A remarkable new species of gecko (Squamata: Gekkonidae: Hemidactylus) from scrublands at the southern tip of India

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Abstract

We describe a new species of Hemidactylus based on an integrative taxonomic framework from scrub habitats at the southern tip of India, in Thoothukudi District, Tamil Nadu. The new species has the most densely packed tubercles among Indian Hemidactylus, almost resembling the most tuberculate Indian Cyrtopodion. Hemidactylus quartziticolus sp. nov. is phylogenetically placed within the brookii group of Indian Hemidactylus, where it is sister to the H. gleadowi complex from western-central India. The new species is 14.5–23.7% divergent in ND2 mitochondrial sequence data from other brookii group members, and can be easily diagnosed from regional congeners by its unique dorsal scalation, the number and arrangement of precloacal-femoral pores, the number of dorsal tubercle rows at midbody, number of lamellae under digit I and IV of manus and pes. The new species is currently known only from two isolated, low quartzite hillocks 45 km apart with scrubby, thorn forests and loose, stony soil.

Keywords

Hemidactylus brookii, morphology, peninsular India, taxonomy, Tamil Nadu

Introduction

The globally distributed gekkonid genus Hemidactylus Goldfuss, 1820 includes ~188 currently recognised species (Uetz et al. 2023). Global phylogenies of the genus reveal five deeply divergent clades that are each more or less broadly geographically circumscribed – the angulatus and Afro-Atlantic radiations in Africa and South America, Arid radiation in Saharo-Arabia, bowringii radiation in Southeast Asia, and finally the Indo-Sri Lankan radiation (hereafter Indian radiation) in India and Sri Lanka (Carrranza and Arnold 2006; Bansal and Karanth 2010; Bauer et al. 2010). India has over 50 species of Hemidactylus and is one of the few countries where three of the broad global clades are naturally distributed — the Arid radiation with three species in northwest India, the bowringii radiation with three species in northeast India and one in western peninsular India, while the Indian radiation in-
includes the remaining species in India and Sri Lanka (Car-
ranza and Arnold 2006; Bansal and Karanth 2010; Bauer
et al. 2010; Lajmi et al. 2018a, b; Amarasinghe et al. 2021;
Pal and Mirza 2022; Uetz et al. 2023). Phylogenies of the
Indian radiation consistently reveal four major groups: flavi-
viridis, prashadi, frenatus and brooki (Bansal and Karanth
2010; Lajmi et al. 2018a; Agarwal et al. 2019). The brooki
group includes 23 species and has been further
divided into four clades: gleadowi, malcolmsmithi + parvi-
macularus, murrayi and ground-dwelling (Agarwal
et al. 2019; Lajmi et al. 2020; Adhikari et al. 2022).

The ground-dwelling clade is morphologically unique
within the brooki group, with species lacking fe-
meral pores in both sexes, undivided or notched subdigital
lamellae, small body size (snout to vent length, SVL < 46
mm) and varied dorsal tuberculation and colour pattern
(Smith 1935; Giri and Bauer 2008; Mirza 2018). Though
the species from the other three clades of the brooki
group are not monophyletic, they have been collectively
referred to as brookish geckos, as they are all small to
medium-sized (SVL < 80 mm), tuberculate, with a light
brown dorsum with darker spots or X-shaped markings
(Agarwal et al. 2019). Though the brookish geckos have	heralded taxonomic history and lack recently col-
ccted toptotypic material for many nomina, 12 species have
been described in just the last 15 years (Mahony
Chaitanya et al. 2019; Adhikari et al. 2022). The recent
uptick in species discovery of brookish geckos is in part
due to the redesription of all name-bearing types of the
group, the use of DNA sequence data as well as concerted
fieldwork (Mahony 2009, 2011; Lajmi et al. 2016; Agar-
wal et al. 2019, 2020; Chaitanya et al. 2019; Adhikari et al.
2022). Most species in the three clades of brookish
gckos are distributed in dry and rocky habitats across
India (Fig. 1), and the most morphologically distinct spec-
ies of the group, Hemidactylus flavicaudus Lajmi, Giri,
Singh & Agarwal and H. xericolus Lajmi, Giri, Singh &
Agarwal, with yellow tails and unique dorsal scalation
were recently described from such habitats in Telangan
(Lajmi et al. 2020).

As part of a survey of geckos in Tamil Nadu, we were
 surveying open, scrubby habitats in Thoothukudi (former-
ly Tuticorin) District in April 2022, when we encountered
what seemed to be an incredibly tuberculate, brooki
Hemidactylus. Mitochondrial sequence data suggest that
this is a distinct lineage, and we describe and diagnose
Hemidactylus quartziticolus sp. nov. using morphologi-
da below.

Materials and Methods

Taxon sampling

Ten specimens of the new species were hand-collected,
photographed using a Canon 70D DSLR camera mounted
with 100 mm macro lens and two external flashes, and
later euthanized using isoflurane. Liver tissues of six indi-
viduals (three from each locality) of the new species were
collected in molecular grade ethanol and subsequently
stored at ~20° C for genetic analysis. Later, specimens
were fixed in 4% formaldehyde for ~24 hours, washed in
water, and transferred to 70% ethanol for long-term stor-
age. Specimens are deposited in the museum and research
collection facility at the National Centre for Biological
Sciences, Bengaluru (NCBS/NRC).

Molecular data

We extracted DNA from liver tissues of four specimens
of the new species from two localities using the Qiagen
DNeasy extraction kit (Table 1). Partial ND2 sequences
were obtained commercially from Medauxin (Bangalore,
India) using the primers L4437 and H5540/ H5934 for
PCR amplification and L4437 for sequencing (Macey et
al. 1997). Preliminary Maximum Likelihood (ML) anal-
yses with the codon-partitioned data and the GTR + G
model of sequence evolution on a dataset including
members from all groups of Indian Hemidactylus (Table
S1) confirmed the initial impression that the species is a
member of the brooki group (Figs 2, S1). We therefore
combined the new sequences with published sequences
for all members of the brooki group using H. frenatus
Duméril & Bibron as the outgroup (Table 1; after Agar-
wal et al. 2019). Sequences were aligned using ClustalW
(Thompson et al. 1994) with default settings and uncor-
corrected pairwise % sequence divergence was calculated in
MEGA 5.2.2 (Tamura et al. 2011; Table 2). We used Part-
titionFinder 2.1.1 (Lanfear et al. 2012) to select the best
partitioning scheme and models of sequence evolution for
both ML and Bayesian Inference (BI) using BIC. The best
partitioning scheme was by codon position and the model
selected were GTR+1 +G, GTR+G, GTR+G models for
codon positions 1–3, respectively. Maximum Likelihood
analyses were carried out in the raxmlGUI 2.0.10 (Edler
et al. 2020) and used RAxML 8.2.12 (Stamatakis 2014)
with the GTR + G model applied across partitions, sup-
port assessed through 1000 thorough bootstrap replicates,
and 10 independent starting trees. MrBayes 3.2.7 (Ron-
quist and Huelsenbeck 2003) was used to run partitioned
BI analyses with two parallel runs and four chains each
(one cold and three hot) for 2,000,000 generations sam-
ing every 2000 generations. The first 25% of trees were
discarded as burn-in with convergence determined based
on the standard deviation of split frequencies (<0.01). We
used TreeAnnotator 1.10.4 (Drummond et al. 2012) to
generate a Maximum Clade Credibility tree. Branches re-
covered with posterior probability 1 and bootstrap value
>95 were considered ‘strongly supported’.

Morphological and meristic data

Morphological data were collected from 10 specimens
of the new species. As preliminary phylogenetic analy-
yses placed the new species within the Hemidactylus

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brookii group, we restrict morphological comparisons to members of the brookii group. Comparative data on most of the described species of Hemidactylus brookii group were taken from type specimens, and/or topotypical specimens and other museum specimens (listed in the material examined section Appendix 1), with data

Figure 1. Elevation map showing the distribution of the new species and other members of the brookii group distributed in peninsular India (stars, new species; triangles, gleadowi clade; circles, murrayi clade; diamonds, malcolsmithi-parvimaculatus clade; squares, ground-dwelling clade). The type locality is marked for H. murrayi.
for some species (H. brookii Gray, 1845, H. gleadowi Murray, 1884, H. kushmorenensis Murray, 1884, H. mahonyi Adhikari et al., 2022, H. srikanthani Adhikari et al., 2022, H. tenkatei Lidh De Jeude, 1895, H. treutleri Mahony, 2009) taken from descriptions of the types (Mahony 2009, 2011; Adhikari et al. 2022). Mensural and meristic data were collected under a ZEISS Stemi 305 stereo dissecting microscope and on the left side of the body where possible. The following measurements were taken with a Mitutoyo digital vernier caliper (to the nearest 0.1 mm): snout vent length (SVL, from tip of snout to vent); axilla to groin length (TRL, from posterior margin of forelimb insertion to anterior margin of hindlimb insertion); body width (BW, maximum body width); body height (BH, maximum body height); forearm length (FL, from elbow to distal end of wrist); crus length (CL, from knee to heel); tail length (TL, from vent to tip of tail); tail width (TW, measured at widest point of tail); head length (HL, distance between retroarticular process of jaw and snout-tip); 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 nare distance (EN, distance between anterior margin of eye and posterior edge of nare); 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); inter-
Table 2. Pairwise uncorrected ND2 sequence divergence within the gleadowi clade and between the gleadowi clade and other broad clades within the Hemidactylus brookii group.

<table>
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<tr>
<th>Species</th>
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<tbody>
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<td>1 Hemidactylus quartziticolus sp. nov.</td>
<td>0.5</td>
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<td>2 Hemidactylus cf. gleadowi 1</td>
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<td>3 Hemidactylus cf. gleadowi 2</td>
<td>16.1</td>
<td>7.4</td>
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<td>4 Hemidactylus flavicaudus</td>
<td>19.4</td>
<td>22.6</td>
<td>21.5</td>
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<td>5 Hemidactylus xericolorus</td>
<td>17.5</td>
<td>21.6</td>
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<td>13.0</td>
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<td>6 malcolmssmithi + parvimaculatus</td>
<td>19.1</td>
<td>21.9</td>
<td>23.0</td>
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<td>21.4</td>
<td>9.1</td>
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<td>7 murrayi clade</td>
<td>20.6</td>
<td>21.1</td>
<td>21.2</td>
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<td>21.2</td>
<td>19.6</td>
<td>14.1</td>
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<td>8 Ground-dwelling clade</td>
<td>23.7</td>
<td>26.6</td>
<td>26.9</td>
<td>25.5</td>
<td>25.6</td>
<td>23.7</td>
<td>23.1</td>
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Results

Phylogenetic relationships

We recover the brookii group and all constituent clades with high support, though relationships among the clades are not well-supported (Fig. 2). Hemidactylus quartziticolus sp. nov. is a member of the gleadowi clade, sister to two lineages allied to H. gleadowi, which are collectively sister group to the clade containing H. flavicaudus and H. xericolorus (Fig. 2). Hemidactylus quartziticolus sp. nov. is 14.5–19.4% divergent in uncorrected ND2 sequence data from the other sampled members of the H. gleadowi group and 19.1–23.7% divergent from other clades in the brookii group (Table 2). We describe this deeply divergent lineage as a new species below.

Systematics

Hemidactylus quartziticolus sp. nov.


Figs 3–7; Tables 3 and 4

Holotype. NRC-AA-1256 (AK-R 1215), adult male, from near Jeya Parvathi Amman Kovil, Vallanadu Reserve Forest, Manakkarai (8.6848° N, 77.8519° E; ca. 120 m asl.), Thoothukudi district, Tamil Nadu state, India, collected by Akshay Khandekar, Ishan Agarwal, Swapnil Pawar and team on 12 April 2022.

Paratypes. (n = 9) NRC-AA-1257 (AK-R 1214), NRC-AA-1258 (AK-R 1218), adult males, same data as holotype; NRC-AA-1259 (AK-R 1220), NRC-AA-1260 (AK-R 1221) adult males, NRC-AA-1264 (AK-R 1216), adult female, same data as holotype except collected from the other side of Jeya Parvathi Amman Kovil, Manakkarai (8.6771° N, 77.8722° E; ca. 90 m asl.); NRC-AA-1261 (AK-R 1206), NRC-AA-1262 (AK-R 1207), NRC-AA-1263 (AK-R 1208), adult males, from Kurumalai Reserve Forest, Kurumalai (9.0919° N, 77.8543° E; ca. 130 m asl.); NRC-AA-1265 (AK-R 1209), adult female, from near Perumal Kovil, Kurumalai (9.0927° N, 77.8519° E; ca. 90 m asl.), Thoothukudi district, Tamil Nadu state, India, collected by same team on 10 April 2022.

Etymology. The specific epithet is a combination of the German noun “quartz” + the Latin suffix -ite (used to denote rocks and minerals) and the Latin suffix -cola that means inhabitant or dweller of, referring to the quartzite rock formations the new species inhabits.

Suggested Common Names. Quartzite brookii gecko or Thoothukudi brookii gecko.

Diagnosis. A small-sized Hemidactylus, snout to vent length less than 57 mm (n = 10); a single internasal scale behind rostral and between supranasals. Dorsal pholidosis heterogenous, composed of much smaller, subcircular, smooth and flattened granular scales intermixed with 18 regularly arranged rows of distinctly enlarged, subcircular...
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lar, strongly keeled and pointed tubercles at midbody; tubercles largest on flanks; 18–20 paravertebral tubercles between forelimb and hindlimb insertions; ventral scales much larger than dorsal body granular scales, smooth, subimbricate, sub-equal from chest to vent, 24–29 scales across belly at mid-body, 48–54 longitudinal scales from fore arm insertions to anterior margin of cloaca; subdigital scanners smooth, mostly divided in oblique series; four lamellae under digit I of manus and pes; six or seven lamellae under digit IV of manus and pes; males with continuous series of 35–38 precloacal-femoral pores (n = 8/10); dorsal scales at tail base heterogeneous, granular scales similar in size and shape to those on mid-body dor-

Comparison with members of the brookii group. Hemidactylus quartziticus sp. nov. can be easily distinguished from the Indian members of the brookii group based on the following differing or non-overlapping

Figure 2. Left, inset, backbone maximum likelihood phylogeny of Indian Hemidactylus with major groups marked in different colours; Hemidactylus quartziticus sp. nov. is marked by a red rectangle within the brookii group (see Table S1 for GenBank accession numbers). Main figure, Maximum Likelihood phylogeny of the brookii group of Indian Hemidactylus based on the ND2 gene. Posterior Probability = 1/ bootstrap support ≥75 shown at nodes, outgroups not shown.
characters: 18 regularly arranged rows of distinctly enlarged, subcircular, strongly keeled and pointed tubercles at midbody (versus enlarged tubercles completely absent from dorsal in *H. imbricatus* Bauer et al., 2008; tubercles only slightly larger than surrounding granular scales in *H. albofasciatus* Grandison & Soman, 1963, *H. gracilis* Blanford, 1870, *H. reticulatus* Beddome, 1870, and *H. vijayaraghavani* Mirza, 2018; 15 rows of dorsal tubercles at mid-body in *H. chikhaldaraensis* Agarwal, Bauer, Giri & Khandekar, 2019, 15 or 16 in *H. chipkali* Mirza & Raju, 2017, *H. rishivalleysensis* Agarwal, Thackeray & Khandekar, 2020 and *H. treutleri*, 11–14 in *H. flavicaudus*, 19 or 20 in *H. kushmorensis*, 13 or 14 in *H. mahonyi*, 11–17 in *H. parvimaculatus* Deranyagala, 1953, 15–17 in *H. sankariensis* Agarwal, Bauer, Giri & Khandekar, 2019, 14 or 15 in *H. srikanthani*, and 6–8 in *H. xericola*); males with continuous series of 35–38 precloacal-femoral pores (versus femoral pores absent, only precloacal pores present in *H. albofasciatus*, *H. gracilis*, *H. imbricatus*, *H. reticulatus*, *H. sartaenas* Giri & Bauer, 2008, and *H. vijayaraghavani*; precloacal-femoral pores series separated medially by more than four poreless scales in *H. chikhaldaraensis*, *H. chipkali*, *H. mahonyi*, *H. murrayi* Gleadow, 1887, *H. rishivalleysensis*, *H. sankariensis*, *H. srikanthani*, *H. tenkatei*, *H. treutleri*, and *H. varadgiri* Chaitanya, Agarwal, Lajmi & Khandekar, 2019; precloacal-femoral pores series separated medially by at least 1–3 poreless scales in *H. brookii*, *H. gleadowi*, *H. flavicaudus*, *H. kushmorensis*, *H. malcolmsmithi* (Constable, 1949), *H. parvimaculatus*, and *H. xericola*); 24–29 scales across belly at mid-body (versus enlarged tubercles completely absent from dorsal in *H. imbricatus* Bauer et al., 2008; tubercles in strong contact with nostril, first supralabial, supranasals and internasal; nostrils small (0.4 mm), oval; surrounded by supranasals, rostral, first supralabial and upper postnasal on either side; a single row of scales separate or from supralabials on each side. Mental subtriangular, slightly wider (2.2 mm) than high (1.9 mm); two pairs of well-developed postmentals, both roughly rectangular; the inner pair slightly shorter (1.5 mm) than the mental, and in strong contact with each other (0.9 mm) below mental, outer pair slightly smaller (1.1 mm) than inner pair and separated from each other by five small, granular chin scales below inner pair (Fig. 4B). Inner postmentals bordered by mental, infralabial I and II, outer postmental on either side and five small, granular chin scales below; outer postmentals bordered by inner postmental, infralabial II and seven chin scales on left and five on right side; two rows of enlarged, slightly elongate scales below second to fourth infralabials, inner row bordering infralabial with scales slightly larger and elongate than lower row; rest of the gular region with small, subcircular, smooth, more or less flattened, granular scales, becoming slightly larger and imbricate on lateral aspect on either side (Fig. 4B). Twelve supralabials up to angle of jaw and eight at mid-orbital position on either side; nine infralabials up to angle of jaw and seven at mid-orbital position on both sides (Fig. 4C).

Body relatively stout (BW/SVL 0.24), trunk relatively short (TRL/SVL 0.43), without ventrolateral fold on either side (Fig. 5A–C). Dorsal pholidosis heterogenous, composed of much smaller, subcircular, smooth and flattened granular scales intermixed with 18 regularly arranged rows of distinctly enlarged, subcircular, strongly keeled and pointed tubercles at midbody; tubercles increasing in size up to flank and then gradually decreasing ventrolaterally; 19 paravertebral tubercles between limb insertions on either side (Fig. 5A–C). Enlarged tubercles on nape and shoulder slightly smaller and conical than

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**Description of holotype.** The holotype is in good condition except tail slightly bent towards left, tail tip regenerated, and a 4.7 mm long incision in abdomen for tissue collection (Fig. 3A–E). Adult male, SVL 53.9 mm. Head short (HL/SVL 0.26), moderately elongate (HW/HL 0.79), not strongly depressed (HD/HL 0.42), distinct from neck. Loreal region inflated, canthus rostralis indistinct (Fig. 4A, C). Snout short (ES/HL 0.42); slightly longer than twice eye diameter (ED/ES 0.49); scales on snout, canthus rostralis, forehead, and inter-orbital region heterogeneous, mostly enlarged and conical; scales on loreal region bordering eye anterior to orbit much larger, more strongly conical, weakly keeled; scales on occiput and temporal region heterogeneous, granular scales intermixed with enlarged, weakly and conical tubercles, enlarged tubercles becoming pronounced, strongly conical and slightly more spaced out on temporal region (Fig. 4A, C). Eye small (ED/HL 0.20); pupil vertical with crenulated margins; supraciliaries small, mucronate, gradually increasing in size towards front of the orbit (Fig. 4C). Ear opening oval (greatest diameter 1.5 mm); eye to ear distance greater than diameter of eye (EE/ED 1.70). Rostral wider (2.1 mm) than high (1.3), divided dorsally by a weakly developed rostral groove for about half of its length; two enlarged supranasals, separated from each other by a single, slightly smaller internasal; upper postnasal present, lower postnasal absent on either side; rostral in contact with nostril, first supralabial, supranasals and internasal; nostrils small (0.4 mm), oval; surrounded by supranasals, rostral, first supralabial and upper postnasal on either side; a single row of scales separate orbit from supralabials on each side. Mental subtriangular, slightly wider (2.2 mm) than high (1.9 mm); two pairs of well-developed postmentals, both roughly rectangular; the inner pair slightly shorter (1.5 mm) than the mental, and in strong contact with each other (0.9 mm) below mental, outer pair slightly smaller (1.1 mm) than inner pair and separated from each other by five small, granular chin scales below inner pair (Fig. 4B). Inner postmentals bordered by mental, infralabial I and II, outer postmental on either side and five small, granular chin scales below; outer postmentals bordered by inner postmental, infralabial II and seven chin scales on left and five on right side; two rows of enlarged, slightly elongate scales below second to fourth infralabials, inner row bordering infralabial with scales slightly larger and elongate than lower row; rest of the gular region with small, subcircular, smooth, more or less flattened, granular scales, becoming slightly larger and imbricate on lateral aspect on either side (Fig. 4B). Twelve supralabials up to angle of jaw and eight at mid-orbital position on either side; nine infralabials up to angle of jaw and seven at mid-orbital position on both sides (Fig. 4C).
Figure 3. *Hemidactylus quartziticolus* sp. nov. (holotype, NRC-AA-1256): A dorsal view of body, B ventral view of body, C dorsal view of tail, D ventral view of tail, and E lateral view of tail. Scale bars 10 mm; photos by Akshay Khandekar.
Figure 4. *Hemidactylus quartziticola* sp. nov. (holotype, NRC-AA-1256): A dorsal view of head, B ventral view of head, C lateral view of head, D view of cloacal region showing precloacal-femoral pores and post cloacal spurs, E ventral view of left manus, and F ventral view of left pes. Scale bars 5 mm; photos by Akshay Khandekar.
Figure 5. Details at mid-body of *Hemidactylus quartziticus* sp. nov. (holotype, NRC-AA-1256): A dorsal view, B ventral view, and C lateral view. Scale bars 5 mm; photos by Akshay Khandekar.
those on parasagittal rows, those on occiput still smaller and blunt (Figs 2A, 3A). Ventral scales much larger than granular scales on dorsum, smooth, subimbricate, subequal from pectoral region to cloaca; 27 transverse ventral scales across belly at mid-body; 48 longitudinal scales from forefemur insertion to anterior margin of cloaca (Fig. 5B). A continuous series of 35 precloacal-femoral pores on the lower-most enlarged row of femoral scales (Fig. 4D).

Scales on palm and sole similar in size or marginally larger than dorsal body granules, subcircular, smooth and flattened; those on dorsal aspect of forearm heterogenous, composed of granular scales intermixed with enlarged tubercles that are similar to the enlarged tubercles on dorsum in shape and size, weakly keeled and pointed; scales on dorsal aspect of palm and wrist much larger than those on granular scales on body dorsum, smooth, flattened and subimbricate; scales on ventral aspect of forearm granular, smooth, marginally larger than dorsal body granules (Fig. 2A, B). Scales on dorsal aspect of thigh and shank heterogenous, consisting of granular scales intermixed with enlarged, weakly keeled and pointed tubercles except those on knee slightly smaller; scales near limb insertions granular, slightly smaller than dorsal body granules; scales on dorsal aspect of sole heterogenous, slightly larger, flattened, smooth, subimbricate scales intermixed with slightly enlarged weakly keeled and weakly pointed tubercles; scales on ventral aspect of thigh and shank similar to body ventrals, subequal, smooth and subimbricate on thigh and imbricate on shank (Fig. 2A, B).

Fore and hind limbs relatively short, stout; forearm short (FL/SVL 0.11); tibia short (CL/SVL 0.13); digits moderately short, strongly clawed; all digits of manus and digits 1–IV of pes indistinctly webbed at base; terminal phalanx of all digits curved, arising angularly from distal portion of expanded lamellar pad, half or more than half as long as associated lamellae pad; scanners beneath each digit in oblique series (the number of undivided basal lamellae excluding apical lamella in parentheses): 4(1)-6(0)-7(1)-7(1)-6(1) (left manus; Fig. 4E), 4(1)-6(0)-7(1)-7(1)-6(1) (right manus); 4(1)-7(1)-7(1)-7(1)-6(1) (left pes; Fig. 4F), 4(1)-7(1)-7(1)-7(1)-6(1) (right pes). Relative length of digits (measurements in mm in parentheses): IV (3.9) > III (3.4) = V (3.4) > II (3.0) > I (2.1) (left manus); IV (4.7) > III (4.2) > V (3.9) > II (3.4) > I (2.7) (left pes).

Tail original except tip (15.4 mm) which is regenerated, depressed, flat beneath, verticillate, with median furrow; tail equal to snout-vent length (TL/SVL 1.00; Fig. 2C–E). Dorsal scales at tail base and on original tail heterogeneous, granular scales similar in size and shape to those on mid-body dorsum, gradually becoming larger, pointed and subimbricate posteriorly, intermixed with series of 4–10 much enlarged, keeled, conical tubercles forming whorls; tubercles in ventrolateral aspect weakly keeled to smooth; 10 enlarged tubercles in first three whorls, eight in fourth whorl, seven in fifth and sixth whorls, six in 7–11 whorls; rest with four enlarged tubercles (Fig. 2C–E). Ventral scales at tail base subequal, smooth, imbricate, slightly larger than midbody ventral scales; three subequal, smooth postcloacal spurs on each side, smaller than dorsal tubercles at mid-body; slightly increasing in size posteriorly; rest of original tail with large, undivided, roughly rectangular, plate-like subcaudal scales (median row) covering almost entire portion of the tail; median row bordered laterally by one or two rows of large, smooth, imbricate scales (Fig. 2D, E).

**Colouration in life (Fig. 6A).** Dorsal ground colour of head, body, limbs and tail brown. Two short preorbital streaks anterior to eye; postorbital streaks distinct, upper terminating on temporal region and lower extending onto neck to form a discontinuous collar. Labials with fine black spots and ochre streaks. Head, body and tail with black blotches — few scattered on head, four along vertebral midline between limb insertions — with two X-shaped markings running through spots across centre of back and anterior to hindlimb insertions, and one incomplete X-shaped marking at forelimb insertions; tail with about 11 narrow, black markings which may be paired spots, single spots or crossbars; limbs with dark reticulation and digits with a few crossbars. Venter off-white.

**Variation and additional information from paratypes (Figs 6B, C, 7A, B).** Mensural and meristic data for the type series is given in Table 3 and 4 respectively. There are eight adult male and two adult female specimens, SVL ranging from 47.0–55.9 mm. All specimens resemble the holotype male (NRC-AA-1256) except for the following variations: inner postmental bordering infralabial I and II on left and infralabial I on right side in NRC-AA-1264, inner postmental bordering infralabial I and II on right and infralabial I on left side in NRC-AA-1261 and NRC-AA-1263, inner postmental bordering infralabial I on either side in NRC-AA-1262 and NRC-AA-1265; chin scales bordering inner postmental (six in NRC-AA-1257, NRC-AA-1260, four in NRC-AA-1264, NRC-AA-1263, three in NRC-AA-1258). Outer postmental bordering infralabial II on left and infralabial I and II on right side in NRC-AA-1264, outer postmental bordering infralabial I on right and infralabial I and II on left side in NRC-AA-1261 and NRC-AA-1263, outer postmental bordering infralabial I and II on either side in NRC-AA-1262 and NRC-AA-1265; chin scales separating left and right outer postmental below inner pair (six in NRC-AA-1257, NRC-AA-1260, four in NRC-AA-1258, NRC-AA-1263. Seven paratypes (NRC-AA-1257, NRC-AA-1264, NRC-AA-1258, NRC-AA-1259, NRC-AA-1260, and NRC-AA-1265) have an original and complete tail, marginally or slightly longer than body (TL/SVL 1.12, 1.03, 1.04, 1.12, 1.14, 1.07 respectively), NRC-AA-1261 and NRC-AA-1262 with complete but partially regenerated tail, and NRC-AA-1263 with partially incomplete tail (Fig. 7A, B). Dorsal ground colouration varies from light pinkish to ochre-brown; dorsal colour pattern varies from series of X-shaped markings to indistinct cross-bars to spots; 12–15 dark markings on original tail; regenerated tail mottled brown.
Figure 6. *Hemidactylus quartziticus* sp. nov. in life: A male, holotype NRC-AA-1256, B female, paratype NRC-AA-1264, and C uncollected juvenile. Photos by Akshay Khandekar.
Table 3. Mensural data (in mm) for the type series of *Hemidactylus quartziticolus* sp. nov. Abbreviations are listed in Materials and Methods except * = incomplete tail.

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Table 4. Meristic data for type series of *Hemidactylus quartziticolus* sp. nov. Abbreviations are listed in Materials and Methods. L and R = left and right; abs. = absent. Numbers in parenthesis indicates undivided lamellae excluding the apical lamella, left and right.

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<th>Type</th>
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Distribution and Natural History. *Hemidactylus quartziticolus* sp. nov. is known from the type locality Vallenadu Reserve Forest and an additional locality 45 km north, Kurumalai Reserve Forest, both in Thoothukudi District, Tamil Nadu, India (Fig. 1). Both localities have low (<310 m asl.), narrow quartzite ridges with exposed rocks along the ridgeline, and generally stony soil and low, scrubby vegetation (Southern Thorn Forests: 6A/DSI; Champion and Seth 1968) (Fig. 8A–C). The team of five visited these two areas on one night each from about an hour before sunset to two hours after sunset. At Vallenadu, the new species was found in abundance (>15 in one hour). Individuals were seen on quartzite rock formations approximately 0.5–2.0 meter height above from the ground. All the female individuals we spotted (n = 5) were gravid, and only a single subadult individual was observed during the entire survey. Sympatric lizards encountered during the survey were *Hemidactylus* cf. *frenatus*, *H.* cf. *leschenaultii*, *H.* cf. *acanthopholis*, *H.* cf. *scabriceps*, *Eutropis* cf. *carinata*, *Psammophilus* cf. *dorsalis*, and *Calotes versicolor* (Daudin, 1802). At Kurumalai it had been raining and was drizzling when we visited and only four individuals of the new species were observed. Two paratypes (an adult male and gravid female) were seen about 50 cm above the ground on the wall of a small temple situated among the quartzite rock formations, and the other two individuals were observed on rocks about 1–2 m above the ground. Sympatric congeners at Kurumalai includes *Hemidactylus* cf. *frenatus*, *H.* cf. *leschenaultii*, *H.* cf. *triedrus*, Eutropis cf. *carinata*, Psammophilus cf. *dorsalis*, and *Calotes versicolor*.

Discussion

*Hemidactylus quartziticolus* sp. nov. is one of the most morphologically distinctive among brookiiid congeners, as no other species has such enlarged dorsal tubercles, a continuous series of 34–38 precloacal-femoral pores, and such few lamellae (four) under digit I of manus and pes. This is the 53rd species of *Hemidactylus* known from India, and the seventh that is endemic to Tamil Nadu based on currently available data (Mirza and Sanap 2014; Chaitanya et al. 2018; Agarwal et al. 2019; Khandekar et al. 2020; Pal and Mirza 2022). There are now 37 *Hemidactylus* species of the Indian radiation that are endemic to peninsular India, including 10 from the Western Ghats, two from the Eastern Ghats, and 25 from other regions of
Figure 8. Habitat of *Hemidactylus quartziticus* sp. nov.: A general habitat at the type locality, B quartzite rock formation on which individuals of the new species were seen at the type locality, and C general habitat at Kurumalai, from where a few paratypes of the new species were collected. Photos by Akshay Khandekar (A and B), and Ishan Agarwal (C).
peninsular India (Uetz et al. 2023). This discovery adds another species to the rapidly growing lizard diversity from the Indian dry zone (e.g. Deepak et al. 2016; Agarwal et al. 2020; Lajmi et al. 2020; Adhikari et al. 2022).

Vallanadu Reserve Forest and the contiguous Black- buck Sanctuary is the most southern population of the Blackbuck Antilope cervicapra (Linnaeus). These scrub habitats are not known for their overall or endemic biodiversity, though Vallanadu is the type locality for an endemic species of shrub Barleria durairajii Ravikumar, Narasimhan, Devanathan & Gnanasekaran (Ravikumar et al. 2016) and there are records of the south Indian endemic Madras Hedgehog Paraechinus nudiventris (Horsfield) from Vallanadu (Saravanan et al. 2016). The broad habitats that Hemidactylus quartziticolus sp. nov. was found in are southern thorn forests which are found widely across arid regions of southern India. There are many low hills scattered across scrub and thorn forests in the vast dry zone that could harbour more undiscovered species. Reiterating what has been stated previously, systematic field surveys are needed across the Indian dry zone to understand basic patterns of species diversity and distribution.

The three clades of brookiish geckos within the brookii group of Indian Hemidactylus have contrasting patterns of morphological variation and distribution: the malcolm-smithi + parvimaculatus clade has the generic brookiish colour pattern of a light brown dorsum with darker spots or X-shaped markings, slightly enlarged, keeled dorsal tubercles, precloacal-femoral pore series separated by one or two poreless scales, and finally two species neither of which is endemic to India (Agarwal et al. 2018); the murrayi clade has the generic brookiish colour pattern, enlarged, keeled dorsal tubercles and pore series separated by at least four poreless scales with nine species endemic to peninsular India and the widespread commensal H. murrayi (Agarwal et al. 2019, 2020; Adhikari et al. 2022). Finally, the H. gleadowi clade is perhaps the most diverse in morphology, including a typical brookiish morph with enlarged, keeled dorsal tubercles and precloacal-femoral pores separated by a single poreless scale (H. gleadowi), the yellow-tailed H. flavicaudus and H. xericolus that have flattened dorsal tubercles and pore series separated by one or two poreless scales, and finally Hemidactylus quartziticolus sp. nov., which is the most tuberculate of all brookiish Hemidactylus and with a continuous series of pores. The distributional range of the H. gleadowi clade was thought to be central India and interior arid regions of southern India and Pakistan (type locality of H. gleadowi), and is now extended by over 800 km to the southern tip of India. It remains to be seen, which, if any, of the Indian H. cf. gleadowi lineages represent nominotypical H. gleadowi.

Acknowledgements

We thank the Chief Wildlife Warden, Tamil Nadu for permits and the Tamil Nadu Forest Department for the tremendous logistic and personal support extended by them without which this survey would not have been possible. Specifically, the Divisional Forest Officer, Thoothukudi Abhishek Tomar, Forester Vallanadu L. Kannan, Forester Kovidpatti K. Kesavan and forest guards and watchers of Vallanadu and Kurumalai. Tarun Karmakar and Yeshwanth HM (NCBS field station and museum facility, Bengaluru) helped with the specimen registrations. We are thankful to Uma Ramakrishnan (NCBS) for lab support. We thank R. Chaitanya and two anonymous reviewers for improving the manuscript.

References


Champion SH, Seth SK (1968) A revised survey of the forest types of India (Delhi: Manager of Publications).


Appendix 1

Material examined

Museum and institutional abbreviations are as follows: National Centre for Biological Sciences, Bengaluru (NCBS-AU/ NCBS-BH/ NCBS-NRC-A/ Akshay Khandekar field series [AK/ AK R]); Bombay Natural History Society, Mumbai (BNHS); Centre for Ecological Sciences, Bangalore (CES/ CES G).

Hemidactylus albofasciatus: AK 1353–AK 1357 adult males and females, from Dorle, Ratnagiri District, Maharashtra, India.

Hemidactylus chikhaldaraensis: Holotype, NCBS-BH684, adult male; AK 1340, adult male, AK 1337–AK 1340, adult females, from Gagilgarh Fort, Chikhaldara, Amravati District Maharashtra, India.

Hemidactylus chipkali: Holotype, NCBS AT107, adult male; paratypes, NCBS AT109 adult male, NCBS AT 108, adult female, from Pachmarhi, Hoshangabad District, Madhya Pradesh, India.

Hemidactylus flavicaudus: Holotype, NCBS NRC-AA-1105, adult female; paratypes, CES 17029, CES 17031, adult males, CES 17028,
adult female, from near Guddeguda, Mahabubnagar District, Telangana, India.  

**Hemidactylus gracilis**: AK 1419, adult male, from Devhari, Aurangabad District, Maharashtra, India.  

**Hemidactylus malcolmsmithi**: CES11055, CES11057, CES11059, adult males, Kangra-Jwalamukhi Road, Kangra District, Himachal Pradesh; CES11065, adult male, Sujanpur, Hamirpur District, Himachal Pradesh; CES11072, adult male, Chamba, Chamba District, Himachal Pradesh; CES11073, adult male, Reasi, Reasi District, Jammu, India.  

**Hemidactylus murrayi**: AK 1329–AK 1332, adult males and AK 1328, adult female, from Pimpri, Dang District, Gujarat, India.  

**Hemidactylus parvimaculatus**: CES11024, adult male, from Hassan, Hassan District, Karnataka; CES11018, adult male, from Coimbatore, Coimbatore District, Tamil Nadu; CES11029, adult male, from Molem, South Goa District, Goa, India.  

**Hemidactylus reticulatus**: AK 587, adult male, AK 588, adult female, from IISc campus, Challakere, Chitradurga District; AK 594, adult male, AK 595, adult female, from Ballari, Bellary District, Karnataka; AK 901, adult male, AK 902, adult female, from Sirumalai, Dindigul District, India.  

**Hemidactylus rishivalleyensis**: Holotype, NCBS-BH728, adult male; paratypes, NCBS-BH731, NCBS-BH732, adult males, NCBS-BH729, NCBS-BH730, NCBS-BH733, NCBS-BH734, NCBS-BH735, adult females, from Cave Rock Hill, Rishi Valley school, Chittoor District, Andhra Pradesh, India.  

**Hemidactylus sankariensis**: Holotype, NCBS-BH682, adult male; paratypes, NCBS-BH681, BNHS 2535, adult males, NCBS-BH683, BNHS 2536, adult females, from mined hillock near Kidayurr road, Sankari, Salem District, Tamil Nadu, India.  

**Hemidactylus sataraensis**: Holotype, BNHS 1743, adult female; paratype, BNHS 1742, adult female, from Chalkewadi, Satara District, Maharashtra, India.  

**Hemidactylus vijayraghavani**: Holotype, NCBS-BH 643, adult male; paratype, NCBS-BH 644, adult female, from Bagalkot, Bagalkot District, Karnataka, India.  

**Hemidactylus varadgirii**: Holotype, BNHS 2377, adult male; paratypes, BNHS 2375, BNHS 2378, adult males, BNHS 2374, BNHS 2376, adult females, from Amboli, Sindhudurg District, Maharashtra, India.  

**Hemidactylus xericolus**: Holotype, NCBS NRC-AA-1110, adult male; paratypes, CES 16170, adult male, NCBS NRC-AA-1111 adult female, from near Marrigudda, Nalgonda District, Telangana, India.

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**Supplementary Material 1**

**Table S1**

**Authors:** Khandekar A, Thackeray T, Mariappan R, Gangalmale S, Waghe V, Pawar S, Agarwal I (2023)  
**Data type:** .pdf  
**Explanation note:** List of sequences used for inset, backbone phylogeny in Fig. 2.  
**Copyright notice:** This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.  
**Link:** https://doi.org/vz.73.e101871.suppl1

**Supplementary Material 2**

**Figure S1**

**Authors:** Khandekar A, Thackeray T, Mariappan R, Gangalmale S, Waghe V, Pawar S, Agarwal I (2023)  
**Data type:** .pdf  
**Explanation note:** Maximum Likelihood phylogeny of Indian Hemidactylus based on the ND2 gene partitioned by codon position and with the GTR + G model applied, bootstrap support ≥60 shown at nodes.  
**Copyright notice:** This dataset is made available under the Open Database License (http://opendatacommons.org/licenses/odbl/1.0). The Open Database License (ODbL) is a license agreement intended to allow users to freely share, modify, and use this dataset while maintaining this same freedom for others, provided that the original source and author(s) are credited.  
**Link:** https://doi.org/vz.73.e101871.suppl2