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A NEW RUPICOLOUS DAY GECKO SPECIES (SQUAMATA: GEKKONIDAE: *Cnemaspis*) FROM TAMIL NADU, SOUTH INDIA

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Abstract

We here describe a new rupicolous day gecko species nested within the *C. gracilis* clade from Madurai, Tamil Nadu, India. The new species differs with a combination of morphological characters and molecular phylogenetics, from other closely related congeners. The sequence divergence of the new species in comparison with the congeners from the *gracilis* clade is 6.1–15.2% for the ND2 gene. The new species can also be differentiated from the congeners based on the following combination of morphological characters: conical and spine-like tubercles absent on flanks; adult SVL less than 35.0 mm; two precloacal pores; precloacal pores separated medially by two poreless scales; four femoral pores; number of mid-ventral scales 110–120; and a small black colour spot on the occiput.

Keywords: dwarf geckos, *gracilis* clade, molecular phylogeny, ND2, rock-dwelling, systematics

Introduction

Cnemaspis Strauch, 1887 is known to have initially diversified during the transition between the Cretaceous and Tertiary periods of geological time characterized by the Deccan Volcanic Eruptions and the Paleocene-Eocene

Thermal Maximum (Pal *et al.* 2021). Pal *et al.* (2021) defined ten clades and described twelve new species from southern peninsular India. Amongst these ten clades, the *gracilis* is known to have a broad distribution (Khandekar *et al.* 2022). Agarwal *et al.* (2022) described five new

species within this clade from the Shevaroy hill massifs drawing attention to the micro-endemism within the genus. The subsequent description of another new species by Narayanan *et al.* (2022) from the Male Mahadeshwara Wildlife Sanctuary in the Eastern Ghats, raised the total number of species in the *gracilis* clade to twelve.

During our recent herpetological surveys in southern India, we discovered a population of *Cnemaspis* on Thiruparankundram Hill, Madurai, Tamil Nadu that was similar to *C. pachamalaiensis* Agarwal *et al.*, 2022, but after detailed comparison of morphology with the support of genetic data, it became clear that this population represents a distinct, unnamed species. Hence, we describe it as a new species.

Material and Methods

Sampling. Specimens were collected in January 2023 from Thiruparankundram Hill, Madurai, Tamil Nadu, India. Two adult males and an adult female were collected by hand, photographed in life, and then euthanized using halothane following the guidelines of Leary *et al.* (2013). Thigh tissue was used for further molecular work. The specimens were subsequently fixed in 4% formaldehyde for ~24 hours, washed in water and later transferred to 70% ethanol for long-term preservation. Scapulation and other morphological characters were recorded using a Lensele stereo microscope. The material referred to in this study is deposited in the collection of the Bombay Natural History Society (BNHS), Mumbai, Maharashtra, India.

Morphological data. Morphological data were taken using a Yamayo (Mitutoyo-500) digimatic calliper to the nearest 0.1 mm. For the geographical coordinates, altitude, and temperature readings, we used a Kestrel 4500 receiver. Morphological data was recorded as snout-vent length (SVL), distance from tip of snout to anterior margin of vent; axilla-groin length (AG), distance from axilla to groin; trunk width (TW), maximum width of the body; eye diameter (ED), horizontal diameter of the orbit; eye-to-nares (EN), distance between anterior point of the orbit to the posterior part of the nostril; snout length (ES), distance from anterior margin of the orbit to the tip of the snout; eye-to-ear (ET), distance from posterior margin of the orbit to the anterior margin of the ear opening; internarial distance (IN), least distance between the inner margins of the nostrils; ear

opening diameter (EOD), horizontal distance from the anterior to posterior margin of the ear opening; head length (HL), distance from tip of snout to posterior edge of mandible; head width (HW), maximum width of the head; head depth (HD), maximum depth of the head; interorbital distance (IO), shortest distance between the superciliary scale rows; upper arm length (UAL), distance from axilla to elbow, lower arm length (FAL), distance from elbow to wrist; palm length (PAL), distance from wrist to the tip of the longest finger; Finger length (FL), distance from the tip of the finger to the nearest fork; femur length (FEL), distance from groin to the knee; tibia length (TBL), distance from knee to heel toe length (TOL), distance from tip of 1st toe to the nearest fork; tail length (TL), distance between posterior margin of vent to the tip of the tail.

Meristic data recorded for all specimens includes number of supralabials (SupL) and infralabials (InfL) on left (L) and right (R) sides; number of supraciliaries (SuS); number of interorbital scales (InO); number of scales between eye to tympanum (BeT), from posterior-most point of the orbit to anterior-most point of the tympanum; number of the postnasal (PoN), all scales posterior to the naris; number of postmentals (PoM); number of posterior postmentals (PoP), scales that are surrounded by the posterior-postmentals and between infralabials; number of supranasals (SuN), excluding the smaller scales between the larger supranasals; number of canthal scales (CaS), number of scales from posterior-most point of naris to anterior most point of the orbit; number of dorsal paravertebral scales (PvS), between pelvic and pectoral limb insertion points along a straight line immediately left of the vertebral column; number of mid-dorsal scales (MbS), from the centre of mid-dorsal row diagonally towards the ventral scales; number of mid-ventral scales (MvS), from the first scale posterior to the mental to last scale anterior to the vent; number of midbody scales (BIS), across the ventral between the lowest rows of dorsal scales; preanal pores (PPores), the number preanal pores; femoral pores (FPores), the number of femoral pores; poreless scales (PS), number of poreless scales between left and right femoral pores; scales between preanal pores (SBP), number of scales between preanal pores; lamellae under digits of manus (MLam) and pes (PLam) on right (R) side, counted from first proximal enlarged scapular greater than

twice the width of the largest palm scale, to distal-most lamella at tip of digits; lamellae under fourth digit of pes (LampIV). Morphometric data are given as % of SVL.

Molecular analysis. DNA extraction, amplification and sequencing: Genomic DNA of two *Cnemaspis* specimens (male BNHS 3158, female BNHS 3159) was extracted from thigh tissue samples that were preserved in 100% ethanol. The DNA extraction was carried out using a DNeasy (Qiagen™) blood and tissue kit following the manufacturer's instructions. Partial sequences of the mitochondrial NADH dehydrogenase 2 (ND2) gene were amplified. The amplification was carried out in three steps of polymerase chain reaction (PCR) using primers MetF1 (Forward) and H5934 (Reverse) (Macey *et al.* 1997). The fragments were amplified with the following conditions: 95°C – 3 min, 1 cycle, 95°C – 30 sec, 56–58°C – 30 sec, 72°C – 45 sec, 35 Cycles, 72°C – 7 min. We then sequenced the forward and reverse DNA

strands using a BDT v3.1 Cycle sequencing kit on ABI 3730xl Genetic Analyzer.

Sequence alignments: The ND2 sequences generated in the study were cleaned manually with MEGA v.7 (Kumar *et al.* 2016) using chromatograms visualised in Chromas v.2.6.5 (Technelysium Pty. Ltd.). Comparative ND2 sequences comprising members of the *Cnemaspis* were downloaded from GenBank following Pal *et al.* (2021), Agarwal *et al.* (2022), and Narayanan *et al.* (2022); (see Table 1). *Phelsuma ornata* Gray, 1825 (EU423282.1); *Phelsuma lineata* Gray, 1842 (EU423283.1); and *Lygodactylus picturatus* Peters, 1870 (MZ772396.1) were used as outgroups in the analysis. The sequences were aligned using MUSCLE (Edgar 2004) in MEGA7 (Tamura & Nei 1993, Kumar *et al.* 2016) with default parameter settings. The final ND2 alignment contained 82 sequences (79 ingroups and 3 outgroups) with 1047 base pair lengths that were further used for phylogenetic analysis.

Table 1. List of GenBank accession numbers of ND2 sequences of the *Gracilis* clade (see Fig. 1); newly generated sequences in this study were deposited in the GenBank® nucleotide sequence database <www.ncbi.nlm.nih.gov> with the accession numbers: OQ925814 and OQ925815

Species	Locality	Genbank Accession No.
<i>C. agarwali</i> 1	India, Tamil Nadu, Salem District, Sankari	MK792467
<i>C. agarwali</i> 2	India, Tamil Nadu, Salem District, Sankari	MK792466
<i>C. agayagangai</i> 1	India, Tamil Nadu, Namakkal District, Agaya Gangai Waterfalls	OP709694
<i>C. agayagangai</i> 2	India, Tamil Nadu, Namakkal District, Agaya Gangai Waterfalls	OP709695
<i>C. fantastica</i> 1	India, Tamil Nadu, Namakkal District, Kollimalai ghat	OP709698
<i>C. fantastica</i> 2	India, Tamil Nadu, Namakkal District, Kollimalai ghat	OP709699
<i>C. fantastica</i> 3	India, Tamil Nadu, Namakkal District, Kollimalai ghat	OP709700
<i>C. ganeshaiahi</i> 1	India, Karnataka, MM Hills	OQ555723
<i>C. ganeshaiahi</i> 2	India, Karnataka, MM Hills	OQ555724
<i>C. gracilis</i> 1	India, Tamil Nadu, Coimbatore District, Valparai	MK792470
<i>C. gracilis</i> 2	India, Tamil Nadu, Salem District, Yercaud	MK792465
<i>C. gracilis</i> 3	India, Kerala, Palakkad District, near Chittur River	MZ701820
<i>C. gracilis</i> 4	India, Kerala, Palakkad District, near Chittur river	OP709696
<i>C. gracilis</i> 5	India, Kerala, Palakkad District, near Chittur river	OP709697
<i>C. jackieii</i>	India, Tamil Nadu, Vairavankulam RF, near Karuppan-adhi dam	MZ701804
<i>C. mundanthuraiensis</i>	India, Tamil Nadu, Tirunelveli District, Mundanthurai forest range	ON494557
<i>C. pachaimalaiensis</i>	India, Tamil Nadu, Tiruchirapalli District, Pachaimalai	OP709702
<i>C. reticulata</i> sp.nov. 1	India, Tamil Nadu, Madurai District near Thiruparankundram dargah	OQ925814
<i>C. reticulata</i> sp.nov. 2	India, Tamil Nadu, Madurai District near Thiruparankundram dargah	OQ925815
<i>C. rudhira</i> 1	India, Tamil Nadu, Salem District, Yercaud	MK792462
<i>C. rudhira</i> 2	India, Tamil Nadu, Salem District, Yercaud	MK792463
<i>C. rudhira</i> 3	India, Tamil Nadu, Salem District, Yercaud	MK792464
<i>C. rudhira</i> 4	India, Tamil Nadu, Salem District, Yercaud	MK792461
<i>C. salimalii</i> 1	India, Tamil Nadu, Namakkal District, Kollimalai	OP709703
<i>C. salimalii</i> 2	India, Tamil Nadu, Namakkal District, Kollimalai	OP709704
<i>C. shevaroyensis</i> 1	India, Tamil Nadu, Salem District, Yercaud	MK792469
<i>C. shevaroyensis</i> 2	India, Tamil Nadu, Salem District, Yercaud	MK792468
<i>C. thackerayi</i>	India, Tamil Nadu, Salem District, Yercaud	MK792471

Molecular Phylogenetic analysis: ND2 is a protein-coding gene hence the dataset was partitioned by codon positions. The generated alignment was implemented for the Maximum Likelihood (ML) phylogenetic analysis. ML analysis was performed using the web implementation of IQ-tree (Nguyen *et al.* 2015) under the TN+F+I+G4 models of sequence evolution for all the positions. The model of sequence evolution was determined using ModelFinder (Kalyaanamoorthy *et al.* 2017) on the IQ- tree web platform, and branch support was tested using 1000 non-parametric rapid ultrafast bootstrap pseudo-replicates (Minh *et al.* 2020). The ML tree was generated using the complete alignment of 82 sequences, however only 28 sequences belonging to the *gracilis* clade including two sequences of the new species are shown (Fig. 1). Pairwise sequence divergences (*p*-distance) were also calculated only for species from the *gracilis* clade using Mega 7, and the complete deletion option was selected to treat gaps/missing data.

Results

Phylogenetic relationship. The tree topology did not differ from the trees generated in recent studies (Agarwal *et al.* 2022, Narayanan *et al.* 2023). The ML phylogenetic inference based on the ND2 gene (Fig. 1) shows the species to be a member of the *gracilis* clade (Khandekar 2019, Khandekar *et al.* 2019, Pal *et al.* 2021, Agarwal 2022, Narayanan *et al.* 2022). The new species recovered is a sister to the *C. gracilis*+*C. mundanthuraiensis*+*C. jackieii* clade with a moderate bootstrap (bp) support of 62. Based on the uncorrected *p*-distance (Table 2), the following genetic distances were recorded between the new species and the other members of *gracilis* clade: 6.1% with *C. jackieii*; 12.1% with *C. gracilis*; 9.1% with *C. mundanthuraiensis*; 9.1% with *C. agarwali*; 9.1% with *C. shevaroyensis*; 15.2 % with *C. fantastica*; 12.1% with *C. pachaimalaiensis*; 9.1% with *C. agayagangai*; 9.1% with *C. ganेशaiahi*; 9.1% with *C. thackerayi*; 9.1% with *C. rudhira* and 12.1% with *C. salimalii*.

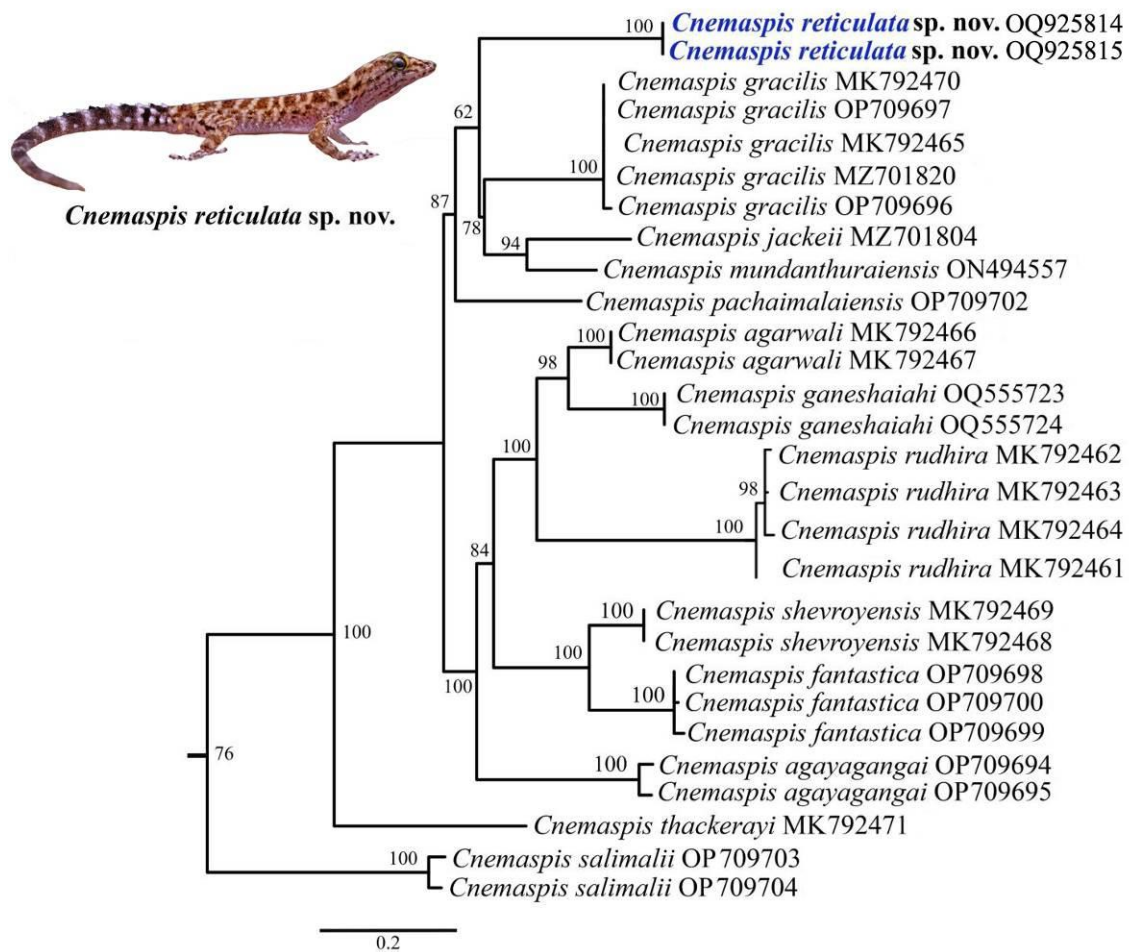


Figure 1. Maximum Likelihood phylogenetic tree showing the relationships among the species of the *Cnemaspis* from the *gracilis* clade. The values along the node represent the ultrafast bootstrap support for 1000 iterations. The lineage in bold indicates the the new species

Table 2. Uncorrected pairwise genetic distances between species in *C. gracilis* clade

No	Species	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	<i>C. reticulata</i> sp. nov. 1														
2	<i>C. reticulata</i> sp. nov. 2	0													
3	<i>C. gracilis</i> 1	0.121	0.121												
4	<i>C. gracilis</i> 2	0.121	0.121	0											
5	<i>C. gracilis</i> 3	0.121	0.121	0	0										
6	<i>C. gracilis</i> 4	0.121	0.121	0	0	0									
7	<i>C. gracilis</i> 5	0.121	0.121	0	0	0	0								
8	<i>C. agarwali</i> 1	0.091	0.091	0.091	0.091	0.091	0.091	0.091							
9	<i>C. agarwali</i> 2	0.091	0.091	0.091	0.091	0.091	0.091	0.091	0						
10	<i>C. ganeshaiahi</i> 1	0.091	0.091	0.091	0.091	0.091	0.091	0.091	0.061	0.061					
11	<i>C. ganeshaiahi</i> 2	0.091	0.091	0.091	0.091	0.091	0.091	0.091	0.061	0.061	0				
12	<i>C. rudhira</i> 1	0.091	0.091	0.03	0.03	0.03	0.03	0.03	0.061	0.061	0.061	0.061			
13	<i>C. rudhira</i> 2	0.091	0.091	0.03	0.03	0.03	0.03	0.03	0.061	0.061	0.061	0.061	0		
14	<i>C. rudhira</i> 3	0.091	0.091	0.03	0.03	0.03	0.03	0.03	0.061	0.061	0.061	0.061	0	0	
15	<i>C. rudhira</i> 4	0.091	0.091	0.03	0.03	0.03	0.03	0.03	0.061	0.061	0.061	0.061	0	0	0
16	<i>C. jackieii</i>	0.061	0.061	0.061	0.061	0.061	0.061	0.061	0.03	0.03	0.03	0.03	0.03	0.03	0.03
17	<i>C. shevaroyensis</i> 1	0.091	0.091	0.152	0.152	0.152	0.152	0.152	0.061	0.061	0.121	0.121	0.121	0.121	0.121
18	<i>C. shevaroyensis</i> 2	0.091	0.091	0.152	0.152	0.152	0.152	0.152	0.061	0.061	0.121	0.121	0.121	0.121	0.121
19	<i>C. agayagangai</i> 1	0.091	0.091	0.091	0.091	0.091	0.091	0.091	0.061	0.061	0.061	0.061	0.061	0.061	0.061
20	<i>C. agayagangai</i> 2	0.091	0.091	0.091	0.091	0.091	0.091	0.091	0.061	0.061	0.061	0.061	0.061	0.061	0.061
21	<i>C. fantastica</i> 1	0.152	0.152	0.212	0.212	0.212	0.212	0.212	0.121	0.121	0.182	0.182	0.182	0.182	0.182
22	<i>C. thackerayi</i>	0.091	0.091	0.152	0.152	0.152	0.152	0.152	0.121	0.121	0.121	0.121	0.121	0.121	0.121
23	<i>C. fantastica</i> 2	0.152	0.152	0.212	0.212	0.212	0.212	0.212	0.121	0.121	0.182	0.182	0.182	0.182	0.182
24	<i>C. fantastica</i> 3	0.152	0.152	0.212	0.212	0.212	0.212	0.212	0.121	0.121	0.182	0.182	0.182	0.182	0.182
25	<i>C. pachaimalaiensis</i>	0.121	0.121	0.121	0.121	0.121	0.121	0.121	0.091	0.091	0.091	0.091	0.091	0.091	0.091
26	<i>C. salimalii</i> 1	0.121	0.121	0.121	0.121	0.121	0.121	0.121	0.091	0.091	0.091	0.091	0.091	0.091	0.091
27	<i>C. salimalii</i> 2	0.121	0.121	0.121	0.121	0.121	0.121	0.121	0.091	0.091	0.091	0.091	0.091	0.091	0.091
28	<i>C. mundanthuraiensis</i>	0.091	0.091	0.091	0.091	0.091	0.091	0.091	0.061	0.061	0.061	0.061	0.061	0.061	0.061

No	Species	15	16	17	18	19	20	21	22	23	24	25	26	27	28
1	<i>C. reticulata</i> sp nov 1														
2	<i>C. reticulata</i> sp nov 2														
3	<i>C. gracilis</i> 1														
4	<i>C. gracilis</i> 2														
5	<i>C. gracilis</i> 3														
6	<i>C. gracilis</i> 4														
7	<i>C. gracilis</i> 5														
8	<i>C. agarwali</i> 1														
9	<i>C. agarwali</i> 2														
10	<i>C. ganeshaiahi</i> 1														
11	<i>C. ganeshaiahi</i> 2														
12	<i>C. rudhira</i> 1														
13	<i>C. rudhira</i> 2														
14	<i>C. rudhira</i> 3														
15	<i>C. rudhira</i> 4														
16	<i>C. jackieii</i>	0.03													
17	<i>C. shevaroyensis</i> 1	0.121	0.091												
18	<i>C. shevaroyensis</i> 2	0.121	0.091	0											
19	<i>C. agayagangai</i> 1	0.061	0.03	0.121	0.121										
20	<i>C. agayagangai</i> 2	0.061	0.03	0.121	0.121	0									
21	<i>C. fantastica</i> 1	0.182	0.152	0.061	0.061	0.121	0.121								
22	<i>C. thackerayi</i>	0.121	0.091	0.061	0.061	0.121	0.121	0.121							
23	<i>C. fantastica</i> 2	0.182	0.152	0.061	0.061	0.121	0.121	0	0.121						
24	<i>C. fantastica</i> 3	0.182	0.152	0.061	0.061	0.121	0.121	0	0.121	0					
25	<i>C. pachaimalaiensis</i>	0.091	0.061	0.152	0.152	0.03	0.03	0.152	0.152	0.152	0.152				
26	<i>C. salimalii</i> 1	0.091	0.061	0.152	0.152	0.091	0.091	0.182	0.152	0.182	0.182	0.121			
27	<i>C. salimalii</i> 2	0.091	0.061	0.152	0.152	0.091	0.091	0.182	0.152	0.182	0.182	0.121	0		
28	<i>C. mundanthuraiensis</i>	0.061	0.03	0.121	0.121	0.061	0.061	0.182	0.121	0.182	0.182	0.091	0.091	0.091	

Taxonomy

Cnemaspis reticulata sp. nov.

[urn:lsid:zoobank.org:act:518A10C8-BD63-40CC-AE35-32A33B1B950E] (Figs. 2–4, Tables 3, 4)

Holotype. Adult male, BNHS 3157, collected from Thiruparankundram Hill (9°52'35.79"N, 78°4'9.03"E; alt. 311 m a.s.l.), Madurai District, Tamil Nadu, India, by Amit Sayyed and Samson Kirubakaran on 27 January 2023.

Paratypes (n=2). adult male, BNHS 3158, and adult female, BNHS 3159; collection details the same data as holotype.

Diagnosis. A small-bodied *Cnemaspis* with adult SVL less than 35.0 mm; 7 supralabials; 7 or 8 infralabials; dorsal scales heterogeneous; dorsal scales small, granular, weakly keeled, intermixed with randomly arranged, weakly keeled, slightly larger tubercles; conical and

spine-like tubercles absent on either side of the flanks; paravertebral scales 91–95; mid-dorsal scales 75–77; scales on snout, dorsal head, neck and body small, granular, juxtaposed, not keeled; scales on ventral surface of head, neck, pectoral, abdominal region, under limbs, and tail smooth; mid-ventral scales 110–120; ventral scales across midbody 28–30; subdigital lamellae under fourth digit of manus 13–14, under fourth digit of pes 17; males with 4 femoral pores on each thigh, 2 precloacal pores separated medially by 2 poreless scales, 9–10 poreless scales on either side between precloacal and femoral pores; dorsal scales of limbs granular, weakly keeled; a single enlarged postcloacal spur on each side. dorsal scales on tail keeled, granular, sub imbricate posteriorly, intermixed with enlarged, strongly keeled tubercles forming whorls; scales on ventral aspect of original tail imbricate, smooth, a series of enlarged sub-caudal scales; a single enlarged postcloacal spur on each side.

Comparisons. *Cnemaspis reticulata* sp. nov. is a member of the *gracilis* clade and can be easily distinguished from all twelve members of the clade by a combination of the following differing or non-overlapping characters: conical and spine-like tubercles absent on flanks (vs. present in *C. agarwali* Khandekar *et al.*, 2019, *C. agayagangai* Agarwal *et al.*, 2022, *C. fantastica* Agarwal *et al.*, 2022, *C. ganeshaiahi* Narayanan *et al.*, 2023, *C. gracilis* Beddome, 1870, *C. jackeii* Pal *et al.*, 2021, *C. mundanthuraiensis* Khandekar *et al.*, 2022, *C. rudhira* Agarwal *et al.*, 2022, *C. salimalii* Agarwal *et al.*, 2022, *C. shevaroyensis* Khandekar *et al.*, 2019, and *C. thackerayi* Khandekar *et al.*, 2019); SVL <35mm (vs. 41.3 mm in *C. salimalii*, and 41 mm in *C. thackerayi*); two precloacal pores (vs. 4–6 in *C. ganeshaiahi*, 2–4 in *C. thackerayi*, 3 or 4 in *C. jackeii*, 2–4 in *C. fantastica*); four femoral pores (vs. 5 or 6 in *C. jackeii*).

A small black spot on occiput, a half circular central black dorsal ocellus on posterior neck flanked anteriorly and posteriorly on each side by three dark ocelli (vs. ocellus on occiput flanked one each side by a smaller ocellus, ocellus on neck flanked anteriorly on each side by a slightly larger ocellus in *C. agayagangai*, ocellus on neck flanked posteriorly by a pair of much larger squarish blotches and anteriorly by a pair of subequal squarish blotches in *C. fantastica*, ocellus paired with two darker

anterior ocelli and two faint posterior ocelli in *C. ganeshaiahi*, a single large ocellus at anterior of forelimb insertion in *C. gracilis*, a single ocellus on neck in *C. salimalii* and *C. rudhira*, a single large ocellus at anterior of forelimb insertion, two pairs of smaller spots on each side just anterior and posterior to forelimb insertions in *C. shevaroyensis*, a single ocellus at the anterior of forelimb insertion in *C. thackerayi*). The new species is morphologically close for *C. pachamalaiensis* from which it can be differentiated by having non-overlapping characters; conical and spine-like tubercles absent on flanks (vs. present); less numbers of mid-ventral scales <120 (vs. 125); and a small black spot on occiput (vs. an ocellus on occiput flanked on each side by a smaller ocellus).

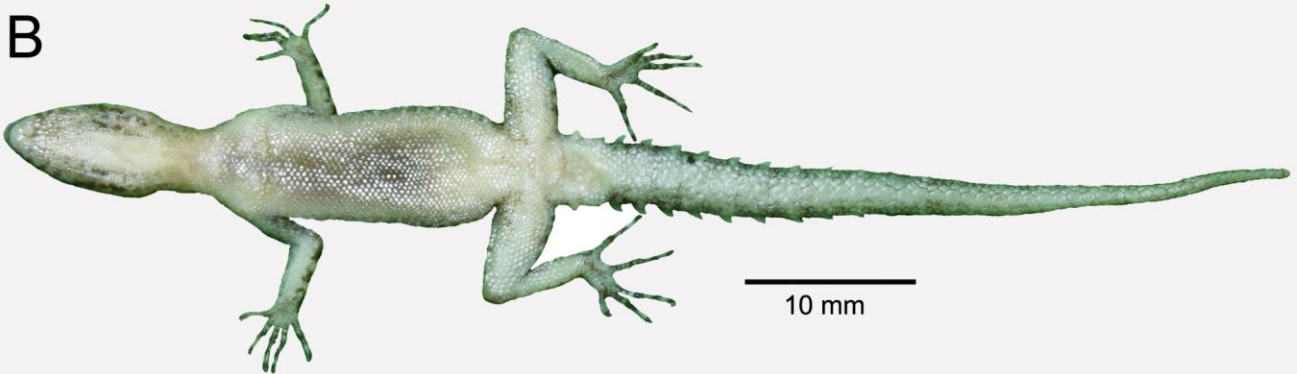
Description of the holotype. Adult male generally in a good state of preservation. 32.71 mm SVL, head short (HL/SVL 0.27), slightly wide (HW/HL 0.74), not depressed (HD/HL 0.39), distinctly larger from the neck. Loreal region slightly inflated, canthus rostralis not prominent. Snout slightly longer than half of head length (ES/HL 0.42); scales on snout and canthus rostralis small, round, juxtaposed, not keeled, larger than those on forehead and interorbital region; occipital and temporal region with much smaller, not keeled, granular scales. Eye small (ED/HL 0.11), with round pupil; supraciliaries not elongate. Tympanum deep, ear-opening very small (EOD/HL 0.09); eye to ear distance much longer than diameter of eye (ET/EOD 3.07). Rostral much wider (1.42 mm) than high (0.75 mm), not divided dorsally, rostral groove absent; single enlarged supranasal on each side, twice the size of postnasals, separated from each other by round enlarged single internasal scales; rostral in contact with supralabial I, nasal, supranasal and internasal; nostrils very small, oval, bordered by postnasals, supranasal and rostral; three rows of small scales separate the orbit from the supralabials. Mental enlarged, subtriangular, not pointed posteriorly, longer (1.89 mm) than wide (1.16 mm); two pairs of postmentals, inner pair slightly large, separated by single large scale, postmentals bordered posteriorly by five smaller, rounded scales; gular scales granular, juxtaposed, smooth; throat scales, flat, cycloid, smaller than those on gular. Supralabials up to angle of jaw seven on both side; supralabial I slightly smaller than II, slightly decreasing in size posteriorly; infralabials up to angle of jaw seven on the right and left side; infralabial I smaller than II in size.

Plate 4

A



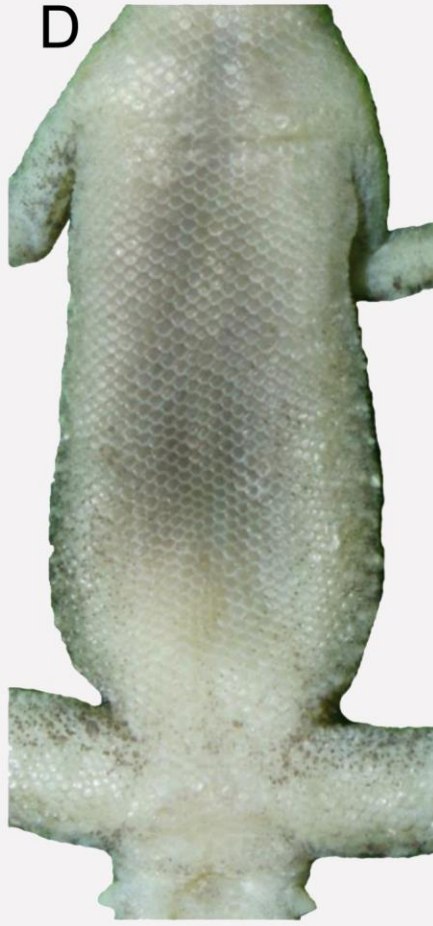
B



C



D



E



5 mm

Figure 2. *Cnemaspis reticulata* sp. nov. holotype (BNHS 3157): (A) dorsal and (B) ventral views of the full body; (C) dorsal, (D) ventral, and (E) lateral views of the mid body

Plate 5

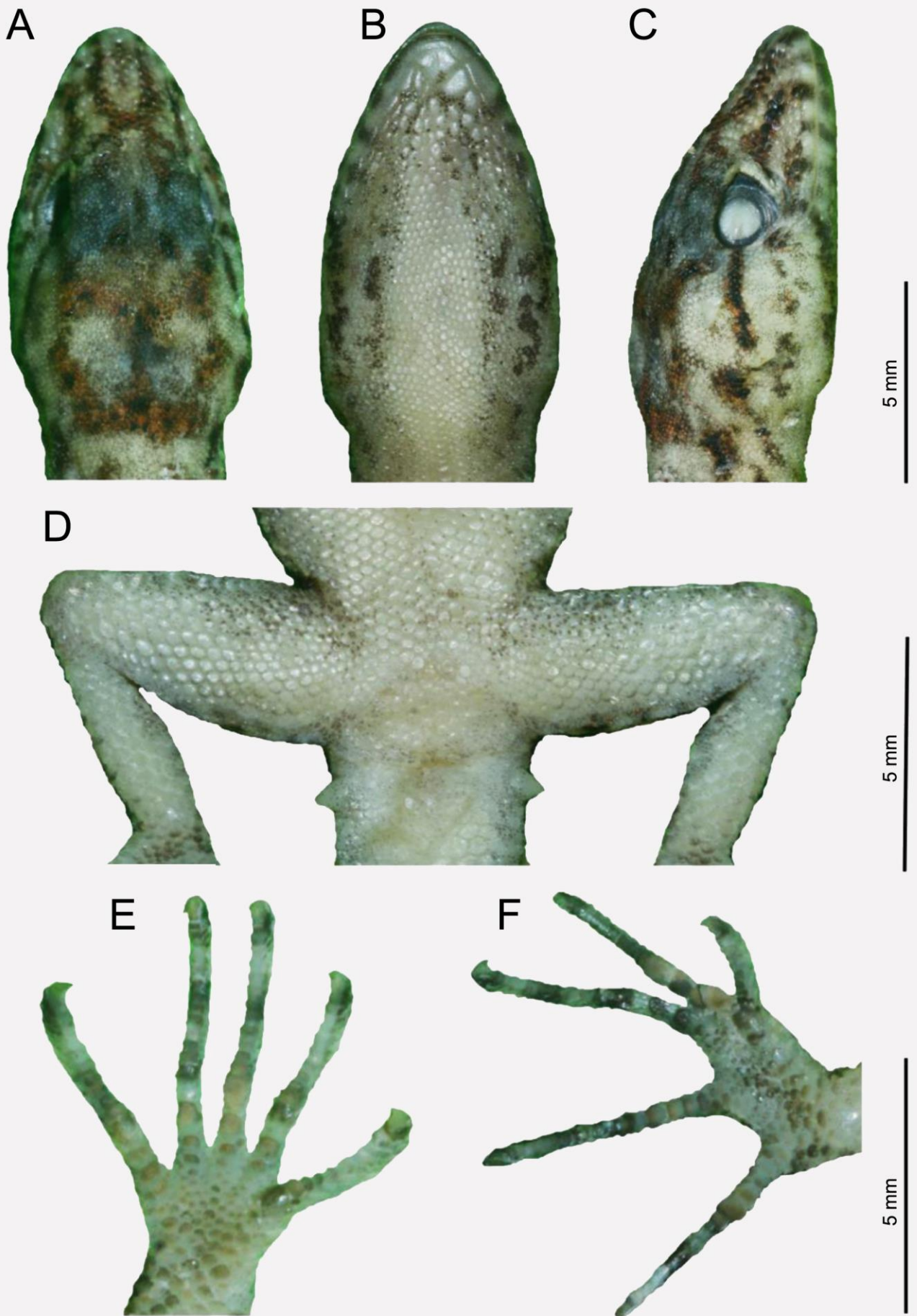


Figure 3. *Cnemaspis reticulata* sp. nov. holotype (BNHS 3157): (A) dorsal, (B) ventral, and (C) lateral views of head, (D) femoral and preloacal region, and ventral view of (E) right manus and (F) right pes

Canthal region with 10 scales on both sides; supraciliaries separated by 16 scales at midorbit.

Body relatively short, trunk less than half of SVL (AG/SVL 0.40) without ventrolateral folds. Dorsal pholidosis heterogeneous; scales small, granular, weakly keeled, intermixed with randomly arranged, weakly keeled, slightly larger tubercles, few slightly large on flanks; dorsal paravertebral scales 93; number of mid-dorsal scales 77; conical and spine-like tubercles absent on either side of the flanks. Granular scales on nape not keeled, slightly smaller than those on paravertebral rows, smaller still on occiput. Scales on ventral surface of neck, chest, arm, pes and tail smooth; mid-ventral scales 110, midbody scales 29 across the ventral between the lowest rows of dorsal scales; four femoral pores on each thigh, two precloacal pores separated medially by two poreless scales, nine poreless scales on either side between precloacal and femoral pores.

Forelimbs moderately long, slender; dorsal scales of brachium weakly keeled, imbricate; scales of forearm weakly keeled, imbricate, smaller than those on brachials; ventral scales of brachium smooth, rounded, juxtaposed, smaller than those on forearm; scales beneath forearm, smooth, flat, cycloid; palmar scales smooth, juxtaposed, raised; claws slightly recurved; dorsal scales of thigh and tibia weakly keeled, imbricate; ventral scales of thigh and tibia flat, cycloid; subtibial scales weakly keeled, imbricate; plantar scales smooth, juxtaposed, raised; digits long with an inflected joint; subdigital lamellae unnotched; lamellae beneath first phalanges slightly widened; subdigital lamellae on fingers: 9, 12, 14, 14, and 12; on toe: 9, 12, 13, 17 and 15. Relative length of fingers: IV (3.04 mm) > III (2.99 mm) > V (2.82mm) > II (2.24 mm) > I (1.73 mm); toes: IV (4.17 mm) > V (3.44mm) > III (3.37 mm) > II (2.63 mm) > I (1.13 mm).

Tail entire and original, cylindrical, moderately slender, flattened beneath, longer than snout-vent length (TL/SVL 1.33). Dorsal scales at tail keeled, granular, slightly large in size and shape than those on midbody dorsum, gradually becoming larger, subimbricate posteriorly, intermixed with enlarged, strongly keeled tubercles forming whorls; scales on ventral aspect of original tail imbricate, smooth, a series of enlarged sub-caudal scales, larger in size than those on dorsal tail; scales on tail base smaller, imbricate and smooth, a single enlarged postcloacal spur on each side.

Table 3. Mensural data (in mm) for the type series of *Cnemaspis reticulata* sp. nov., * regenerated tail

Character	Holotype		Paratypes	
	BNHS 3157	BNHS 3158	BNHS 3159	
Sex	male	male	female	
SVL	32.71	33.44	34.76	
AG	13.15	13.05	14.91	
TW	7.43	7.63	8.81	
ED	0.99	1.09	1.08	
EN	3.16	3.70	3.87	
ES	3.75	4.34	4.45	
ET	2.61	2.71	2.50	
IN	0.74	0.82	0.81	
EOD	0.85	0.86	0.87	
HL	8.92	9.00	9.32	
HW	6.62	6.26	6.21	
HD	3.48	4.39	3.87	
IO	3.24	3.47	4.02	
UAL	5.45	4.55	4.09	
FAL	6.40	5.70	4.51	
PAL	4.02	4.30	4.37	
FL1	1.73	1.94	1.75	
FL2	2.24	3.20	2.38	
FL3	2.99	2.75	3.01	
FL4	3.04	3.36	3.10	
FL5	2.82	2.64	2.49	
FEL	5.84	5.66	6.62	
TBL	7.40	6.96	7.19	
TOL1	1.13	1.31	1.10	
TOL2	2.63	3.54	3.09	
TOL3	3.37	3.56	3.58	
TOL4	4.17	4.24	4.11	
TOL5	3.44	3.74	3.41	
TL	43.54	34.43	*33.72	

Table 4. Meristic data of the type series of *Cnemaspis reticulata* sp. nov., — data not present

Character	Holotype		Paratypes	
	BNHS 3157	BNHS 3158	BNHS 3159	
Sex	male	male	female	
SupL R/L	7/7	7/7	7/7	
InfL R/L	7/7	7/7	8/7	
SuS	16	15	15	
InO	32	30	30	
BeT	21	22	20	
PoN	3	3	3	
PoM	2	2	2	
PoP	5	5	4	
SuN	3	3	3	
CaS	10	10	11	
PvS	93	91	95	
MbS	77	75	76	
MvS	110	111	120	
BIS	29	28	30	
FPores	4/4	4/4	—	
PPores	2	2	—	
PS	9/9	9/10	—	
SBP	2	2	—	
MLam R	9,12,14,14,12	8,10,14,13,12	9,12,14,14,12	
PLam R	9,12,13,17,15	7,11,12,17,15	9,13,16,17,17	

Plate 6

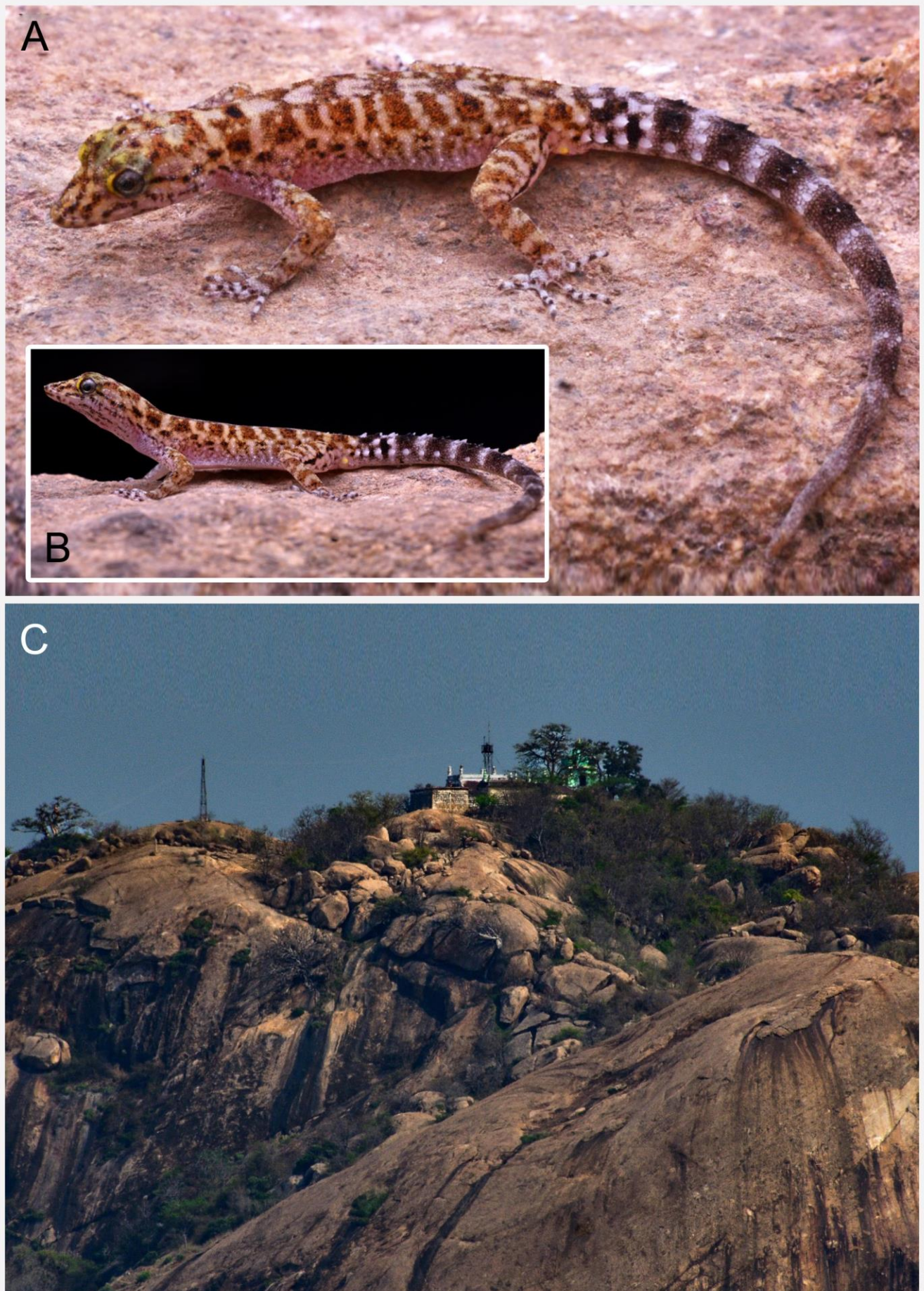


Figure 4. *Cnemaspis reticulata* sp. nov. (A) Dorsolateral and (B) lateral views of the holotype (BNHS 3157) in life; and (C) rocky habitat at the type locality (Thiruparankundram Hill, Madurai, Tamil Nadu, India)

Colouration. In life (Fig. 4), the dorsal aspect of the body is orangish, intermixed with yellowish-grey bands on dorsal body forming a net like structure; a half circular central black dorsal ocellus on posterior neck flanked anteriorly and posteriorly on each side by three dark ocelli, very small ocellus on occiput. Head overall orangish, two yellowish-grey patches on occipital, three small, black spots, surrounded with orangish scales on the dorsal head, forehead and supraciliaries yellow, yellowish-grey bands on snout. Tail with ten or eleven alternating white and black bands. dorsal aspect of tail white with black bands. The limbs are orangish above with irregular yellowish-grey bands; digits are white with irregular black spots. The ventral side of the head whitish with irregular brown spots, ventral side of body and tail is whitish. In preservative, the dorsum of the body and limbs orangish, which turns into gray, yellow and white markings in life, turns into grey in preservation; ventral side of head, body and tail grayish-white.

Etymology. The specific epithet *reticulata* is an adjective in feminine referring to the net-

like dorsal colour pattern of the gecko. Suggested English Name: Reticulated dwarf Gecko.

Natural History. The type series was collected during 16.00–19.00 hr on rock boulders near the dargah situated on Thiruparankundram Hill (Fig. 5). The hill is a monolithic rock with a circumference of over 3.2 km located in Madurai district, Tamil Nadu state. The hill is known for its Islamic dargah and is one of the six abodes of Lord Murugan. The hill is also archaeologically important as it has many historic temples, monuments, old paintings and Jain caves thus highly protected by the Archeological Survey of India (ASI). The surrounding area of the hill is covered with grassland and shrubland with a few big trees of *Azadirachta* sp. (Meliaceae) and *Wrightia tinctoria* (Apocynaceae). The individuals of *C. reticulata* sp. nov. were found to be sympatric with *Hemidactylus* sp.

Distribution. Currently, *Cnemaspis reticulata* sp. nov. is only known from its type locality (Fig. 5) Thiruparankundram Hill, Madurai District, Tamil Nadu state, India.

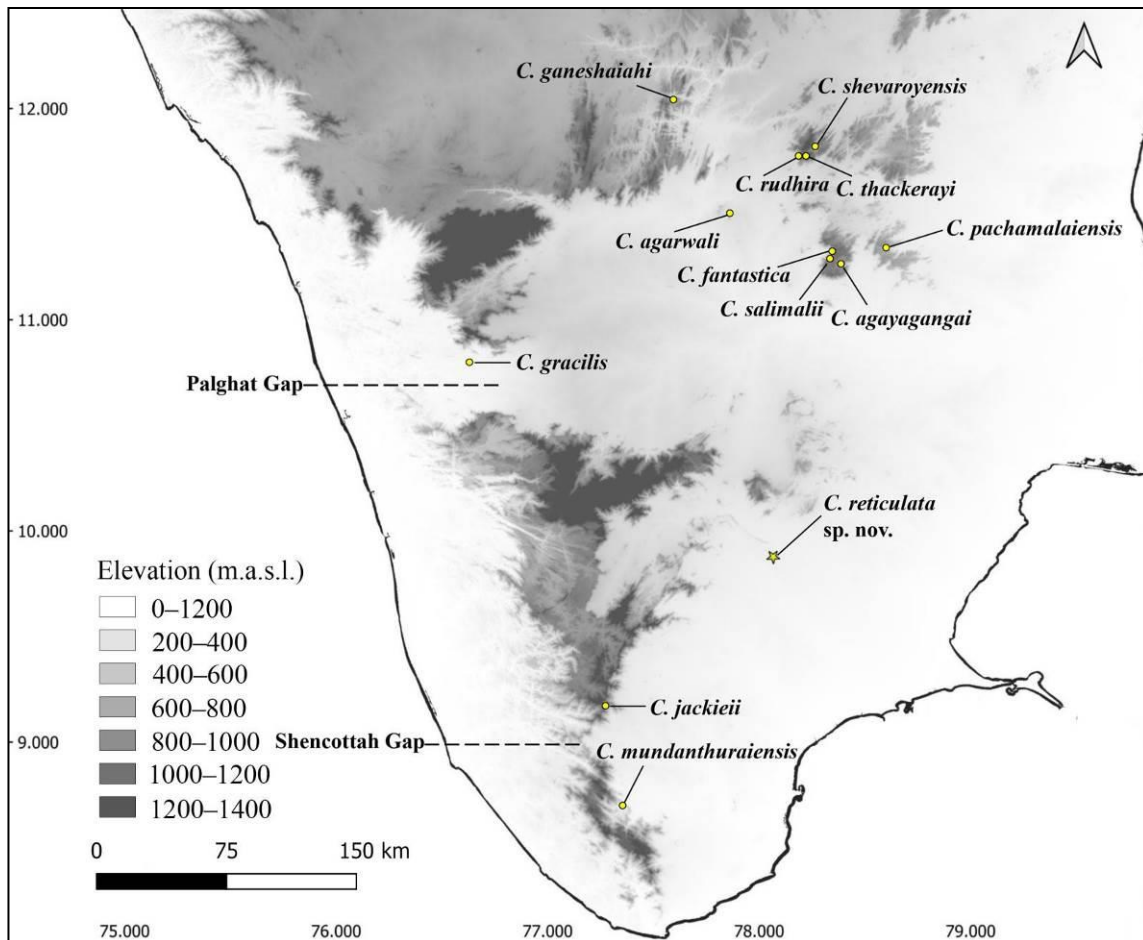


Figure 5. Map showing the distribution of *Cnemaspis* species from *gracilis* clade in peninsular India

Discussion

The new species has unique morphological and molecular characters. The presence of the new species on a monolithic rock indicates micro-endemism within the genus. Agarwal *et al.* (2022) highlighted this micro-endemism within the *gracilis* clade by sampling various localities in the Shevaroy hill massif. Agarwal *et al.* (2022) proposed that micro-endemism would have been influenced by various factors such as differences in elevation and intrinsic habitat heterogeneity, dispersal, and sexual selection. The dispersal patterns of the species within these microhabitats would be worth examining by testing for correlations between environmental parameters and molecular data. With extensive sampling and data collection, it is possible that additional, undescribed, micro-endemic lineages will be discovered. This scenario, thus calls for more localised conservation efforts.

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