



A new species of rupicolous *Cnemaspis* Strauch, 1887 (Squamata: Gekkonidae) from the Biligirirangan Hills of Southern India

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Abstract

We describe a new species of small-sized (SVL 24.6–28.8 mm) rupicolous *Cnemaspis* from the Biligirirangan Hills (BR Hills), Karnataka based on morphology and molecular (mitochondrial 16S and ND2) data. The new species is nested within the *monticola*, *mysoriensis* and *gracilis* clades, where it is basal to *monticola* and *gracilis* clades in the Maximum Likelihood analysis and is basal to the *monticola* clade in the Bayesian phylogenetic analysis.

Keywords

Endemic, gecko, molecular, morphology, taxonomy

Introduction

The gekkonid genus *Cnemaspis* Strauch, 1887 is one of the most speciose groups of geckos in the world, with 192 known species distributed across the south and southeast Asia, of which around 100 species are known from peninsular India (including the Western Ghats) and 40 from Sri Lanka (Uetz et al. 2022). Among these, 59 species from India were described in the last two decades (Cyriac et al. 2020; Pal et al. 2021; Sayyed et al. 2021; Khandekar et al. 2021, 2022a, 2022b). Recent studies provided novel insights and added to our understanding of the cryptic diversity, biogeography and diversification of *Cnemaspis* (Manamendra-Arachchi et al. 2007; Agarwal et al. 2020a; Agarwal et al. 2021; Pal et al. 2021). Agarwal et al. 2020a postulated the isolated microclimatic refugia as a driver for the diversification of species in the dry zone restricted

bangara clade. As for the wet zone clades and other dry zone species in the Western Ghats, Pal et al. (2021) postulate multiple possible drivers like micro-refugia, geographical barrier and Miocene aridification.

Although many of these descriptions are primarily from the Western Ghats (Pal et al. 2021; Cyriac et al. 2020), followed by some parts of the Eastern Ghats (Agarwal et al. 2020b, 2021) and the Mysore plateau (Khandekar et al. 2022a), many parts of the latter regions remain poorly studied. Pal et al. (2021) recently divided the peninsular Indian and Sri Lankan *Cnemaspis* into ten different nominal clades based on molecular and morphological data. Among these, three clades (*mysoriensis*, *bangara* and *gracilis*) are largely distributed in the Eastern Ghats and the Mysore plateau. The *mysoriensis* and *bangara* clades

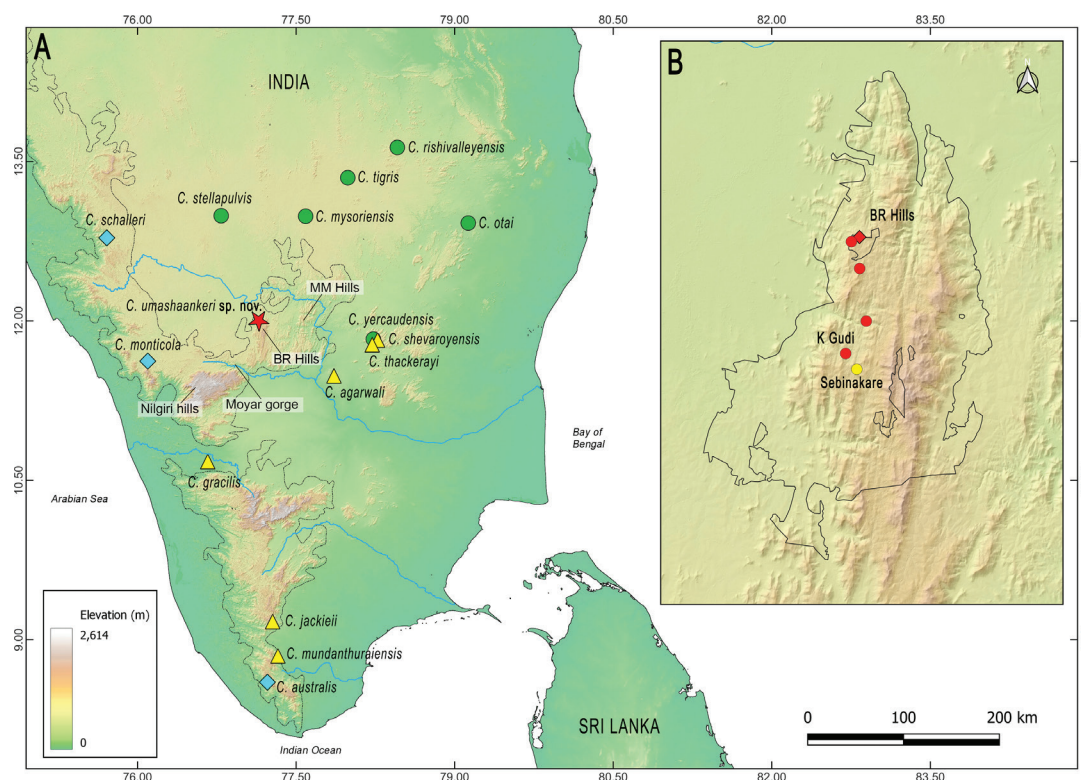


Figure 1. A Map showing the type localities of the members of *mysoriensis* (green circle), *monticola* (Indian) (blue square), *gracilis* (yellow triangle) clades and *Cnemaspis umashaankeri* sp. nov. (red star). B Map showing the extent of BR Hills Tiger Reserve and known locations of *C. umashaankeri* sp. nov.

have their members distributed in the Mysore plateau and the Eastern Ghats and members of *gracilis* clade are more widely distributed across Central and Southern Western Ghats, the Mysore plateau and the Eastern Ghats. Furthermore, the *monticola* clade is closely related to these clades and has two described species in the Western Ghats and all other members are distributed in Sri Lanka and Southeast Asia.

The BR Hills is situated at the union of the Eastern and the Western Ghats and act as a crucial corridor between both hill ranges (Ganeshiah and Shankar 1998). Geographically, it lies to the northeast of the Nilgiri massif but is separated by the deeper Moyar gorge to its south and to its east lies Mala Mahadeshwara hills (MM hills). During recent fieldwork in the BR Hills Tiger Reserve, we found a population of *Cnemaspis* sp. that we were unable to assign to any of the described species, but morphologically resembled the members of the *mysoriensis* clades that are known from the vicinity of BR Hills. In this paper, using both morphological and molecular data, we confirm that this population is distinct which we describe here as a new species.

Materials and Methods

Fieldwork was carried out between August and October 2021 in the BR Hills and Kyathadevara Gudi (K Gudi) villages within the Biligiri Ranganathaswamy Temple

Tiger Reserve (BRT) in Chamarajanagar District, Karnataka state (Fig. 1). Four specimens of *Cnemaspis* sp. were collected during the study from BR Hills and the specimens from K Gudi were observed and released. The entire landscape of the tiger reserve is heterogeneous and undulating terrain with an altitude ranging from 600 m to 1,800 m above mean sea level. The temperature ranges from 8°C to 25°C and the annual rainfall range from 600 mm in the lower altitude and 3000 mm on the hill-top. The wide range of climatic conditions and altitudinal variations within this small area has resulted in varied forest types, including scrub forest, dry deciduous, moist deciduous, riparian, evergreen, sholas and grasslands (Aravind et al. 2001).

Molecular analysis

Genomic DNA was extracted from tail tissue samples from the specimens collected and 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 from BR Hills (ZSI-R-28301 & BNHS 3127), Karnataka, India. We amplified partial sequences of two mitochondrial 16S rRNA (16S) and NADH dehydrogenase 2 (ND2) genes. PCR amplification for both markers was done following the existing primers and protocols (ND2: MetF1 (Forward) and H5934 (Reverse) (Macey et al. 1997); 16S: primers 16Sar-L (Forward) and 16Sbr-H (Reverse) (Palumbi et al. 1991). PCR conditions were as follows: fragments of the

16s gene were amplified using an initial denaturation at 95°C for 5 min, followed by 39 cycles of denaturation at 95°C for 45 sec, annealing at 50.4°C for 45 sec and extension at 72°C for 1 min 30 sec. The final extension was at 72°C for 10 min. 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. Final extension was at 72°C for 10 min. PCR reactions were carried out in a 25 µl reaction containing 11 µl of Takara emerald RR310B mastermix, 12 µl of PCR grade H₂O, 0.5 µl of each forward and reverse primers and 1 µl (60–80 ng) 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 protein-coding gene ND2 by translating nucleotide alignments to amino acids in MEGA7 (Kumar et al. 2016). The newly generated sequences were 925 base pairs for ND2 and 491 base pairs for 16S. The final concatenated dataset was 1579 base pairs. Newly generated sequences were aligned with 82 other *Cnemaspis* species downloaded from GenBank (supplementary Table S1).

We used PartitionFinder2 to identify the best-fit partition scheme for the concatenated dataset and the best-fit model of sequence evolution for each partition as determined by the Bayesian Information Criterion (BIC), using the default greedy algorithm linked to branch lengths (Lanfear et al. 2012). The best-fit scheme for the concatenated dataset comprises four partitions, by gene and by codon position (supplementary Table S1). Maximum Likelihood analysis for the concatenated dataset was carried out in the IQTREE web server implemented in (<http://iqtree.cibiv.univie.ac.at>) (Trifinopoulos et al. 2016). IQTREE uses an inbuilt program Modelfinder (Kalyaanamoorthy et al. 2017) to find the best-fit partitions scheme and models of sequence evolution for the partitioned dataset (supplementary Table S1). Bayesian Inference (BI) analysis for the concatenated dataset was carried out using the program MrBayes 3.2 (Ronquist et al. 2012), with default prior settings. 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 50% majority consensus rule. We obtained ESS values using the Tracer v1.7 software (Rambaut et al. 2018) and confirmed the convergence for all the priors (ESS > 200). Support for the internal branches for the ML and BI was

quantified using Ultrafast bootstrap (UFB) approximation (1000 replicates and 3000 iterations) (Hoang et al. 2018) and posterior probabilities, respectively. Bayesian posterior probabilities (BPP) values above 0.95 and UFB values above 95 are considered strong support (Huelsenbeck et al. 2001; Minh et al. 2013). The resulting tree was edited in Figtree. We used the *wynadensis* clade to root the phylogeny following the phylogeny inferred from Pal et al (2021). 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 (measurements and meristic) follow Agarwal et al. (2019). Measurements and meristic data for the specimens used in this study were taken under a Nikon SMZ1270 microscope under 8X magnification. Measurements were taken using a Mitutoyo digital vernier calliper to the nearest 0.1 mm. Photographs were taken using Canon EOS 7D mounted with a 100 mm macro lens and two external flashes. Measurements and meristic characters include, snout vent length (SVL, from tip of snout to vent); axilla to groin length (AGL, from posterior margin of forelimb insertion to anterior margin of hindlimb insertion); body width (BW, maximum body width); forearm length (FL, from 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 the posterior margin of the retroarticular process of jaw and snout-tip); head width (HW, maximum width of head at the widest range); 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 SL: supralabials; IL: infralabials; DTR: longitudinal rows of enlarged dorsal tubercles at midbody between the venterolateral folds; VS: ventral scales counted between the posterior of the mentum till the anterior of cloacal opening; 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: preanal pores; FP: femoral pores on the femoral region; SBPP: number of medial poreless scales between the preanal pores; SB FP&PP: the number of poreless scales between the series of femoral pores and the preanal pores.

Comparative data for the species from *monticola*, *gracilis* and *mysorensis* clades were obtained from the lit-

erature (Manamendara-Arachchi et al. 2007; Khandekar 2019; Agarwal et al. 2020b; Pal et al. 2021; Khandekar et al. 2021; Khandekar et al. 2022a, 2022b). Museum abbreviations: BNHS: Bombay Natural History Society, Mumbai, India; ZSI-R: Zoological Survey of India, Kolkata, India; ZSI-SRC: Southern Regional Centre, Zoological Survey of India, Chennai, India.

Results

Molecular analysis

Our ML and BI phylogenies recovered different sets of relationships for the new species. In the Bayesian analysis, the new species is sister to the *monticola* clade with strong support (BPP 0.98). However, in the ML analysis, the new species described here is nested between *mysoriensis*, *gracilis* and *monticola* clades, and recovered as basal to the latter two clades (*gracilis* and *monticola*) with low support (UFB 71) (Fig. 2) and the monophyly of *gracilis* and *monticola* clade is also recovered with low support (UFB 52) similar to that of the previous studies. The new species has a genetic divergence of 13.9–24% from the *mysoriensis* clade, 15.8–18.1% from the *gracilis* clade and 13.2–14.9% from the *monticola* clade in the mitochondrial ND2 gene (supplementary Table S2). In the 16S gene, the new species has a genetic divergence of 5.9–8.9% from the *mysoriensis* clade, 5.4–6.1% from the *gracilis* clade and 7–7.3% in *monticola* clade (supplementary Table S3).

Cnemaspis umashaankeri sp. nov.

<http://zoobank.org/2784859C-5B45-45C2-B682-E52E1C-939F1A>

Figs 3–6

Type locality. Biligiri Rangan Hills village, Biligiri Ranganathaswamy Temple Tiger Reserve, Karnataka, India (12.002204°N and 77.145234°E, 1161 m asl).

Holotype. ZSI-R-28301, SVL 25.7 mm, adult male, collected from the type locality by Aravind N.A. and Surya Narayanan on 14th October 2021 (Figs 3, 4, 6A).

Paratypes (n=3). ZSI-R-28302, SVL 24.6 mm, adult male (Fig. 5A); BNHS 3127, SVL 27.7 mm, adult female (Fig. 5B); BNHS 3126, SVL 28.8 mm, adult male (Fig. 5C). Collection details same as holotype.

Etymology. The specific epithet is a patronym honouring Dr R. Uma Shaanker, Retired Professor of Plant Physiology, University of Agricultural Sciences, Bangalore and Founder of Ashoka Trust for Research in Ecology and the Environment (ATREE), Bangalore. He has contributed

immensely to understanding plant and animal evolution, ecology, and conservation biology.

Suggested common name. Umashaanker's Dwarf Gecko.

Diagnosis. A small-sized *Cnemaspis*, SVL up to 29 mm (n=4). Dorsal pholidosis heterogeneous; moderately keeled, granular scales in the vertebral and paravertebral region irregularly arranged, weakly keeled tubercles on each side of flank, tubercles in lowest row largest, spine-like; 6–8 rows of dorsal tubercles; ventral scales smooth, imbricate, 20 or 21 scales across the belly, 90–96 longitudinal scales from mental to cloacal opening, subdigital scancers smooth, entire, unnotched; 6–9 lamellae under digit I of manus and eight lamellae under digit I of pes, 15–17 and 12–15 lamellae under digit IV of pes and manus, respectively; males with 4 or 5 femoral pores on each thigh separated on either side by 4 or 5 poreless scales from a series of 6–8 precloacal pores; tail with enlarged, strongly keeled, distinctly pointed, conical tubercles forming whorls; median row of subcaudals smooth, slightly enlarged; subdigital scancers smooth, entire, unnotched.

Comparison with *gracilis*, *mysoriensis* and *monticola* clades. *Cnemaspis umashaankeri* sp. nov. differs from the members of the *monticola* clade (Pal et al. 2021), including its members from Sri Lanka and Southeast Asia by the absence of spine-like tubercles in the flanks (versus spine like tubercles present in all the members of *monticola* and *kandiana* clades). Additionally, from the Indian members of this clade *C. umashaankeri* sp. nov. can be distinguished by the presence of 90–94 ventral scales (versus 113–129 in *C. monticola* Manamendra-Arachchi, Batuwita and Pethiyagoda, 2007; 130–136 in *C. australis* Manamendra-Arachchi, Batuwita and Pethiyagoda, 2007; 111–124 *C. schalleri* Khandekar, Thackeray and Agarwal, 2021); by a combination of 6–8 PP and 4 or 5 FP separated by 4 or 5 poreless scales (versus 3 or 4 PP and 3–5 FP separated by 9–12 poreless scales in *C. monticola*; 2 or 3 PP and 4 or 5 FP separated by 11–13 poreless scales in *C. australis*; 2 or 3 PP and 3–5 FP separated by 8–10 poreless scales in *C. schalleri*).

Among the members of the *mysoriensis* clade, *Cnemaspis umashaankeri* sp. nov. closely resembles *C. yercaudensis* Das and Bauer, 2000 and *C. otai* Das and Bauer, 2000 in having 20 or 21 MVS and 90–94 ventral scales (versus 18–20 MVS and 90–105 ventrals in *C. yercaudensis*; 18 MVS and 93–98 ventrals in *C. otai*), but it differs from all the members in the *mysoriensis* clade by the following characters. It can be easily distinguished from the members of the clade by having a combination of 6–8 PP and 4 or 5 FP separated by 4 or 5 poreless scales (versus 2 PP and 2 FP separated by 12–14 poreless scales in *C. adii* Srinivasulu, Kumar and Srinivasulu, 2015; 4 PP and 3 FP separated by 9 or 10 poreless scales in *C. otai*; 2 PP and 2 FP separated by 7 or 8 poreless scales in *C. mysoriensis* (Jerdon, 1853); 2 PP and 3 femoral pores separated by 5 or 6 poreless scales in *C. yercaudensis*; 2 PP and 2 or 3 FP on each side separated by 8 poreless scales in *C. stellapulvis* Khandekar,

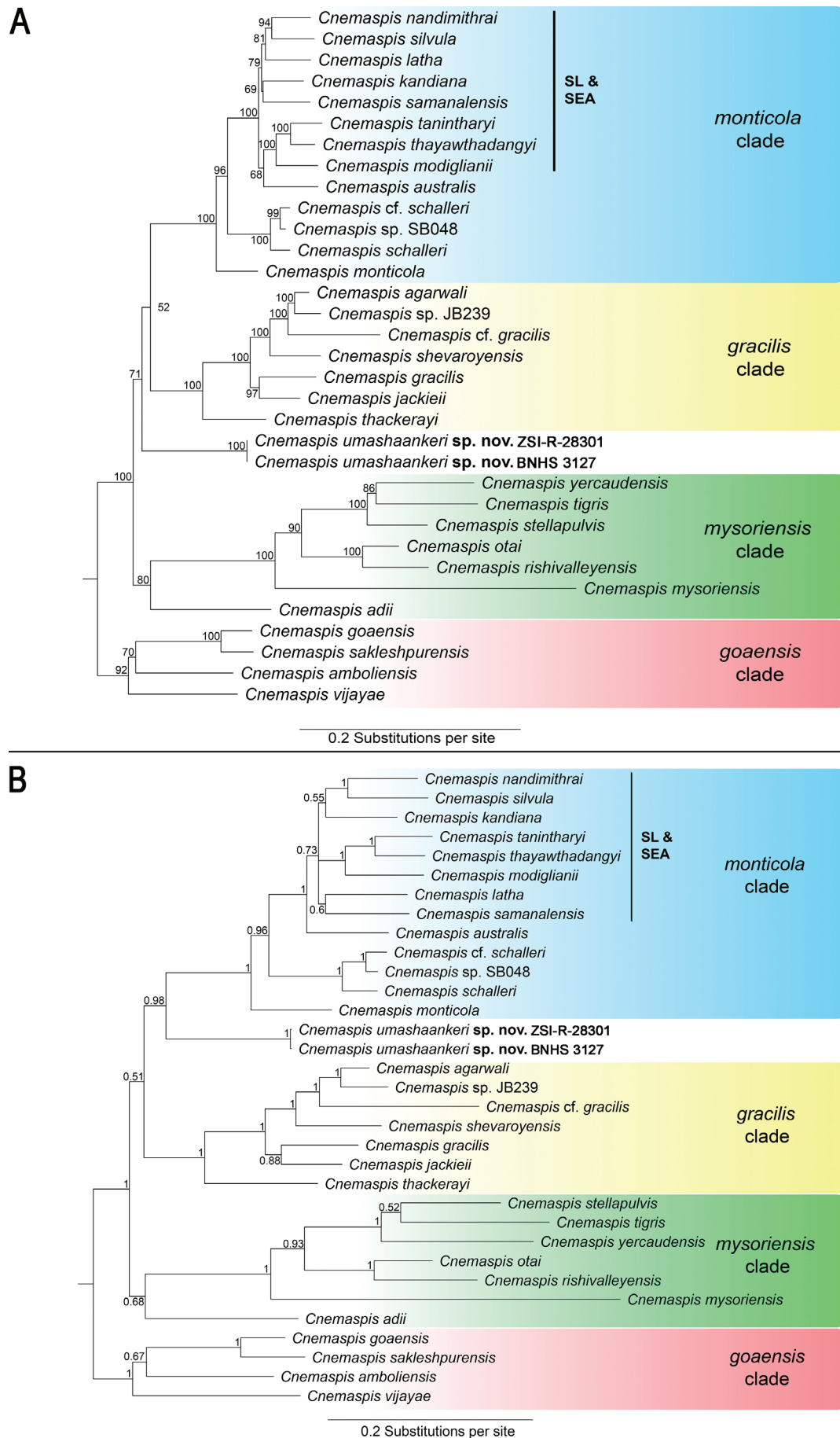


Figure 2. ML (A) and Bayesian phylogenies (B) with the concatenated dataset showing the relationship of the new species with the *mysoriensis*, *monticola*, *gracilis* and *goaensis* clades. SL = Sri Lanka and SEA = Southeast Asia. Complete trees with root are provided in the supplementary material Fig. 1.



Figure 3. Dorsal (upper) and ventral (lower) aspects of the Holotype (ZSI-R-28301) of *Cnemaspis umashaankeri* **sp. nov.** Scale bar = 10 mm.

Thackeray and Agarwal, 2020; 3 PP and 1 FP on each side separated by 10 poreless scales in *C. rishivalleyensis* Agarwal, Thackeray and Khandekar, 2020; FP absent and 2–5 PP in *C. avasabinae* Agarwal, Bauer and Khandekar, 2020; 2 (3 in one specimen) PP and 2 FP on each side separated by 6–9 poreless scales in *C. tigris* Khandekar, Thackeray and Agarwal, 2022.

From the members of the *gracilis* clade, *Cnemaspis umashaankeri* **sp. nov.** can be easily distinguished by a combination of 6–8 PP and 4 or 5 FP separated by 4 or 5 poreless scales (versus 4 PP and 4–6 FP separated by 8 poreless scales in *C. agarwali* Khandekar, 2019; 1 or 2 PP and 4 FP separated by 7–9 poreless scales in *C. shevaroyensis* Khandekar, Gaitonde and Agarwal, 2019; 2–4 PP and 5–9 FP separated by 1–6 poreless scales in *C. thackerayi* Khandekar, Gaitonde and Agarwal 2019; 3 or 4 PP and 5 or 6 FP separated by 1 or 2 poreless scales in *C. jackeii* Pal, Mirza, Dsouza and Shanker 2021; 2 PP and 3–5 FP separated by 9–11 poreless scales in *C. mundanthuraiensis* Khandekar, Thackeray and Agarwal, 2022). Furthermore, *C. umashaankeri* **sp. nov.** differs from all the members of this clade in having a lower ventral 90–96 and MVSR 20 or 21 (versus 24–26 MVSR and 136–140

ventrals in *C. agarwali*; 21–24 MVSR and 111–118 ventrals in *C. shevaroyensis*; 22–25 MVSR and 105–122 ventrals in *C. agarwali*).

Additionally, *Cnemaspis umashaankeri* **sp. nov.** can be distinguished from *Cnemaspis boiei* (Gray, 1842) by the presence of femoral and preanal pores (versus both femoral and preanal pores absent in *C. boiei*). From *Cnemaspis jerdoni* (Theobald, 1868), the new species can be distinguished by the presence of 4 or 5 femoral pores and 6–8 preanal pores (versus 8 femoral pores and preanal pores absent in *C. jerdoni*).

Description of the holotype (ZSI-R-28301). Adult male in good state of preservation, the tip of the tail clipped for the tissue collection (Fig. 3). SVL 25.7 mm, head short (HL/SVL 0.29), wide (HW/ HL 0.64), not strongly depressed (HD/HL 0.48), distinct from neck. Loreal region slightly inflated, canthus rostralis not prominent. Snout roughly one-third of the head length (ES/HL 0.35), 2.5 × eye diameter (ED/ES 0.40); scales on snout and canthus rostralis large, round; slightly larger than the scales those on forehead and interorbital region; occipital and temporal region with much smaller granules (Fig. 4A).

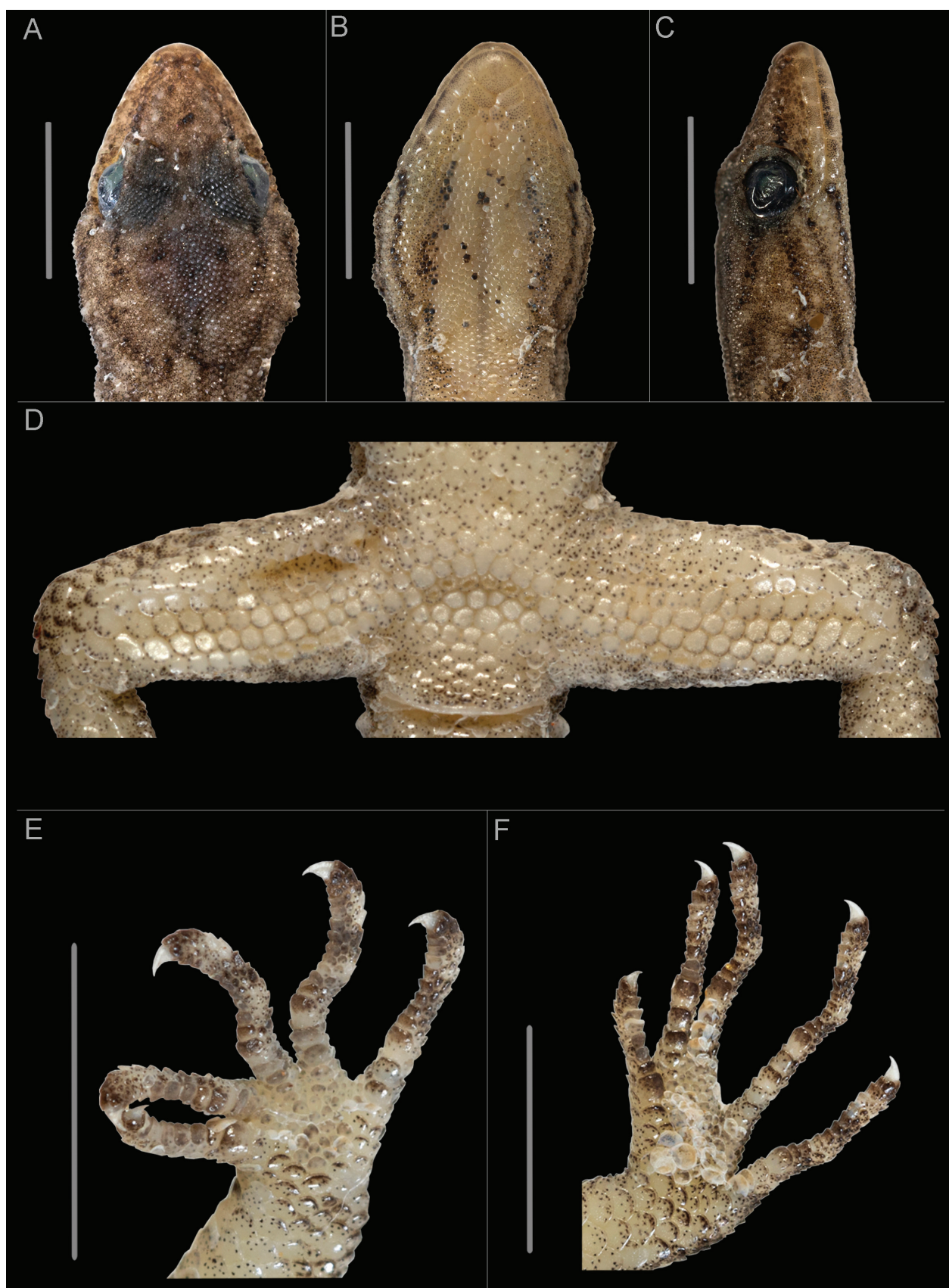


Figure 4. *Cnemaspis umashaankeri* sp. nov. (Holotype, ZSI-R-28301); **A** head in dorsal view, **B** ventral view, **C** lateral view, **D** view of the femoral region, **E**, ventral view of right manus and **F**, right pes. Scale bar = 5mm.

Eye small (ED/HL 0.14); with round pupil; orbit with fringe scales that are largest anteriorly; supraciliaries not elongate. Ear-opening deep, vertical, small (EL/HL 0.06);

eye to ear distance greater than diameter of eye (EE/ED 2.18). Rostral much wider (1.7 mm) than long (0.8 mm), partially divided dorsally by a strongly developed rostral

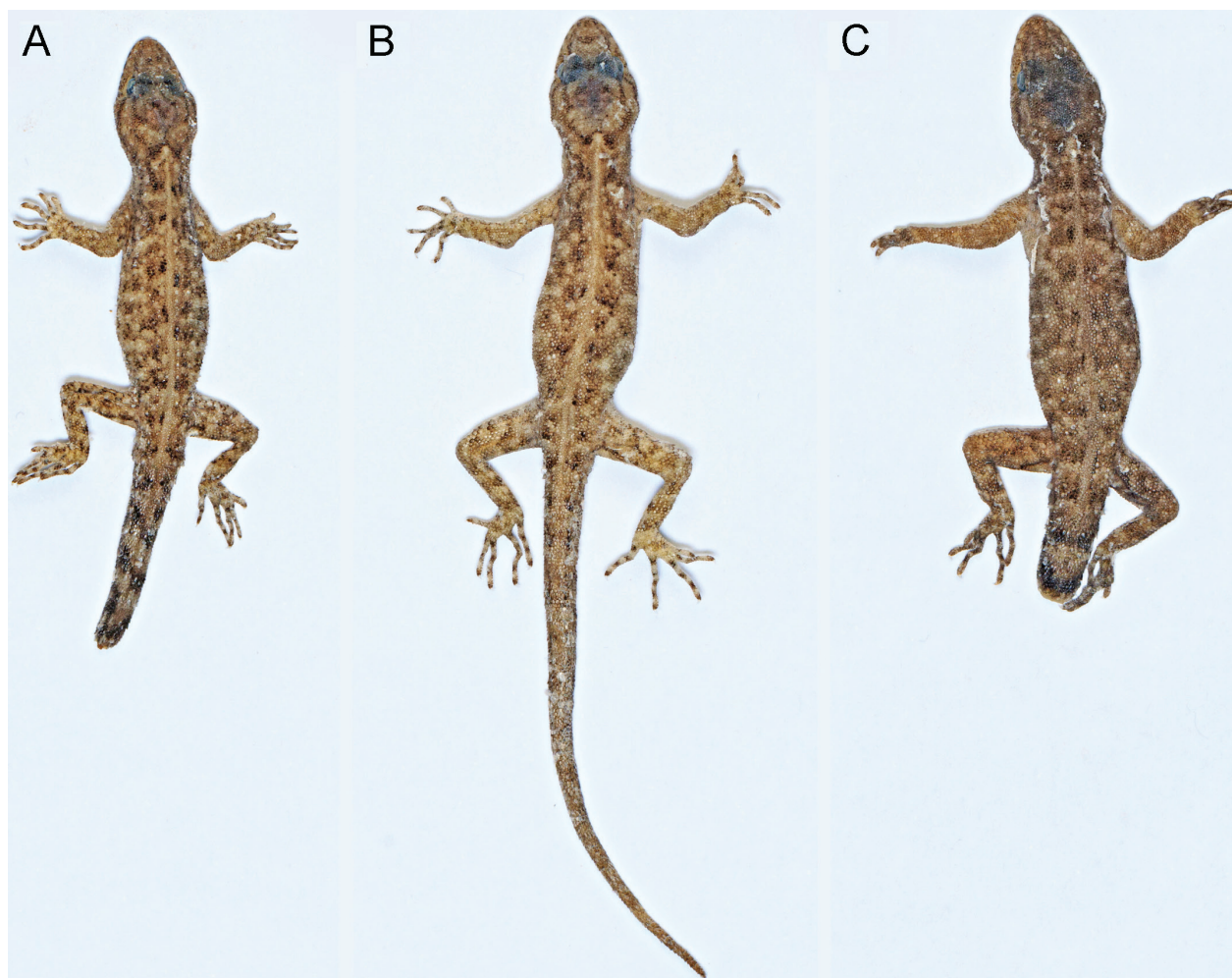


Figure 5. Dorsal aspect of the paratypes of *C. umashaankeri* sp. nov.; **A** ZSI-R-28302, **B** BNHS 3127, **C** BNHS 3126.

groove for more than half of its length; single enlarged supranasal on each side, slightly larger than postnasals; a small scale present at the juncture of rostral and internasals; rostral in contact with supralabial 1, nasal, supranasal, internasal, briefly contacting post nasal; nostrils oval, each surrounded by postnasal, supranasal and rostral; three rows of scales separate the orbit from the supralabials (Fig. 4A).

Mental enlarged, subtriangular, wider than long; two pairs of postmentals, inner pair large, roughly rectangular, bordered by mental, infralabial I, outer postmentals and two enlarged chin shields; outer postmentals slightly smaller than inner postmentals, roughly circular, bordered by inner postmentals and eight enlarged chin shields; inner postmentals in contact with each other and two small gular scales prevent contact of left and right outer postmentals; chin shields bordering postmentals flat, smooth, smaller than outermost postmentals. Eight Supralabials on each side and seven supralabials on left and six on right side at midorbit; supralabial I largest, supralabials decreasing in size posteriorly; seven infralabials to angle of jaw on each side and six at midorbit on either side; infralabial I largest, infralabials decreasing in size posteriorly (Fig. 4C). Extra-brillar fringe scales seven or eight on each side; 24–26 scale rows between left and right supraciliaries at midorbit.

Body relatively slender (BW/SVL 0.23), trunk less than half of SVL (AGL/SVL 0.42); spine-like scales on flank absent. Dorsal scales on trunk heterogeneous, moderately keeled anteriorly and strongly keeled posteriorly; granular scales intermixed with much larger, strongly keeled, conical tubercles; approximately eleven tubercles in paravertebral row from above forelimb insertion to the hind limb insertion. Scales on nape are slightly smaller than those on paravertebral rows and smaller on the occiput. Scales on flank slightly larger than those on dorsum, granular and strongly keeled, intermixed with more tubercles than that of the dorsum. Ventral much larger than those on the dorsum, those on belly smooth, imbricate, subequal from chest to vent; midbody scale rows across belly 21; 90 scales from mental to anterior border of cloaca. Scales on throat and pectoral region slightly smaller than those on belly, flat and imbricate; gular region with much smaller, flattened scales with those on chin bordering postmentals. Four femoral pores on each thigh separated four poreless scales on the left and five poreless scales on the right from six continuous precloacal pores (Fig. 4D).

Scales on palm and sole smooth, flat and roughly circular; scales on dorsal aspect of manus and pes heterogeneous, moderately keeled, imbricate; those near forelimb insertion much smaller; dorsal aspect of forearm



Figure 6. Live images of *C. umashaankeri* sp. nov.; **A** Holotype (ZSI-R-28301), **B** Live uncollected female.

and elbow with scales smaller than those on upper arm, strongly keeled, roughly rounded; dorsal aspect of hand predominantly bearing large, strongly keeled, imbricate scales. Ventral aspect of upper arm with smooth, roughly rounded. Scales on dorsal aspect of thigh subequal to those on dorsal granules, strongly keeled, imbricate. Scales on dorsal aspect of knee and shank slightly smaller than those on dorsum of thigh, subimbricate, strongly keeled; dorsal aspect of foot predominantly bearing small to large, moderate to strongly keeled, imbricate scales; scales on ventral aspect of thigh and shank similar to those on midbody ventrals (Fig. 3). Fore and hind limbs moderately long, slender; (CL/SVL 0.16); digits long, with a strong, recurved claw, distal portions laterally compressed conspicuously. Series of unpaired lamellae on basal portion of digits, separated from narrower distal lamellae by a single large scale at the inflection; proximal lamellae series: 1–3–3–4–3 (right manus; Fig. 4E), 1–4–4–6–5 (right pes; Fig. 4F), 1–3–4–4–3 (left manus),

1–4–4–6–3 (left pes); distal lamellae series: 7–8–11–10–9 (right manus; Fig. 4E), 7–9–10–10–10 (right pes; Fig. 4F), 7–8–10–11–9 (left manus), 7–8–10–11–10 (left pes). Relative length of digits (measurements in mm in parentheses): IV (2.1) > III (1.9) > V (1.8) > II (1.6) > I (1.1) (right manus); III (3.3) > IV (3.1) > II (2.3) > V (2.2) > I (1.7) (right pes).

Tail incomplete, cylindrical in cross-section, relatively slender, longer than snout-vent length (TL/SVL 0.87). Dorsal scales at tail base granular, strongly keeled, similar in size and shape to those on midbody dorsum, gradually becoming larger, flatter, subimbricate posteriorly, intermixed with two rows of distinctly enlarged, conical, strongly keeled paravertebral tubercles; four to six tubercles in dorsolateral, lateral and ventrolateral rows, distinctly enlarged, strongly keeled, imbricate, which are restricted only at the anterior portion of the tail, forming whorls. Scales on the ventral aspect of the original tail much larger than those on the dorsal, imbricate, smooth,

Table 1. Mensural data for the type series of *Cnemaspis umashaankeri* **sp. nov.** * denote incomplete tail.

Species	<i>Cnemaspis umashaankeri</i> sp. nov.			
Voucher no.	ZSI-R-28301	ZSI-R-28302	BNHS 3126	BNHS 3127
Type status	Holotype	Paratype	Paratype	Paratype
Sex	Male	Male	Male	Female
SVL	25.7	24.6	28.8	27.7
TL	22.6*	14*	7.9*	34.9
TW	2.1	2.2	3.1	2.5
CL	4.3	3.7	4.7	5.2
AGL	11	9	12.3	11.23
BH	2.8	2.9	3.3	3.7
BW	6	5.3	6.5	6.3
HL	7.7	7.8	7.7	8.1
HW	5	4.6	5.7	5.2
HD	2.4	3.1	2.8	3
ED	1.1	1.3	1.2	1.3
EE	2.4	2.5	2.4	2.6
ES	2.7	2.8	3.3	3.3
EN	2.2	2.1	2.4	2.8
IN	0.9	0.8	0.9	1
IO	2.6	2.8	3	3.2
EL	0.5	0.3	0.5	0.5

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

	<i>Cnemaspis umashaankeri</i> sp. nov.			
Voucher no.	ZSI-R-28301	ZSI-R-28302	BNHS 3126	BNHS 3127
Type status	Holotype	Paratype	Paratype	Paratype
Sex	Male	Male	Male	Female
SL L&R	7&7	7&7	7&7	7&7
IL L&R	7&7	7&7	6&7	6&7
SL M L&R	6&6	6&6	6&7	6&7
IL M L&R	5&5	5&5	5&6	5&6
PVT	irr. arr	irr. arr	irr. arr	irr. arr
DTR	6	8	8	6
MVSR	21	21	20	21
VS	90	92	94	96
LamF1 L&R	8&8	8&9	8&8	8&6
LamF4 L&R	15&14	12&13	15&dam	15&15
LamT1 L&R	8&8	8&8	8&8	8&8
LamT4 L&R	17&16	15&15	16&16	17&16
LamT5 L&R	13&15	14&13	14&15	15&16
PP L&R	6	8	8	ab
SBPP	0	0	0	0
SB PP&FP L&R	4&5	5&4	4&5	ab
FP L&R	4&4	5&5	5&5	ab

with a series of three enlarged subcaudal scales of which the median series is almost twice the size of adjunct two rows, roughly hexagonal; those on the tail base much smaller, imbricate and smooth, a single enlarged postcloacal spur on each side.

Colour in life. Dorsal aspect of the body is overall dark brown with yellow and black intermixed irregular patch-

es. The weakly keeled granular tubercles on the lateral aspect of the body prominently in yellow. An indistinct pale vertebral stripe extending from the neck to the anterior portion of the tail. The dorsal part of the head is not distinctly different from the dorsal body in colour. One dark preorbital stripe extending from the narial region to the eye, two postorbital stripes running from the posterior of eye to the axillar insertion and the other stripe extends



Figure 7. Overall habitat of the BR Hills village and the BRT Tiger Reserve.

from the posterior of the subocular region extending towards venter. Rostral and first two supralabials are predominantly darker, rest yellowish. Infralabials predominantly darkish bordered by yellow, except the last which is fully yellowish. Black and greyish dorsal transverse caudal bands encircling the tail. Black bands generally 7 or 8 scales thicker and greyish bands thicker by 4 or 5 scales. All the black separate except the third to fifth that is connected dorsally. Post cloacal spur yellowish on either side. Ventral surface dull white and gular region distinctly yellowish. Few ventral scales along the coastal and the scales in the thigh indistinctly yellowish. In preservative, all the colour remains same except the yellow, that turned paler on both dorsal and ventral sides.

Variation in paratypes. Mensural and meristic data for the type series are provided in Table 1 & 2. Paratypes range in size of the SVL from 24.6 mm to 28.8 mm ($n=3$). Paratypes ZSI-R-28302 and BNHS 3126 are males and ZSI-R-28302 is a female. All paratypes overall resemble the holotype except in the following characters. Tail complete in the paratype BNHS 3127 and incomplete in all other paratypes ZSI-R-28302, BNHS 3126 with varying degrees in length, all of which have original tails. Post mentals in brief contact in the paratype ZSI-R-28302 and are separated by a single small scale in paratype BNHS 3126. Outer postmentals are separated by a series of three scales in ZSI-R-28302 and by four scales in BNHS 3126. The overall colouration of all the male specimens (ZSI-R-28302 & BNHS 3126) is similar to the holotype. The dark mottling in the gu-

lar scales is absent in BNHS 3126 and less prominent in ZSI-R-28302. The dorsal colouration of the only female paratype BNHS 3127 is brownish overall including the tail.

Distribution and natural history. *Cnemaspis umashaankeri* **sp. nov.** is currently known only from four localities within the BRT Tiger Reserve (Fig. 7). During our fieldwork we found this species in the settlements largely intermixed with coffee plantations in BR Hills and K Gudi villages (11.906001°N, 77.133290°E) and Basavanakadu stream (11.941572°N, 77.155268°E). Beyond these areas, we also found *C. umashaankeri* **sp. nov.** commonly in semi-evergreen, moist deciduous forests around the coffee estates within the Tiger Reserve mainly in habitats associated with the rocky granite boulders and crevices. The holotype and the paratypes were collected from building walls of the ATREE field station situated amidst the human settlements and coffee plantations, indicating that this species can survive human disturbances. The type series was collected at night around 20:00 hrs during which individuals were highly active. Within the sampled sites, several other individuals of *C. umashaankeri* **sp. nov.** were observed foraging, mostly in the evenings or later in the night. These uncollected individuals were identified based on the dorsal pholidosis and number of femoral and preanal pores. Eggs of the new species were seen in the rock and building crevices. *Hemidactylus graniticolus* Agarwal, Giri and Bauer, 2011 and *Hemidactylus* sp. are found syntopically with the new species within the known range.

Discussion

Biligiri Rangan Hills situated in the vicinity of the Nilgiri Hills and Mysore city, both of which are known to be important regions for plantations and as administrative zones during colonial era. However, this region received limited attention from the explorers, especially in terms of the herpetofauna. Beddome (1870) described the first new species *Cyrtodactylus collegalensis* [as *Gymnodactylus*] of reptile from from “Balarangans (= BR Hills) in dry forests near Yellundur (=Yelandur)” (also see Agarwal et al. 2016). The British naturalist and coffee planter Ralph Camroux Morris (1894–1977) who lived in the Honnametti estate (now part of the BRT Tiger Reserve) was the subsequent person to explore this region. His interest was broadly in mammals and birds, on which he had published several natural history notes between 1922–1958 (Ali 1978), and only one of his notes dealt with snakes pertaining to the BR Hills (Morris 1958). After this, only a handful of studies in the recent past have dealt with inventorying (Murthy and Thirumalai 2006) or reported the sightings of herpetofauna of BR Hills (Ganesh et al. 2018). Apart from these, two amphibian species *Microhyla sholigari* Dutta and Ray, 2000 and *Raorchestes honnametti* Gururaja, Priti, Roshmi and Aravind, 2016 have been described from the BR Hills. After the work of Beddome (1870), *Cnemaspis umashaankeri* **sp. nov.** is the second reptile species to be described from the BRT Tiger Reserve.

Murthy and Thirumalai (2006) reported *Cnemaspis indica* Gray 1846 from “Sebinkare to Doraisami Park” based on two examples without any morphological data, in their checklist. Two of these specimens (ZSI/SRS/VRL-487, 488) were traced during this study. Due to the poor state of preservation, we could not collect information on the number of femoral and precloacal pores, but we refer to these specimens as *C. umashaankeri* **sp. nov.** based on the presence of irregularly arranged dorsal tubercles, which is absent in *C. indica* (Gray 1846; Pal et al. 2021). Also, the type locality and the other known location K Gudi village of the new species is only 12 km and 2 km, respectively from the locality mentioned in Murthy and Thirumalai (2006) with similar habitat type and elevational range. Furthermore, *Cnemaspis indica* was originally described from the Nilgiri Hills and has a restricted distribution in the higher elevations in this region (Pal et al. 2021).

Interestingly, from the existing information, BR Hills appear to harbour some of the range-restricted herpetofauna (forest species) that are found both in the Eastern and the Western Ghats; such as *Draco dussumeiri* Duméril and Bibron, 1837, *Monilestaurus rouxii* (Duméril and Bibron, 1837), *Boiga nuchalis* (Günther, 1875), *Dendrelaphis bifrenalis* (Boulenger 1890), *Craspedocephalus occidentalis* (Pope and Pope, 1933) and *Lycodon flavicollis* Mukherjee & Bhupathy, 2007 (Ganesh et al. 2018; Aengals et al. 2022). This pattern of shared faunal elements from both the Eastern and the Western Ghats and the apparent missing of some wet zone species in the BR Hills has been previously reported for birds (Srinivasan and Prashanth 2006).

In the ML phylogeny, *Cnemaspis umashaankeri* **sp. nov.** is sister to two clades, one restricted to the Eastern and the Western Ghats (*gracilis* clade) and the Western Ghats and in Sri Lanka (*monticola* clade), but with low support. On the other hand, in the BI analysis, *C. umashaankeri* **sp. nov.** is sister to the *monticola* clade with strong support. However, our phylogenetic analyses included all the described species belonging to the three clades of interest (*gracilis*, *mysoriensis* and *monticola*) to which the new species shows affinity. *Cnemaspis umashaankeri* **sp. nov.** could not be positively placed in any of these species' clades, but shares morphological similarity with *mysoriensis* and *gracilis* clades by the absence of spine-like tubercles, while this is present in all the members of *monticola* clade (Pal et al. 2021). Additional sampling from this and nearby regions may resolve the phylogenetic placement and the dispersal patterns of these clades within peninsular India and Sri Lanka. Moyar gorge has been previously postulated as a significant biogeographic barrier for several terrestrial reptilian genera *Sitana* Cuvier, *Hemidactylus* Goldfuss and *Playceps* Blyth (Deepak and Karanth 2018; Srikanthan et al. 2018; Deepak et al. 2021) and the role of this barrier for other herpetofauna in these ranges remains to be tested.

This description of yet another *Cnemaspis* from the BR Hills shows the hidden diversity in this genus and highlights the lack of studies and exploration in this region. Hitherto *Cnemaspis umashaankeri* **sp. nov.** is known only from the vicinity of the BR Hills, mostly in the mid-elevation semi-evergreen and moist deciduous forests and their presence in the evergreen patches of the higher elevations needs to be investigated across the range. Given the poor exploration of herpetofauna in this region and adjacent areas, further extensive surveys are warranted for an updated inventory and to uncover the hidden diversity.

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Supplementary material 1

Table S1

Authors: Narayanan S, Aravind NA (2022)

Data type: .docx

Explanation note: List of sequences and Genbank accession numbers used in this study.

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Link: <https://doi.org/10.3897/vz.72.e89324.suppl1>

Supplementary material 2

Table S2

Authors: Narayanan S, Aravind NA (2022)

Data type: .docx

Explanation note: Uncorrected pairwise distances for the mitochondrial ND2 gene among the *gracilis*, *mysoriensis* and *monticola* clade.

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Supplementary material 3

Table S3

Authors: Narayanan S, Aravind NA (2022)

Data type: .docx

Explanation note: Uncorrected pairwise distances for the mitochondrial 16S gene among the *gracilis*, *mysoriensis* and *monticola* clade.

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Supplementary material 4

Figure S1

Authors: Narayanan S, Aravind NA (2022)

Data type: .pdf

Explanation note: Complete ML phylogeny based on the concatenated dataset showing the relationship of the South Asian *Cnemaspis*.

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Link: <https://doi.org/10.3897/vz.72.e89324.suppl4>

Supplementary material 5

Figure S2

Authors: Narayanan S, Aravind NA (2022)

Data type: .pdf

Explanation note: Complete BI phylogeny based on the concatenated dataset showing the relationship of the South Asian *Cnemaspis*.

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