



A new species of rupicolous *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae) from the Male Mahadeshwara Wildlife Sanctuary, southern Eastern Ghats, India

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Abstract

We describe a new species of rupicolous *Cnemaspis* from the Male Mahadeshwara Wildlife Sanctuary in the Eastern Ghats. The current description is based on a type series of eight specimens that bear a unique combination of morphological and colour pattern characteristics that do not occur in other closely related species. Maximum likelihood and Bayesian analyses based on the mitochondrial gene ND2 recovered the new species to be nested within the *gracilis* clade and the sister species to the recently described *C. agarwali* from the Eastern Ghats.

Keywords

Endemic, gecko, India, integrative taxonomy, MM Hills, morphology

Introduction

The Afro-Asian gekkonid genus *Cnemaspis* Strauch, 1887 known to be one of the most speciose groups, has seen a sudden increase in species diversity with approximately 56 species described in the last ten years across peninsular India, including the Western Ghats (Mirza et al. 2014; Sayyed et al. 2016; Agarwal et al. 2017; Khandekar et al. 2019a, 2019b, 2020, 2022a, 2022b; Pal et al. 2021; Cyriac et al. 2018; Narayanan and Aravind 2022; Agarwal et al. 2022). In a recent revision of the Western Ghats members, Pal et al. (2021) grouped South Asian (SA) *Cnemaspis*

into ten species clades. Among these clades, members of the *gracilis* clade are widespread and are known from both the Western Ghats and the Eastern Ghats (Pal et al. 2021; Agarwal et al. 2022). Agarwal et al. (2022) recently described five new species belonging to the *gracilis* clade from the Shervaroy's landscape of the Eastern Ghats and the vicinity. This work highlighted the micro-endemism within this clade and increased the species diversity from six to eleven.

During our recent fieldwork in the Male Mahadeshwara wildlife sanctuary (MM WLS) in the Eastern Ghats, India (Fig. 1) we collected eight specimens of a population of *Cnemaspis* that were morphologically similar to the members of the *gracilis* clade. Because of this population's disjunct distribution from the other members of the clade and in light of the recent findings of Agarwal et al. (2022), we further investigated the identity of this population and found it to be a distinct species. Based on an integrated taxonomic approach using morphological characteristics and molecular data, we thus present a species description of this new population.

Materials and Methods

Sampling

The specimens were collected inside the Ashoka Trust for Research in Ecology and the Environment (ATREE) campus in the Keeranhola Village situated in the valley within Male Mahadeshwara Wildlife Sanctuary (MM WLS) also known as MM Hills, in Chamarajanagar District, Karnataka, India. Collected individuals were euthanised 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 molecular analysis. Fixed specimens were then washed and kept in water overnight and subsequently transferred to 70 % ethanol

Study site

The Male Mahadeshwara Wildlife Sanctuary was established in 2013 and is surrounded by Cauvery Wildlife Sanctuary to the North and East, Sathyamangalam Tiger Reserve to the South, and Biligiri Rangaswamy Temple Tiger Reserve to the West. The MM WLS is located in the junction of the Eastern and Western Ghats—the two most biologically diverse ranges of Southern India. The area under the MM WLS is approximately 906 km², with a highly undulating terrain. The vegetation types in the MM WLS are largely dominated by the dry deciduous forest (64.34 %) followed by scrub woodland (20.50 %) and moist deciduous and riparian forest (2.47 %) (Uma Shaanker et al. 2004; Aravind et al. 2010). The area has a warm climate throughout the year, with April to June being the hottest, with temperatures reaching beyond 40°C. In contrast, December and January are the coldest months, with minimum temperatures as low as 13°C. The MM WLS receives meagre rainfall from the southwest as well as the northeast monsoons, less than 1000 mm per year (Aravind et al. 2010). There are about 12 human settlements scattered within the wildlife sanctuary. The communities depend on non-timber forest product (NTFP) harvesting, quarrying, and daily wage labour for basic livelihood (Uma Shaanker et al. 2004; Aravind et al. 2010).

Molecular analysis

Genomic DNA was extracted from tail tissue samples stored in absolute ethanol at -20°C , using the DNeasy (Qiagen™) blood and tissue kit. We generated DNA sequence data for two individuals of *Cnemaspis* species (BNHS 3146 and BNHS 3149) from Keeranhola Village, MM WLS, Karnataka, India. We amplified partial sequences of the mitochondrial NADH dehydrogenase 2 (*ND2*) gene. PCR amplification for both markers was done following the existing primers and protocols (*ND2*: MetF1 (Forward) and H5934 (Reverse) (Macey et al. 1997). PCR conditions were as follows: fragments of the *ND2* gene were amplified using an initial denaturation at 95°C for 5 min, followed by 35 cycles of denaturation at 95°C for 45 sec, annealing at 56°C for 45 sec and extension at 72°C for 55 sec. The final extension was at 72°C for 10 min. PCR reactions were carried out in a 25µl reaction containing 11µl of Takara emerald RR310B mastermix, 12µl of PCR grade H₂O, 0.5µl of each forward and reverse primers and 1µl (60–80ng) of template DNA. PCR amplifications were carried out in S1000™ Thermal Cycler (Bio-Rad, USA). Amplified PCR products were run on a 2 % agarose gel and viewed with an Essential V4 (UVITEC Cambridge, UK) gel documentation system to confirm the PCR amplification. PCR products were purified, and Sanger sequenced in both directions at Barcode Biosciences (Bangalore, India).

Bidirectional sequences were manually checked using the CHROMAS (<http://technelysium.com.au/wp/chromas>) and aligned using ClustalW (Higgins et al. 1994) with default prior settings implemented in MEGA 7 (Tamura et al. 2011). We checked for unexpected stop codons in the protein-coding gene *ND2* by translating nucleotide alignments to amino acids in MEGA7 (Kumar et al. 2016). The newly generated sequences were 986 base pairs for *ND2*. Newly generated sequences were aligned with 26 other *Cnemaspis* species downloaded from GenBank (Appendix 1). *Cnemaspis monticola* and *C. australis* were used as the outgroups to root the tree following Agarwal et al. (2022).

Maximum Likelihood (ML) analysis for the final dataset was carried out using the IQTREE web server (<http://iqtree.cibiv.univie.ac.at>) (Trifinopoulos et al. 2016). The data set was partitioned by codon using Modelfinder (Kalyaanamoorthy et al. 2017) to find the best-fit partitions and models of sequence evolution for each partition (Appendix 2). 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. 2012) with default settings to find the best-fit model of sequence evolution (Appendix 2). Four separate runs were set up with eight Markov chains, each initiated from random trees and allowed to run for 10 X 10⁶ 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 the 50 % majority consensus rule. We

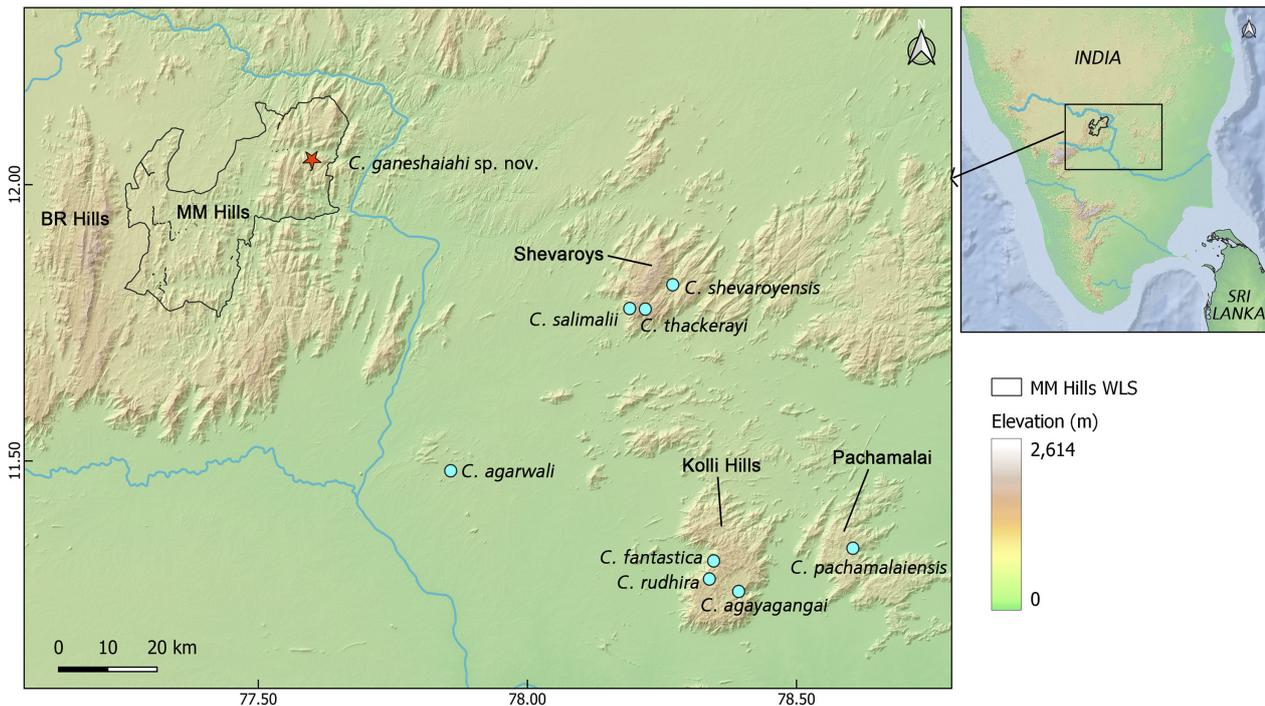


Figure 1. Map showing the type localities of the members of *gracilis* clade from the Eastern Ghats. Species from the Western Ghats are further south and not shown here.

obtained ESS values using the Tracer (v. 1.6) to confirm convergence for all the priors (ESS >200). Support for the internal branches for the ML and BI was quantified using UF Bootstrap (UFB) (1000 replicates and 3000 iterations) (Minh et al. 2013) and posterior probabilities (BI PP), respectively. UFB values of 95 and above and PP values of 0.95 and above were considered evidence of strong support. The resulting tree was visualized and edited in Figtree. Uncorrected pairwise genetic distances were calculated in Mega 7 (Kumar et al. 2016) using the default setting, selecting a pairwise deletion option.

Morphological analysis

All morphological characters (mensural and meristic) follow Agarwal et al. (2019). Measurements and meristic data from the collected specimens for this study were taken under a Nikon SMZ1270 microscope under 8X magnification and were measured using a Mitutoyo digital Vernier calliper to the nearest 0.1mm. Photographs were taken using Canon EOS 7D mounted with a 100mm 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 at the widest region); 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 base of tail); head length (HL, distance from retroarticular process to snout-tip); head width (HW, maximum width of head at the widest region); head depth (HD, maximum head depth at

occiput); eyeball diameter (ED, greatest horizontal diameter of eyeball); Ear to nostril (EN, distance between anterior margin of eyeball and posterior margin of nostril); eye to snout distance (ES, distance from anterior margin of eyeball and tip of snout); eyeball to ear distance (EE, distance from anterior margin of ear opening to posterior margin of eyeball); ear length (EL, maximum length of ear opening); internarial distance (IN, distance between medial margins of nares); interorbital distance (IO, shortest distance between left and right supraciliary scale rows). Additional meristic characters include SL: supralabials (counted from the largest scale at the corner of the mouth or posterior to the eye, to the rostral scale); IL: infralabials (counted from termination of enlarged scales at the corner of the mouth to the mental scale); DTR: longitudinal rows of enlarged dorsal tubercles at midbody; VS: ventral scales (counted along the midline of the body from the postmentals to just anterior to the cloacal opening, stopping where the scales become granular); supraciliaries: large (comparatively larger than the other scales in the head) scales bordering the eye; 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; PP: number preanal pores; FP: number femoral pores; SBPP: number of poreless scales in the diastema between the pore-bearing preanal scales; SB FP&PP: the number of poreless scales between the series of femoral pores and the preanal pores.

Comparative data for the species from *gracilis* clade were obtained from original descriptions and other literature (Beddome 1870; Khandekar 2019; Pal et al. 2021; Agarwal et al. 2022). The museum abbreviation is as follows: BNHS: Bombay Natural History Society, Mumbai, India.

Results

Phylogenetic relationships

The inferred phylogenies from both the ML and BI analyses are congruent with the results provided by Agarwal et al. (2022), except for the position of the new species described here. The new species from the MM Hills is nested within the *gracilis* clade and is sister to *Cnemaspis agarwali* Khandekar, 2019 with moderate to strong support in ML and BI phylogenies (UFB 89 & BI PP 0.95). These two species together form the sister lineage to the recently described *Cnemaspis rudhira* Agarwal et al., 2022 with strong support (UFB 96 & BI PP 1.0). The uncorrected pairwise genetic distance between the new species and its sister species *C. agarwali* ranges from 4.5–4.6 % and between it and *C. rudhira* ranges from 11.4–12.1 % (Appendix 3).

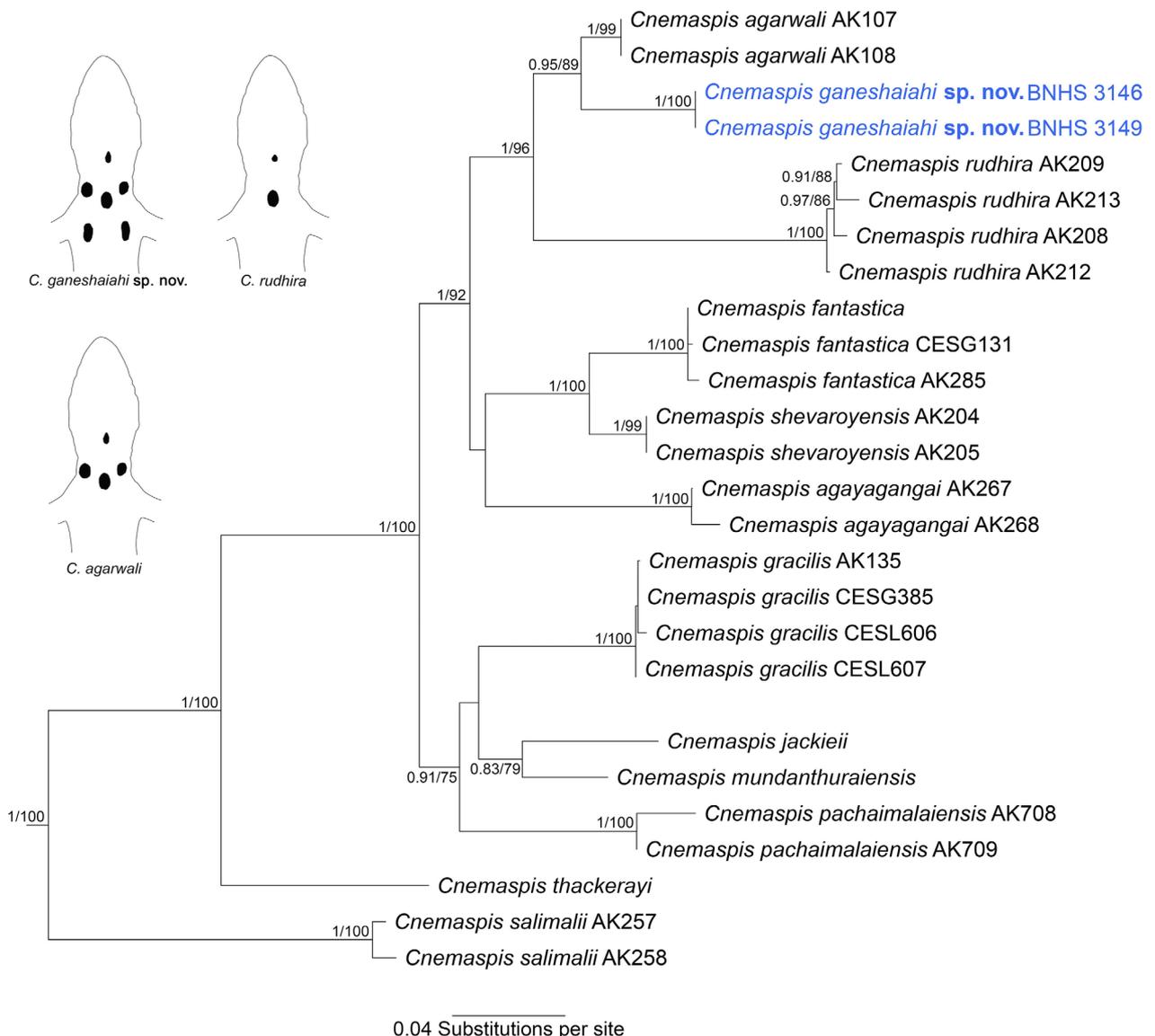


Figure 2. ML phylogeny topology showing the relationship of the new species within the *gracilis* clade. Roots not shown. Node values are BI and UFB, respectively.

Systematics

Cnemaspis ganeshaiahi sp. nov.

<https://zoobank.org/EF7D0D6D-B278-455D-AEF5-EA15D-7A174B5>

Figs 3–6

Suggested common name. Ganeshaiiah's dwarf gecko.

Type locality. Keeranholra Village, Male Mahadeshwara Wildlife Sanctuary, Chamarajanagar district, Karnataka, India (12.045478°N, 77.599490°E, 945 m asl).

Holotype. BNHS 3146, SVL 29.1 mm, adult male collected by Aravind N.A. and Surya Narayanan on 14th December 2021 (Figs 3, 4, 6A).

Paratypes. BNHS 3147, SVL 31.9 mm, adult male (Fig. 5A); BNHS 3148, SVL 29.4 mm, adult male (Fig. 5B), collection details same as holotype; BNHS 3149, SVL 30.6 mm, adult female (Fig. 5C) collected from the granite walls within human settlements, collections details same as holotype. BNHS 3150, SVL 32.2 mm, adult male; BNHS 3151, SVL 32.4 mm, adult male; BNHS 3152, SVL 32.8 mm, adult female; BNHS 3153, SVL 36.2 mm, juvenile female collected from rock boulders from near the type locality.

Etymology. The specific epithet of this new species is a patronym in honour of Professor K.N. Ganeshaiiah, who served as a Professor of Plant Genetics and Breeding at the University of Agricultural Sciences, Bangalore, and was a founding trustee of the Ashoka Trust for Research in Ecology and the Environment (ATREE), Bangalore. Professor Ganeshaiiah has contributed significantly towards plant breeding, ecology, evolutionary biology, and conservation biology. He also popularised science literature in the local language and wrote over 25 books.

Diagnosis. A small-sized *Cnemaspis*, SVL up to 32.8 mm ($n = 8$). Dorsal pholidosis heterogeneous; weakly keeled granular scales intermixed with fairly regularly arranged rows of enlarged, strongly keeled, conical tubercles; last one or two rows of enlarged tubercles on flank keeled, spine-like; 12–14 rows of dorsal tubercles at mid-body, 14–18 tubercles in paravertebral rows, paravertebral rows rarely irregularly arranged; ventral scales smooth, subcircular, subimbricate, subequal from chest to vent, 24–28 scales across belly at mid-body, 118–124 longitudinal scales from mental to cloaca; subdigital scancers smooth, unpaired, unnotched; nine or 10 lamellae under digit I of manus and pes, 15–18 lamellae under digit IV of manus and 17–21 lamellae under digit IV of pes; males ($n = 5/8$) with five femoral pores on each thigh separated by seven or eight poreless scales from series of four to six precloacal pores, precloacal pores separated medially by one or two poreless scales, (precloacal pores rarely not separated, $n = 1/5$); tail with enlarged, strongly keeled, pointed, and spine-like tubercles forming whorls; median row of subcaudals smooth, roughly pentagonal, and distinctly enlarged. Dorsum pale-orange, mottled with small white to light-grey spots and few small black spots with a series of light-grey vertebral blotches extending from neck to tail base; a single central black dorsal ocellus on neck and a smaller one on occiput separated by a light-grey blotch, ocellus on neck flanked anteriorly on each side by a subequal ocellus and posteriorly by a pair of obscure blotches; venter off-white with black speckles, two distinct pairs of black streaks on throat; original tail in males pale-grey, regenerated tail orange-brown.

Comparison among the members of the *gracilis* clade. *Cnemaspis ganeshaiiah* sp. nov. is morphologically placed in the *gracilis* clade based on a combination of characteristics like dorsal pholidosis heterogenous (vs. homogeneous in *littoralis*, *indica* and *wynadensis* clades); presence of precloacal pores (vs. *littoralis*, *giri*,

indica and *wynadensis* clades); presence of femoral pores (vs. absent in *beddomei* clade); presence of spine-like tubercles on the flank (vs. absent in *bangara*, *beddomei*, *girii* and *mysorensis* clades); the presence of strong sexual dichromatism (vs. absent or if present, sparse in *monticola* and *goensis* clades).

From the members of the *gracilis* clade, *Cnemaspis ganeshaiiah* sp. nov. can be easily distinguished by a combination following characteristics: spine-like tubercles present in the flanks (vs. absent in *Cnemaspis thackerayi* Khandekar et al., 2019, *C. jackeii* Pal et al., 2021, *C. agarwali* and *C. shevaroyensis* Khandekar et al., 2019); four to six PP medially separated by one scale ($n = 2/5$) and five FP separated by seven or eight poreless scales (vs. one or two PP medially separated by two or three scales and four FP separated by seven to nine poreless scales in *C. shevaroyensis*; two to four PP medially separated by one or two scales and five to nine FP separated by one to six poreless scales in *C. thackerayi*; three or four PP medially separated by one of two scales and five or six FP separated by one or two poreless scales in *C. jackeii* Pal et al., 2021; two PP medially separated by two to four scale and three to five FP separated by nine to eleven poreless scales in *C. mundanthuraiensis* Khandekar et al., 2022; two PP medially separated by two scales and three to five FP separated by five to seven poreless scales in *C. salimalii* Agarwal et al., 2022; two PP medially separated by one or two scales and four or five FP separated by eight to 10 poreless scales in *C. agayagangai* Agarwal et al., 2022; two PP medially separated by two scales and three to five FP in *C. gracilis* (Beddome, 1870); two to four PP medially separated by one or two scales and four or five FP separated by seven to nine poreless scales in *C. fantastica* Agarwal et al., 2022; two to five PP and four to seven FP separated by seven to 11 poreless scales in *C. pachamalaiensis* Agarwal et al., 2022); by the presence of higher numbers of DTR 13 or 14 (vs. 9–11 in *C. agarwali*) and slightly higher numbers of ventral scales 114–124 (vs. 102–117 in *C. agarwali*). *Cnemaspis ganeshaiiah* sp. nov. is morphologically much similar to and overlaps with *C. rudhira* from which it can be differentiated by having fewer 24–28 ventral scales (vs. 30–32) and in having two pairs of ocelli anterior and posterior to the ocellus in the neck versus the anterior and posterior pairs of ocelli being absent.

Description of the holotype. Adult male in good state of preservation except for tail tip slightly missing. SVL 29.1 mm, head short (HL/SVL 0.29), wide (HW/HL 0.55), not strongly depressed (HD/HL 0.41), distinct from neck. Loreal region marginally inflated, canthus rostralis not distinct. Snout slightly less than half of head length (ES/HL 0.45), slightly more than 2.5 times eyeball diameter (ES/ED 2.9); scales on snout and canthus rostralis subcircular, subequal, and weakly keeled; much larger than those on forehead and interorbital region; scales on forehead similar to those on snout and canthus rostralis except smaller, elongate, and weakly conical; scales in interorbital region even smaller, granular, and weakly keeled; scales on occipital and temporal region heterogeneous with slightly



Figure 3. Dorsal (upper) and ventral (lower) aspects of the Holotype (BNHS 3146) of *Cnemaspis ganeshaihi* sp. nov. Scale bar = 10 mm.

enlarged, weakly keeled, conical tubercles intermixed with smaller, weakly keeled and weakly conical granular scales. Eyeball small (ED/HL 0.14) with round pupil; supraciliaries short, larger anteriorly; 23 or 24 scale rows between left and right supraciliaries at mid-orbit. Ear-opening deep, oval, small (EL/HL 0.04); eyeball to ear distance greater than diameter of eyeball (EE/ED 2.0). Rostral more than two times wider (1.4 mm) than high (0.65 mm), incompletely divided dorsally by a strongly developed rostral groove; a single enlarged supranasal on each side, much larger than postnasals, partly in contact with each other; anteriorly divided by a small internasal scale; two postnasals, upper postnasal marginally larger than lower; rostral in contact with first supralabial, nostril, internasal, supranasal, and lower postnasal on either side; nostrils oval, surrounded by two postnasals, supranasal, and rostral on either side; two rows of scales separate orbit from supralabials. Mental enlarged, subtriangular, slightly wider (1.52 mm) than high (1.17 mm); two pairs of postmentals, inner pair roughly rectangular, right one visually larger than the left one, both much shorter than mental, in strong contact with each other posterior to mental; inner pair bordered by mental, first infralabial,

outer postmental, enlarged median chin shield on either side, and an enlarged chin shield on left side; outer postmentals roughly rectangular, smaller than inner pair, bordered by inner postmentals, first and second infralabials, and three enlarged chin shields on left side, four enlarged chin shield on right side, and median chin shield on left side; three enlarged gular scales between left and right outer postmentals; all chin scales bordering postmentals flat, subcircular, smooth, and smaller than outermost postmentals; scales on rest of throat, smaller, flattened, subequal, and smooth. Infralabials bordered posteriorly by a row or two of slightly enlarged, greatly elongate scales, decreasing in size posteriorly. Nine supralabials up to the angle of the jaw on each side, and seven at the midorbital position on each side; first supralabial largest, supralabials gradually decrease in size posteriorly; eight infralabials up to angle of jaw on each side, five at midorbital position on either side; first infralabial largest, infralabials gradually decrease in size posteriorly.

Body relatively slender (BW/AGL 0.47), trunk less than one-half SVL (AGL/SVL 0.38) lacking ventrolateral folds; spine-like scales on flank present. Dorsal pholidosis heterogeneous; weakly keeled granular scales inter-

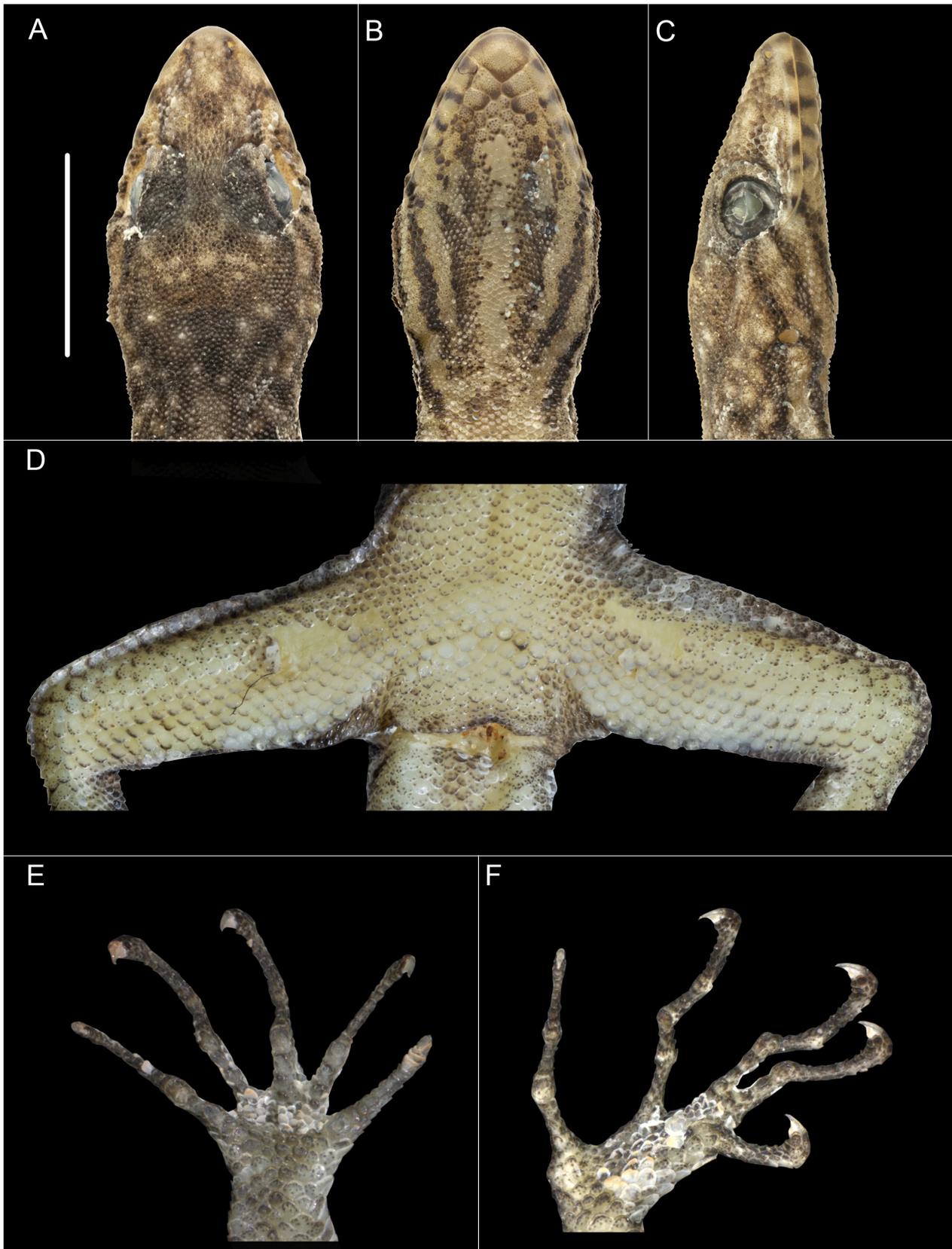


Figure 4. *Cnemaspis ganeshaihi* sp. nov. (Holotype, BNHS 3146). **A** Head in dorsal view, **B** ventral view, **C** lateral view, **D** view of the femoral region, **E** ventral view of right manus, and **F** right pes. Scale bar = 5mm.

mixed with a fairly regularly arranged row of enlarged, strongly keeled, conical tubercles; tubercles in approximately 13 longitudinal rows at mid-body including spine-like scales on lower flank; 18 (left) and 16 (right) tuber-

cles in paravertebral row from forelimb insertion to hind limb insertion. Ventral scales much larger than granular scales on dorsum smooth, subcircular, subimbricate, subequal to pectoral and ventral scales; mid-body scale rows



Figure 5. Dorsal aspect of the paratypes of *Cnemaspis ganeshaihi* sp. nov. **A** BNHS 3147 (upper), **B** BNHS 3148 (middle), **C** BNHS 3149 (lower).

across belly 24; 124 scales from mental to anterior border of cloaca. Scales on base of neck similar to those on belly, marginally smaller; gular region with still smaller, subequal, smooth, flattened scales, those bordering postmentals enlarged, smooth, subcircular, and flattened. Five femoral pores on either thigh, six continuous precloacal pores and six (on right) and seven (on left) poreless scales on either side between precloacal and femoral pores.

Scales on palm and soles granular, smooth, subcircular, subimbricate and flattened; scales on dorsal aspects of limbs heterogeneous; mixture of small granular, weakly keeled, imbricate scales twice the size of granules on dorsum, largest on anterolateral aspect of the hands and feet; posterolateral aspect of limbs with small weakly keeled to smooth granular scales; scales on lower arm and shank

small, subimbricate, and keeled; ventral aspect of forelimbs with small, smooth, subimbricate scales; ventral aspect of hind limb with enlarged, smooth, flattened, subimbricate scales, slightly larger than ventrals. Forelimbs and hind limbs moderately long, slender (LAL/SVL 0.16; CL/SVL 0.18); digits long, with strong, recurved claw, distinctly inflected, portions distal to the inflections laterally conspicuously compressed. Subdigital lamellae unpaired except basal lamella or two pairs on some digits, separated into a basal and narrower distal series by single enlarged lamella at inflection; basal lamellae series: (1-4-4-5-4 right manus, 1-4-6-7-5 right pes), (1-4-4-5-3 left manus; 1-5-6-8-6 left pes); distal lamellae series: (9-10-11-11-9 right manus, 8-9-12-13-12 right pes), (9-10-12-11-9 left manus; 8-10-13-14-11 left pes). Rel-

Table 1. Mensural data for the type series of *Cnemaspis ganeshaihi* sp. nov. * denote incomplete tail, J denote Juvenile.

Voucher no.	BNHS 3146	BNHS 3147	BNHS 3148	BNHS 3150	BNHS 3151	BNHS 3152	BNHS 3149	BNHS 3153
Type status	Holotype	Paratype						
Location	MM Hills							
Sex	Male	Male	Male	Male	Male	Female	Female	Female J
SVL	29.1	31.9	29.4	32.2	32.4	32.8	30.6	26.6
TL	31.2	38.6	25.5*	38.7	45.2	39.5		29.9
TW	3.1	3.4	2.6	3.3	3.4	2.7	2.2	2.1
CL	5.5	6.2	5.6	6	6.1	6.2	5.8	4.3
AGL	11.2	12.4	12.2	14.6	14.1	14.9	12.9	12.6
BH	3.1	2.9	2.7	3	3.1	2.7	3	2.8
BW	5.3	6.5	5.4	5.7	5.6	5.3	7.4	5.4
HL	8.6	8.4	8.7	9.2	9.1	9.4	8.1	7.9
HW	4.8	4.9	4.7	5.4	5.3	5.2	5.1	4.4
HD	3.6	3.3	3.4	3.6	3.3	3.4	3.2	2.5
ED	1.2	1.5	1.5	1.7	1.6	1.7	1.2	1.3
EE	2.4	2.4	1.8	2.7	2.5	2.9	2.5	2.1
ES	3.5	3.8	3	3.9	3.9	4.1	3.49	3.1
EN	2.8	2.6	2.8	3.1	3.5	3.4	2.5	2.4
IN	0.9	0.9	0.9	1.1	1.1	1.2	1	0.8
IO	2.8	2.8	2.4	2.9	2.8	2.7	2.5	2
EL	0.4	0.6	0.5	0.7	0.9	0.7	0.5	0.5

Table 2. Meristic data for the type series of *Cnemaspis ganeshaihi* sp. nov. irr. arr. = irregularly arranged, ab = absent, dam = damaged.

Voucher no.	BNHS 3146	BNHS 3147	BNHS 3148	BNHS 3150	BNHS 3151	BNHS 3152	BNHS 3149	BNHS 3153
Type status	Holotype	Paratype						
Location	MM Hills							
Sex	Male	Male	Male	Male	Male	Female	Female	Female J
SL L&R	9&9	8&7	7&8	8&9	8&8	8&8	7&7	8&8
IL L&R	6&6	7&7	6&7	7&8	7&7	7&7	6&6	7&7
SL M L&R	7&7	7&6	7&7	7&7	7&7	7&7	7&7	7&7
IL M L&R	5&5	6&6	6&6	6&7	6&6	6&6	6&6	6&6
PVT	18	14	16	16	15	14	14	15
DTR	14	13	13	13	13	12	13	13
MVSR	24	24	25	28	26	27	28	26
VS	124	114	118	122	120	119	121	121
LamF1 L&R	10&10	10&10	10&10	10&10	9&9	10&10	9&9	9&10
LamF4 L&R	16&17	15&15	16&18	15&16	15&16	16&16	16&16	16&16
LamT1 L&R	9&9	9&9	10&10	10&10	9&9	9&9	9&9	10&9
LamT4 L&R	19&20	*&17	20&21	19&19	21&21	21&20	19&20	20&19
LamT5 L&R	16&16	16&16	18&19	16&17	16&17	16&16	16&16	16&16
PP L&R	6	2&2	2&2	2&2	2&2	NA	NA	NA
SBPP	0	1	1	2	1	NA	NA	NA
SB PP&FP L&R	7&7	7&7	8&8	7&8	8&8	NA	NA	NA
FP L&R	5&5	5&5	5&5	5&5	5&5	NA	NA	NA

ative length of digits (measurements in mm in parentheses): IV (2.7) > III (2.4) > II (2.2) > V (2.1) > I (1.6) (left manus); IV (3.4) > V (3.3) > III (3.1) > II (2.6) > I (1.6) (left pes).

Tail partly original except the posterior end (15 mm) which is regenerated, about 2–3mm dissected for analysis, subcylindrical, slender, slightly longer than snout-vent length (TL/SVL 1.07). Dorsal scales on tail base weak-

ly keeled, granular, similar in size and shape to granular scales on mid-body dorsum, gradually becoming larger, flattened, imbricate posteriorly, intermixed with enlarged, strongly keeled, distinctly pointed, conical tubercles; enlarged tubercles on tail forming whorls; six tubercles each on first five whorls, five in 6th–8th whorls, rest of tail regenerated and lacking tubercles. Subcaudal scales much larger than those on dorsal aspect, subimbricate, smooth;

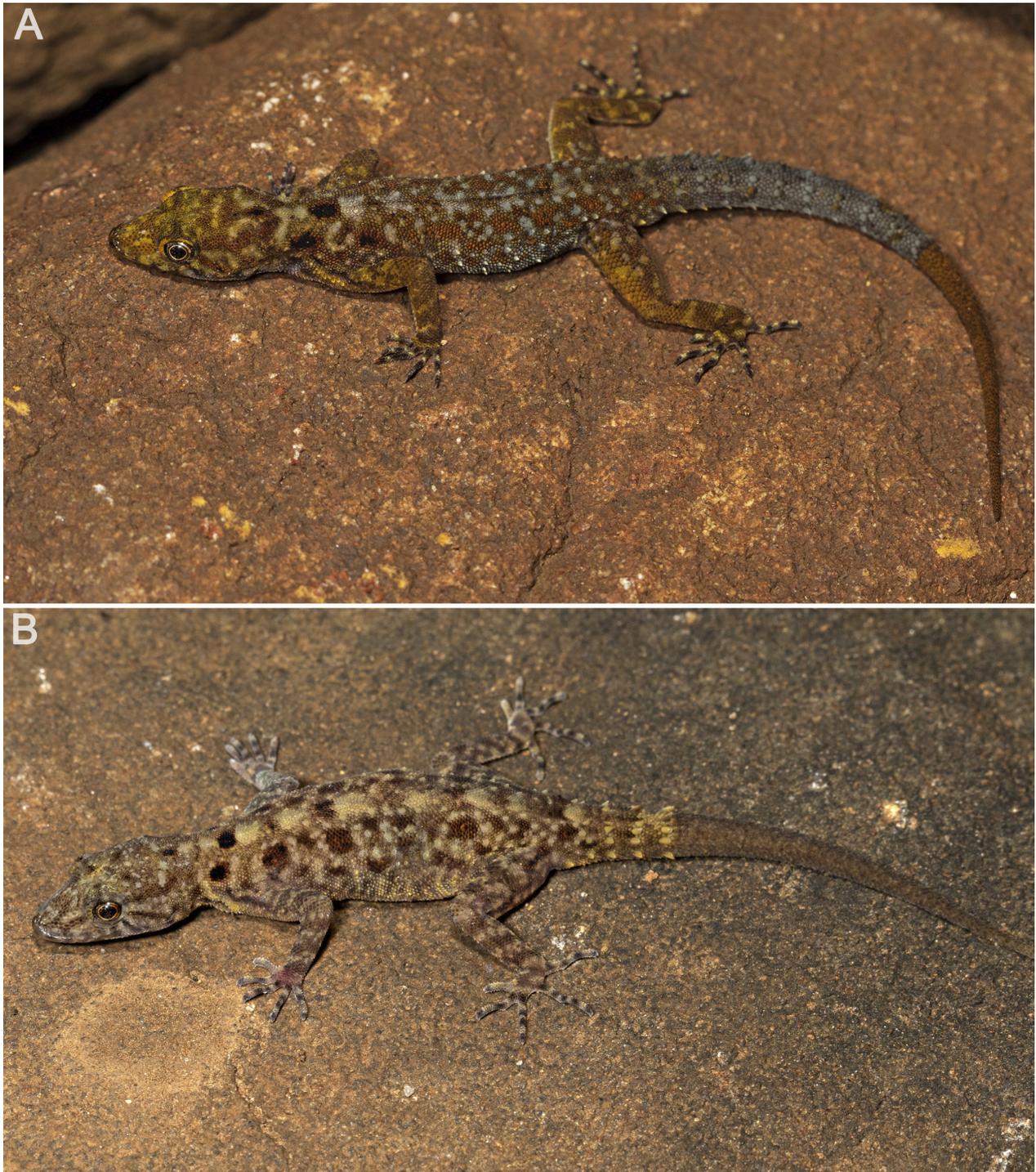


Figure 6. Live images of *Cnemaspis ganeshiahi* sp. nov. **A** Paratype (BNHS 3148), **B** live uncollected female.

median series distinctly enlarged, roughly rectangular; scales on tail base slightly larger than those on mid-body ventrals, smooth, imbricate; a single enlarged, weakly keeled and conical postcloacal spur on each side.

Colouration in life and preservative. The dorsal aspect of the body is overall yellowish and orangish, intermixed with numerous grey irregular spots on the body. The well-developed tubercles are greyish, and brighter along the lateral side of the body. Head overall yellowish with irregular brownish patches. The dorsum apart from the greyish tubercles and ocelli, possesses several irregularly

shaped orange patches. One roughly rhomboidal ocellus on the occiput, a single thick black ocellus slightly posterior to the neck, paired with two darker anterior ocelli and two faint posterior ocelli. The central ocellus on the neck is much closer to the anterior pair than it is to the posterior ones. The limbs are brownish above with conspicuous irregularly shaped patches; digits are blackish with irregularly shaped yellow spots. The ventral side of the head is whitish in the middle and covered by a yellowish border along the sides starting from the infralabials and extending to the neck where it is prominent, three pairs of parallel black streaks, one starting from below the ocular and



Figure 7. A. Overall habitat of the MM Hills WLS. Inset image showing the microhabitat from where the holotype was collected.

other from the posterior of the ocular region extending till the base of the neck and the third and innermost starting below the outer postmentals and extending till the base of the neck where both streaks are connected; body mostly creamish white. The original tail is greyish including the tubercles that form a series of whorls. The regenerated portion is orangish with numerous tiny black speckles. In preservatives, the colour remains the same except for the yellow and orange which turned paler on both the dorsal and ventral surfaces.

Variation in paratypes. Morphometric and meristic differences are provided in Table 1 and Table 2. Paratypes range in size SVL from 29.4 mm to 32.8 mm ($n = 7$). Paratypes BNHS 3147, BNHS 3148, BNHS 3150 and BNHS 3151 are males and BNHS 3149, BNHS 3152 and BNHS 3153 are females. Overall the paratypes resemble the holotype except for the following characters. Tail complete in the paratype BNHS 3147, BNHS 3150, BNHS 3152, BNHS 3151 and incomplete in all other paratypes BNHS 3153, BNHS 3148, and BNHS 3149 h varying degrees in length; BNHS 3149 has a completely regenerated tail. Supranasals are divided by a tiny scale in the holotype and an elongated internasal in the paratypes. All the male paratypes have one (BNHS 3147, BNHS 3148 and BNHS 3151) or two (BNHS 3150) poreless scales between the preloacal pores.

Ecology, natural history and distribution. *Cnemaspis ganeshaiahi* **sp. nov.** is currently known only from the type locality and the nearby vicinity. The habitat is dry deciduous and scrub forests with large granite boulders. They are found in the crevices of walls or in boulders. *Cnemaspis ganeshaiahi* **sp. nov.** appears to be a diurnal

species and the type series was collected during the day at approximately 11:00 hrs from rocky outcrops amidst human settlements and the farmlands. During our survey, we found *C. ganeshaiahi* **sp. nov.** mostly in the rocky outcrops, walls made of granite stones within the forest patches in the valley, and human settlements. A few individuals were found within buildings. *Cnemaspis ganeshaiahi* **sp. nov.** seems abundant locally and within these microhabitats, we observed several uncollected individuals during our fieldwork ($n = 40$). We also found some individuals ($n = 5$) within the buildings, indicating their tolerance to human presence. At the type locality, *Hemidactylus whitakeri* Mirza et al., 2018 and *H. cf. frenatus* are found syntopically with *C. ganeshaiahi* **sp. nov.**

Discussion

The taxonomy of Indian *Cnemaspis* was long static with only fifteen described species until the description of three new species from the Eastern Ghats and northeast India by Das and Sengupta (2000) and Das and Bauer (2000). The advent of molecular taxonomy and intensive fieldwork has resulted in several new species descriptions and resolution of the cryptic species of several reptile genera in the recent past (Lajmi et al. 2016; Deepak et al. 2016; Agarwal et al. 2019). This appears to be true for Indian *Cnemaspis* as well, as 53 new species have been described since 2018 (Uetz et al. 2022). Sayyed et al. (2018) first used molecular data (16S) for the Indian *Cnemaspis* in their description of four new species and added sequences for other Indian species. Subsequently,

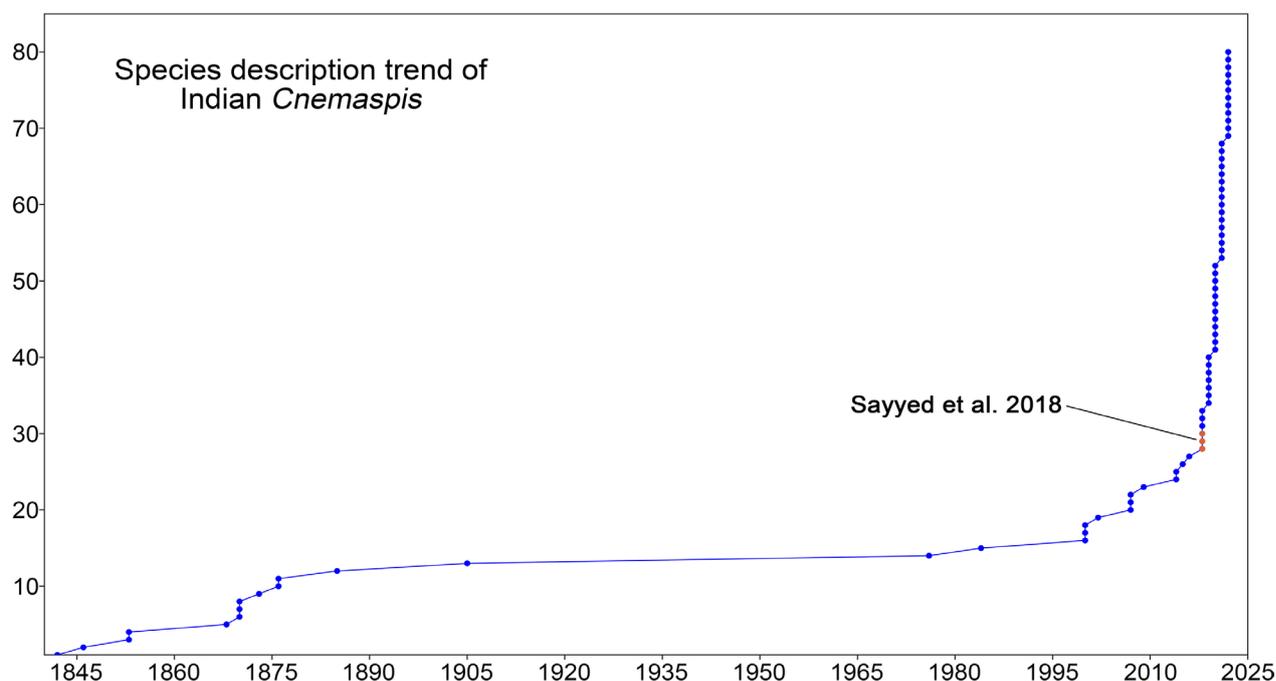


Figure 8. Graph showing the species discovery pattern of the Indian *Cnemaspis*. Red points indicate the work first used the molecular data for the Indian *Cnemaspis*.

many other works used either 16S or ND2 for their new descriptions that resulted in an increase of over 60 % of the total of Indian *Cnemaspis* (Cyriac et al. 2020; Pal et al. 2021; Agarwal et al. 2022), mostly from peninsular India. The description of *C. ganeshiahi* **sp. nov.** adds to the diversity of the *gracilis* clade from eleven to twelve and the total number of Indian *Cnemaspis* to eighty-one.

Agarwal et al. (2022) proposed several explanations such as elevation, habitat heterogeneity, dispersal, and sexual selection as possible drivers for the high diversity within the *gracilis* clade. The current description complements the findings of Agarwal et al. (2022) by adding one more species to the *gracilis* clade from a distance of not more than 70 km from the other closest member. The type locality of *Cnemaspis ganeshiahi* **sp. nov.** (MM Hills) is 65 km away from the type locality of the closely related *C. agarwali* (Sankari in Tamil Nadu state). The latter is an isolated massif in the vicinity of MM Hills but disconnected from it by the intervening lower plains and the river Kaveri, a significant biogeographic barrier (Deepak and Karanth 2018; Deepak et al. 2021; Das et al. 2022). This locality also falls within the vicinity (47 km) of the Sheravoy's landscape, where Agarwal et al. (2022) recently described five microendemic species of *Cnemaspis*, including the other closely related *C. rudhira*. This highlights the possible presence of more divergent lineages within the *gracilis* clade in Peninsular India. Further exploration of similar landscapes in the surrounding regions might provide better clarity on the distribution of this species and possibly reveal more undescribed species.

Although most recent studies used a minimum of 5 % as the genetic cut-off within gekkonids, Agarwal et al. (2022) discussed a fine cut-off of 3.7 % within morphologically diagnosable south Asian *Cnemaspis*. Further, within the *gracilis* clade, they described *Cnemaspis*

fantastica based on a low divergence from its sister *C. shevaroyensis* (4.5 % in ND2) but showed strong variation in the morphological characteristics. Similar to the aforementioned sister pair, *C. ganeshiahi* **sp. nov.** and its phylogenetic sister *C. agarwali* also share a low genetic divergence of 4.6 % but show strong variations in the morphological characteristics. In addition to the morphology, we also clearly demonstrated the allopatric distribution of *C. ganeshiahi* **sp. nov.** with its closely related species.

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Appendix 1

List of genbank accession numbers used for the phylogenetic analyses in this study.

Species	Voucher	Genbank no.	Locality
<i>Cnemaspis agarwali</i>	AK 107	MK792466	India, Tamil Nadu, Salem District, Sankari
<i>Cnemaspis agayagangai</i>	NRC-AA-1215 (AK 267)	OP709694	India, Tamil Nadu, Namakkal District, Agaya Gangai Waterfalls
<i>Cnemaspis agayagangai</i>	NRC-AA-1214 (AK 268)	OP709695	India, Tamil Nadu, Namakkal District, Agaya Gangai Waterfalls
<i>Cnemaspis australis</i>	ZM003	MZ701834	India, Kerala
<i>Cnemaspis australis</i>	ZM003	MZ701834	India, Kerala, Peppara
<i>Cnemaspis cf. gracilis</i>	AK 212	MK792463	India, Tamil Nadu, Salem District, Yercaud
<i>Cnemaspis fantastica</i>	NRC-AA-1223 (AK 284)	OP709698	India, Tamil Nadu, Namakkal District, Kollimalai ghat
<i>Cnemaspis fantastica</i>	NRC-AA-1224 (AK 285)	OP709699	India, Tamil Nadu, Namakkal District, Kollimalai ghat
<i>Cnemaspis fantastica</i>	CESG 131	OP709700	India, Tamil Nadu, Namakkal District, Kollimalai ghat
<i>Cnemaspis ganeshaihi</i> sp. nov.	BNHS 3146	OQ555723	India, Karnataka, MM Hills
<i>Cnemaspis ganeshaihi</i> sp. nov.	BNHS 3149	OQ555724	India, Karnataka, MM Hills
<i>Cnemaspis gracilis</i>	CESL607	MZ701820	India, Kerala, Palakkad District, near Chittur River
<i>Cnemaspis gracilis</i>	AK 135	MK792470	India, Tamil Nadu, Coimbatore District, Valparai
<i>Cnemaspis gracilis</i>	CES L 606	OP709696	India, Tamil Nadu, Palakkad District, Chennathanair RF
<i>Cnemaspis gracilis</i>	CES L 607	OP709697	India, Tamil Nadu, Palakkad District, Chennathanair RF
<i>Cnemaspis gracilis</i>	CES G 385	MK7924	India, Kerala, Palakkad District, near Chittur river
<i>Cnemaspis jackieii</i>	CES L192	MZ701804	India, Tamil Nadu, Vairavankulam RF, near Karuppanadhi dam
<i>Cnemaspis monticola</i>	CES L 044	MZ701803	India, Kerala, Wayanad District, Manikunjmalai
<i>Cnemaspis mundanthuraiensis</i>	NRC-AA-1176 (AKR 443)	ON494557	India, Tamil Nadu, Tirunelveli District, Mundanthurai forest range
<i>Cnemaspis pachaimalaiensis</i>	NRC-AA-1231 (AK 708)	OP709701	India, Tamil Nadu, Tiruchirapalli District, Pachaimalai
<i>Cnemaspis pachaimalaiensis</i>	NRC-AA-1232 (AK 709)	OP709702	India, Tamil Nadu, Tiruchirapalli District, Pachaimalai
<i>Cnemaspis rudhira</i>	NRC-AA-1239 (AK 208)	MK792461	India, Tamil Nadu, Salem District, Yercaud
<i>Cnemaspis rudhira</i>	NRC-AA-1240 (AK 209)	MK792462	India, Tamil Nadu, Salem District, Yercaud
<i>Cnemaspis rudhira</i>	NRC-AA-1241 (AK 212)	MK792463	India, Tamil Nadu, Salem District, Yercaud
<i>Cnemaspis rudhira</i>	NRC-AA-1242 (AK 213)	MK792464	India, Tamil Nadu, Salem District, Yercaud
<i>Cnemaspis salimalii</i>	NRC-AA-1205 (AK 257)	OP709703	India, Tamil Nadu, Namakkal District, Kollimalai
<i>Cnemaspis salimalii</i>	NRC-AA-1206 (AK 258)	OP709704	India, Tamil Nadu, Namakkal District, Kollimalai
<i>Cnemaspis shevaroyensis</i>	NCBS-BH674 (AK 204)	MK792468	India, Tamil Nadu, Salem District, Yercaud
<i>Cnemaspis shevaroyensis</i>	NCBS-BH674 (AK 204)	MK792469	India, Tamil Nadu, Salem District, Yercaud
<i>Cnemaspis thackerayi</i>	CES G143	MK792471	India, Tamil Nadu, Salem District, Yercaud

Appendix 2

Partition schemes and models used for the phylogenetic analyses.

Codon position	ML (IQ-TREE)	Bayesian Inference
ND2 Position 1	HKY+F+G4	TVM+I+G
ND2 Position 2	TN+F+G4	GTR+I+G
ND2 Position 3	TIM+F	GTR+G

