



# A new species of rock-dwelling *Hemidactylus* Goldfuss, 1820 (Squamata: Gekkonidae) from the southern Eastern Ghats, India

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## Abstract

A new large-bodied (SVL 101–109 mm) gecko of the genus *Hemidactylus* is described from the Gingee Hills in the Eastern Ghats of India. The new species is closely related to *H. graniticolus* and the recently described *H. easai*, from which it can be distinguished by its lower femoral pores count. The new species described here was previously identified as *H. cf. graniticolus* based only on the molecular data, pending its formal description. Our findings were consistent with the results from the molecular DNA analyses, showing that this population is morphologically distinct from other closely related species. As a result, we formally describe this lineage as a new species, providing a comprehensive description of its morphological characteristics based on a type series of five specimens and compare it with its congenics.

## Keywords

Femoral pores, gecko, Gingee, ND2 phylogeny, species complex, taxonomy

## Introduction

The Eastern Ghats of India comprises a discontinuous series of mountains and hills, along the eastern coast of peninsular India extending from the state of Odisha in the

north to Tamil Nadu in the south. The forested regions of peninsular India, which were once ancestral, became more arid during the early Oligocene epoch, followed

by accelerated aridification in Miocene (Dettman et al. 2001). This trend continued into the Pleistocene and Holocene, because of the weakening of the Indian monsoon (Riedel et al. 2021). This resulted in the fragmentation of the forests, now primarily confined to small hill ranges and isolated hillocks, with a few remaining isolated forest blocks on the plains. These isolated hillocks have been previously claimed to act as microclimatic refugia (Agarwal et al. 2020) and are known to harbor several micro-endemic geckonids (Agarwal et al. 2019a, 2022).

The speciose gekkonid genus *Hemidactylus* Goldfuss, 1820 comprises 188 species of which 54 are known from India (Pal and Mirza 2022; Kumar et al. 2022; also see Uetz et al. 2023). Among the South Asian *Hemidactylus*, the well-supported *prashadi* group comprise twenty-two species of large-bodied geckos with a snout vent length (SVL) > 100 mm distributed throughout peninsular India and Sri Lanka (Agarwal et al. 2019b; Pal and Mirza 2022). Members of this group primarily inhabit granitic boulders, except for *H. scabriceps* (Annandale, 1906), which is terrestrial (Lajmi et al. 2020). Among the Indian members of this group, nine species are restricted to the Western Ghats, while the rest are distributed throughout peninsular India (Agarwal et al. 2019b, 2011; Das et al. 2022; Pal and Mirza, 2022) with two species more widely reported from the Western Ghats, the Eastern Ghats and the Mysore plateau (Mirza et al. 2018). Within the *prashadi* group, the *graniticolus* clade (sensu Agarwal et al. 2019b) currently comprises three described species *Hemidactylus graniticolus* Agarwal et al., 2011 and *H. kolliensis* Agarwal et al., 2019 from the eastern Ghats and Mysore plateau and the recently described *H. easai* Das et al., 2022 from the Western Ghats. Both Agarwal et al. (2019b) and Das et al. (2022) recognized three undescribed lineages from the Eastern Ghats in their phylogenetic analysis and tentatively identified them as *H. cf. graniticolus*.

In this study, we analyzed the morphological features of one of these three undescribed lineages, utilizing fresh materials from the Gingee Hills in the southern Eastern Ghats. Additionally, we obtained mitochondrial *ND2* sequences from fresh specimens. Based on our results from both morphological and molecular analysis, we herein describe the monophyletic lineage from the Gingee Hills as a new species.

## Materials and Methods

### Specimen collection

Five specimens (BNHS 2907–BNHS 2911) of *Hemidactylus* sp. were collected from Pakkamalai Hill, Tamil Nadu, India (12.164819°N, 79.250909°E) (Fig. 1). Collected individuals were euthanized using isoflurane after taking live photographs. Specimens were then fixed in 4% formalin after collecting liver/tail tissues that are stored in absolute ethanol (99.9%) at –20°C for molecu-

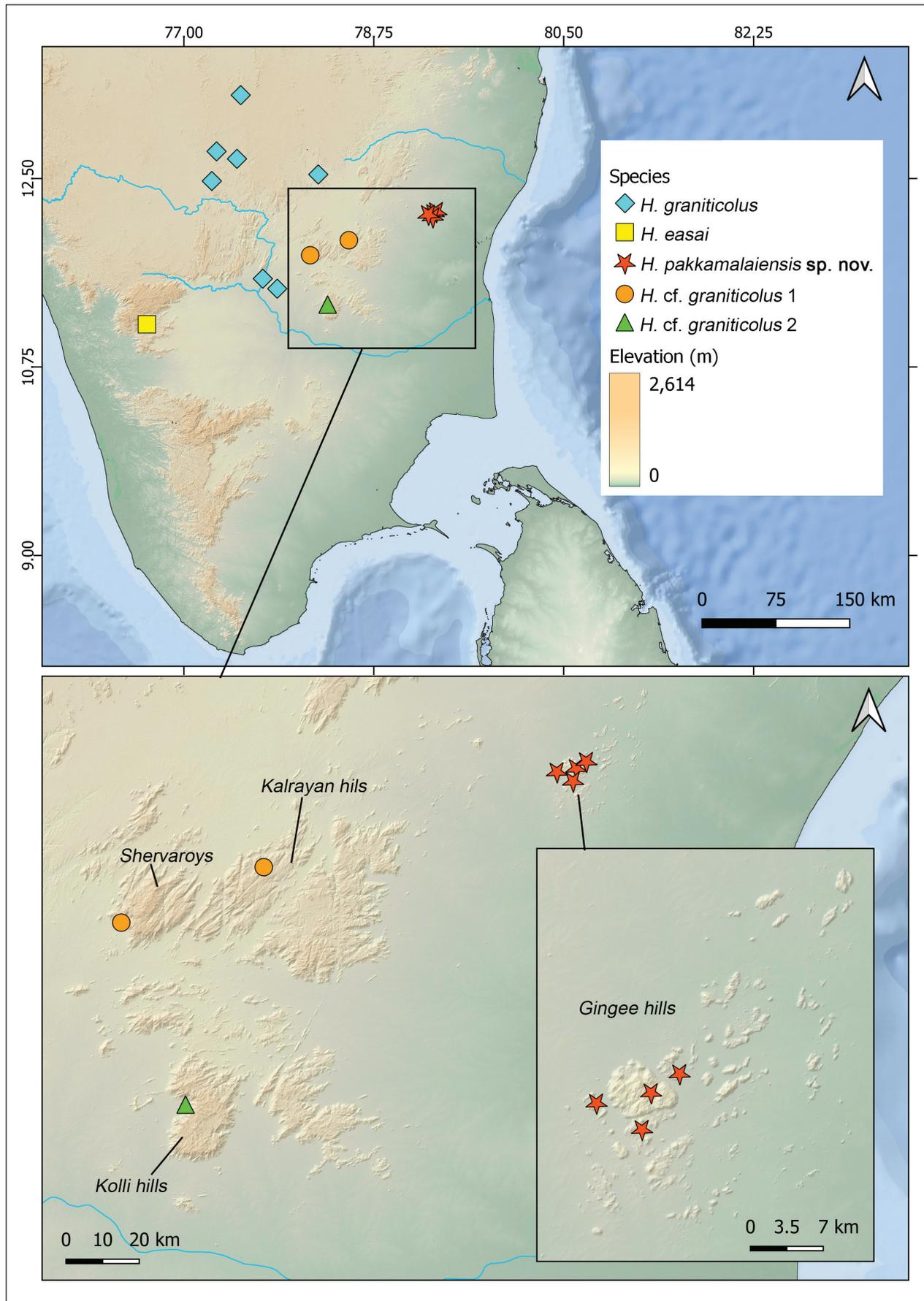
lar analysis. Fixed specimens were then washed and kept in water overnight and subsequently transferred to 70% ethanol.

### Molecular analysis

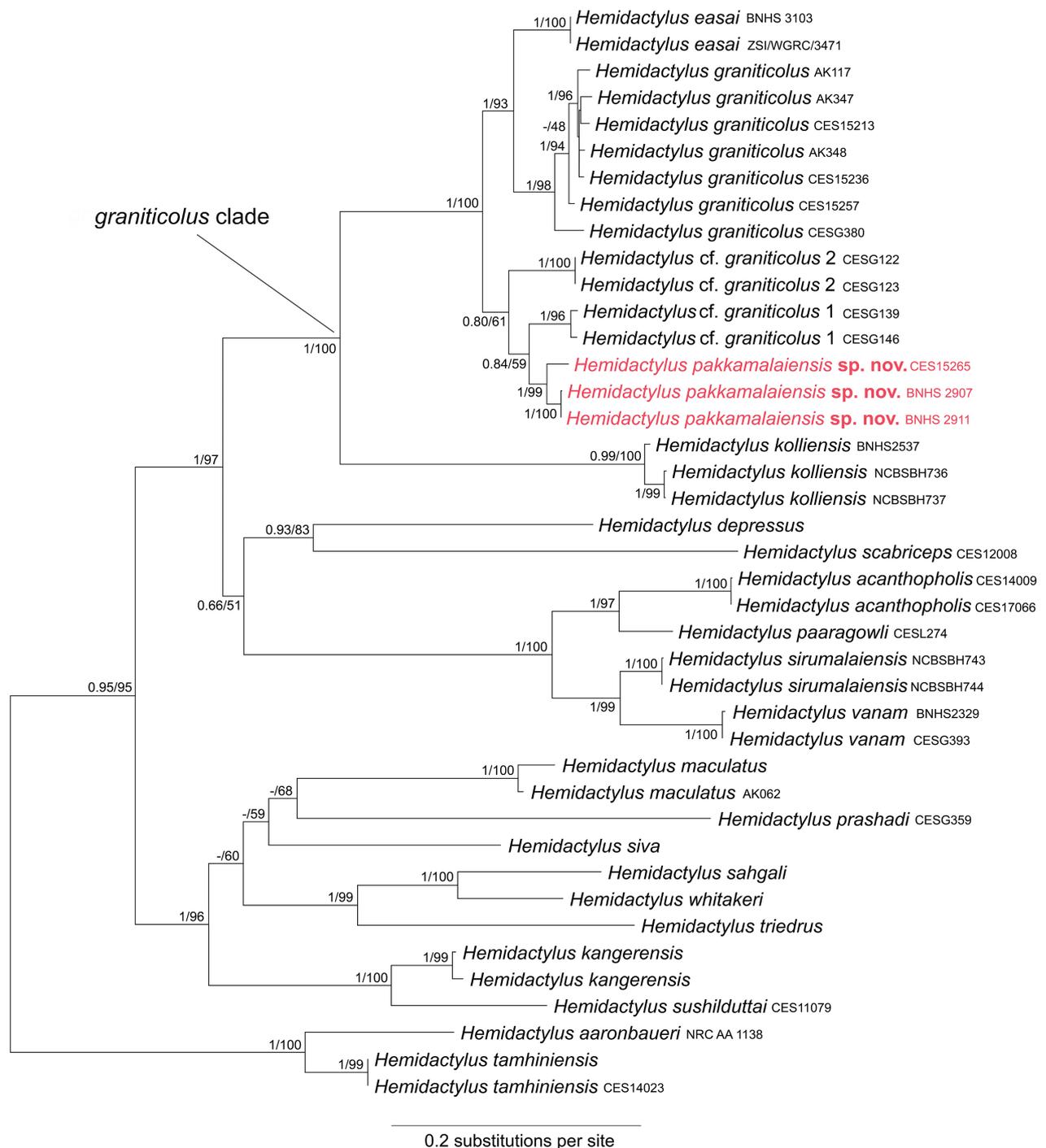
We extracted genomic DNA from liver tissue samples stored in absolute ethanol at –20°C, using the DNeasy (Qiagen™) blood and tissue kit. We amplified the partial sequence (1041 base pairs) of the mitochondrial *ND2* gene, for two specimens (BNHS 2907 & BNHS 2911) using the following primers: MetF1 and H5934 (Macey et al. 1997). PCR conditions were as described in Das et al. (2022).

Bidirectional sequences were manually checked using the CHROMAS v.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 v.7 (Kumar et al. 2016). We checked for unexpected stop codons by translating the sequence to amino acids in MEGA v.7 (Kumar et al. 2016). The new sequences generated in this study was aligned with 39 sequences of *Hemidactylus* from the *prashadi* group deposited in Genbank and two other species, *Dravidogecko septentrionalis* Chaitanya et al., 2019 and *D. douglasadamsi* Chaitanya et al., 2019 that are used as outgroups for the phylogenetic analysis (see Supplementary Material 1: Table S1).

Maximum Likelihood (ML) analysis for the final dataset was carried out using IQTREE (<http://iqtree.cibiv.univie.ac.at>) (Trifinopoulos et al. 2016). The best-fit models for partition scheme suggested by the Partitionfinder v1.1.1 (Lanfear et al. 2017) were determined using the in-built Modelfinder (Kalyaanamoorthy et al. 2017) for the ML analysis. The best-fit models for the ML analysis are as follows, *ND2* position1: TVM+F+G4, *ND2* position2: TPM3u+F+G4, *ND2* position3: TIM+F+I+G4. A Bayesian Inference (BI) analysis was carried out using MrBayes v.3.2 (Ronquist et al. 2012), with default prior settings. For this analysis, we used the best-fit models suggested by Partitionfinder for each partition as follows, *ND2* position1: TVM+I+G, *ND2* position2: TVM+G, *ND2* position3: TrN+I+G. Four separate runs were set up with eight Metropolis-Coupled Markov Chain (MC3) Monte Carlo 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 pseudoreplicates (ultrafast bootstrap UFB) and posterior probability PP, respectively. We considered PP above 0.95 and UFB above 95 as strong support. The uncorrected pairwise genetic distance (p-distance) was calculated in MEGA7 using default settings (pairwise deletion).



**Figure 1.** Topographic map showing the distribution of *Hemidactylus pakkamalaiensis* sp. nov. and other members of the *graniticolus* clade from the peninsular India (Top). *Hemidactylus pakkamalaiensis* sp. nov. and the two lineages identified as *H. cf. graniticolus* from the southern Eastern Ghats (Bottom). The inset map shows the known distribution of *H. pakkamalaiensis* sp. nov. in the Gingee Hills cluster.



**Figure 2.** ML phylogeny showing the phylogenetic relationships of the *prashadi* group. Numbers at internal branches are Bayesian posterior probabilities (left) and ML bootstrap support values (right).

## Morphological analysis

All the morphological characters (morphometric and meristic) examined in this work were implemented following Agarwal et al. (2019). Measurements and meristic data from the collected specimens for this study were taken under a Nikon SMZ1270 stereo microscope and using a Mitutoyo digital vernier caliper (accuracy 0.1mm). Measurements and meristic characters were as follows: snout vent length (SVL, from tip of snout to the cloacal opening; axilla to groin length (AGL, from posterior margin of forelimb insertion to anterior margin of hind-limb

insertion); 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 the cloacal opening to tip 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: longitudinal rows of enlarged dorsal tubercles at midbody (DTR); number of paravertebral tubercles between limb insertions (PVT); the number of ventral scale rows at midbody between the lowest rows of dorsal scales (MVSR); 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 and other morphological data for the large-bodied *prashadi* group were obtained from literature and the original descriptions (Chaitanya et al. 2018; Giri, 2008; Khandekar et al. 2021; Mirza et al. 2018; Mirza and Sanap 2014; Srikanthan et al. 2018; Amarasinghe et al. 2021; Das et al. 2022). The museum abbreviation are as follows: BNHS: Bombay Natural History Society, Mumbai, India; CES: Centre for Ecological Sciences, Indian Institute of Science, Bengaluru, India.

## Results

### Molecular analysis

Both ML and BI analyses recovered similar topology for the *prashadi* group. The *graniticolus* clade is recovered as a strongly supported (UFB: 100, PP: 1.0) monophyletic clade with two subclades, one that includes *H. easai* + *H. graniticolus* and the other clade that includes the new species here described with two other undescribed lineages (Fig. 2). The new species described here is nested together with a sample reported in Lajmi and Karanth (2020) collected from a hillock within the Gingee Hills cluster, with strong support (UFB: 100, PP: 1.0). These three samples are together sister to two other samples identified as *H. cf. graniticolus* 1 from the adjacent Shevaroy landscape with low support in ML and BI (UFB: 59, PP: 0.86). The uncorrected pairwise genetic distance between the new species and other lineages (including the two undescribed lineages) within the *graniticolus* clade range between 5.6% and 10.3%, in the mitochondrial ND2 gene (Table 1).

### Morphological analysis

Morphological measurements and counts are summarised in Table 2 and in the comparison section below. The overall morphology and colour pattern for the members of the *graniticolus* clade and the new species described here are similar. We found significant differences in the femoral pores between these species and dorsal pholidosis. The new species described here is characterized by a combination of non-overlapping characteristics like the number

of femoral pores, dorsal tubercle rows and ventral scales along the midbody.

## Systematics

### *Hemidactylus pakkamalaiensis* Narayanan, Christopher, Raman, Mukherjee, Vimalraj, Deepak sp. nov.

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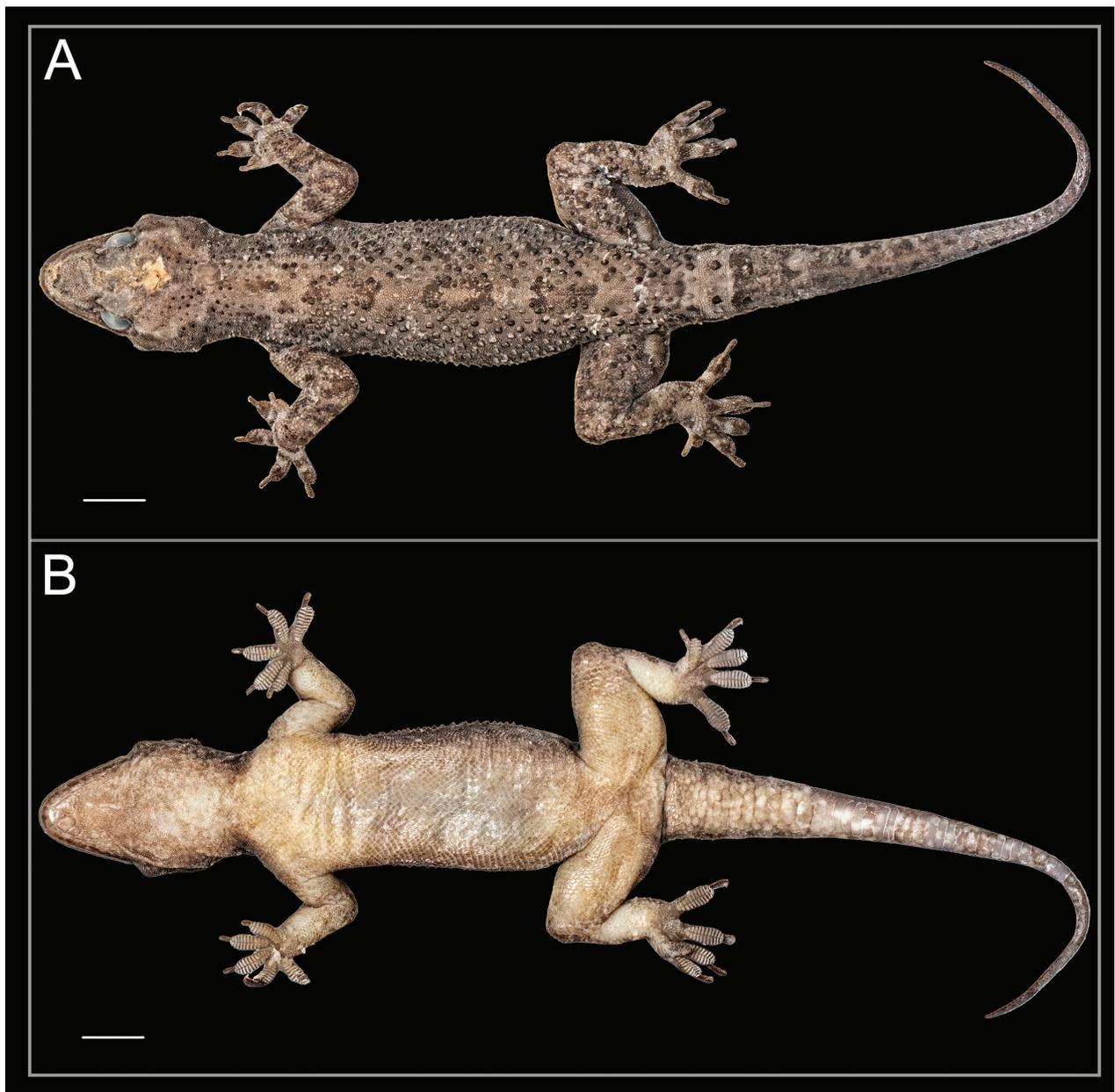
Figs 3–6

**Holotype.** BNHS 2907 (Figs 3, 4, 6A) adult male, collected from Pakkamalai Hill, Gingee Hills range, Villupuram district, Tamil Nadu, India (12.164819°N, 79.250909°E, 335m asl) by Peter Christopher and Surya Narayanan on 27 November 2022.

**Paratypes (n = 4).** BNHS 2908 & BNHS 2909 (adult males), BNHS 2910 & BNHS 2911 (adult females), collections details same as the holotype (Figs 5, 6B).

**Etymology.** The specific epithet is a toponym named after its type locality Pakkamalai Hill. We suggest an English name Pakkamalai rock gecko and a Tamil name பாக்கமலை பாறைப்பல்லி.

**Diagnosis.** A large-sized gecko of the genus *Hemidactylus*, snout–vent length up to a maximum SVL of 109 mm (n = 5). Dorsal pholidosis heterogeneous, composed of roughly circular, granular scales intermixed with much enlarged, fairly regularly arranged longitudinal rows of 19–22 striated subtriangular tubercles at midbody. Enlarged 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. Paravertebral rows with 21–24 tubercles; 34–38 transverse ventral scale rows at mid-body. Digits with enlarged scansors, lamellae in straight transverse series; two or three undivided basal lamellae beneath first finger and two or three beneath first toe; one or two undivided basal lamellae beneath fourth toe; ten or 11 lamellae (including undivided and divided) beneath first finger and nine or ten beneath first toe; 12 or 13 lamellae (including undivided and divided) beneath fourth finger and 12–14 beneath fourth toe; males with series of 19–21 femoral pores on each side separated by four or five 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 4–8 large, keeled, striated, posteriorly pointed tubercles.



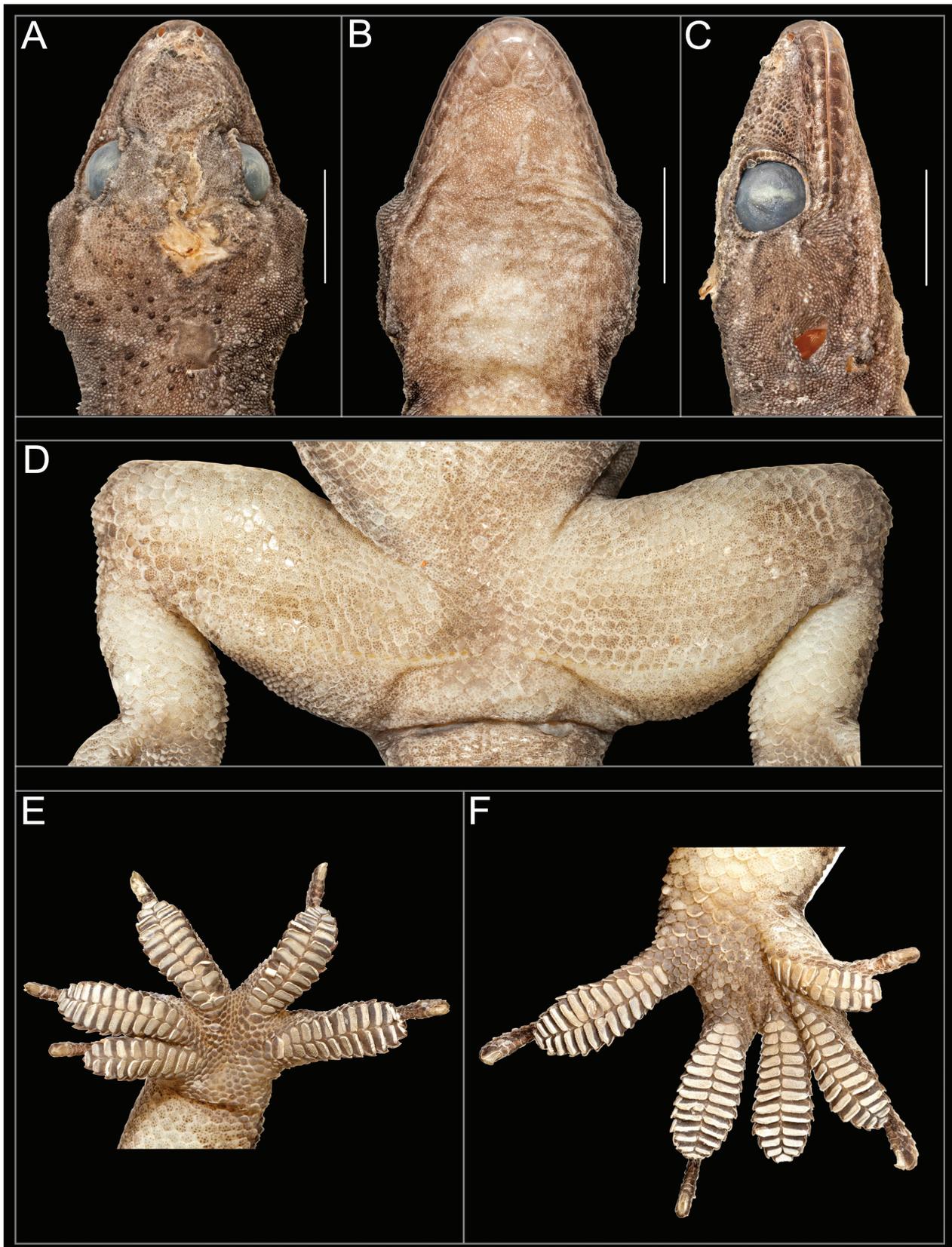
**Figure 3.** Holotype of *Hemidactylus pakkamalaiensis* sp. nov. (BNHS 2907) in the dorsal (A) and ventral (B) view. Scale bar = 10mm.

Dorsal colouration dull-brown with a series of four or five transverse pale saddles from occiput to sacrum, tail with distinct alternating light and dark bands.

**Comparison with other members of prashadi group.**

*Hemidactylus pakkamalaiensis* sp. nov. differs from the other large-bodied congeners by several non-overlapping morphological characters. It can be distinguished by the presence of 19–21 femoral pores (FP) separated by 4 or 5 pore-less scales in males (vs. 23–28 FP separated by 1–3 pore-less scales in *H. graniticolus*; 19–21 FP separated by 13 or 14 pore-less scales in *H. acanthopholis* Mirza & Sanap, 2014; 26–28 FP separated by 7–9 pore-less scales in *H. hunae* Deraniyagala, 1937; 16–18 FP separated by 13 or 14 pore-less scales in *H. sirumalaiensis* Khandekar et al., 2020; 17–22 FP separated by 10 or 11 pore-less scales in *H. vanam* Chaitanya et al., 2018; 15–19 FP sep-

arated by three pore-less scales in *H. depressus* Gray, 1842; 17 or 18 FP separated by five pore-less scales in *H. siva* Srinivasalu et al., 2018; 7–9 FP separated by 1–3 pore-less scales in *H. triedrus* (Daudin, 1802); 11–15 FP separated by 1–3 pore-less scales in *H. sahgali* Mirza et al., 2018; 7 or 8 FP separated by three pore-less scales in *H. whitakeri* Mirza et al., 2018; 15–19 FP separated by six pore-less scales in *H. aaronbaueri* Giri, 2008; 17 or 18 FP separated by seven pore-less scales in *H. tamhiniensis* Khandekar et al., 2021; 18–21 FP separated by four pore-less scales in *H. kangerensis* Mirza et al., 2017; 24–30 FP separated by 2–4 pore-less scales in *H. easai*; 14–15 FP separated by 11 pore-less scales in *H. hegdei* Pal & Mirza, 2022); by the presence of 19–22 rows of moderately keeled subtriangular tubercles in both sex (vs. 16 or 17 in *H. sushilduttai* Giri et al., 2017; 12–14 in *H. kimbulae*; 15 or 16 in *H. kolliensis*; 17 or 18 in *H. easai*;



**Figure 4.** *Hemidactylus pakkamalaiensis* sp. nov. (Holotype, BNHS 2907), **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.

18–20 in *H. kangerensis*; 14–16 in *H. hunae*; 16 in *H. siva*; 16–18 in *H. sushilduttai*); presence of 34–38 transverse ventral scale rows at mid-body in both sex (vs. 40–13 in *H. hunae*, 41 or 42 in *H. easai*; 40–46 in *H. graniti-*

*colus*; 28–30 in *H. kangerensis*; 30–33 in *H. sushilduttai*; 27–30 in *H. siva*); dorsal pholidosis heterogeneous with enlarged tubercles (vs. dorsal pholidosis homogeneous with no enlarged tubercles in *H. scabriceps*).

**Description of holotype (BNHS 2907).** The holotype, an adult male, (SVL 104 mm) is well preserved. Head short (HL/SVL 0.29), slightly elongated (HW/HL 0.66), not strongly depressed (HH/HL 0.29), distinct from neck. Loreal region slightly inflated, and canthus rostralis indistinct (Fig. 4C). Snout short (SE/HL 0.40); slightly longer than twice eye diameter (OD/SE 0.45); scales on the snout, canthus rostralis, forehead and inter-orbital region heterogeneous, mostly granular and conical; scales on the snout and canthus rostralis much larger than those on occiput, forehead and inter-orbital regions; skin in the frontal slightly damaged. Eye small (OD/HL 0.18); pupil vertical with crenulated margins; supraciliaris small, mucronate, gradually increasing in size towards the front of the orbit, largest about one-third the way from the anterior edge of orbit; a few supraciliaris in the suprocular region in the left eye damaged and missing. Ear opening elliptical (2.8 mm); a row of small keeled tubercles above the ear.

Rostral scale wider than deep (RL/RW 0.68), partially divided dorsally by a weakly developed rostral groove; nasals, 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 three postnasals on either side; five (on the anterior) and three (on the posterior) rows of scales separate orbit from supralabials.

Mental triangular; two well-developed pair of postmentals, the inner pair smaller (3.4 mm) than the mental (4.6 mm), and in strong contact with each other (1.2 mm) behind mental, outer pair shorter (2.2 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 10 small gular scales on each side; outer postmentals bordered by infralabial II on the right and left, inner postmental, and five gular scales on the right and six gular scales in the left along with two other large scales between the gular scales and the infralabials; one to three additional rows of scales below infralabials III to VIII are enlarged and weakly imbricate. Supralabials (on both sides) to mid orbital position 10, to angle of jaw 12 on right and left; infralabials 10 and nine on right and left side, respectively. Body relatively stout (BW/SVL 0.22), ventrolateral folds not very distinct.

Dorsal pholidosis heterogeneous, composed of sub-circular granular scales intermixed with enlarged, fairly regularly arranged strongly keeled. Pointed tubercles in 21 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 13–16 small granules with 2–5 granules between two

longitudinally adjacent enlarged tubercles (5–11 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 granular scales on the dorsum, smooth, imbricate, slightly larger on precloacal and femoral region than on chest and abdominal region; mid-body scale rows across belly 34; 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 slightly smaller than the 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, imbricate, intermixed with enlarged, conical tubercles, which are larger on thigh compared to shank that are subequal to those tubercles in the dorsal aspect of the body; anterior aspect of thigh with flatter scales, posterior aspect with granular scales.

Twenty pores in an enlarged row of femoral scales on both sides, 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 0.13); tibia short (CL/SVL 0.15); 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: 10-13-13-12-13 (left manus), 10-12-13-12-13 (right manus) (Fig. 4E), 10-13-13-13-13 (left pes), 10-14-13-13-13 (right pes) (Fig. 4F). Relative length of digits (measurements in mm in parentheses): I (6.8) < II (8.7) < III (8.3) < IV (8.2) < V (8) (left manus); I (6.8) < V (9.6) < IV (8.7) < II (9.3) < III (6.6 damaged) (left pes).

Tail complete regenerated (about 30% of the tail original); 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 4–6 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. Two indistinct postcloacal spurs on each side, much smaller than dorsal tubercles at midbody.

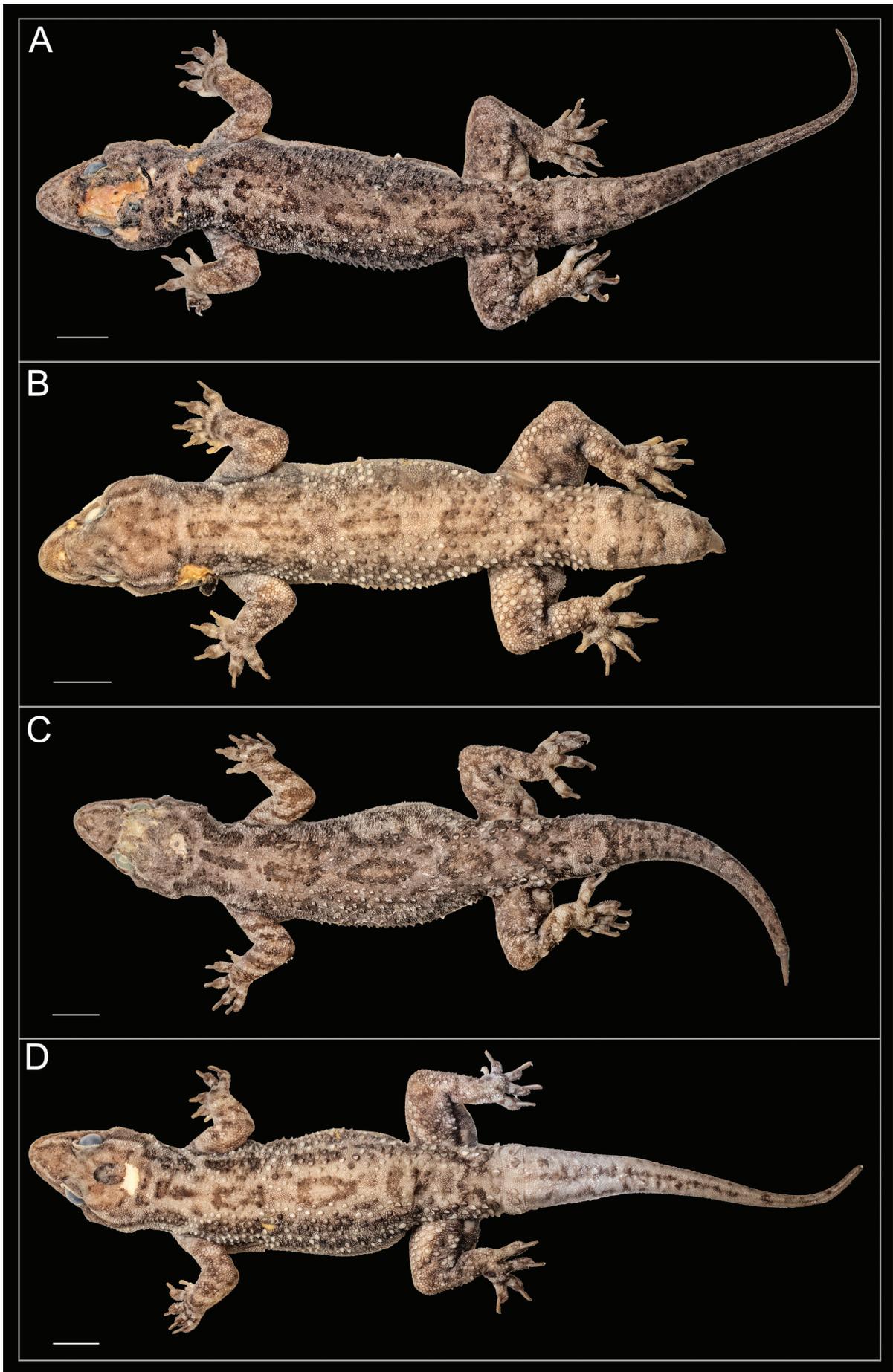
**Variations in the paratypes.** Variations among the meristic and morphometric characters in the paratypes are provided in the Table. 2. Two paratypes BNHS 2910 & 2911 are females. BNHS 2909 has a very short tail among all the type series. Up to eight enlarged tubercles in the tail in paratype BNHS 2909. postcloacal spur distinct in

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

	Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	<i>H. pakkamalaiensis</i> sp. nov. CES15265															
2	<i>H. pakkamalaiensis</i> sp. nov. BNHS 2911	2.8														
3	<i>H. pakkamalaiensis</i> sp. nov. BNHS 2907	2.7	0.1													
4	<i>Hemidactylus</i> cf. <i>graniticolus</i> 2 CESH122	7.7	7.2	7.1												
5	<i>Hemidactylus</i> cf. <i>graniticolus</i> 2 CESH123	7.7	7.2	7.1	0.0											
6	<i>Hemidactylus</i> cf. <i>graniticolus</i> 1 CESH139	5.6	5.3	5.2	7.9	7.9										
7	<i>Hemidactylus</i> cf. <i>graniticolus</i> 1 CESH146	5.9	5.6	5.5	8.2	8.2	1.1									
8	<i>H. easai</i> BNHS 3103	8.5	8.6	8.5	9.3	9.3	8.5	8.8								
9	<i>H. easai</i> ZSI/3471	8.5	8.5	8.5	9.3	9.3	8.5	8.8	0.0							
10	<i>H. graniticolus</i> AK117	9.5	9.7	9.6	9.4	9.4	10.1	10.6	6.6	6.6						
11	<i>H. graniticolus</i> AK347	9.4	9.5	9.4	9.7	9.7	9.9	10.4	7.2	7.2	2.0					
12	<i>H. graniticolus</i> AK348	10.3	10.2	10.1	9.8	9.8	10.1	10.6	7.0	7.0	1.2	1.4				
13	<i>H. graniticolus</i> CES15213	9.6	9.8	9.7	9.7	9.7	9.8	10.4	7.1	7.1	1.6	1.4	1.2			
14	<i>H. graniticolus</i> CES15236	9.8	9.9	9.7	10.0	10.0	10.1	10.7	7.2	7.2	1.5	1.4	0.7	1.0		
15	<i>H. graniticolus</i> CES15257	9.6	9.6	9.5	9.2	9.2	9.5	10.0	6.6	6.6	1.8	1.8	1.6	1.9	1.6	
16	<i>H. graniticolus</i> CESH380	9.1	9.5	9.3	9.2	9.2	10.0	10.1	7.1	7.1	4.4	4.0	3.9	3.9	3.9	3.1

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

Voucher no.	BNHS 2907	BNHS 2908	BNHS 2909	BNHS 2910	BNHS 2911
	<i>Hemidactylus pakkamalaiensis</i> sp. nov.				
	Holotype	Paratype	Paratype	Paratype	Paratype
Sex	Male	Male	Male	Female	Female
SVL	104	109.2	101.2	109	101
AGL	42.2	46.4	41.6	50	43.3
TL	95	90.3	30.1*	76.7	84.3
HL	30.5	32.2	30	31	28.4
HW	20.3	22.7	22	21	21.1
HD	9.1	9.5	7.9	8.8	7.4
FL	14.5	15.4	13.7	15.4	12.6
CL	16	16.1	15.1	16.4	14.6
ED	5.6	5.9	5.6	6.4	6
EN	10.1	11	9.6	10.1	9.2
ES	12.4	12.9	11.4	13.4	11.4
EE	8.2	8.2	7.9	8.1	7.1
EL	2.8	3.8	3.2	3.4	2.4
IN	3.3	3.2	2.8	3.1	3
IO	8.6	9.4	8.1	8.7	9.5
Femoral pores (poreless scales separating series)	20&20(4)	21&20(4)	19&19(5)	NA	NA
DTR	21	19	22	20	22
PVT	23	21	24	21	22
MVSR	34	34	38	38	38
Supralabials (L&R)	12,12	12,11	12,11	12,12	12,12
Infralabials (L&R)	10,9	9,9	10,10	10,10	10,9
Supralabials to midorbit (L&R)	10,10	10,10	10,10	10,10	10,10
Infralabials to midorbit (L&R)	8,7	7,7	8,8	8,8	8,7
Manus left	10-13-13-12-13	10-12-12-12-12	10-12-12-12-13	11-12-12-13-13	11-12-13-13-14
Manus right	10-12-13-12-13	10-11-12-12-12	9-12-12-13-13	11-12-12-13-13	10-12-14-13-14
Pes left	10-13-13-13-13	10-13-13-12-13	10-13-13-13-13	10-14-12-12-13	10-13-13-13-13
Pes right	10-14-13-13-13	9-13-12-13-13	10-13-13-13-13	10-13-13-14-11	10-13-13-13-13



**Figure 5.** Paratypes of *Hemidactylus pakkamalaiensis* sp. nov. in dorsal view, **A** BNHS 2908, **B** BNHS 2909, **C** BNHS 2910, **D** BNHS 2911. Scale bar = 10mm.



**Figure 6.** Dorsolateral view of the **A** holotype (BNHS 2907) and **B** one of the paratypes (BNHS 2911) of *Hemidactylus pakkamalaiensis* **sp. nov.** in life from Pakkamalai Hill, Tamil Nadu, India.

paratypes BNHS 2908 & BNHS 2909. Other differences include the number of undivided lamellae at the base of pes and manus that varies between three (BNHS 2908) to five (BNHS 2910 & BNHS 2911) in the paratypes and occasionally in the middle in BNHS 2910 & 2909. Gular scales that are in contact with the outer postmental much larger on the right side in BNHS 2909. The total number of the gular scales contacting the outer postmentals vary between eight and thirteen.

**Colour in life and preservative (based on holotype).** Dorsal aspect of the body, uniformly brownish with three indistinct transverse bands from the neck to the hind limb insertion and one on the tail, bordered by discontinuous brownish patches extending towards the lateral side of the body (Fig. 6A). Dorsal aspect of the head is brownish with inconspicuous white markings on the parietal and neck region. Ventral aspect of the head is mostly cream-coloured with light brown mottling on the gular region and mental, infralabials, postmentals and a few other adjacent scales mottled with dark brown. Fore and

hindlimbs are brownish speckled with irregular black patches and a few scattered brownish-yellow spots on the dorsal side. Ventral aspect of the body, forelimbs and hindlimbs predominantly cream coloured with sprinkled and or mottled with brown colour. In preservative, the overall colouration is the same as in life except in dark transverse bands on the dorsum that became less prominent.

**Distribution and natural history.** *Hemidactylus pakkamalaiensis* **sp. nov.** is currently known from the Gingee Hills cluster. This species is nocturnal and appears to be locally abundant. In addition to the collected specimens, we encountered 56 live individuals in and around the collection site during our four-day fieldwork. All the specimens in the type series were gathered from rock boulders within a limited area at the type locality, mostly after 19:00 hrs. These hills are predominantly formed of granitic rock boulders and feature native vegetation, including thorny scrub jungle, moist deciduous forest, and tropical dry evergreen forest (Arulappan et al. 2015).



**Figure 7.** Habitat at the type locality (Pakkamalai Hill, Tamil Nadu, India) of *Hemidactylus pakkamalaiensis* **sp. nov.**

## Discussion

The description of *Hemidactylus pakkamalaiensis* **sp. nov.** expands the known diversity of *Hemidactylus* in India to 55 and the *prashadi* group to 23 (Kumar et al. 2022; Uetz et al. 2023). Although this lineage was previously identified through phylogenetic data, it had not been formally described until now (Lajmi and Karanth 2019; Agarwal et al. 2019; Das et al. 2022).

The Gingee Hills are part of the larger Southern Granulitic Terrain (SGT), which consists mostly of granitic gneiss with an origin in the mid-Archean to the Neoproterozoic era (Fermor 1936). The Gingee Hills are characterized by a significant presence of granitic rock boulders that provide a suitable micro-habitat for rock-dwelling geckos. These hills are unique in this regard, and despite being situated in the drier part of peninsular India, Pakkamalai Hill is home to a diverse range of vegetation types, including the distinctive Tropical Dry Evergreen Forest (Arullappan et al. 2009). This combination of vegetation and the microhabitats availability likely provided an ambient microclimatic condition that facilitated the diversification of this species. However, our survey found that *H. pakkamalaiensis* **sp. nov.** was present in all habitat types. This would suggest that the substrate (rock boulders) is the primary requirement of this species rather than the type of vegetation. Previous studies have demonstrated a high diversity in other gekkonid genera that are also restricted to small hill ranges within this region (Agarwal et al. 2019a, 2022). Agarwal et al. (2020) proposed that microclimatic conditions within the granitic hill ranges in the region were a potential reason for the diversifica-

tion in the genus *Cnemaspis*. The current study concurs with the previous recognition of this lineage as a distinct species based on morphological evidence. We follow the evolutionary species concept to delimit the monophyletic lineage from Gingee Hills as a distinct species (Simpson 1951; Wiley 1978; de Queiroz 2007).

Although *Hemidactylus pakkamalaiensis* **sp. nov.** is genetically related to *H. easai* and *H. graniticolus*, it differs significantly from these closely related species by having fewer femoral pores, with a count of 19–21 as compared to 24–28 in the latter two species. One of the samples (CES 12565) used here in the molecular analyses, collected from the adjacent hill to the Pakkamalai (Lajmi and Karanth 2020), shows a shallow divergence (2.8%) with the samples of *H. pakkamalaiensis* **sp. nov.** collected in the present study. While this specimen could not be located and examined, we recover it as *H. pakkamalaiensis* **sp. nov.** solely based on the low level of divergence, which is consistent with the intraspecific divergence observed within the *H. graniticolus* sensu stricto.

In our phylogeny, we recovered two sister lineages to *H. pakkamalaiensis* **sp. nov.** that could potentially represent distinct lineages. Previously, Agarwal et al. 2019b recognized these two as distinct lineages based on their species delimitation analyses and the genetic divergence cut-off. *Hemidactylus pakkamalaiensis* **sp. nov.** is geographically separated from the sister lineage *H. cf. graniticolus* 1 from the Shervaroys landscape by the intervening plains which are an unsuitable habitat for these large rock-dwelling geckos. We concur with the aforementioned hypothesis as these lizards have disjunct distributions and are isolated by geographical separation with no obvious contact zones. However, as previously stated in

Das et al. (2022), we failed to locate these specimens in the collections and their morphological affinity with *H. pakkamalaiensis* sp. nov. remains unclear.

Globally nine new species of *Hemidactylus* were described in the year 2022 out of which seven were from peninsular India (Adhikari et al. 2022; Kumar et al. 2022; Pal and Mirza 2022; also see Uetz et al. 2023). Additional surveys are required to uncover the true species diversity of *Hemidactylus* in peninsular India. Furthermore, fine-scale sampling is required to understand genetic structuring within species occurring in isolated hillocks across this landscape.

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## References

- Adhikari OD, Achyuthan N, Kumar GC, Khot RV, Shreeram M, Ganesh S (2022) Two new species of *Hemidactylus* Goldfuss, 1820 (Squamata: Gekkonidae) from the rocky outcrops of the Deccan plateau, peninsular India. *Zootaxa* 5129: 227–249. <https://doi.org/10.11646/zootaxa.5129.2.4>
- Agarwal I, Giri VB, Bauer AM (2011) A new cryptic rock-dwelling *Hemidactylus* (Squamata: Gekkonidae) from south India. *Zootaxa* 2765: 21–37. <https://doi.org/10.11646/zootaxa.2765.1.2>
- Agarwal I, Khandekar A, Giri VB, Ramakrishnan U, Karanth KP (2019a) The hills are alive with geckos! A radiation of a dozen species on sky islands across peninsular India (Squamata: Gekkonidae, *Hemiphyllodactylus*) with the description of three new species. *Organisms Diversity and Evolution* 19: 341–361. <https://doi.org/10.1007/s13127-019-00392-5>
- Agarwal I, Bauer AM, Giri VB, Khandekar A (2019b) An expanded ND2 phylogeny of the *brookii* and *prashadi* groups with the description of three new Indian *Hemidactylus* Oken (Squamata: Gekkonidae). *Zootaxa* 4619: 431–458. <https://doi.org/10.11646/zootaxa.4619.3.2>
- Agarwal I, Thackeray T, Pal S, Khandekar A (2020) Granite boulders act as deep-time climate refugia: A Miocene divergent clade of rupicolous *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae) from the Mysore Plateau, India, with descriptions of three new species. *Journal of Zoological Systematics and Evolutionary Research* 58(4): 1234–1261. <https://doi.org/10.1111/jzs.12391>
- Agarwal I, Thackeray T, Khandekar A (2022) A multitude of spots! Five new microendemic species of the *Cnemaspis gracilis* group (Squamata: Gekkonidae) from massifs in the Shevaroy landscape, Tamil Nadu, India. *Vertebrate Zoology* 72: 1137–1186. <https://doi.org/10.3897/vz.72.e94799>
- Amarasinghe AAT, Karunarathna S, Campbell PD, Madawala M, de Silva A (2021) A new species of *Hemidactylus* Goldfuss, 1820 (Reptilia: Gekkonidae) from Sri Lanka with redescription of *H. hunae* Deraniyagala, 1937. *Herpetologica* 77: 259–272. <https://doi.org/10.1655/Herpetologica-D-21-00003.1>
- Arulappan M, Britto SJ, Ruckmani K, Mohankumar R (2015) An ethnobotanical study of medicinal plants used by ethnic people in Gingee, Villupuram District, Tamil Nadu, India. *American Journal of Ethnomedicine* 2: 84–102.
- Chaitanya R, Lajmi A, Giri VB (2018) A new cryptic, rupicolous species of *Hemidactylus* Oken, 1817 (Squamata: Gekkonidae) from Meghamalai, Tamil Nadu, India. *Zootaxa* 4374: 49–70. <https://doi.org/10.11646/zootaxa.4374.1.3>
- Das S, Pal S, Siddharth S, Palot MJ, Deepak V, Narayanan S (2022) A new species of large-bodied *Hemidactylus* Goldfuss, 1820 (Squamata: Gekkonidae) from the Western Ghats of India. *Vertebrate Zoology* 72: 81–94. <https://doi.org/10.3897/vz.72.e76046>
- Dettman DL, Kohn MJ, Quade J, Ryerson FJ, Ojha TP, Hamidullah S (2001) Seasonal stable isotope evidence for a strong Asian monsoon throughout the past 10.7my. *Geology* 29: 31–34. [http://dx.doi.org/10.1130/0091-7613\(2001\)029%3C0031:SSIEFA%3E2.0.CO;2](http://dx.doi.org/10.1130/0091-7613(2001)029%3C0031:SSIEFA%3E2.0.CO;2)
- deQueiroz K (2007) Species concepts and species delimitations. *Systematic Biology* 56: 879–886. <https://doi.org/10.1080/10635150701701083>
- Fermor LL (1936) An attempt at the correlation of the ancient schistose formations of peninsular India. *Geological Survey of India*, 70, Calcutta, India.
- Giri VB (2008) A new rock dwelling *Hemidactylus* (Squamata: Gekkonidae) from Maharashtra, India. *Hamadryad* 32: 25–33.
- Higgins D, Thompson J, Gibson T, Thompson JD, Higgins DG, Gibson TJ (1994) CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Research* 22: 4673–4680. <https://doi.org/10.1093/nar/22.22.4673>
- Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, Jermiin LS (2017) ModelFinder: Fast model selection for accurate phylogenetic estimates. *Nature Methods* 14: 587–589. <https://doi.org/10.1038/nmeth.4285>
- Kumar S, Stecher G, Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. *Molecular Biology and Evolution* 33: 1870–1874. <https://doi.org/10.1093/molbev/msw054>
- Kumar GC, Srinivasalu A, Srinivasalu C (2022) Redescription of *Hemidactylus giganteus* Stoliczka, 1871 with the description of three new allied species (Squamata: Gekkonidae: *Hemidactylus* Goldfuss, 1820) from peninsular India. *Zootaxa* 5115: 301–341. <https://doi.org/10.11646/zootaxa.5115.3.1>
- Khandekar A, Thackeray T, Pawar S, Agarwal I (2020) A new medium-bodied rupicolous *Hemidactylus* Goldfuss, 1820 (Squamata: Gekkonidae) from the Sirumalai massif, Tamil Nadu, India. *Zootaxa* 4852: 83–100. <https://doi.org/10.11646/zootaxa.4852.1.4>
- Khandekar A, Thackeray T, Agarwal I (2021) A cryptic new species of rupicolous *Hemidactylus* Goldfuss, 1820 (Squamata: Gekkonidae) allied to *H. aaronbaueri* Giri, 2008 from the northern Western Ghats of Maharashtra, India. *Zootaxa* 5020: 434–456. <https://doi.org/10.11646/zootaxa.5020.3.2>
- Lajmi A, Bansal R, Giri V, Karanth P (2019) Phylogeny and biogeography of the endemic *Hemidactylus* geckos of the Indian subregion suggest multiple dispersals from Peninsular India to Sri Lanka. *Zoological Journal of the Linnean Society* 186: 286–301. <https://doi.org/10.1093/zoolinnean/zly047>
- Lajmi A, Karanth PK (2020) Eocene–Oligocene cooling and the diversification of *Hemidactylus* geckos in Peninsular India. *Molecular*

- Phylogenetics and Evolution 142: 106637. <https://doi.org/10.1016/j.ympev.2019.106637>
- Lajmi A, Verma A, Karanth KP (2020) Repeated evolution of terrestrial lineages in a continental lizard radiation. *Journal of Evolutionary Biology* 33: 57–66. <https://doi.org/10.1111/jeb.13544>
- Lanfear R, Frandsen PB, Wright AM, Senfeld T, Calcott B (2017) PartitionFinder 2: New methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. *Molecular Biology and Evolution* 34: 772–773. <https://doi.org/10.1093/molbev/msw260>
- Macey JR, Larson A, Ananjeva NB, Fang Z, Papenfuss TJ (1997) Two novel gene orders and the role of light-strand replication in rearrangement of the vertebrate mitochondrial genome. *Molecular Biology and Evolution* 14: 91–104. <https://doi.org/10.1093/oxfordjournals.molbev.a025706>
- Mirza ZA, Sanap RV (2014) A new cryptic species of gecko of the genus *Hemidactylus* Oken, 1817 (Reptilia: Gekkonidae) from Southern India. *Taprobanica* 6: 12–20.
- Mirza ZA, Gowande GG, Patil R, Ambekar M, Patel H (2018) First appearance deceives many: Disentangling the *Hemidactylus triedrus* species complex using an integrated approach. *PeerJ* 6: e5341. <https://doi.org/10.7717/peerj.5341>
- Pal S, Mirza ZA (2022) A new species of Large-bodied Gecko of the genus *Hemidactylus* Goldfuss, 1820 from southern Western Ghats of Tamil Nadu, India. *Journal of the Bombay Natural History Society* 119: 167364. <https://doi.org/10.17087/jbnhs/2022/v119/167364>
- Riedel N, Fuller DQ, Marwan N, Poretschkin C, Basavaiah N, Menzel P, Ratnam J, Prasad S, Sachse D, Sankaran M, Sarkar S, Stebich M (2021) Monsoon forced evolution of savanna and the spread of agro-pastoralism in peninsular India. *Scientific Reports* 11: 9032. <https://doi.org/10.1038/s41598-021-88550-8>
- Ronquist F, Teslenko M, Mark VDP, Ayres D, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) MrBayes 3.2: Efficient Bayesian phylogenetic inference and model choice across a large model space. *Systematic Biology* 61: 539–542. <https://doi.org/10.1093/sysbio/sys029>
- Simpson GG (1951) The species concept. *Evolution* 5: 285–298. <https://doi.org/10.1111/j.1558-5646.1951.tb02788.x>
- Srikanthan AN, Swamy P, Mohan AV, Pal S (2018) A distinct new species of riparian rock-dwelling gecko (genus: *Hemidactylus*) from the southern Western Ghats. *Zootaxa* 4434: 141–157. <https://doi.org/10.11646/zootaxa.4434.1.9>
- Trifinopoulos J, Nguyen LT, von Haeseler A, Minh BQ (2016) W-IQ-TREE: A fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Research* 44: W232–W235. <https://doi.org/10.1093/nar/gkw256>
- Tamura K, Peterson D, Peterson N, Stecher G, Nei M, Kumar S (2011) MEGA 5: Molecular Evolutionary Genetics Analysis using maximum likelihood, evolutionary distance and maximum parsimony methods. *Molecular Biology and Evolution* 28: 2731–2739. <https://doi.org/10.1093/molbev/msr121>
- Uetz P, Freed P, Aguilar R, Hošek J (eds.) (2023) The Reptile Database, <http://www.reptile-database.org> [accessed 20 January 2023].
- Wiley EO (1978) The evolutionary species concept reconsidered. *Systematic Zoology* 27: 17–26. <https://doi.org/10.2307/2412809>

## Supplementary Material 1

### Table S1

**Authors:** Narayanan S, Christopher P, Raman K, Mukherjee N, Prabhu P, Lenin M, Vimalraj S, Deepak V (2023)

**Data type:** .xlsx

**Explanation note:** Genbank voucher numbers for the samples used in the study.

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