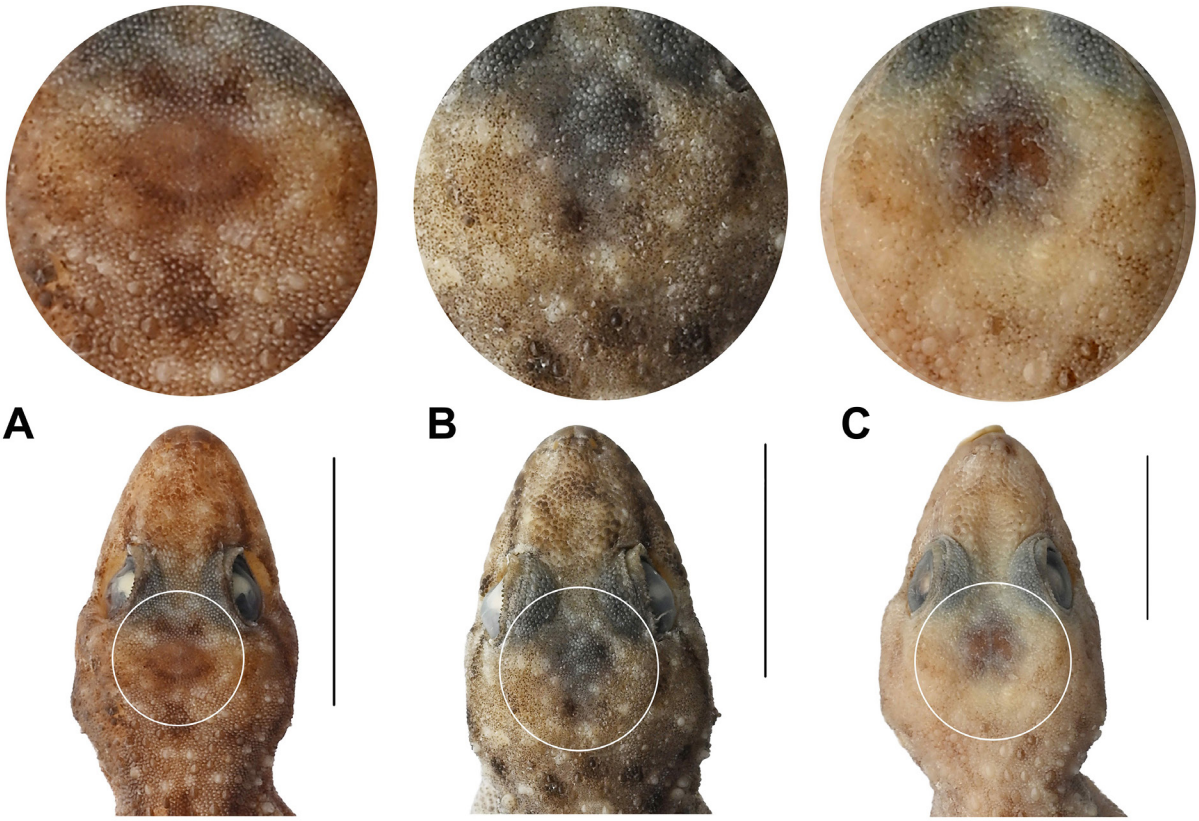


Fig. 8. Comparisons of head scalation on occipital region among three closely allied species. **A**. *Hemidactylus koyaorum* sp. nov. (mostly homogenous and without any keeled scales). **B**. *Hemidactylus cairnicola* sp. nov. **C**. *Hemidactylus treutleri* Mahony, 2009 with heterogeneous, granular scales intermixed with enlarged keeled scales.

series, divided except for one to two basal scansors on digit I and single distal on all digits and some single basal ones too: 7-9-9-9-9 (right manus), 7-9-9-9-9 (left manus), 7-9-10-10-9 (right pes), 7-9-10-10-8 (left pes). Relative length of digits (measurements in mm in parentheses): IV (4.67) > III (4.62) > V (4.53) > II (4.07) > I (3.0) (left manus); IV (5.30) > V (4.80) > III (4.67) > II (4.08) > I (3.35) (left pes). Two postcloacal spurs of subequal size on each side those are smooth and much smaller than dorsal tubercles at mid-body. Tail depressed, flat beneath, verticillate, with well-defined median furrow; length of regenerated tail slightly longer than snout-vent length (TL/SVL ratio 1.0); dorsal and lateral scales on the tail subimbricate, granular, larger than granules on dorsum, with a series of much enlarged, strongly pointed and keeled conical tubercles; ventral scales enlarged, imbricate, median row (subcaudal plates) covering almost entire base of tail after seven rows of smaller scales.

Coloration (Fig. 5C). In life, dorsal coloration grey with four prominent white flower-like patterns on body, surrounded by darker margins; head and nape dotted with white spots; some tubercles on dorso-lateral sides randomly spottsed with white; pair of faint preocular streaks present; tail with white pattern and with scattered dark spots; ventral lighter and unpatterned. In preservative, white pattern not visible in some specimens.

Variation

Mensural data for the type series is given in Table 4. There are seven paratypes (five males and two females) ranging in SVL from 39.7 mm to 55.6 mm. They agree with the description of the holotype in most of the morphological characters except as follows: supralabials 9–11; scales across midbody 29–34; longitudinal ventral scales 120–133; femoral pores 7–9; porless scales between femoral pores 6–7; 4th toe lamellae 9–10.

Comparison with members of the *murrayi* clade

Hemidactylus koyaorum sp. nov. can be easily distinguished from other members of the *murrayi* clade based on the following characters: MVSR 27–34 (vs 37 or 38 in *H. srikanthani*); male with 7–9 FP and six or seven SBFP (vs eight SBFP in *H. chipkali* and *H. cairnicola* sp. nov., six or seven FP and six SBFP in *H. murrayi*, six or seven FP in *H. chikhaldaraensis*, 15 FP and four SBFP in *H. sankariensis*, 16 or 17 FP and seven SBFP in *H. srikanthani*, 10–12 FP and nine or 10 SBFP in *H. rishivalleyensis*, nine or 10 FP and 4–6 SBFP in *H. varadgirii*); 15 or 16 DTR (vs 13–15 in *H. cairnicola* sp. nov., 16–20 in *H. murrayi*, 13 or 14 in *H. mahonyi*, 14 or 15 in *H. srikanthani* and 17 or 18 in *H. varadgirii*); sub-digital lamellae beneath digit I of manus and pes six or seven (vs five in *H. chipkali* and five or six in *H. mahonyi* and *H. varadgirii*); sub-digital lamellae beneath digit IV of manus nine (vs 10 in *H. chikhaldaraensis*, eight in *H. sankariensis* and *H. varadgirii* and seven in *H. chipkali*); sub-digital lamellae beneath digit IV of pes 10 (rarely nine, in one specimen) (vs nine in *H. treutleri*, 7–9 in *H. sankariensis* and *H. murrayi*, 11 in *H. chikhaldaraensis* and seven or eight in *H. chipkali* and *H. varadgirii*).

Additionally, *H. koyaorum* sp. nov. can be easily distinguished from its two closest species *H. treutleri* and *H. cairnicola* sp. nov. by: scales on occipital region mostly homogenous without any keeled scales (vs heterogeneous, granular scales intermixed with enlarged keeled scales in *H. treutleri* and *H. cairnicola* sp. nov.) (Fig. 8); outer postmentals bordered by infralabial II (vs infralabial II and III in *H. cairnicola* sp. nov.); VS 120–133 (vs 133–136 in *H. treutleri* and 137–145 in *H. cairnicola* sp. nov.); supralabials 9–11 (vs 11 or 12 in *H. treutleri*); infralabials eight or nine (vs nine or 10 in *H. treutleri*); SVL up to 55.6 mm (vs 49.0 mm in *H. cairnicola* sp. nov. and 70.2 mm in *H. treutleri*).

Distribution and natural history

Hemidactylus koyaorum sp. nov. is endemic to the Deccan Peninsula biogeographic zone and is currently known only from its type locality in Warangal District, Telangana State, India. The species was recorded

Table 4 (continued on next page). Morphological and meristic data for type specimens of *Hemidactylus koyaorum* sp. nov. * denotes damaged body parts.

Voucher No.	**ZSI-R-28421 (holotype)**	**ZSI-R-28422 (paratype)**	**ZSI-R-28423 (paratype)**	**ZSI-R-28424 (paratype)**
Sex	male	female	male	male
SVL	55.1	47.7	55.6	55.2
AGL	23.3	19.3	24.6	25.5
BW	14.0	11.5	15.2	14.0
TL	55.2	*	*	57.0
TW	8.8	6.5	8.6	8.0
HL	17.4	14.8	17.4	16.8
HW	11.7	10.4	11.8	11.7
HD	6.3	6.1	6.4	6.9
FL	7.7	6.2	7.3	8.0
CL	8.7	8.1	9.6	9.1
ED	3.4	3.2	3.7	3.7
IO	5.1	*	6.5	6.0
EN	5.3	4.6	5.8	5.1
ES	7.1	6.4	7.5	6.8
EE	4.5	3.8	4.6	4.8
EL	1.3	1.3	1.2	1.5
IN	1.6	1.3	1.7	1.7
ML	2.2	2.2	2.1	2.0
1st PML	2.8	2.0	2.5	2.7
1st PC	1.6	1.0	1.1	1.5
2nd PML	1.7	1.3	1.7	2.1
MVSR	27	31	29	29
VS	123	127	120	123
LamF1 (L/R)	7/7	6/6	*/7	7/7
LamF2 (L/R)	9/9	9/9	*/9	9/9
LamF3 (L/R)	9/9	9/9	*/9	9/9
LamF4 (L/R)	9/9	9/9	*/9	9/9
LamF5 (L/R)	9/9	9/9	*/9	9/9
LamT1 (L/R)	7/7	6/6	7/7	*/6
LamT2 (L/R)	9/9	9/9	9/9	9/9
LamT3 (L/R)	10/10	10/10	10/10	10/10
LamT4 (L/R)	10/10	10/10	10/10	10/10
LamT5 (L/R)	8/9	9/9	9/*	9/9
FP	7/7	–	8/8	7/7
SBFP	7	–	7	7
SL (L/R)	10/11	10/9	10/11	*/10
IL (L/R)	8/9	8/8	8/8	8/8
DTR	15	16	15	15

from an extended portion of Pakhal Wildlife Sanctuary characterized by scattered boulders of varying sizes on lateritic red soil (Fig. 5D). During the time of observation, the soil was slightly moist following

Table 4 (continued).

Voucher No.	**ZSI-R-28425 (paratype)**	**ZSI-R-28426 (paratype)**	**ZSI-R-28428 (paratype)**	**FBRC-ZSI-VS-30 (paratype)**
Sex	male	female	male	male
SVL	45.6	39.7	53.1	49.0
AGL	18.6	17.8	22.1	22.3
BW	11.7	8.7	14.4	11.2
TL	*	*	*	*
TW	6.8	5.0	9.9	6.8
HL	14.7	12.7	17.2	16.2
HW	9.9	8.1	11.9	10.3
HD	5.8	5.1	7.0	6.2
FL	5.8	5.6	7.2	6.9
CL	7.3	6.0	8.7	7.6
ED	2.9	2.5	3.3	3.0
IO	5.3	4.5	6.0	5.6
EN	4.9	3.9	5.2	5.1
ES	6.5	5.5	6.8	6.8
EE	4.1	3.4	5.0	4.2
EL	1.2	1.0	1.3	1.2
IN	1.7	1.3	1.8	1.7
ML	1.9	1.9	2.2	2.2
1st PML	2.1	1.7	2.8	2.2
1st PC	1.1	0.9	1.6	1.2
2nd PML	1.6	1.4	1.8	1.9
MVSR	32	30	30	34
VS	133	132	123	130
LamF1 (L/R)	7/7	7/7	*/6	6/6
LamF2 (L/R)	9/9	8/9	*/8	8/8
LamF3 (L/R)	9/9	9/9	*/9	9/9
LamF4 (L/R)	9/9	9/9	*/9	9/9
LamF5 (L/R)	9/9	9/9	*/9	9/9
LamT1 (L/R)	7/7	7/7	6/6	6/6
LamT2 (L/R)	9/9	9/9	9/9	9/9
LamT3 (L/R)	10/10	10/10	9/10	10/10
LamT4 (L/R)	10/10	9/9	10/10	10/10
LamT5 (L/R)	9/9	8/8	8/9	9/9
FP	7/7	–	7/7	9/8
SBFP	7	–	6	7
SL (L/R)	11/11	10/10	10/10	11/10
IL (L/R)	8/9	8/8	8/8	9/9
DTR	16	15	16	16

Table 5. PCA factor loadings.

Characters	PC1	PC2	PC3	PC4	PC5	PC6
SVL	-0.225	0.232	0.083	0.605	-0.62	-0.354
AGL	-0.251	-0.119	-0.179	0.26	0.004	0.362
BW	-0.248	-0.091	0.037	-0.113	-0.321	0.467
TW	-0.31	-0.208	-0.128	-0.394	-0.377	0.094
HL	-0.162	0.14	-0.085	-0.113	0.0872	-0.14
HW	-0.217	0.135	0.028	-0.146	-0.03	0.03
HD	-0.236	0.019	-0.137	-0.054	-0.043	0.081
FL	-0.223	0.005	0.316	0.228	0.312	0.156
CL	-0.148	0.175	0.135	-0.083	-0.042	0.225
ED	-0.22	0.251	0.167	0.083	0.041	0.306
EN	-0.198	0.33	-0.066	-0.127	0.158	-0.134
ES	-0.175	0.158	-0.067	-0.106	0.045	0.083
EE	-0.225	0.07	-0.092	-0.099	0.128	-0.152
IN	-0.168	-0.08	-0.583	-0.082	-0.009	-0.244
ML	-0.251	0.421	0.26	-0.172	0.182	-0.201
1st PML	-0.227	0.024	-0.121	-0.123	0.017	-0.239
1st PC	-0.357	-0.622	0.479	-0.08	0.061	-0.335
2nd PML	-0.3	-0.197	-0.32	0.447	0.423	0.059

Table 6. PERMANOVA summary statistics based only on the morphometric data. $p < 0.05$ indicates statistical significance.

Species pairs	F. Model	R^2	p-value	p-adjusted
H. cairnicola sp. nov. vs *H. koyaorum* sp. nov.	11.3337	0.56	0.008	0.024*
H. cairnicola sp. nov. vs *H. treutleri*	57.6743	0.91	0.017	0.051
H. koyaorum sp. nov. vs *H. treutleri*	25.6665	0.70	0.001	0.003*

light morning drizzle. Most individuals were encountered beneath a boulder, positioned slightly above the ground surface. Upon disturbance, the animals exhibited rapid serpentine locomotion through the grass and leaf litter, suggesting an adaptation for movement within dense ground cover. The new species occurs sympatrically with several other reptiles, including *Hemidactylus flaviviridis* Rüppell, 1835, *H.* cf. *giganteus* Stoliczka, 1871, *H. leschenaultii* Duméril & Bibron, 1836, and *H. murrayi* Gleadow, 1887 (Gekkonidae); *Eutropis allapallensis* (Schmidt, 1926) (Scincidae); *Sitana spinaecephalus* Deepak, Vyas & Giri, 2016 (Agamidae); and snakes such as *Oligodon taeniolatus* (Jerdon, 1853) (Colubridae), *Naja naja* (Linnaeus, 1758) (Elapidae), and *Indotyphlops braminus* (Daudin, 1803) (Typhlopidae).

Multivariate analyses

A Principal Component Analysis (PCA) based on 18 morphometric variables revealed patterns of morphological variation among three closely related *Hemidactylus* lineages from Telangana, India. Clear separation among the lineages was observed in the morphospace (Fig. 9), and the first two principal component axes together explained 86.45% of the total variance. Factor loadings for each morphometric variable are presented in Table 5.

PCA loadings revealed relatively uniform contributions of most morphometric characters along PC1, indicating that overall morphological variation was driven collectively by multiple traits rather than by a single dominant character. The highest contributions to PC1 were observed for 1st PC, TW and 2nd PML, whereas PC2 and PC3 were primarily influenced by 1st PC, ML, EN, and IN. It suggest that the observed morphometric differentiation among the three *Hemidactylus* taxa is associated with variation in overall body proportions and head morphology (Table 5).

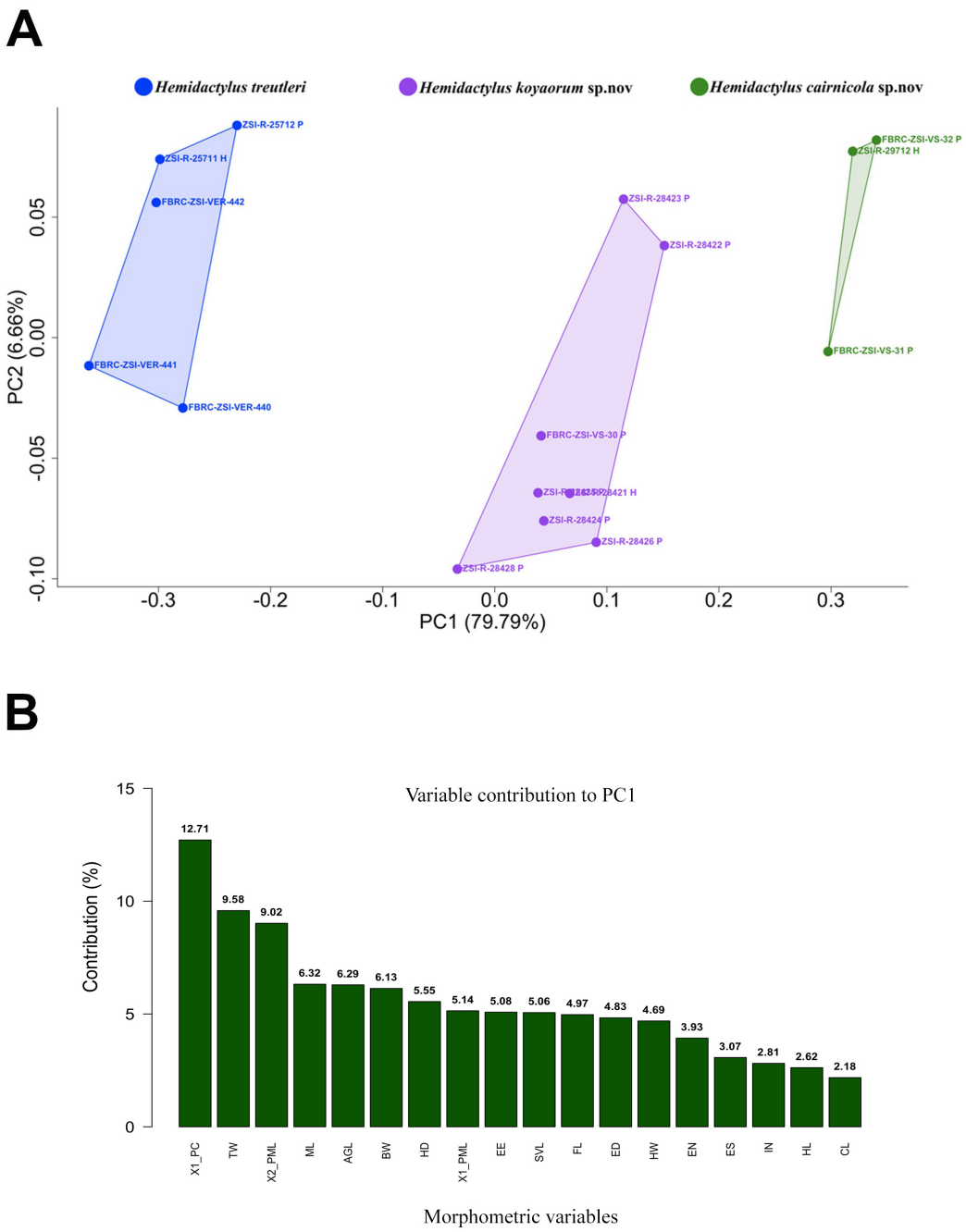


Fig. 9. A. Principal Component Analysis (PCA) results showing clear separation in morphometric characters between the three closely allied species of *Hemidactylus* found in Telangana state of India. **B**. PCA variable contribution.

Pairwise PERMANOVA revealed significant morphometric differentiation between *Hemidactylus cairnicola* sp. nov. and *H. koyaorum* sp. nov. ($F = 11.33$, $R^2 = 0.56$, p_adj = 0.024), and between *H. koyaorum* sp. nov. and *H. treutleri* ($F = 25.66$, $R^2 = 0.70$, p_adj = 0.003). The comparison between *H. cairnicola* sp. nov. and *H. treutleri* yielded an extremely high effect size ($R^2 = 0.91$), indicating pronounced morphometric divergence. However, the Bonferroni-adjusted p-value was marginally non-significant (p_adj = 0.051). Overall, the large effect sizes observed across comparisons support substantial morphological structuring among the three species (Table 6).

A PERMDISP analysis indicated differences in multivariate dispersion among the three species of *Hemidactylus* (Fig. 10). *Hemidactylus cairnicola* sp. nov. exhibited relatively lower dispersion around the group centroid, suggesting comparatively lower intraspecific morphological variation, whereas *H. koyaorum* sp. nov. showed the highest dispersion, indicating greater morphological heterogeneity. *Hemidactylus treutleri* displayed intermediate levels of dispersion. Nevertheless, the clear separation observed in PCA morphospace, together with significant PERMANOVA results, supports distinct morphometric differentiation among the three taxa.

The significant PERMANOVA results, coupled with high effect sizes, indicate strong morphometric differentiation among the three species of *Hemidactylus*. The clearcut separation in PCA morphospace,

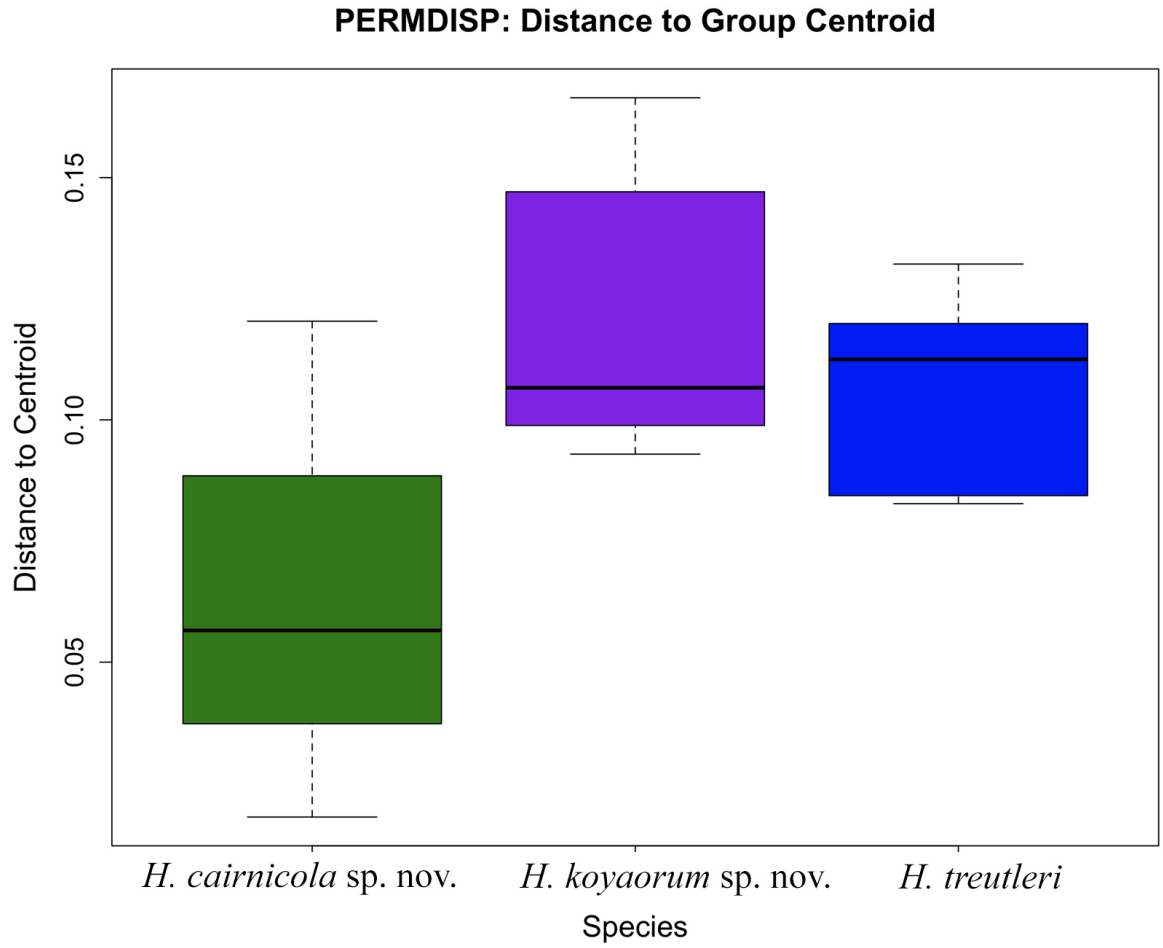


Fig. 10. PERMDISP box plot showing differences in multivariate dispersion among the two new species and *Hemidactylus treutleri* Mahony, 2009.

with the first two components explaining a substantial proportion of total variance, further supports distinct morphological structuring. Together, these findings provide robust quantitative evidence for species-level delimitation among the studied species.

Discussion

With the descriptions of *Hemidactylus cairnicola* sp. nov. and *H. koyaorum* sp. nov., the current number of endemic reptile species in Telangana State increases to six (Mohapatra *et al.* 2025b). The remaining four endemic species include *Hemidactylus aemulus* Kumar, Srinivasulu & Srinivasulu, 2022, *H. flavicaudus* Lajmi, Giri, Singh & Agarwal, 2020, *H. treutleri*, and *H. xericolus* Lajmi, Giri, Singh & Agarwal, 2020. Biogeographically, both new species are restricted to the Central Plateau biogeographic province (Fig. 6D) within the Deccan Peninsula biogeographic zone (Rodgers *et al.* 2000), further highlighting the region as an important centre of endemism.

The *Hemidactylus brookii* group in India has long been recognised as harbouring some of the most cryptic diversity among congeners (Carranza & Arnold 2006; Bansal & Karanth 2010; Bauer *et al.* 2010; Mahony 2011; Lajmi *et al.* 2016, 2019; Agarwal *et al.* 2019; Agashe *et al.* 2025). Within this group, the *murrayi* clade has received comparatively extensive taxonomic attention (Mirza & Raju 2017; Agarwal *et al.* 2019, 2020; Chaitanya *et al.* 2019; Adhikari *et al.* 2022). Nevertheless, the discovery of the two new species described herein suggests that substantial hidden diversity persists even within this relatively well-studied clade. In contrast, species complexes within other clades of the *H. brookii* group, particularly the *brookii-malcolmsmithii-parvimaculatus* clade, remain poorly resolved, warranting systematic sampling and focused integrative taxonomic investigations.

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