



# A new species of large-bodied *Hemidactylus* Goldfuss, 1820 (Squamata: Gekkonidae) from the Western Ghats of India

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## Abstract

A new large (94–107mm SVL) species of gecko of the genus *Hemidactylus* is described from the drier parts of the Western Ghats of India. The new species is closely related to *H. graniticolus*, from which it can be distinguished based on dorsal pholidosis at mid-body, the structure of tubercles on the dorsum, dorsal pholidosis on the tail. The new species is also 6.6–7.2% divergent from *H. graniticolus* in the ND2 mitochondrial gene.

## Keywords

Gecko, Kerala, morphology, ND2, new species, phylogeny, taxonomy

## Introduction

The gekkonid genus *Hemidactylus* Goldfuss, 1820 is one of the most speciose groups of geckos with 180 known species distributed across the globe (Uetz et al. 2021). Nearly one-third of this diversity, 48 species, is found in India (Uetz et al. 2021). A recent study showed the role

of the Eocene–Oligocene cooling that facilitated the early diversification of *Hemidactylus* spp. in peninsular India (Lajmi and Karanth 2020). Furthermore, it is shown that most of the diversification in the endemic Indian radiation of *Hemidactylus* spp. occurred in the drier zones with

multiple dispersals into Sri Lanka (Lajmi et al. 2019). Among the south Asian *Hemidactylus*, *prashadi* clade is well-supported (Agarwal et al. 2019a and Lajmi et al. 2019) and comprises 20 described species that are largely restricted to peninsular India and Sri Lanka (Khandekar et al. 2021). This group can be differentiated from the other members of the genus by their having mostly medium to large adult body size (SVL 77–128 mm).

Among these larger geckos (SVL >100 mm), seven species are restricted to the Western Ghats, namely: *Hemidactylus aaronbaueri* Giri, 2008; *H. maculatus* Duméril & Bibron, 1836; *H. prashadi* Smith 1935; *H. paaragowli* Srikanthan, Swamy, Mohan & Pal, 2018; *H. acanthopholis* Mirza & Zanap, 2014; *H. vanam* Chaitanya, Lajmi & Giri, 2018; and *H. tamhiniensis* Khandekar, Thackeray & Agarwal, 2021. Three species, *H. graniticolus* Agarwal, Giri & Bauer 2011; *H. triedrus* Daudin, 1802; and *H. whitakeri* Mirza, Gowande, Patil, Ambekar & Patel 2018 seems to be widespread and are reported from the Western Ghats, the Eastern Ghats and the Mysore plateau (Agarwal et al. 2011; Mirza et al. 2018; Agarwal et al. 2019a; Lajmi et al. 2019).

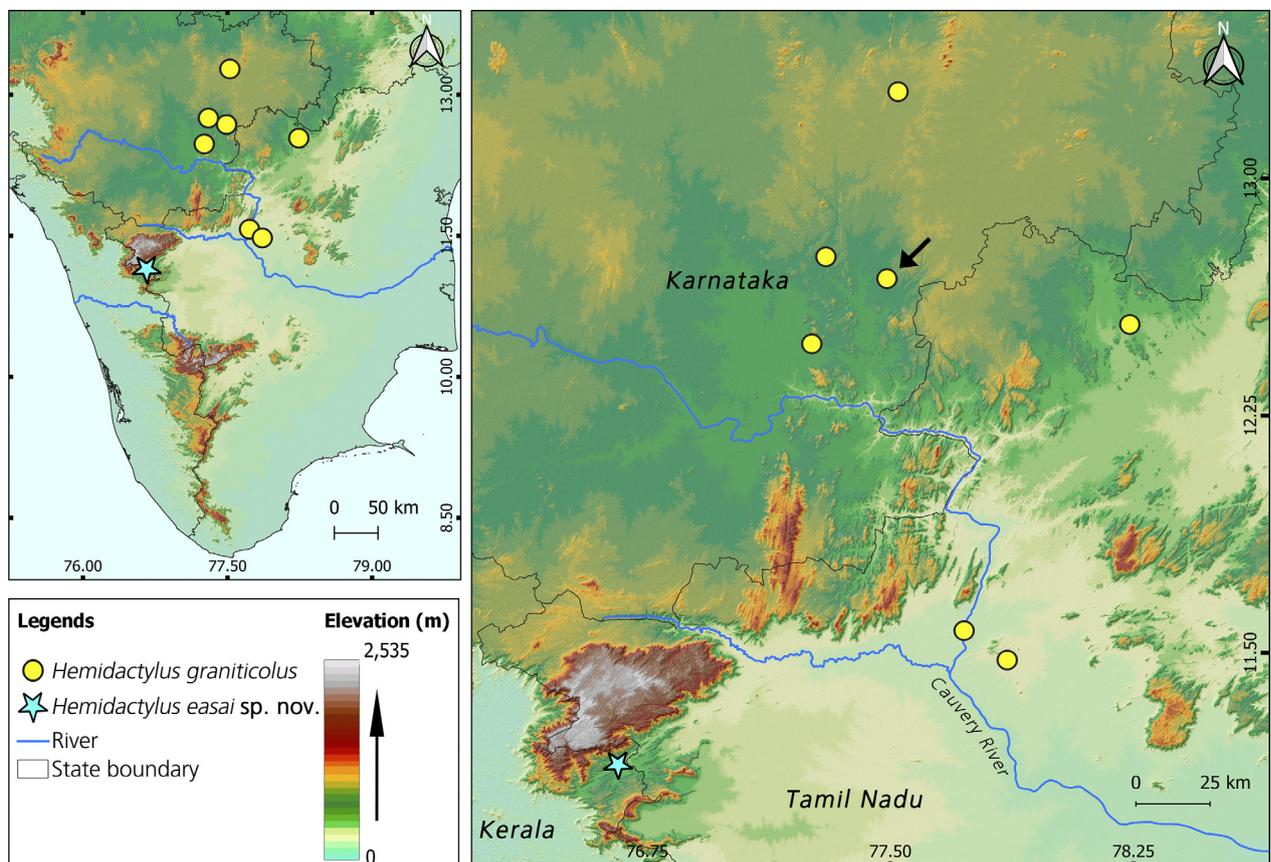
Agarwal et al. (2019a) recognised three other lineages as *H. cf. graniticolus* in their phylogeny, all from the Eastern Ghats and no representative samples were included for the Western Ghats. In this paper, we describe a distinct new species from the Western Ghats, that is closely related to *Hemidactylus graniticolus*, based on morphology and molecular data.

## Materials and Methods

### Molecular analysis

We collected four specimens of *Hemidactylus* sp. and generated DNA sequence for two specimens of *Hemidactylus* sp. (ZSI/WGRC/IR.V/3471 & BNHS 3103) from Pattimalam, Attapadi, Palakkad district, Kerala, India (11.146397°N, 76.65939°E, 530m asl) (Fig. 1). Specimens were euthanized and fixed in 4% formalin and later washed and transferred to 70% ethanol for preservation. We extracted genomic DNA from liver tissue sample stored in absolute ethanol at  $-20^{\circ}\text{C}$ , using the DNeasy (Qiagen™) blood and tissue kit. We amplified the complete sequence (1041 base pairs) of the mitochondrial *ND2* gene using the following primers: MetF1 (Forward) and H5934 (Reverse) (Macey et al. 1997). PCR conditions were as follows: initial denaturation at  $95^{\circ}\text{C}$  for 3 min, followed by 39 cycles of denaturation at  $95^{\circ}\text{C}$  for 35 sec, annealing at  $55^{\circ}\text{C}$  for 40 sec and extension at  $72^{\circ}\text{C}$  for 1 min 30 sec. The final extension was at  $72^{\circ}\text{C}$  for 5 min.

Bidirectional sequences were manually checked using the CHROMAS 2.6.6 software (<http://technelysium.com.au/wp/chromas>) and aligned using ClustalW (Higgins et al. 1994) with default prior settings implemented in MEGA 7 (Kumar et al. 2016). We checked for unexpected stop codons by translating the sequence to amino acids in MEGA7 (Kumar et al. 2016). The new sequence



**Figure 1.** Map showing the distribution of *Hemidactylus easai* sp. nov. and *H. graniticolus*. Black arrow represents the type locality of *H. graniticolus*.

generated in this study were aligned with data for 71 other *Hemidactylus* and two outgroups (*Dravidogecko septentrionalis* Chaitanya, Giri, Deepak, Roy, Murthy & Karanth 2019 & *D. douglasadamsi* Chaitanya, Giri, Deepak, Roy, Murthy & Karanth 2019) (Supplementary Table 1).

A Maximum Likelihood (ML) analysis was carried out with RAxML GUI version 2.0 (Edler et al. 2021) implementing the GTRGAMMAI for the dataset partitioned by codon position. A Bayesian Inference (BI) analysis was carried out using the program MrBayes 3.2 (Ronquist et al. 2012), with default prior settings. The dataset was partitioned by codon positions using PartitionFinder v1.1.1 (Lanfear et al. 2017) with default settings to find the best-fit model of sequence evolution. Partition finder suggested three partitions as follows, position1: TVM+I+G, position2: TVM+G, position3: TrN+I+G. Four separate runs were set up with eight Markov chains each initiated from random trees and allowed to run for  $10 \times 10^6$  million generations, sampling every 100 generations. Analyses were terminated when the standard deviation of split frequencies was less than 0.001, the first 25% of trees were discarded as “burn-in”, and trees were constructed under 50% majority consensus rule. We obtained ESS values using the Tracer software and confirmed the convergence for all the priors (ESS > 200). Support for internal branches in ML and BI trees was quantified using 1000 replicates (thorough bootstrap) and posterior probability, respectively. We considered BI > 0.95, ML > 85 as strong support. The uncorrected pairwise genetic distance was calculated in MEGA7 using default settings (pairwise deletion).

## Morphological analysis

All the morphological characters examined (mensural and meristic) follow Agarwal et al. (2019a). Measurements and meristic data from the collected specimens for this study were taken under a Nikon microscope and were measured using a Mitutoyo digital Vernier calliper to the nearest 0.1 mm. Photographs were taken using Canon EOS 7D mounted with a 100 mm macro lens and two external flashes. Measurements and meristic characters include: snout vent length (SVL, from tip of snout to vent); axilla to groin length (AGL, from posterior margin of forelimb insertion to anterior margin of hindlimb insertion); body width (BW, maximum body width); forearm length (FL, from posterior margin of elbow while flexed 90° to distal end of wrist); crus length (CL, from the posterior surface of the knee while flexed 90° to the base of the heel); tail length (TL, from vent to tip of tail); tail width (TW, measured at widest point of tail); head length (HL, distance from the posterior margin of the retroarticular process to the tip of the snout); head width (HW, maximum width of head); head depth (HD, maximum head depth at occiput); eye diameter (ED, greatest horizontal diameter of eye); eye to naris distance (EN, distance between anterior margin of eye and posterior edge of nostril); eye to snout distance (ES, distance between anterior margin of eye and tip of snout); eye to ear distance (EE, distance

from anterior edge of ear opening to posterior margin of eye); ear length (EL, maximum length of ear opening); internarial distance (IN, distance between nares); interorbital distance (IO, shortest distance between left and right supraciliary scale rows). Additional meristic characters include DTR: longitudinal rows of enlarged dorsal tubercles at midbody; PVT: number of paravertebral tubercles between limb insertions; MVSR: the number of ventral scale rows at mid-body between the lowest rows of dorsal scales; femoral pores in the femoral region in males; the number of pore-less scales between the series of femoral pores and the number of undivided lamellae on all the digits in manus and pes.

Comparative data for the *Hemidactylus graniticolus* were obtained from Agarwal et al. (2011). We considered data from only five specimens (BNHS 1850, BNHS 1858, BNHS 1859, BNHS 1859, BMNH 1946.8.23.76) of *H. graniticolus* reported in Agarwal et al. (2011) since some of the samples from the other locations (Yercaud, Salem district) are identified as *H. cf. graniticolus* in the recent studies (see discussion) (Agarwal et al. 2019a; Khandekar et al. 2020). Morphological data for the other large bodied *Hemidactylus* were obtained from literature and the original descriptions (Chaitanya et al. 2018; Giri, 2008; Khandekar et al. 2021, Mirza et al. 2018; Mirza & Sanap 2014; Srikanthan et al. 2018; Amarasinghe et al. 2021)

**Museum abbreviations** are as follows: BNHS: Bombay Natural History Society, Mumbai, India; BMNH: Natural History Museum, London; ZSI-WGRC: Zoological Survey of India, Western Ghats Regional Centre, Kozhikode, India.

## Results

### Molecular analysis

In both ML and BI analyses, the new species is recovered as a sister to the *Hemidactylus graniticolus sensu stricto* clade with strong support (ML 88, BI 1.0) and are together forming a strongly supported (ML 100, BI 1.0) monophyletic group with three other putative species identified as *H. cf. graniticolus* (see, Agarwal et al. 2019a) (Fig. 2). The uncorrected pairwise genetic distance is 6.6–7.2% between the new species and other samples of *H. graniticolus* (Table 1).

### *Hemidactylus easai* sp. nov.

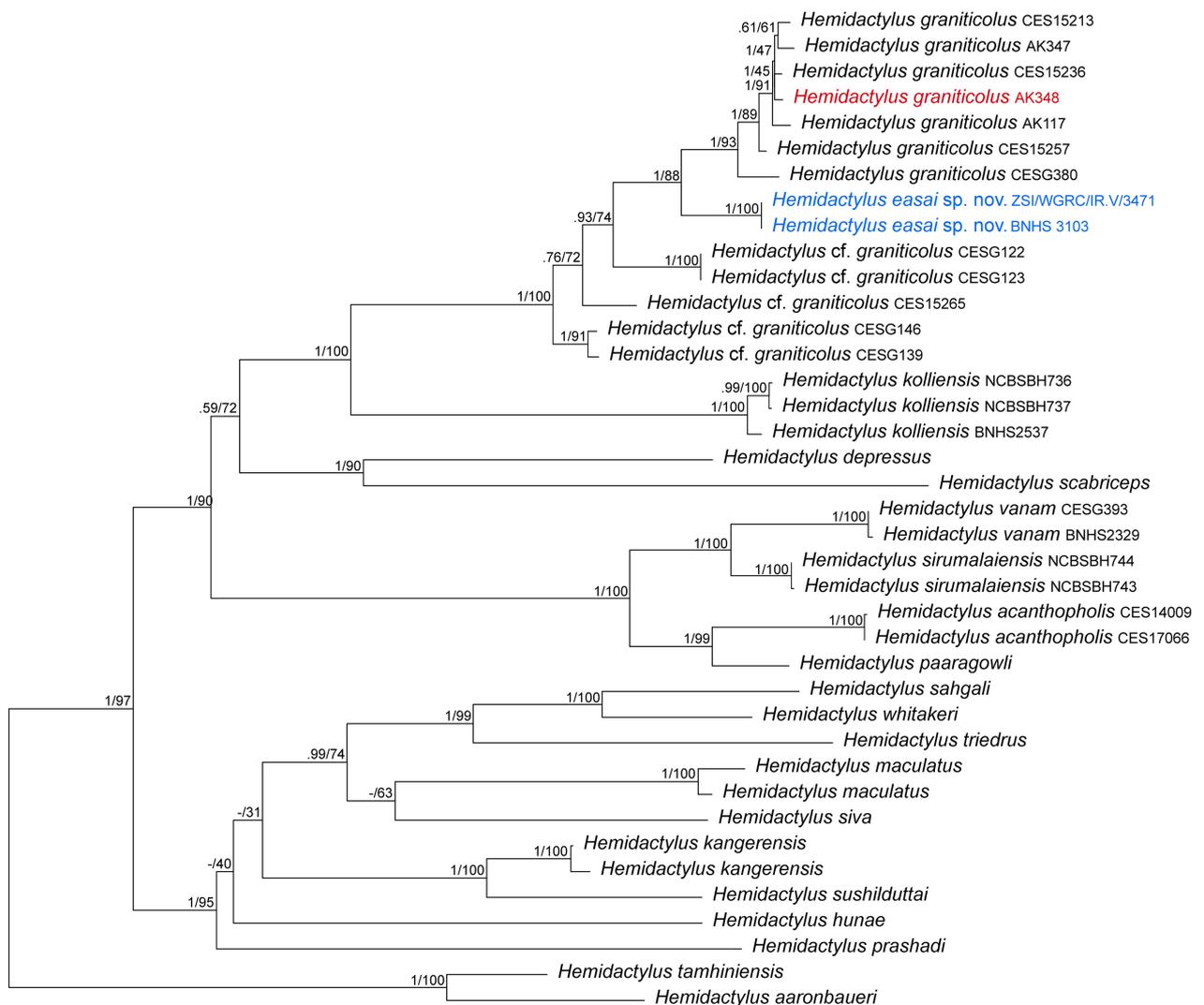
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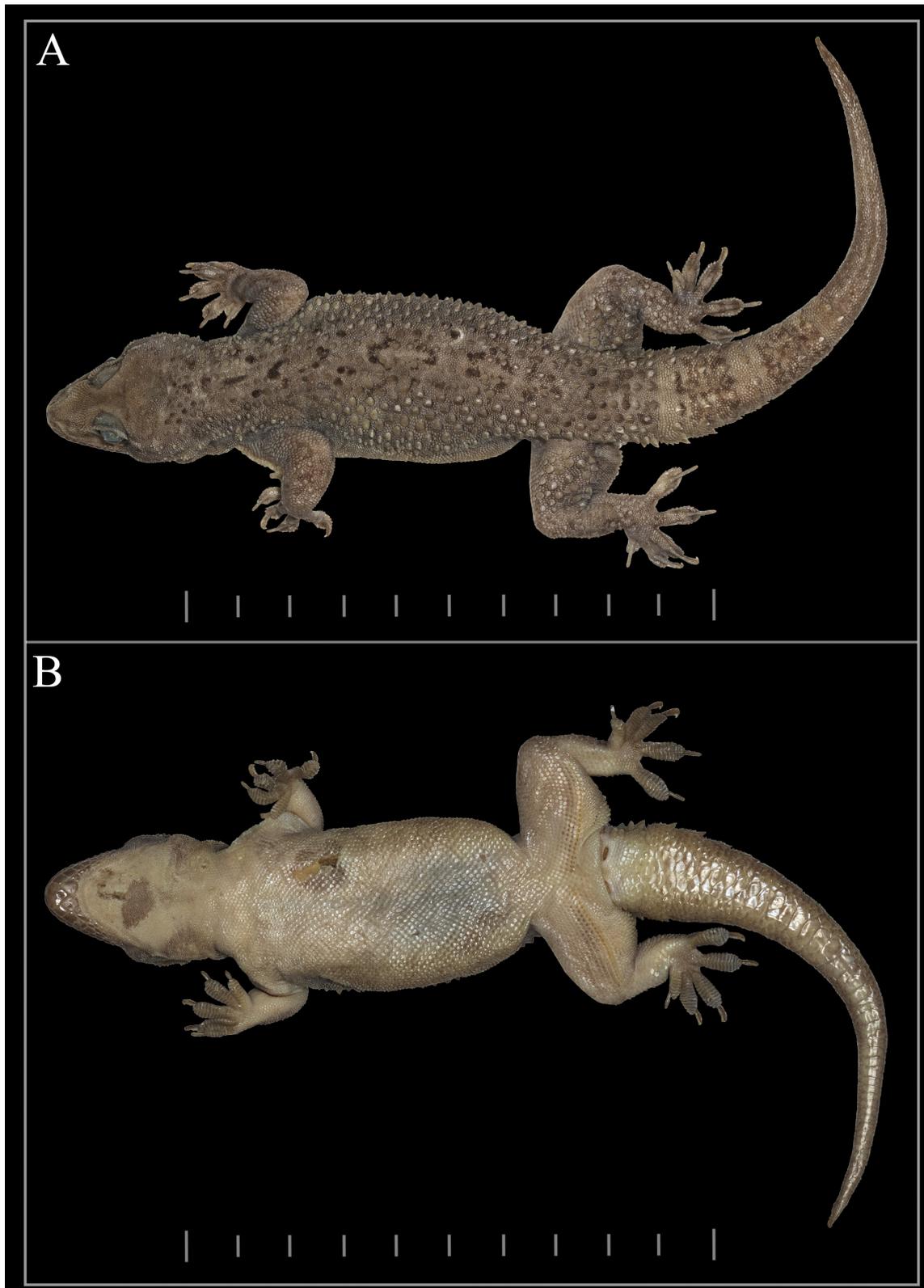
Figs 3–4, 5A, 6, 7; Tables 1–2

**Holotype.** ZSI/WGRC/IR.V/3471 (Figs 2–5A, 6A, 7A) adult male, from Attapadi, Palakkad district, Kerala,

**Table 1.** Uncorrected pairwise distances for mitochondrial *ND2* gene among the *graniticolus* clade.

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1 <i>Hemidactylus graniticolus</i> AK348														
2 <i>Hemidactylus graniticolus</i> AK347	1.4													
3 <i>Hemidactylus graniticolus</i> CES15213	1.2	1.4												
4 <i>Hemidactylus graniticolus</i> CES15236	0.7	1.4	1.0											
5 <i>Hemidactylus graniticolus</i> AK117	1.2	2.0	1.6	1.5										
6 <i>Hemidactylus graniticolus</i> CESH380	3.9	4.0	3.9	3.9	4.4									
7 <i>Hemidactylus graniticolus</i> CES15257	1.6	1.8	1.9	1.6	1.8	3.1								
8 <i>Hemidactylus easai</i> sp. nov. ZSI/WGRC/IR.V/3471	7.0	7.2	7.1	7.2	6.6	7.1	6.6							
9 <i>Hemidactylus easai</i> sp. nov. BNHS 3103	7.0	7.2	7.1	7.2	6.6	7.1	6.6	0.0						
10 <i>Hemidactylus</i> cf. <i>graniticolus</i> CESH146	10.6	10.4	10.4	10.7	10.6	10.1	10.0	8.8	8.8					
11 <i>Hemidactylus</i> cf. <i>graniticolus</i> CESH139	10.1	9.9	9.8	10.1	10.1	10.0	9.5	8.5	8.5	1.1				
12 <i>Hemidactylus</i> cf. <i>graniticolus</i> CESH122	9.8	9.7	9.7	10.0	9.4	9.2	9.2	9.3	9.3	8.2	7.9			
13 <i>Hemidactylus</i> cf. <i>graniticolus</i> CESH123	9.8	9.7	9.7	10.0	9.4	9.2	9.2	9.3	9.3	8.2	7.9	0.0		
14 <i>Hemidactylus</i> cf. <i>graniticolus</i> CES15265	10.4	9.6	9.7	10.0	9.6	9.3	9.7	8.7	8.7	6.0	5.7	7.8	7.8	
15 <i>Hemidactylus kolliensis</i> BNHS2537	17.2	17.0	16.3	16.2	16.0	14.9	17.0	16.9	16.9	17.6	17.2	18.0	18.0	18.3

**Figure 2.** ML phylogeny showing the phylogenetic relationships of *Hemidactylus easai* sp. nov. Numbers at internal branches are posterior probability and ML bootstrap support values, respectively. Sample marked in blue is generated in this study and sample from the type locality of *H. graniticolus* is marked in red.

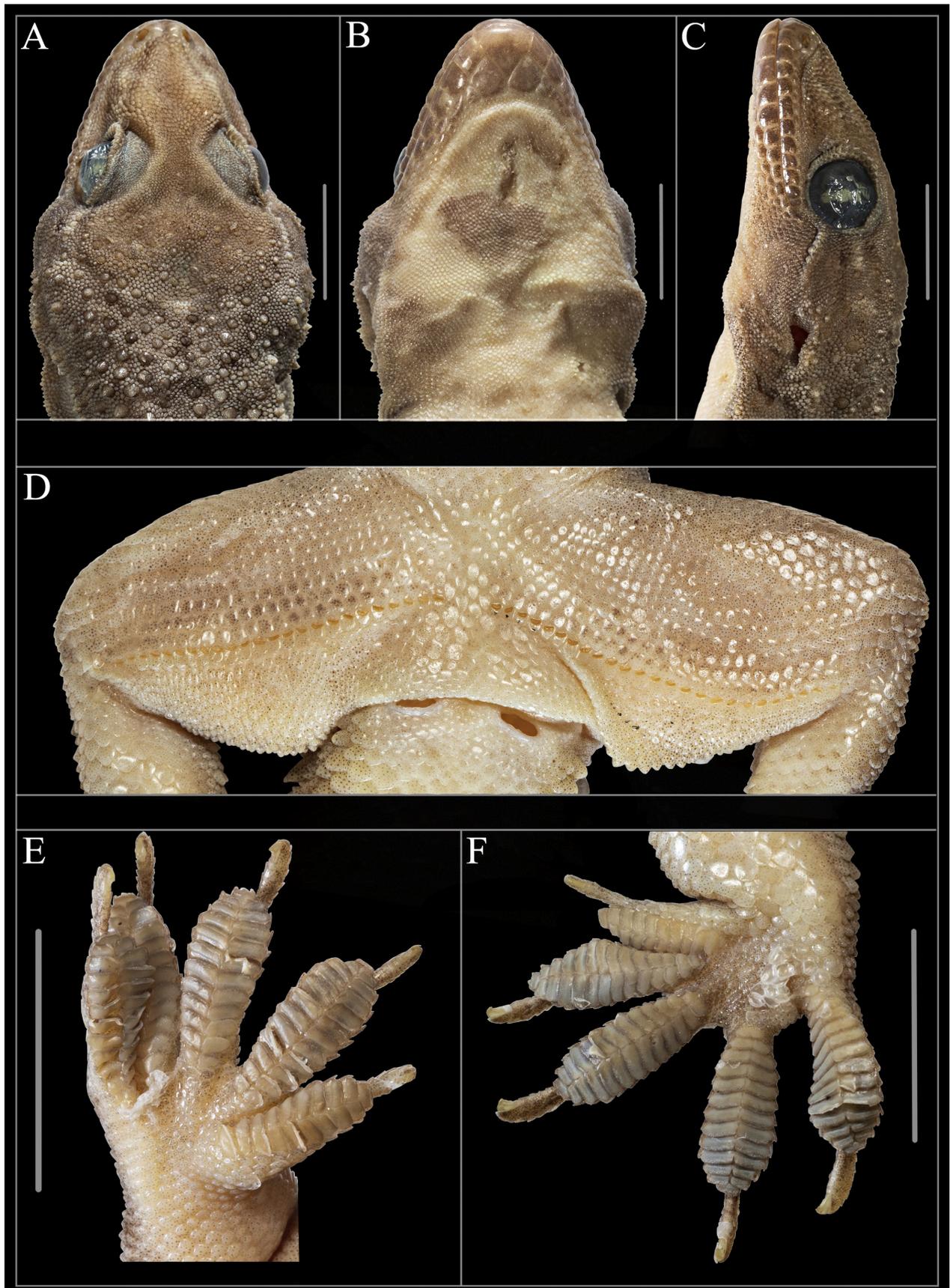


**Figure 3.** Holotype of *Hemidactylus easai* sp. nov. (ZSI/WGRC/IR.V/3471) in dorsal (A) and ventral (B) aspect. Scale bar = 10cm.

India (11.146397°N, 76.65939°E, 530m asl), collected by Muhamed Jafer Palot and Sandeep Das on 12 June 2020.

**Paratypes (n=3).** ZSI/WGRC/IR.V/3472 (adult male), BNHS 3103 & BNHS 3104 (adult females), collections details same as the holotype (Figs 5B–C, 6 & 7B).

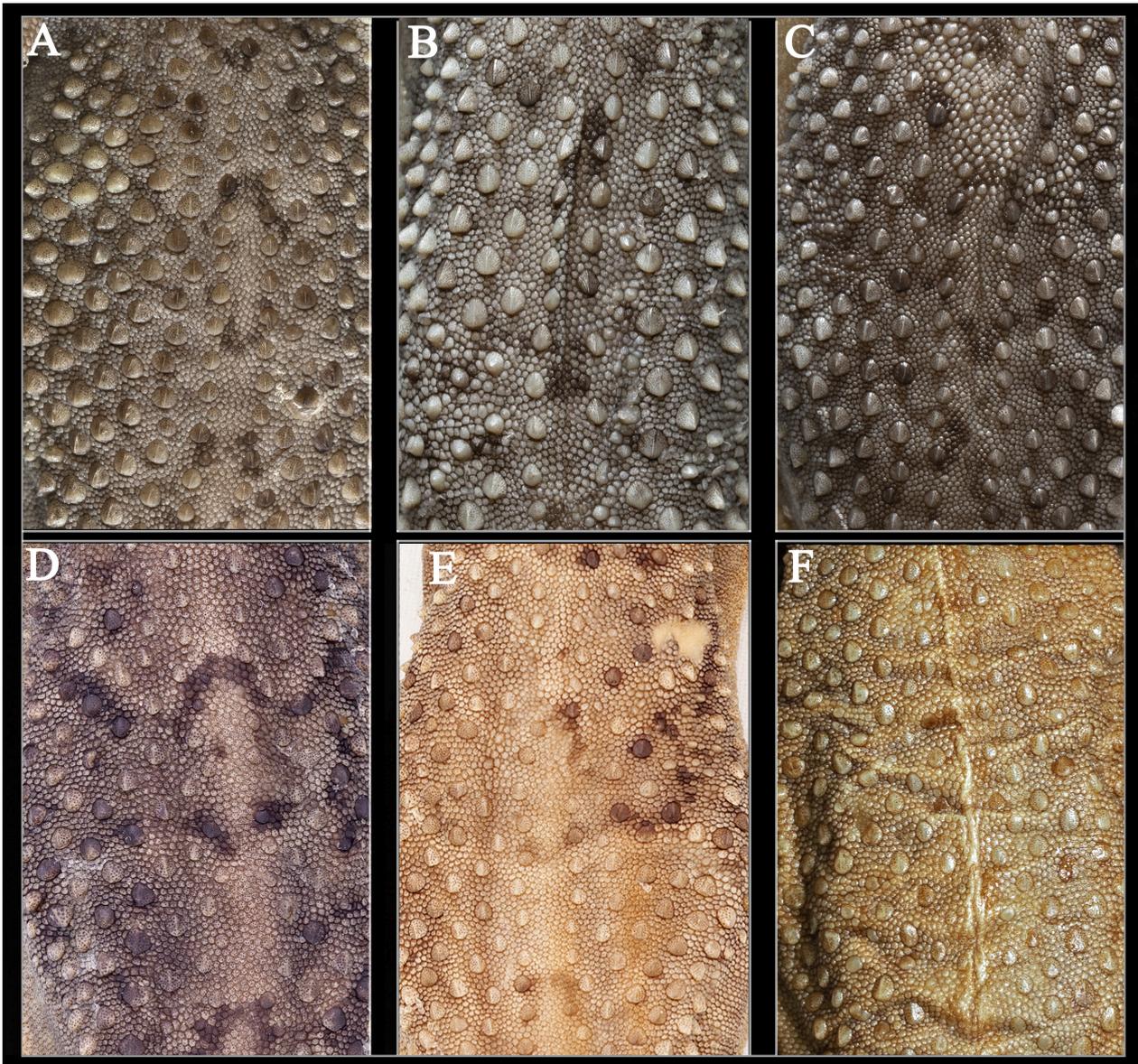
**Etymology.** The specific epithet is a patronym honouring Dr P. S. Easa, former director of Kerala Forest Research Institute, Thrissur, Kerala for his contributions towards wildlife research, conservation and management, primarily in the Western Ghats over the last four decades and for mentoring SD. We suggest Easa's rock gecko as common name.



**Figure 4.** *Hemidactylus easai* sp. nov. (holotype, ZSI/WGRC/IR.V/3471), A. head in dorsal view, B. ventral view, C. lateral view, D. view of the femoral region, E. ventral view of right manus and F. right pes. Scale bar = 10mm.

**Diagnosis.** A large-sized gecko of the genus *Hemidactylus*, snout-vent length up to SVL 107 mm (n=4). Dorsal pholidosis heterogeneous, composed of roughly circular,

granular scales intermixed with much enlarged, fairly regularly arranged longitudinal rows of 17 or 18 striated subtriangular tubercles at midbody (Fig. 5A-C). Enlarged



**Figure 5.** Plate showing the dorsal pholidosis of *Hemidactylus easai* sp. nov. (A, ZSI/WGRC/IR.V/3471, B, ZSI/WGRC/IR.V/3472 & C, BNHS 3103) and *H. graniticolus* (D, BNHS 1850, E, BNHS 1858 & F, BMNH 1946.8.23.76).

tubercles on the two most medial parasagittal rows are small, subconical, strongly keeled and rounded, gradually increasing in size and becoming conical towards flanks, last two to three rows on flanks smaller, conical. Two well-developed pairs of postmentals, the inner pair longer than the outer pair and mental, and in broad contact behind the mental. 20–23 tubercles in paravertebral rows; ventrolateral folds distinct; 41 or 42 transverse ventral scale rows at mid-body. Digits with enlarged scancers, lamellae in straight transverse series; 2–5 undivided basal lamellae beneath first finger and 2–5 beneath first toe; 0 or 1 undivided basal lamellae beneath fourth toe; 10–12 lamellae (including undivided and divided) beneath first finger and 10 or 11 beneath first toe; 11–13 lamellae (including undivided and divided) beneath fourth finger and 13 beneath fourth toe; males with series of 24–30 femoral pores on each side separated by 2–4 pore-less scales. Original tail depressed, oval in transverse section with a median dorsal furrow; scales on the tail slightly

larger than dorsals, striated, with longitudinal series of 6–8 large, keeled, striated, posteriorly pointed tubercles. Dorsal coloration dull-brown with a series of four or five transverse pale saddles from occiput to sacrum, tail with distinct alternating light and dark bands.

**Description of holotype.** The holotype, an adult male, (SVL 105.8 mm) well preserved and is in good condition. Head short (HL/SVL 0.30), slightly elongate (HW/HL 0.76), not strongly depressed (HH/HL 0.41), distinct from neck. Loreal region slightly inflated, canthus rostralis indistinct (Fig. 4C). Snout short (SE/HL 0.46); slightly longer than twice eye diameter (OD/SE 0.45); scales on snout, canthus rostralis, forehead and inter-orbital region heterogenous, mostly granular and conical; scales on the snout and canthus rostralis much larger than those on occiput, forehead and inter-orbital regions. Eye small (OD/HL 0.19); pupil vertical with crenulated margins; supraciliaries small, mucronate, gradually increasing in size

towards the front of the orbit, largest about one-third the way from anterior edge of orbit. Ear opening elliptical (greatest diameter 2.2 mm); a row of small pointed tubercles above the ear; eye to ear distance slightly greater than the diameter of eye (EE/OD 0.71). Rostral wider than deep (RL/RW 0.65), partially divided dorsally by a weakly developed rostral groove; two internasals, enlarged and separated by three small scales; one supranasal on each side, smaller than internasals; two diminutive postnasals on each side; rostral in contact with nasal scale, supralabial I, internasals and the anterior small scale separating the internasals; nostrils small (0.8 mm), oval; nasal scale surrounded by supranasal, internasal, rostral, supralabial I and two postnasals on either side; 4–6 rows of scales separate orbit from supralabials. Mental triangular; two well-developed postmentals, the inner pair smaller (3.3 mm) than the mental (4.4 mm), and in strong contact with each other (1.1 mm) behind mental, outer pair shorter (1.7 mm) than the inner pair and separated from each other by inner pair (Fig. 4B). Inner postmentals bordered by mental, infralabial I and II on left and right, outer postmental and six small gular scales on each side; outer postmentals bordered by infralabial II on the right and separated by a large scale on the left, inner postmental, and five gular scales on both side along with one large scale on the right side between the third infralabial and the outer postmental; four to five additional rows of scales below infralabials III to VIII are enlarged and weakly imbricate. Supralabials (on both sides) to mid orbital position nine, to angle of jaw 11 on right and left; infralabials 9 on each side. Body relatively stout (BW/SVL 0.20), ventrolateral folds distinct.

Dorsal pholidosis heterogeneous, composed of sub-circular granular scales intermixed with enlarged, fairly regularly arranged strongly keeled, pointed tubercles in 18 longitudinal rows, extending from occiput to tail, that are heterogeneous in shape and size; enlarged tubercles on the two most medial parasagittal rows slightly smaller than rest on dorsum and the rows most broadly spaced from one another, gradually increasing in size and becoming conical towards flanks, last two rows on flanks slightly smaller than medial parasagittal rows and strongly conical; each enlarged tubercle surrounded by a rosette of 12–15 small granules with 2–5 granules between two longitudinally adjacent enlarged tubercles (3–6 between parasagittal rows at midbody); enlarged tubercles on nape and shoulder smaller and conical, those on occiput and the temporal region still smaller, conical.

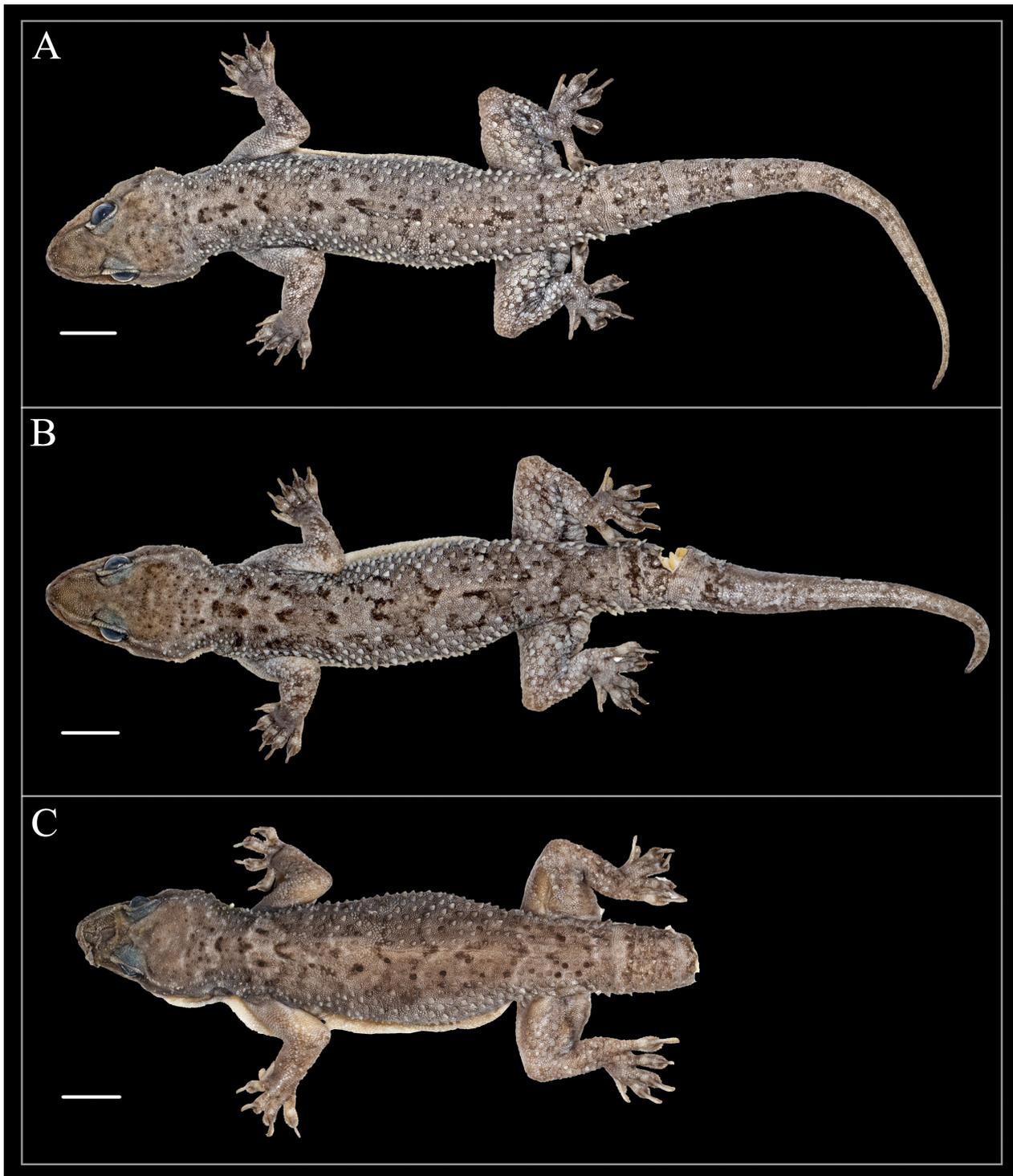
Ventral scales larger than dorsal granular scales, smooth, imbricate, slightly larger on precloacal and femoral region than on chest and abdominal region; midbody scale rows across belly 42; gular region with small, granular scales, becoming slightly larger and imbricate on anterior and lateral aspect. Scales on palm and sole smooth, imbricate, subcircular; scales on the dorsal aspect of upper arm subequal last row of enlarged tubercles on dorsum, flat, weakly pointed, imbricate, keeled; dorsal aspect of forearm with smaller, granular scales, intermixed with a few enlarged, conical tubercles, those on anterior aspect are smooth, flat, imbricate; scales on dorsal part of

thigh and shank granular, except those on knee flat, imbricate, intermixed with enlarged, conical tubercles, which are larger on thigh compared to shank; anterior aspect of thigh with flatter scales, posterior aspect with granular scales. Twenty-five and twenty-four pores in an enlarged row of femoral scales on left and right side respectively, separated medially by a diastema of four pore-less scales; subequal row of enlarged scales anterior to pore-bearing scales (Fig. 4D). Fore and hind limbs relatively short, stout; forearm short (FL/SVL 0.15); tibia short (CL/SVL 0.17); digits moderately short, strongly clawed; all digits of manus and digits I–IV of pes indistinctly webbed; terminal phalanx of all digits curved, arising angularly from distal portion of expanded lamellar pad, half or more than half as long as associated toepad; scancers beneath each toe in a straight transverse series, divided except for distal and four to five basal scancers on digit I: 11-12-12-12 (left manus), 10-13-12-12-11 (right manus) (Fig. 4E), 10-14-13-13-12 (left pes), 10-14-13-13-13 (right pes) (Fig. 4F). Relative length of digits (measurements in mm in parentheses): I (5.8) < II (6.7) < III (7.2) < IV (7.4) < V (8.1) (left manus); I (3.9.) < V (9.2) < IV (8.4) < II (8.3) < III (8.2) (left pes).

Tail regenerated; depressed, flat beneath, verticillate, with well-defined median furrow; scales on the dorsal aspect of tail subimbricate, larger than granules on dorsum, with a series of 4–10 much enlarged, strongly pointed, moderately keeled tubercles; ventral scales enlarged, imbricate, median row (subcaudal plates) covering almost entire base of the tail, bordered laterally by two or three rows of larger pointed, smooth, imbricate scales; those close to vent small, smooth, flat and imbricate (Fig. 3D). Two subequal rounded postcloacal spurs on each side are much smaller than dorsal tubercles at midbody (Fig. 3D).

**Variations in the paratypes.** Variations in the paratypes in some of the meristic and mensural characters are provided in the Table 2. Two paratypes are females. BNHS 3104 has an incomplete tail and partially broken in BNHS 3103 at the base, but intact (Fig. 6B). Internasals in BNHS 3103 are separated by two small scales. In ZSI/WGRC/IR.V/3472 & BNHS 3104 outer post mental on the left side is in contact with the third supralabial and a distinct small scale is present between the mental and the inner post mental on the right side in ZSI/WGRC/IR.V/3472. Skin in the frontal region of the head in BNHS 3104 is slightly damaged but intact (Fig. 6C). In life, all the paratypes were comparatively lighter in dorsal colouration and this, however, is not significant in preservative.

**Color in life (based on holotype).** Dorsal aspect of the body, uniformly brownish with four indistinct transverse bands from the neck to the hind limb insertion and two on the tail, bordered by discontinuous black patches (Fig. 7A). Dorsal aspect of the head without any dark markings in the parietal and frontal region. A preorbital yellow streak extends from the posterior of the naris to the anterior of the eye on both sides. Ventral aspect of the head mostly cream coloured with light brown mottling on the



**Figure 6.** Paratypes of *Hemidactylus easai* sp. nov. in dorsal aspects, A. ZSI/WGRC/IR.V/3472, B. BNHS 3103, C. BNHS 3104. Scale bar = 10mm.

gular region and mental, infralabials, post mentals and few other adjacent scales mottled with dark brown. Fore and hindlimbs brownish speckled with irregular black patches on the dorsal side. Ventral aspect of the body, forelimbs and hindlimbs predominantly cream coloured with sprinkled and or mottled with brown colour.

**Comparison with other members of prashadi group.** *Hemidactylus easai* sp. nov. differs from the other large-bodied congeners by several non-overlapping

morphological characters. It can be distinguished by the presence of 24–30 femoral pores (FP) separated by 2–4 pore-less scales (vs. 21 FP separated by two pore-less scales in *H. kolliensis*; 19–21 FP separated by 13–14 pore-less scales in *H. acanthopholis*; 22–24 FP separated by 3–6 pore-less scales in *H. hunae*; 16–18 FP separated by 13–14 pore-less scales in *H. sirumalaiensis*; 17–22 FP separated by 10–11 pore-less scales in *H. vanam*; 21–24 PF separated by four pore-less scales in *H. sushilduttai*; 15–19 FP separated by 3 pore-less scales in *H. depres-*

**Table 2.** Meristic and mensural data for the type series of *Hemidactylus easai* sp. nov. \* denotes incomplete tail.

Voucher no.	Holotype: ZSI/WGRC/ IR.V/3471	Paratype 1: ZSI/WGRC/ IR.V/3472	Paratype 2: BNHS 3103	Paratype 3: BNHS 3104
Sex	Male	Male	Female	Female
SVL	105	104.6	107	94.3
AGL	43.3	39.7	43	38.3
BW	30.1	21.8	21.8	23.4
TL	101	102	87.8	19*
TW	17.6	14.2	12.1	12.1
HL	30.5	30.8	30.1	26.9
HW	23.3	22.6	21.5	19.1
HD	12.8	12.6	12	11.3
FL	14.7	14.1	13.4	13.5
CL	17.8	17.4	17	15.9
ED	5.9	6.1	5.6	4.8
EN	10.1	9.3	9.5	8.7
ES	12.9	12.5	12.5	10.6
EE	8.3	8.9	8.1	8
EL	2.1	2.4	2.2	2
IN	2.7	2.4	2.6	2.5
IO	9.6	10	9.8	9.3
Femoral pores (pore-less scales separating series)	25&24(4)	30&28(2)		
DTR	18	18	17	18
PVT	20	21	23	22
MVSR	42	41	42	42
Supralabials (L&R)	11&11	13&12	12&12	12&10
Infralabials (L&R)	10&10	10&10	10&10	10&10
Supralabials to midorbit (L&R)	9&9	9&9	9&9	9&9
Infralabials to midorbit (L&R)	8&8	8&8	8&8	8&8
Manus left	11-12-12-12-12	12-13-13-13-13	10-12-13-11-13	10-11-12-12-13
Manus right	10-13-12-12-11	12-13-13-12-13	10-12-12-12-12	10-12-12-12-11
Pes left	10-14-13-13-12	11-13-13-13-13	11-13-13-13-14	11-13-13-13-13
Pes right	10-14-13-13-13	11-13-13-13-13	11-13-13-13-13	10-13-13-13-13

*sus*; 17–18 FP separated by 5 pore-less scales in *H. siva*; 7–9 FP separated by 1–3 pore-less scales in *H. triedrus*; 11–15 FP separated by 1–3 pore-less scales in *H. sahgalii*; 7–8 FP separated by 3 pore-less scales in *H. whitakeri*; 21–24 FP separated by 5–7 pore-less scales in *H. kimbulae*; 15–19 FP separated by 6 pore-less scales in *H. aaronbaueri*, 17–18 FP separated by 7 pore-less scales in *H. tamhiniensis*, 18–21 FP separated by 4 pore-less scales in *H. kangerensis*); by the presence of 16–18 rows of moderately keeled subtriangular tubercles (vs. 22–24 in *H. paaragowli*; 14–16 in *H. prashadi*; 15–16 in *H. kolliensis* and homogeneous dorsal pholidosis with no enlarged tubercles in *H. scabriceps*); .

From the closely related *Hemidactylus graniticolus*, *H. easai* sp. nov. can be differentiated by the presence of moderate to strongly keeled tubercles on the dorsum (vs. weakly keeled or smooth tubercles on the dorsal aspect) (Fig. 5); enlarged tubercles on the two most medial parasagittal rows subconical, strongly keeled (vs. tubercles on the two most medial parasagittal rows flattened, smooth to weakly keeled); dorsal pholidosis of tail with slightly larger granular, striated scales and longitudinal series of 6–8 large, keeled, striated, posteriorly pointed

tubercles (vs. dorsal pholidosis of tail with small, imbricate, striated scales and a series of four enlarged, keeled weakly striated and flattened tubercles).

**Distribution and natural history notes.** *Hemidactylus easai* sp. nov. is currently known only from the type locality in the Kerala parts of the Western Ghats. The type series was collected from human settlements, inside buildings on the banks of the river Bhavani, which originates from the Nilgiri Hills of Western Ghats (Fig. 8), flows very close to Silent Valley National Park and joins the Cauvery River near Tamil Nadu. The locality is a rain shadow area dominated by dry zone vegetation interspersed with riparian vegetation. The mean annual rainfall in Palakkad district is 2135 mm (Prasad et al. 2021). The holotype and the paratypes were found at night, actively foraging for insects. Several uncollected individuals of *H. easai* sp. nov. were observed in human settlements and rock crevices in the vicinity of the type locality. *Hemidactylus easai* sp. nov. was found in sympatry with *Cnemaspis gracilis* in the same microhabitat and, *H. cf. whitakeri* and *Cyrtodactylus* sp. was also found in the type locality.



**Figure 7.** *Hemidactylus easai* sp. nov. showing colour in life, A. Holotype ZSI/WGRC/IR.V/3471, B. Paratype ZSI/WGRC/IR.V/3472.

The type locality of *H. easai* sp. nov. is in a close proximity to the Silent Valley National Park (SVNP) but not under any legal protection. It is however possible that the new species is found within the SVNP and adjacent Nilgiris mountain range, given that the habitat is contiguous.

**Correct spelling of *Hemidactylus paaragowli* Srikanthan, Swamy, Mohan & Pal 2018.** Srikanthan et al. (2018), in the original description, included two different spellings, „*Hemidactylus paaragowlipaaragowli*“ (abstract) or „*Hemidactylus paaragowli*“ (keywords, description). However, the original authors or the subsequent authors working on the systematics of *Hemidactylus* from India did not correct this nomenclatural error but used the name “*Hemidactylus paaragowli*” (Mirza et al. 2018; Agarwal et al. 2019a; Lajmi and Karanth 2020; Khandekar et al. 2020). Here in this work, according to the provisions of articles 19.3, 24.2 & 32.2.1 of the International Code for Zoological Nomenclature (ICZN,

1999), we act as the first reviser and choose *Hemidactylus paaragowli* as the correct spelling since this spelling is used in the formal description part and higher usage (20 times) over the incorrect „*Hemidactylus paaragowli-paaragowli*“ which is cited only once in the abstract of the original description (Srikanthan et al. 2018).

## Discussion

The rate at which *Hemidactylus* are being described from India is high in the last decade, with 16 new descriptions of the total 48 known species (Uetz et al. 2021; Khandekar et al. 2021). However, only two large-bodied species, *Hemidactylus prashadi* and *H. paaragowli* (Srikanthan et al. 2018; Cyriac & Umesh 2021) are known from Kerala to date. The description of *Hemidactylus easai* sp. nov.



**Figure 8.** A. Abandoned building from the type locality where holotype was collected and B. General habitat of the type locality of *Hemidactylus easai* sp. nov.

makes it the eighth large-bodied *Hemidactylus* from the Western Ghats and the third for Kerala, adding one more to the list of vertebrates to the state. This also emphasizes our poor understanding of these fauna in the lesser explored drier regions of the Western Ghats.

Beyond the specimens reported here, few other specimens previously identified as *H. graniticolus* or *H. cf. graniticolus* required a closer look. One specimen (BMNH 1946.8.23.76: paratype of *H. graniticolus*, Fig.

5F) collected from “Malabar”, is morphologically similar to *H. graniticolus* than to the new species but a precise location for this specimen is lacking. We also examined the specimen (CES08026) reported as *H. graniticolus* by Lajmi and Karanth (2020) from the Nilgiri Hills in the Western Ghats and we tentatively refer to this specimen as *H. easai* sp. nov., because of the presence of prominent and moderately keeled tubercles along the paravertebral rows but, we were unable to check its phylogenetic posi-

tion since there is no *ND2* sequence data. Furthermore, in our phylogeny, five samples representing three distinct lineages, previously identified as “*H. cf. graniticolus*” are closely related to *H. easai* **sp. nov.** We were unable to trace these specimens at the CES collections and hence the identity of these specimens remains unknown. However, all these three lineages, phylogenetically appear to be independent lineages and the genetic pairwise distance between any of these pairs including *H. easai* **sp. nov.** is 5.7%–10% and thus do not challenge our hypothesis of *H. easai* **sp. nov.** as a new species.

The dry zones of peninsular India are known for its high endemism in many squamate reptiles (*Hemidactylus*: Lajmi et al. 2019, 2020; *Hemiphyllocladactylus*: Agarwal et al. 2019b; *Sitana*: Deepak & Karanth 2018; *Cnemaspis*: Agarwal et al. 2020), largely due to the landscape heterogeneity. The isolated hills in peninsular India have played an important role in speciation of lizards (Agarwal et al. 2019b, 2020). Furthermore, in some cases the rivers in peninsular India have also played a role in reproductive isolation and speciation (e.g. *Sitana*: Deepak & Karanth 2018; *Platyceps*: Deepak et al. 2021). *Hemidactylus easai* **sp. nov.** and *Hemidactylus graniticolus sensu stricto* (including samples identified as *H. cf. graniticolus*) are also geographically separated by the river Cauvery.

With the current description and the available distributional data, it is likely that *H. graniticolus* may be restricted to the Mysore plateau and parts of the southern Eastern Ghats. *Hemidactylus easai* **sp. nov.** is currently known from the north of the Palghat gap and is nested within the clade containing species from the Mysore plateau and the southern Eastern Ghats, in our phylogenetic analyses (Fig. 2). Although *H. easai* **sp. nov.** is currently known only from the type locality, it is likely that this species is distributed in the adjacent regions with similar habitat. However, we have not sampled extensively in the Palghat gap nor immediately south of the gap for *Hemidactylus* species. Given the patchy sampling and incomplete data, we refrain from commenting on the relationships of these species and their distribution in the south of Palghat gap. Additional sampling in this region and the eastern slopes of southern Western Ghats may unveil actual distribution of *H. easai* **sp. nov.** and the true diversity of *Hemidactylus* in peninsular India and their systematic relationships.

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## Supplementary material

### Supplementary figures and tables

**Authors:** Das S, Pal S, Siddharth S, Palot MJ, Deepak V, Narayanan S (2022)

**Data type:** .zip

**Explanation note:** Supplementary tables and figures for *Hemidactylus easai* sp. nov.

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